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Anti-STEAP2 antibodies, antibody-drug conjugates, and bispecific antigen-binding molecules that bind STEAP2 and CD3, and uses thereof

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(54) Title: ANTI-STEAP2 ANTIBODIES, ANTIBODY-DRUG CONJUGATES, AND BISPECIFIC ANTIGEN-BINDING MOLECULES THAT BIND STEAP2 AND CD3, AND USES THEREOF

H1H7814N-7 efficacy on C4-2 tumors in SCID mice

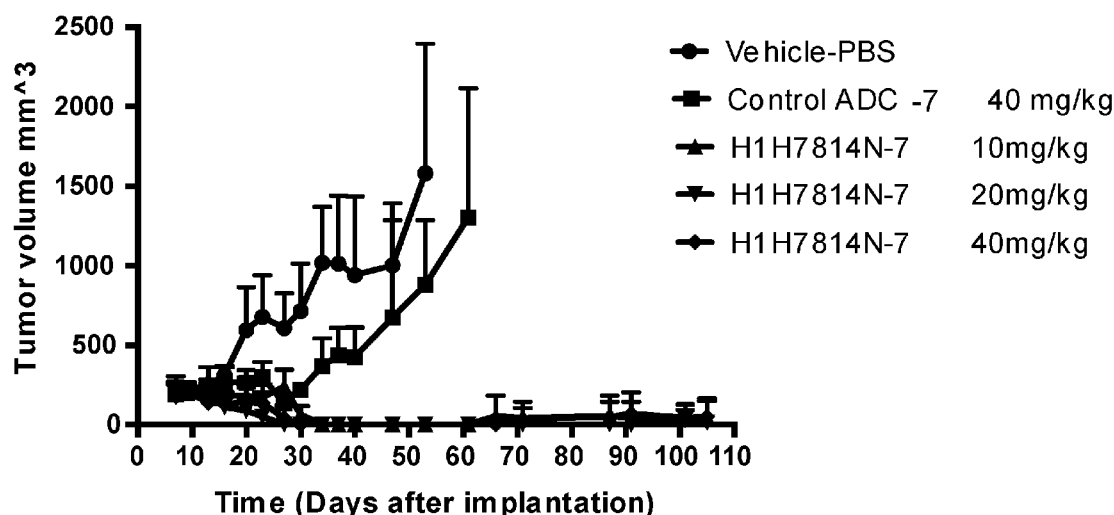


FIG. 1

(57) Abstract: The protein known as six-transmembrane epithelial antigen of prostate 2 (STEAP2) is highly expressed in prostate cancer and is associated with the expression of other prostate cancer-associated genes. The present invention provides novel full-length human IgG antibodies that bind to human STEAP2 (monospecific antibodies). The present invention also provides novel bispecific antibodies (bsAbs) that bind to both STEAP2 and CD3 and activate T cells via the CD3 complex in the presence of STEAP2 -expressing tumors. According to certain embodiments, the present invention provides bispecific antigen-binding molecules comprising a first antigen-binding domain that specifically binds human and monkey CD3, and a second antigen-binding molecule that specifically binds human STEAP2. In certain embodiments, the bispecific antigen-binding molecules of the present invention are capable of inhibiting the



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growth of tumors expressing STEAP2. The bispecific antigen-binding molecules of the invention are useful for the treatment of prostate diseases and disorders in which an upregulated or induced STEAP2 -targeted immune response is desired and/or therapeutically beneficial. For example, the bispecific antibodies of the invention are useful for the treatment of prostate cancers, including castrate-resistant prostate cancer. The present invention also includes anti-STEAP2 antibody drug conjugates which inhibit tumor growth in vivo.

ANTI-STEAP2 ANTIBODIES, ANTIBODY-DRUG CONJUGATES, AND BISPECIFIC ANTIGEN-BINDING MOLECULES THAT BIND STEAP2 AND CD3, AND USES THEREOF

REFERENCE TO A SEQUENCE LISTING

[0001] This application incorporates by reference the Sequence Listing submitted in Computer Readable Form as file 10296WO01-Sequence.txt, created on September 22, 2017 and containing 739,964 bytes.

FIELD OF THE INVENTION

[0002] The present invention relates to antibodies, and antigen-binding fragments thereof, which are specific for six-transmembrane epithelial antigen of prostate 2 (STEAP2), and methods of use thereof. The present invention also relates to bispecific antigen-binding molecules that bind STEAP2 and CD3, and methods of use thereof. The present invention further relates to antibody-drug conjugates comprising an anti-STEAP2 antibody or fragment thereof and a therapeutic agent (e.g., a cytotoxic agent).

BACKGROUND

[0003] Six-transmembrane epithelial antigen of prostate 2 (STEAP2), also known as STEAP-2, metalloreductase STEAP2, prostate cancer-associated protein 1, protein up-regulated in metastatic prostate cancer, SixTransMembrane protein of prostate 1 (STAMP1), and 098P4B6, is an integral, six-transmembrane-spanning protein, which is upregulated in normal and malignant prostate cells. STEAP2, which works as a shuttle between the Golgi complex and the plasma membrane, is a metalloreductase which reduces iron and copper, facilitating their import into the cell. STEAP2 is mainly localized to epithelial cells of the prostate. STEAP2 is also expressed in normal heart, brain, pancreas, ovary, skeletal muscle, mammary gland, testis, uterus, kidney, lung, trachea, colon, and liver. STEAP2 is over-expressed in cancerous tissues, including prostate, bladder, cervix, lung, colon, kidney, breast, pancreatic, stomach, uterus, and ovarian tumors (Gomes, I.M. et al., 2012, Mol. Cancer Res. 10:573-587; Challita-Eid- P.M., et al., 2003, WO 03/087306; Emtage, P.C.R., 2005, WO 2005/079490).

[0004] CD3 is a homodimeric or heterodimeric antigen expressed on T cells in association with the T cell receptor complex (TCR) and is required for T cell activation. Functional CD3 is formed from the dimeric association of two of four different chains: epsilon, zeta, delta and gamma. The CD3 dimeric arrangements include gamma/epsilon, delta/epsilon and zeta/zeta. Antibodies against CD3 have been shown to cluster CD3 on T cells, thereby causing T cell activation in a manner similar to the engagement of the TCR by peptide-loaded MHC molecules. Thus, anti-CD3

antibodies have been proposed for therapeutic purposes involving the activation of T cells. In addition, bispecific antibodies that are capable of binding CD3 and a target antigen have been proposed for therapeutic uses involving targeting T cell immune responses to tissues and cells expressing the target antigen.

[0005] Antigen-binding molecules that target STEAP2, including antibody-drug conjugates, as well as bispecific antigen-binding molecules that bind both STEAP2 and CD3 would be useful in therapeutic settings in which specific targeting and T cell-mediated killing of cells that express STEAP2 is desired.

BRIEF SUMMARY OF THE INVENTION

[0006] In a first aspect, the present invention provides antibodies and antigen-binding fragments thereof that bind to human STEAP2. The antibodies according to this aspect of the invention are useful, *inter alia*, for targeting cells expressing STEAP2. The present invention also provides bispecific antibodies and antigen-binding fragments thereof that bind human STEAP2 and human CD3. The bispecific antibodies according to this aspect of the invention are useful, *inter alia*, for targeting T cells expressing CD3, and for stimulating T cell activation, *e.g.*, under circumstances where T cell-mediated killing of cells expressing STEAP2 is beneficial or desirable. For example, the bispecific antibodies can direct CD3-mediated T cell activation to specific STEAP2-expressing cells, such as prostate tumor cells.

[0007] Exemplary anti-STEAP2 antibodies of the present invention are listed in Tables 1 and 2 herein. Table 1 sets forth the amino acid sequence identifiers of the heavy chain variable regions (HCVRs) and light chain variable regions (LCVRs), as well as heavy chain complementarity determining regions (HCDR1, HCDR2 and HCDR3), and light chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) of the exemplary anti-STEAP2 antibodies. Table 2 sets forth the sequence identifiers of the nucleic acid molecules encoding the HCVRs, LCVRs, HCDR1, HCDR2 HCDR3, LCDR1, LCDR2 and LCDR3 of the exemplary anti-STEAP2 antibodies.

[0008] The present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCVR comprising an amino acid sequence selected from any of the HCVR amino acid sequences listed in Table 1, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0009] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising an LCVR comprising an amino acid sequence selected from any of the LCVR amino acid sequences listed in Table 1, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0010] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising an HCVR and an LCVR amino acid sequence pair (HCVR/LCVR) comprising any of the HCVR amino acid sequences listed in Table 1 paired with any of the LCVR amino acid sequences listed in Table 1. According to certain embodiments, the present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCVR/LCVR amino acid sequence pair contained within any of the exemplary anti-STEAP2 antibodies listed in Table 1. In certain embodiments, the HCVR/LCVR amino acid sequence pair is selected from the group consisting of SEQ ID NOs: 250/258 (e.g., H2M11162N).

[0011] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a heavy chain CDR1 (HCDR1) comprising an amino acid sequence selected from any of the HCDR1 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0012] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a heavy chain CDR2 (HCDR2) comprising an amino acid sequence selected from any of the HCDR2 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0013] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a heavy chain CDR3 (HCDR3) comprising an amino acid sequence selected from any of the HCDR3 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0014] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a light chain CDR1 (LCDR1) comprising an amino acid sequence selected from any of the LCDR1 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0015] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a light chain CDR2 (LCDR2) comprising an amino acid sequence selected from any of the LCDR2 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0016] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a light chain CDR3 (LCDR3) comprising an amino acid sequence selected from any of the LCDR3 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0017] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising an HCDR3 and an LCDR3 amino acid sequence pair (HCDR3/LCDR3) comprising any of the HCDR3 amino acid sequences listed in Table 1 paired with any of the LCDR3 amino acid

sequences listed in Table 1. According to certain embodiments, the present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCDR3/LCDR3 amino acid sequence pair contained within any of the exemplary anti-STEAP2 antibodies listed in Table 1. In certain embodiments, the HCDR3/LCDR3 amino acid sequence pair is selected from the group consisting of SEQ ID NOs: 256/264 (e.g., H2M11162N).

[0018] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a set of six CDRs (*i.e.*, HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3) contained within any of the exemplary anti-STEAP2 antibodies listed in Table 1. In certain embodiments, the HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences set is selected from the group consisting of SEQ ID NOs: 252-254-256-260-262-264 (e.g., H2M11162N).

[0019] In a related embodiment, the present invention provides antibodies, or antigen-binding fragments thereof, comprising a set of six CDRs (*i.e.*, HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3) contained within an HCVR/LCVR amino acid sequence pair as defined by any of the exemplary anti-STEAP2 antibodies listed in Table 1. For example, the present invention includes antibodies, or antigen-binding fragments thereof, comprising the HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences set contained within an HCVR/LCVR amino acid sequence pair selected from the group consisting of SEQ ID NOs: 250/258 (e.g., H2M11162N). Methods and techniques for identifying CDRs within HCVR and LCVR amino acid sequences are well known in the art and can be used to identify CDRs within the specified HCVR and/or LCVR amino acid sequences disclosed herein. Exemplary conventions that can be used to identify the boundaries of CDRs include, *e.g.*, the Kabat definition, the Chothia definition, and the AbM definition. In general terms, the Kabat definition is based on sequence variability, the Chothia definition is based on the location of the structural loop regions, and the AbM definition is a compromise between the Kabat and Chothia approaches. See, *e.g.*, Kabat, "Sequences of Proteins of Immunological Interest," National Institutes of Health, Bethesda, Md. (1991); Al-Lazikani *et al.*, *J. Mol. Biol.* 273:927-948 (1997); and Martin *et al.*, *Proc. Natl. Acad. Sci. USA* 86:9268-9272 (1989). Public databases are also available for identifying CDR sequences within an antibody.

[0020] The present invention also provides nucleic acid molecules encoding anti-STEAP2 antibodies or portions thereof. For example, the present invention provides nucleic acid molecules encoding any of the HCVR amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0021] The present invention also provides nucleic acid molecules encoding any of the LCVR amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule

comprises a polynucleotide sequence selected from any of the LCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0022] The present invention also provides nucleic acid molecules encoding any of the HCDR1 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR1 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0023] The present invention also provides nucleic acid molecules encoding any of the HCDR2 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR2 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0024] The present invention also provides nucleic acid molecules encoding any of the HCDR3 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR3 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0025] The present invention also provides nucleic acid molecules encoding any of the LCDR1 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR1 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0026] The present invention also provides nucleic acid molecules encoding any of the LCDR2 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR2 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0027] The present invention also provides nucleic acid molecules encoding any of the LCDR3 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR3 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0028] The present invention also provides nucleic acid molecules encoding an HCVR, wherein the HCVR comprises a set of three CDRs (*i.e.*, HCDR1-HCDR2-HCDR3), wherein the HCDR1-

HCDR2-HCDR3 amino acid sequence set is as defined by any of the exemplary anti-STEAP2 antibodies listed in Table 1.

[0029] The present invention also provides nucleic acid molecules encoding an LCVR, wherein the LCVR comprises a set of three CDRs (*i.e.*, LCDR1-LCDR2-LCDR3), wherein the LCDR1-LCDR2-LCDR3 amino acid sequence set is as defined by any of the exemplary anti-STEAP2 antibodies listed in Table 1.

[0030] The present invention also provides nucleic acid molecules encoding both an HCVR and an LCVR, wherein the HCVR comprises an amino acid sequence of any of the HCVR amino acid sequences listed in Table 1, and wherein the LCVR comprises an amino acid sequence of any of the LCVR amino acid sequences listed in Table 1. In certain embodiments, the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto, and a polynucleotide sequence selected from any of the LCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto. In certain embodiments according to this aspect of the invention, the nucleic acid molecule encodes an HCVR and LCVR, wherein the HCVR and LCVR are both derived from the same anti-STEAP2 antibody listed in Table 1.

[0031] The present invention also provides recombinant expression vectors capable of expressing a polypeptide comprising a heavy or light chain variable region of an anti-STEAP2 antibody. For example, the present invention includes recombinant expression vectors comprising any of the nucleic acid molecules mentioned above, *i.e.*, nucleic acid molecules encoding any of the HCVR, LCVR, and/or CDR sequences as set forth in Table 1. Also included within the scope of the present invention are host cells into which such vectors have been introduced, as well as methods of producing the antibodies or portions thereof by culturing the host cells under conditions permitting production of the antibodies or antibody fragments, and recovering the antibodies and antibody fragments so produced.

[0032] The present invention includes anti-STEAP2 antibodies having a modified glycosylation pattern. In some embodiments, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

[0033] In another aspect, the invention provides a pharmaceutical composition comprising a recombinant human antibody or fragment thereof which specifically binds STEAP2 and a

pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of an anti-STEAP2 antibody and a second therapeutic agent. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with an anti-STEAP2 antibody. Additional combination therapies and co-formulations involving the anti-STEAP2 antibodies of the present invention are disclosed elsewhere herein.

[0034] In another aspect, the invention provides therapeutic methods for targeting/killing tumor cells expressing STEAP2 using an anti-STEAP2 antibody of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an anti-STEAP2 antibody of the invention to a subject in need thereof. In some cases, the anti-STEAP2 antibodies (or antigen-binding fragments thereof) can be used for treating prostate cancer, or may be modified to be more cytotoxic by methods, including but not limited to, modified Fc domains to increase ADCC (see e.g. Shield et al. (2002) JBC 277:26733), radioimmunotherapy, antibody-drug conjugates, or other methods for increasing the efficiency of tumor ablation.

[0035] The present invention also includes the use of an anti-STEAP2 antibody of the invention in the manufacture of a medicament for the treatment of a disease or disorder (e.g., cancer) related to or caused by STEAP2-expressing cells. In one aspect, the invention relates to a compound comprising an anti-STEAP2 antibody or antigen-binding fragment, or a STEAP2xCD3 bispecific antibody, as disclosed herein, for use in medicine. In one aspect, the invention relates to a compound comprising an antibody-drug conjugate (ADC) as disclosed herein, for use in medicine.

[0036] In yet another aspect, the invention provides monospecific anti-STEAP2 antibodies for diagnostic applications, such as, e.g., imaging reagents.

[0037] In yet another aspect, the invention provides therapeutic methods for stimulating T cell activation using an anti-CD3 antibody or antigen-binding portion of an antibody of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an antibody

[0038] In another aspect, the present invention provides an isolated antibody or antigen-binding fragment thereof that binds STEAP2-expressing C4-2 cells with an EC₅₀ of less than 50 nM as measured by FACS analysis. In another aspect, the present invention provides an isolated antibody or antigen-binding fragment thereof that binds and is internalized by STEAP2-expressing C4-2 cells.

[0039] The invention further provides an antibody or antigen-binding fragment that competes for binding to human STEAP2 with a reference antibody comprising an HCVR/LCVR amino acid sequence pair as set forth in Table 1. In another aspect, the invention provides an antibody or antigen-binding fragment that competes for binding to human STEAP2 with a reference antibody

comprising an HCVR/LCVR amino acid sequence pair selected from the group consisting of SEQ ID NOs:2/10; 18/26; 34/42; 50/58; 66/58; 74/58; 82/58; 90/58; 98/58; 106/114; 122/130; 138/146; 154/162; 170/178; 186/194; 202/210; 218/226; 234/242; 250/258; 266/274; 282/290; 298/306; 314/322; 330/338; 346/354; 362/370; and 378/386.

[0040] The invention furthermore provides an antibody or antigen-binding fragment, wherein the antibody or antigen-binding fragment thereof binds to the same epitope on human STEAP2 as a reference antibody comprising an HCVR/LCVR amino acid sequence pair as set forth in Table 1. In another aspect, the antibody or antigen-binding fragment binds to the same epitope on human STEAP2 as a reference antibody comprising an HCVR/LCVR amino acid sequence pair selected from the group consisting of SEQ ID NOs:2/10; 18/26; 34/42; 50/58; 66/58; 74/58; 82/58; 90/58; 98/58; 106/114; 122/130; 138/146; 154/162; 170/178; 186/194; 202/210; 218/226; 234/242; 250/258; 266/274; 282/290; 298/306; 314/322; 330/338; 346/354; 362/370; and 378/386.

[0041] The invention further provides an isolated antibody or antigen-binding fragment thereof that binds human STEAP2, wherein the antibody or antigen-binding fragment comprises: the complementarity determining regions (CDRs) of a heavy chain variable region (HCVR) having an amino acid sequence as set forth in Table 1; and the CDRs of a light chain variable region (LCVR) having an amino acid sequence as set forth in Table 1. In another aspect, the isolated antibody or antigen-binding fragment comprises the heavy and light chain CDRs of a HCVR/LCVR amino acid sequence pair selected from the group consisting of: SEQ ID NOs:2/10; 18/26; 34/42; 50/58; 66/58; 74/58; 82/58; 90/58; 98/58; 106/114; 122/130; 138/146; 154/162; 170/178; 186/194; 202/210; 218/226; 234/242; 250/258; 266/274; 282/290; 298/306; 314/322; 330/338; 346/354; 362/370; and 378/386. In yet another aspect, the isolated antibody or antigen-binding fragment comprises HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, selected from the group consisting of: SEQ ID NOs:4-6-8-12-14-16; 20-22-24-28-30-32; 36-38-40-44-46-48; 52-54-56-60-62-64; 68-70-72-60-62-64; 76-78-80-60-62-64; 84-86-88-60-62-64; 92-94-96-60-62-64; 100-102-104-60-62-64; 108-110-112-116-118-120; 124-126-128-132-134-136; 140-142-144-148-150-152; 156-158-160-164-166-168; 172-174-176-180-182-184; 188-190-192-196-198-200; 204-206-208-212-214-216; 220-222-224-228-230-232; 236-238-240-244-246-248; 252-254-256-260-262-264; 268-270-272-276-278-280; 284-286-288-292-294-296; 300-302-304-308-310-312; 316-318-320-324-326-328; 332-334-336-340-342-344; 348-350-352-356-358-360; 364-366-368-372-374-376; and 380-382-384-388-390-392.

[0041a] In one aspect, there is provided an antibody or antigen-binding fragment thereof that specifically binds human six-transmembrane epithelial antigen of prostate 2 (STEAP2)-expressing cells, wherein the antibody or antigen-binding fragment thereof comprises a heavy chain variable region (HCVR) comprising complementarity determining regions HCDR1, HCDR2, and HCDR3

comprising the amino acid sequences of SEQ ID NOs: 220, 222, and 224, respectively, and a light chain variable region (LCVR) comprising complementarity determining regions LCDR1, LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NOs: 228, 230, and 232, respectively.

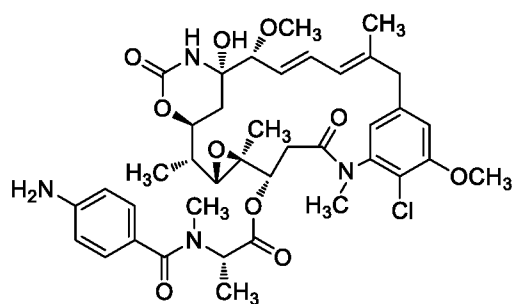
[0042] In another aspect, the invention provides an isolated antibody or antigen-binding fragment thereof that binds human STEAP2, wherein the antibody or antigen-binding fragment comprises: (a) a heavy chain variable region (HCVR) having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 18, 34, 50, 66, 74, 82, 90, 98, 106, 122, 138, 154, 170, 186, 202, 218, 234, 250, 266, 282, 298, 314, 330, 346, 362, and 378; and (b) a light chain variable region (LCVR) having an amino acid sequence selected from the group consisting of SEQ ID NOs: 10; 26; 42; 58; 114; 130; 146; 162; 178; 194; 210; 226, 242; 258; 274; 290; 306; 322; 338; 354; 370; and 386. In a further aspect, the isolated antibody or antigen-binding fragment of claim 10, wherein the antibody or antigen-binding fragment comprises a HCVR/LCVR amino acid sequence pair selected from the group consisting of: SEQ ID NOs: 2/10; 18/26; 34/42; 50/58; 66/58; 74/58; 82/58; 90/58; 98/58; 106/114; 122/130; 138/146; 154/162; 170/178; 186/194; 202/210; 218/226; 234/242; 250/258; 266/274; 282/290; 298/306; 314/322; 330/338; 346/354; 362/370; and 378/386.

[0043] According to another aspect, the present invention provides antibody-drug conjugates comprising an anti-STEAP2 antibody or antigen-binding fragment thereof and a therapeutic agent (e.g., a cytotoxic agent). In some embodiments, the antibody or antigen-binding fragment and the cytotoxic agent are covalently attached via a linker, as discussed herein. In various embodiments, the anti-STEAP 2 antibody or antigen-binding fragment can be any of the anti-STEAP 2 antibodies or fragments described herein.

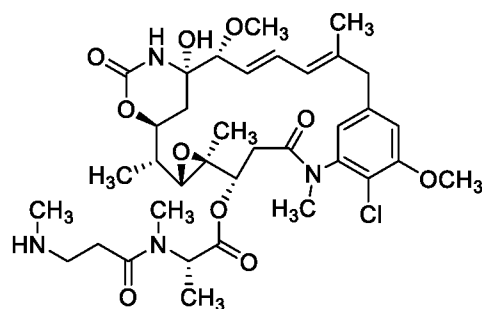
[0043a] In one aspect, there is provided an antibody-drug conjugate (ADC) comprising an antibody or antigen-binding fragment thereof that specifically binds to human six-transmembrane epithelial antigen of prostate 2 (STEAP2), and a cytotoxic agent, wherein the antibody or antigen-binding fragment thereof and the cytotoxic agent are covalently attached via a linker, and wherein the antibody or antigen-binding fragment thereof comprises complementarity determining regions HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 comprising the amino acid sequences of SEQ ID NOs: 220-222-224-228-230-232, respectively.

[0044] In some embodiments, the cytotoxic agent is selected from an auristatin, a maytansinoid, a tubulysin, a tomaymycin derivative, or a dolastatin derivative. In some cases, the cytotoxic agent is an auristatin selected from MMAE or MMAF, or a maytansinoid selected from DM1 or DM4. In some embodiments, the cytotoxic agent is a maytansinoid having the structure of Formula (I) or Formula (II), as discussed herein.

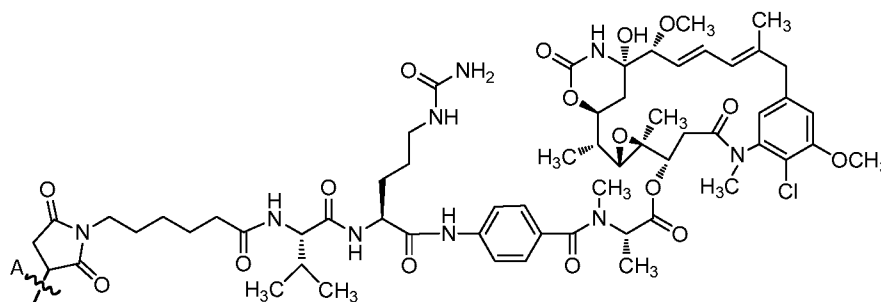
[0045] In some embodiments, the cytotoxic agent is a maytansinoid having the structure:



[0046] In some embodiments, the cytotoxic agent is a maytansinoid having the structure:

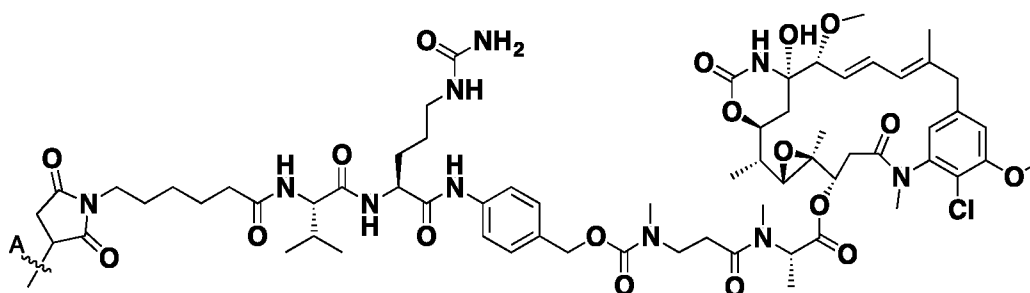


[0047] In some embodiments, the antibody-drug conjugate comprises an anti-STEAP 2 antibody or fragment thereof, and



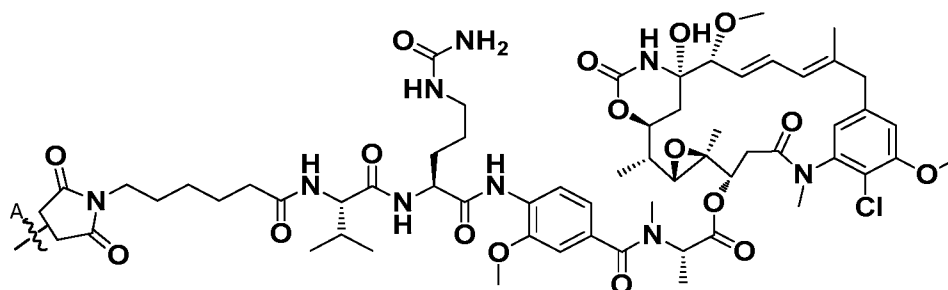
wherein $\text{---}\overset{\text{A}}{\text{---}}$ is a bond to the anti-STEAP 2 antibody or fragment thereof.

[0048] In some embodiments, the antibody-drug conjugate comprises an anti-STEAP 2 antibody or fragment thereof, and



wherein $\text{---}\overset{\text{A}}{\text{---}}$ is a bond to the anti-STEAP 2 antibody or fragment thereof.

[0049] In some embodiments, the antibody-drug conjugate comprises an anti-STEAP 2 antibody or fragment thereof, and

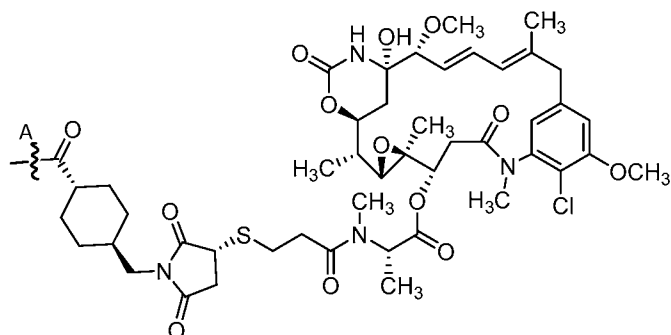


wherein $\text{---}\overset{\text{A}}{\text{---}}$ is a bond to the anti-STEAP 2 antibody or fragment thereof.

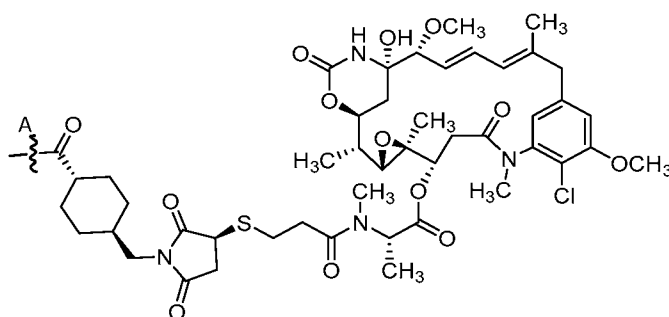
[0050] In some embodiments, the bond contacts the antibody or fragment thereof via a sulfur constituent of a cysteine residue.

[0051] In some embodiments, the antibody-drug conjugate comprises an anti-STEAP 2 antibody

or fragment thereof, and



, or



, or

a mixture thereof,

wherein $\overset{A}{\text{---}}$ is a bond to the anti-STEAP 2 antibody or fragment thereof.

[0052] In some embodiments, the bond contacts the antibody or fragment thereof via a nitrogen constituent of a lysine residue.

[0053] In any of the various embodiments of the antibody-drug conjugates discussed above or herein, the antibody-drug conjugate can comprise from 1 to 4 cytotoxic agents per anti-STEAP 2 antibody or fragment thereof.

[0054] According to another aspect, the present invention provides bispecific antigen-binding molecules (e.g., antibodies) that bind STEAP2 and CD3. Such bispecific antigen-binding molecules are also referred to herein as "anti-STEAP2/anti-CD3 bispecific molecules," "anti-CD3/anti-STEAP2 bispecific molecules," or "STEAP2xCD3 bsAbs." The anti-STEAP2 portion of the anti-STEAP2/anti-CD3 bispecific molecule is useful for targeting cells (e.g., tumor cells) that express STEAP2 (e.g., prostate tumors), and the anti-CD3 portion of the bispecific molecule is useful for activating T-cells. The simultaneous binding of STEAP2 on a tumor cell and CD3 on a T-cell facilitates directed killing (cell lysis) of the targeted tumor cell by the activated T-cell. The anti-STEAP2/anti-CD3 bispecific molecules of the invention are therefore useful, *inter alia*, for treating diseases and disorders related to or caused by STEAP2-expressing tumors (e.g., prostate cancers).

[0055] The bispecific antigen-binding molecules according to this aspect of the present invention comprise a first antigen-binding domain that specifically binds human CD3, and a second antigen-binding domain that specifically binds STEAP2. The present invention includes anti-STEAP2/anti-CD3 bispecific molecules (e.g., bispecific antibodies) wherein each antigen-binding domain comprises a heavy chain variable region (HCVR) paired with a light chain variable region (LCVR). In certain exemplary embodiments of the invention, the anti-CD3 antigen-binding domain and the anti-STEAP2 antigen binding domain each comprise different, distinct HCVRs paired with a common LCVR. For example, as illustrated in Example 4 herein, bispecific antibodies were constructed comprising a first antigen-binding domain that specifically binds CD3, wherein the first antigen-binding domain comprises an HCVR derived from an anti-CD3 antibody paired with an LCVR derived from an anti-STEAP2 antibody (e.g., the same LCVR that is included in the anti-STEAP2 antigen-binding domain); and a second antigen-binding domain that specifically binds STEAP2, wherein the second antigen-binding domain comprises an HCVR/LCVR derived from an anti-STEAP2 antibody. In other words, in the exemplary molecules disclosed herein, the pairing of an HCVR from an anti-CD3 antibody with an LCVR from an anti-STEAP2 antibody creates an antigen-binding domain that specifically binds CD3 (but does not bind STEAP2). In such embodiments, the first and second antigen-binding domains comprise distinct anti-CD3 and anti-STEAP2 HCVRs but share a common anti-STEAP2 LCVR. In other embodiments, the bispecific antigen-binding molecules comprise distinct anti-CD3 and anti-STEAP2 HCVRs, but share a common LCVR. The amino acid sequence of this LCVR is shown, e.g., in SEQ ID NO:1890, and the amino acid sequences of the corresponding CDRs (i.e., LCDR1-LCDR2-LCDR3) are shown in SEQ ID NOs:1892, 1894, and 1896, respectively. Genetically modified mice can be used to produce fully human bispecific antigen-binding molecules comprising two different heavy chains that associate with an identical light chain that comprises a variable domain derived from one of two different human light chain variable region gene segments. Alternatively, variable heavy chains may be paired with one common light chain and expressed recombinantly in host cells. As such, the antibodies of the invention can comprise immunoglobulin heavy chains associated with a single rearranged light chain. In some embodiments, the light chain comprises a variable domain derived from a human Vk1-39 gene segment or a Vk3-20 gene segment. In other embodiments, the light chain comprises a variable domain derived from a human Vk1-39 gene segment rearranged with a human Jk5 or a human Jk1 gene segment.

[0056] The present invention provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises any of the HCVR amino acid sequences, any of the LCVR amino acid sequences, any of the HCVR/LCVR amino acid sequence pairs, any of the heavy chain CDR1-CDR2-CDR3 amino acid sequences, or any of the light chain

CDR1-CDR2-CDR3 amino acid sequences as set forth in US publication 2014/0088295 published March 27, 2014 and and PCT/US2016/044732 filed July 29, 2016.

[0057] In addition, the present invention provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises any of the HCVR amino acid sequences as set forth in Tables 9, 11, and 15 herein. The first antigen-binding domain that specifically binds CD3 may also comprise any of the LCVR amino acid sequences as set forth in Tables 1, 9, 12, and 17 herein. According to certain embodiments, the first antigen-binding domain that specifically binds CD3 comprises any of the HCVR/LCVR amino acid sequence pairs as set forth in Tables 9, 11, 12, 15, and 17 herein. The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises any of the heavy chain CDR1-CDR2-CDR3 amino acid sequences as set forth in Tables 9, 11, and 15 herein, and/or any of the light chain CDR1-CDR2-CDR3 amino acid sequences as set forth in Tables 1, 9, 12, and 17 herein.

[0058] According to certain embodiments, the present invention provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a heavy chain variable region (HCVR) having an amino acid sequence as set forth in Tables 9, 11, and 15 herein or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0059] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a light chain variable region (LCVR) having an amino acid sequence as set forth in Tables 1, 9, 12, and 17 herein, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0060] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a HCVR and LCVR (HCVR/LCVR) amino acid sequence pair as set forth in Tables 9, 11, 12, 15, and 17 herein.

[0061] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a heavy chain CDR3 (HCDR3) domain having an amino acid sequence as set forth in Tables 9, 11, and 15 herein, or a substantially similar sequence thereto having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR3 (LCDR3) domain having an amino acid sequence as set forth in Tables 1, 9, 12, and 17 herein, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0062] In certain embodiments, the first antigen-binding domain that specifically binds CD3 comprises a HCDR3/LCDR3 amino acid sequence pair as set forth in Tables 9, 11, 12, 15, and 17 herein.

[0063] The present invention also provides anti-CD3/anti-STEAP2 bispecific antigen-binding molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a heavy chain CDR1 (HCDR1) domain having an amino acid as set forth in Tables 9, 11, and 15 herein, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR2 (HCDR2) domain having an amino acid as set forth in Tables 9, 11, and 15, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR3 (HCDR3) domain having an amino acid as set forth in Tables 9, 11, and 15, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR1 (LCDR1) domain having an amino acid sequence as set forth in Tables 1, 9, 12, and 17 herein, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR2 (LCDR2) domain having an amino acid sequence as set forth in Tables 1, 9, 12, and 17 herein, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity, and a light chain CDR3 (LCDR3) domain having an amino acid sequence as set forth in Tables 1, 9, 12, and 17 herein, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0064] Certain non-limiting, exemplary anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the invention include a first antigen-binding domain that specifically binds CD3 comprising HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, having the amino acid sequences as set forth in Tables 9, 11, 12, 15, and 17 herein.

[0065] The present invention further provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain that specifically binds human CD3 comprises heavy chain complementarity determining regions (HCDR1, HCDR2 and HCDR3) from a heavy chain variable region (HCVR) comprising an amino acid sequence as set forth in Table 9, Table 11, or Table 15 and light chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) from a light chain variable region (LCVR) comprising an amino acid sequence as set forth in Table 1, Table 9, Table 12, or Table 17.

[0066] In another aspect, the invention provides a bispecific antigen-binding molecule wherein the first antigen-binding domain that specifically binds human CD3 comprises heavy chain complementarity determining regions (HCDR1, HCDR2 and HCDR3) from a heavy chain variable region (HCVR) selected from the group consisting of SEQ ID NOs: 1730, 1762, and 1866, and light

chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) from a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 258.

[0067] The invention further provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain that specifically binds human CD3 comprises three heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) and three light chain complementarity determining regions (A1-LCDR1, A1-LCDR2 and A1-LCDR3), wherein A1-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1732, 1764, and 1868; A1-HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1734, 1766, and 1870; A1-HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1736, 1768, and 1872; A1-LCDR1 comprises an amino acid sequence of SEQ ID NO: 260; A1-LCDR2 comprises an amino acid sequence of SEQ ID NO: 262; and A1-LCDR3 comprises an amino acid sequence of SEQ ID NO: 264.

[0068] In a further aspect, the invention provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain that specifically binds human CD3 comprises the heavy and light chain CDRs of a HCVR/LCVR amino acid sequence pair selected from the group consisting of: SEQ ID NOs: 1730/258, 1762/258, and 1866/258.

[0069] In another aspect, the invention provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain that specifically binds human CD3 comprises three heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) and three light chain complementarity determining regions (A1-LCDR1, A1-LCDR2 and A1-LCDR3), and wherein the second antigen-binding domain that specifically binds human STEAP2 comprises three heavy chain complementarity determining regions (A2-HCDR1, A2-HCDR2 and A2-HCDR3) and three light chain complementarity determining regions (A2-LCDR1, A2-LCDR2 and A2-LCDR3); wherein A1-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1732, 1764, and 1868; A1-HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1734, 1766, and 1870; A1-HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1736, 1768, and 1872; A1-LCDR1 comprises an amino acid sequence of SEQ ID NO: 260; A1-LCDR2 comprises an amino acid sequence of SEQ ID NO: 262; and A1-LCDR3 comprises an amino acid sequence of SEQ ID NO: 264; and wherein A2-HCDR1 comprises an amino acid sequence of SEQ ID NO: 252; A2-HCDR2 comprises an amino acid sequence of SEQ ID NO: 254; A2-HCDR3 comprises an amino acid sequence of SEQ ID NO: 256; A2-LCDR1 comprises an amino acid sequence of SEQ ID NO: 260; A2-LCDR2 comprises an amino acid sequence of SEQ ID NO: 262; and A2-LCDR3 comprises an amino acid sequence of SEQ ID NO: 264.

[0070] Certain non-limiting, exemplary anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the invention include a first antigen-binding domain that specifically binds CD3 comprising a heavy chain comprising variable domain framework regions having an amino acid sequence selected from FR1 (SEQ ID NO: 1903), FR2 (SEQ ID NO: 1904), FR3 (SEQ ID NO: 1905), and FR4 (SEQ ID NO: 1906).

[0071] In more embodiments, exemplary anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the invention include a bispecific antigen-binding molecule wherein the first antigen-binding domain that specifically binds human CD3 comprises a HCVR comprising HCDR1-HCDR2-HCDR3 having the amino acid sequences of SEQ ID NOs: 1907-1908-1909

[0072] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the second antigen-binding domain that specifically binds STEAP2 comprises a heavy chain variable region (HCVR) having the amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 18, 34, 50, 66, 74, 82, 90, 98, 106, 122, 138, 154, 170, 186, 202, 218, 234, 250, 266, 282, 298, 314, 330, 346, 362, and 378, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0073] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the second antigen-binding domain that specifically binds STEAP2 comprises a light chain variable region (LCVR) having the amino acid sequence selected from the group consisting of SEQ ID NOs: 10; 26; 42; **58**; 114; 130; 146; 162; 178; 194; 210; 226, 242; 258; 274; 290; 306; 322; 338; 354; 370; and 386, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0074] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the second antigen-binding domain that specifically binds STEAP2 comprises a HCVR and LCVR (HCVR/LCVR) amino acid sequence pair of SEQ ID NO: 250/258.

[0075] The present invention also provides anti-CD3/anti-STEAP2 bispecific molecules, wherein the second antigen-binding domain that specifically binds STEAP2 comprises a heavy chain CDR3 (HCDR3) domain having an amino acid sequence of SEQ ID NO:256 or a substantially similar sequence thereto having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR3 (LCDR3) domain having an amino acid sequence of SEQ ID NO: 264, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0076] In certain embodiments, the second antigen-binding domain that specifically binds STEAP2 comprises a HCDR3/LCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOs:256/264.

[0077] The present invention also provides anti-CD3/anti-STEAP2 bispecific antigen-binding molecules, wherein the second antigen-binding domain that specifically binds STEAP2 comprises a heavy chain CDR1 (HCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:4, 20, 36, 52, 68, 76, 84, 92, 100, 108, 124, 140, 156, 172, 188, 204, 220, 236, 252, 268, 284, 300, 316, 332, 348, 364, and 380, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR2 (HCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:6, 22, 38, 54, 70, 78, 86, 94, 102, 110, 126, 142, 158, 174, 190, 206, 222, 238, 254, 270, 286, 302, 318, 334, 350, 366, and 382, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR3 (HCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:8, 24, 40, 56, 72, 80, 88, 96, 104, 112, 128, 144, 160, 176, 182, 208, 224, 240, 256, 272, 288, 304, 320, 336, 352, 368, and 384, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR1 (LCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:12, 28, 44, 60, 116, 132, 148, 164, 180, 196, 212, 228, 244, 260, 276, 292, 308, 324, 340, 356, 372, and 388, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR2 (LCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:14, 30, 46, 62, 118, 134, 150, 166, 182, 198, 214, 230, 246, 262, 278, 294, 310, 326, 342, 358, 374, and 390, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; ; and a light chain CDR3 (LCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:16, 32, 48, 64, 120, 136, 152, 168, 184, 200, 216, 232, 248, 264, 280, 296, 312, 328, 344, 360, 376, and 392, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0078] Certain non-limiting, exemplary anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the invention include a second antigen-binding domain that specifically binds STEAP2 comprising HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, having the amino acid sequences selected from the group consisting of: SEQ ID NOs: 252-254-256-260-262-264.

[0079] In a related embodiment, the invention includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules wherein the second antigen-binding domain that specifically binds STEAP2 comprises the heavy and light chain CDR domains contained within heavy and light chain variable region (HCVR/LCVR) sequences selected from the group consisting of SEQ ID NOs: 250/258.

[0080] In another aspect, the invention provides a bispecific antigen-binding molecule comprising a first antigen-binding domain that binds human CD3 and a second antigen-binding domain that binds human STEAP2, wherein the second antigen-binding domain is derived from the antibody or antigen-binding fragment of any one of the anti-STEAP2 antibodies of the invention. In a further aspect, the invention provides a bispecific antigen-binding molecule comprising a first antigen-binding domain that specifically binds human CD3, and a second antigen-binding domain that specifically binds human STEAP2.

[0081] The invention further provides a bispecific antigen-binding molecule which binds human cells expressing human CD3 and cynomolgus monkey cells expressing cynomolgus CD3. In another aspect, the bispecific antigen-binding molecule binds human cells expressing human STEAP2.

[0082] In another aspect the invention provides a bispecific antigen-binding molecule which inhibits tumor growth in immunocompromised mice bearing human prostate cancer xenografts.

[0083] In certain embodiments, anti-CD3 antibodies of the invention, antigen-binding fragments and bispecific antibodies thereof were made by replacing amino acid residues of a parental in a stepwise manner based on differences between the germline sequence and the parental antibody sequence.

[0084] In some embodiments, the invention provides a bispecific antigen-binding molecule, wherein the second antigen-binding domain competes for binding to human STEAP2 with a reference antigen-binding protein comprising three heavy chain complementarity determining regions (A2-HCDR1, A2-HCDR2 and A2-HCDR3) and three light chain complementarity determining regions (A2-LCDR1, A2-LCDR2 and A2-LCDR3), wherein A2-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 252; A2-HCDR2 comprises an amino acid sequence of SEQ ID NO: 254; A2-HCDR3 comprises an amino acid sequence of SEQ ID NO: 256; A2-LCDR1 comprises an amino acid sequence of SEQ ID NO: 260; A2-LCDR2 comprises an amino acid sequence of SEQ ID NO: 262; and A2-LCDR3 comprises an amino acid sequence of SEQ ID NO: 264. In some embodiments, the invention provides a bispecific antigen-binding molecule, wherein the second antigen-binding domain competes for binding to human STEAP2 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising an amino acid sequence of SEQ ID NO: 250, and a light chain variable region (LCVR) comprising an amino acid sequence of SEQ ID NO: 258.

[0085] In some embodiments, the invention provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain competes for binding to human CD3 with a reference antigen-binding protein comprising three heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) and three light chain complementarity determining regions

(A1-LCDR1, A1-LCDR2 and A1-LCDR3), wherein A1-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1732, 1764, and 1868; A1-HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1734, 1766, and 1870; A1-HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1736, 1768, and 1872; A1-LCDR1 comprises an amino acid sequence of SEQ ID NO: 260; A1-LCDR2 comprises an amino acid sequence of SEQ ID NO: 262; and A1-LCDR3 comprises an amino acid sequence of SEQ ID NO: 264. In some embodiments, the invention provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain competes for binding to human CD3 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1730, 1762, and 1866, and a light chain variable region (LCVR) comprising an amino acid sequence of SEQ ID NO:258.

[0086] In some embodiments, the invention provides a bispecific antigen-binding molecule, wherein the first antigen-binding domain competes for binding to human CD3 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1730, 1762, and 1866, and a light chain variable region (LCVR) comprising an amino acid sequence of SEQ ID NO:258; and wherein the second antigen-binding domain competes for binding to human STEAP2 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising an amino acid sequence of SEQ ID NO:250, and a light chain variable region (LCVR) comprising an amino acid sequence of SEQ ID NO: 258.

[0087] In one aspect, the invention provides a pharmaceutical composition comprising an anti-STEAP2 antigen-binding molecule or anti-STEAP2/anti-CD3 bispecific antigen-binding molecule and a pharmaceutically acceptable carrier or diluent. The invention further provides a method for treating a cancer in a subject, the method comprising administering to the subject the pharmaceutical composition comprising an anti-STEAP2 antigen-binding molecule or anti-STEAP2/anti-CD3 bispecific antigen-binding molecule and a pharmaceutically acceptable carrier or diluent. In some embodiments, the cancer is selected from the group consisting of prostate cancer, bladder cancer, cervical cancer, lung cancer, colon cancer, kidney cancer, breast cancer, pancreatic cancer, stomach cancer, uterine cancer, and ovarian cancer. In some cases, the cancer is prostate cancer. In some cases, the prostate cancer is castrate-resistant prostate cancer.

[0088] In another aspect, the present invention provides nucleic acid molecules encoding any of the HCVR, LCVR or CDR sequences of the anti-CD3/anti-STEAP2 bispecific antigen-binding molecules disclosed herein, including nucleic acid molecules comprising the polynucleotide sequences as set forth in Tables 2, 10, 13, 14, 16, and 18 herein, as well as nucleic acid molecules

comprising two or more of the polynucleotide sequences as set forth in Tables 2, 10, 13, 14, 16, and 18 in any functional combination or arrangement thereof. Recombinant expression vectors carrying the nucleic acids of the invention, and host cells into which such vectors have been introduced, are also encompassed by the invention, as are methods of producing the antibodies by culturing the host cells under conditions permitting production of the antibodies, and recovering the antibodies produced.

[0089] The present invention includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules wherein any of the aforementioned antigen-binding domains that specifically bind CD3 are combined, connected or otherwise associated with any of the aforementioned antigen-binding domains that specifically bind STEAP2 to form a bispecific antigen-binding molecule that binds CD3 and STEAP2.

[0090] The present invention includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules having a modified glycosylation pattern. In some applications, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

[0091] In another aspect, the invention provides a pharmaceutical composition comprising an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule as disclosed herein and a pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule and a second therapeutic agent. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule. Exemplary agents that may be advantageously combined with an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule are discussed in detail elsewhere herein.

[0092] In yet another aspect, the invention provides therapeutic methods for targeting/killing tumor cells expressing STEAP2 using an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule of the invention to a subject in need thereof.

[0093] The present invention also includes the use of an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule of the invention in the manufacture of a medicament for the treatment of a disease or disorder related to or caused by STEAP2-expressing cells.

[0094] Other embodiments will become apparent from a review of the ensuing detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0095] FIG. 1 shows efficacy of H1H7814N-7 in a STEAP2 positive prostate cancer xenograft model (SCID mice implanted with C4-2 cells) at a dose of 10, 20, or 40 mg/kg H1H7814N-7 administered on day 13 after implantation.

[0096] FIG. 2 shows efficacy of H1H7814N-7 in a STEAP2 positive prostate cancer xenograft model (SCID mice implanted with C4-2 cells) at a dose of 20 mg/kg H1H7814N-7 administered on day 14 after implantation.

[0097] FIG. 3 shows efficacy of H1H7814N-7 in a STEAP2 positive prostate cancer xenograft model (SCID mice implanted with C4-2 cells) at a dose of 150µg/kg H1H7814N-7 administered on day 17 after implantation.

[0098] FIG. 4 shows efficacy of H1H7814N-60 in a STEAP2 positive prostate cancer xenograft model (SCID mice implanted with C4-2 cells) at a dose of 2.5mg/kg (DAR 3.6 TV) H1H7814N-60 administered on day 29 after implantation.

[0099] FIG. 5 shows the binding of STEAP2xCD3 bispecific antibodies to Jurkat cells.

[0100] FIG. 6 shows the binding of STEAP2xCD3 bispecific antibodies to a human prostate cancer cell line (PC3) engineered to express a STEAP2/1 chimeric construct.

[0101] FIGs. 7 and 8 show the binding of STEAP2xCD3 bispecific antibodies to Cynomolgous T cells.

[0102] FIG. 9 shows the induction of human PBMC proliferation by STEAP2xCD3 bispecific antibodies.

[0103] FIG. 10 shows the induction of cynomolgous PBMC proliferation by STEAP2xCD3 bispecific antibodies.

[0104] FIG. 11 shows C4-2 cell (STEAP2-bearing target cells) depletion in a cytotoxicity assay by representative STEAP2xCD3 bispecific antibodies in the presence of human PBMCs.

[0105] FIG. 12 shows activation of human T cells by representative STEAP2xCD3 bispecific antibodies, which correlates with the observed target-cell lysis shown in FIG. 11.

DETAILED DESCRIPTION

[0106] Before the present invention is described, it is to be understood that this invention is not limited to particular methods and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0107] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used herein, the term "about," when used in reference to a particular recited numerical value, means that the value may vary from the recited value by no more than 1%. For example, as used herein, the expression "about 100" includes 99 and 101 and all values in between (e.g., 99.1, 99.2, 99.3, 99.4, etc.).

[0108] Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All patents, applications and non-patent publications mentioned in this specification are incorporated herein by reference in their entireties. However, it is to be understood that, if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in the art, in Australia or any other country.

Definitions

[0109] The expression "CD3," as used herein, refers to an antigen which is expressed on T cells as part of the multimolecular T cell receptor (TCR) and which consists of a homodimer or heterodimer formed from the association of two of four receptor chains: CD3-epsilon, CD3-delta, CD3-zeta, and CD3-gamma. Human CD3-epsilon comprises the amino acid sequence as set forth in SEQ ID NO:1897; human CD3-delta comprises the amino acid sequence as set forth in SEQ ID NO:1898. All references to proteins, polypeptides and protein fragments herein are intended to refer to the human version of the respective protein, polypeptide or protein fragment unless explicitly specified as being from a non-human species. Thus, the expression "CD3" means human CD3 unless specified as being from a non-human species, e.g., "mouse CD3," "monkey CD3," etc.

[0110] As used herein, "an antibody that binds CD3" or an "anti-CD3 antibody" includes antibodies and antigen-binding fragments thereof that specifically recognize a single CD3 subunit (e.g., epsilon, delta, gamma or zeta), as well as antibodies and antigen-binding fragments thereof that specifically recognize a dimeric complex of two CD3 subunits (e.g., gamma/epsilon, delta/epsilon, and zeta/zeta CD3 dimers). The antibodies and antigen-binding fragments of the present invention may bind soluble CD3 and/or cell surface expressed CD3. Soluble CD3 includes natural CD3 proteins as well as recombinant CD3 protein variants such as, e.g., monomeric and dimeric CD3 constructs, that lack a transmembrane domain or are otherwise unassociated with a cell membrane.

[0111] As used herein, the expression "cell surface-expressed CD3" means one or more CD3 protein(s) that is/are expressed on the surface of a cell *in vitro* or *in vivo*, such that at least a portion of a CD3 protein is exposed to the extracellular side of the cell membrane and is accessible to an antigen-binding portion of an antibody. "Cell surface-expressed CD3" includes CD3 proteins contained within the context of a functional T cell receptor in the membrane of a cell. The

expression "cell surface-expressed CD3" includes CD3 protein expressed as part of a homodimer or heterodimer on the surface of a cell (e.g., gamma/epsilon, delta/epsilon, and zeta/zeta CD3 dimers). The expression, "cell surface-expressed CD3" also includes a CD3 chain (e.g., CD3-epsilon, CD3-delta or CD3-gamma) that is expressed by itself, without other CD3 chain types, on the surface of a cell. A "cell surface-expressed CD3" can comprise or consist of a CD3 protein expressed on the surface of a cell which normally expresses CD3 protein. Alternatively, "cell surface-expressed CD3" can comprise or consist of CD3 protein expressed on the surface of a cell that normally does not express human CD3 on its surface but has been artificially engineered to express CD3 on its surface.

[0112] The expression "STEAP2," as used herein, refers to six-transmembrane epithelial antigen of prostate 2. STEAP2 is an integral, six-transmembrane-spanning protein that is highly expressed in prostate epithelial cells and is a cell-surface marker for prostate cancer, for example STEAP2 was found to be expressed in significant levels on an LNCaP prostate cell line (Porkka, et al. *Lab Invest* 2002, 82:1573–1582). STEAP2 (UniProtKB/Swiss-Prot: Q8NFT2.3) is a 490-amino acid protein encoded by *STEAP2* gene located at the chromosomal region 7q21 in humans, see e.g. the amino acid sequence of human STEAP2 as set forth in SEQ ID NO:1899.

[0113] As used herein, "an antibody that binds STEAP2" or an "anti-STEAP2 antibody" includes antibodies and antigen-binding fragments thereof that specifically recognize STEAP2.

[0114] The term "antigen-binding molecule" includes antibodies and antigen-binding fragments of antibodies, including, e.g., bispecific antibodies.

[0115] The term "antibody", as used herein, means any antigen-binding molecule or molecular complex comprising at least one complementarity determining region (CDR) that specifically binds to or interacts with a particular antigen (e.g., STEAP2 or CD3). The term "antibody" includes immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, as well as multimers thereof (e.g., IgM). Each heavy chain comprises a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region comprises three domains, C_{H1} , C_{H2} and C_{H3} . Each light chain comprises a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region comprises one domain (C_{L1}). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In different embodiments of the invention, the FRs of the anti-STEAP2 antibody or anti-CD3 antibody (or antigen-binding portion thereof) may be identical to the human germline

sequences, or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs.

[0116] The term "antibody", as used herein, also includes antigen-binding fragments of full antibody molecules. The terms "antigen-binding portion" of an antibody, "antigen-binding fragment" of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Antigen-binding fragments of an antibody may be derived, *e.g.*, from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and optionally constant domains. Such DNA is known and/or is readily available from, *e.g.*, commercial sources, DNA libraries (including, *e.g.*, phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

[0117] Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) F(ab')₂ fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (*e.g.*, an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide. Other engineered molecules, such as domain-specific antibodies, single domain antibodies, domain-deleted antibodies, chimeric antibodies, CDR-grafted antibodies, diabodies, triabodies, tetrabodies, minibodies, nanobodies (*e.g.* monovalent nanobodies, bivalent nanobodies, etc.), small modular immunopharmaceuticals (SMIPs), and shark variable IgNAR domains, are also encompassed within the expression "antigen-binding fragment," as used herein.

[0118] An antigen-binding fragment of an antibody will typically comprise at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H-V_H, V_H-V_L or V_L-V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

[0119] In certain embodiments, an antigen-binding fragment of an antibody may contain at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding

fragment of an antibody of the present invention include: (i) V_H - C_H1 ; (ii) V_H - C_H2 ; (iii) V_H - C_H3 ; (iv) V_H - C_H1 - C_H2 ; (v) V_H - C_H1 - C_H2 - C_H3 ; (vi) V_H - C_H2 - C_H3 ; (vii) V_H - C_L ; (viii) V_L - C_H1 ; (ix) V_L - C_H2 ; (x) V_L - C_H3 ; (xi) V_L - C_H1 - C_H2 ; (xii) V_L - C_H1 - C_H2 - C_H3 ; (xiii) V_L - C_H2 - C_H3 ; and (xiv) V_L - C_L . In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (e.g., 5, 10, 15, 20, 40, 60 or more) amino acids which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or hetero-dimer (or other multimer) of any of the variable and constant domain configurations listed above in non-covalent association with one another and/or with one or more monomeric V_H or V_L domain (e.g., by disulfide bond(s)).

[0120] As with full antibody molecules, antigen-binding fragments may be monospecific or multispecific (e.g., bispecific). A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format, including the exemplary bispecific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art.

[0121] The antibodies of the present invention may function through complement-dependent cytotoxicity (CDC) or antibody-dependent cell-mediated cytotoxicity (ADCC). "Complement-dependent cytotoxicity" (CDC) refers to lysis of antigen-expressing cells by an antibody of the invention in the presence of complement. "Antibody-dependent cell-mediated cytotoxicity" (ADCC) refers to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and thereby lead to lysis of the target cell. CDC and ADCC can be measured using assays that are well known and available in the art. (See, e.g., U.S. Patent Nos 5,500,362 and 5,821,337, and Clynes *et al.* (1998) *Proc. Natl. Acad. Sci. (USA)* 95:652-656). The constant region of an antibody is important in the ability of an antibody to fix complement and mediate cell-dependent cytotoxicity. Thus, the isotype of an antibody may be selected on the basis of whether it is desirable for the antibody to mediate cytotoxicity.

[0122] In certain embodiments of the invention, the anti-STEAP2 monospecific antibodies or anti-STEAP2/anti-CD3 bispecific antibodies of the invention are human antibodies. The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the invention

may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[0123] The antibodies of the invention may, in some embodiments, be recombinant human antibodies. The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibodies isolated from an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids Res. 20:6287-6295) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to *in vitro* mutagenesis (or, when an animal transgenic for human Ig sequences is used, *in vivo* somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire *in vivo*.

[0124] Human antibodies can exist in two forms that are associated with hinge heterogeneity. In one form, an immunoglobulin molecule comprises a stable four chain construct of approximately 150-160 kDa in which the dimers are held together by an interchain heavy chain disulfide bond. In a second form, the dimers are not linked via inter-chain disulfide bonds and a molecule of about 75-80 kDa is formed composed of a covalently coupled light and heavy chain (half-antibody). These forms have been extremely difficult to separate, even after affinity purification.

[0125] The frequency of appearance of the second form in various intact IgG isotypes is due to, but not limited to, structural differences associated with the hinge region isotype of the antibody. A single amino acid substitution in the hinge region of the human IgG4 hinge can significantly reduce the appearance of the second form (Angal et al. (1993) Molecular Immunology 30:105) to levels typically observed using a human IgG1 hinge. The instant invention encompasses antibodies having one or more mutations in the hinge, C_H2 or C_H3 region which may be desirable, for example, in production, to improve the yield of the desired antibody form.

[0126] The antibodies of the invention may be isolated antibodies. An "isolated antibody," as used herein, means an antibody that has been identified and separated and/or recovered from at least one component of its natural environment. For example, an antibody that has been separated or removed from at least one component of an organism, or from a tissue or cell in which the antibody naturally exists or is naturally produced, is an "isolated antibody" for purposes of the present invention. An isolated antibody also includes an antibody *in situ* within a recombinant cell. Isolated antibodies are antibodies that have been subjected to at least one purification or isolation step. According to certain embodiments, an isolated antibody may be substantially free of other cellular material and/or chemicals.

[0127] The present invention also includes one-arm antibodies that bind STEAP2. As used herein, a "one-arm antibody" means an antigen-binding molecule comprising a single antibody heavy chain and a single antibody light chain. The one-arm antibodies of the present invention may comprise any of the HCVR/LCVR or CDR amino acid sequences as set forth in Table 1.

[0128] The anti-STEAP2 or anti-STEAP2/anti-CD3 antibodies disclosed herein may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences from which the antibodies were derived. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The present invention includes antibodies, and antigen-binding fragments thereof, which are derived from any of the amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s) of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the residues found in the original germline sequence from which the antibody was derived. In other embodiments, only certain residues are mutated back to the original germline sequence, e.g., only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. In other embodiments, one or more of the framework and/or CDR residue(s) are mutated to the corresponding residue(s) of a different germline sequence (*i.e.*, a germline sequence that is different from the germline sequence from

which the antibody was originally derived). Furthermore, the antibodies of the present invention may contain any combination of two or more germline mutations within the framework and/or CDR regions, *e.g.*, wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antibodies and antigen-binding fragments that contain one or more germline mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity, etc. Antibodies and antigen-binding fragments obtained in this general manner are encompassed within the present invention.

[0129] The present invention also includes anti-STEAP2 or anti-STEAP2/anti-CD3 antibodies comprising variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes anti-STEAP2 or anti-STEAP2/anti-CD3 antibodies having HCVR, LCVR, and/or CDR amino acid sequences with, *e.g.*, 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences set forth in Table 1 herein or as described in Tables 9, 11, 12, 15, and 17 herein.

[0130] The term "epitope" refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

[0131] The term "substantial identity" or "substantially identical," when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95%, and more preferably at least about 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed below. A nucleic acid molecule having substantial identity to a reference nucleic acid molecule may, in certain instances, encode a polypeptide having the same or substantially similar amino acid sequence as the polypeptide encoded by the reference nucleic acid molecule.

[0132] As applied to polypeptides, the term "substantial similarity" or "substantially similar" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) *Methods Mol. Biol.* 24: 307-331, herein incorporated by reference. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet *et al.* (1992) *Science* 256: 1443-1445, herein incorporated by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0133] Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutant thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) *supra*). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of

sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul *et al.* (1990) J. Mol. Biol. 215:403-410 and Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-402, each herein incorporated by reference.

Germline Mutations

[0134] The anti-CD3 antibodies disclosed herein comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy chain variable domains as compared to the corresponding germline sequences from which the antibodies were derived.

[0135] The present invention also includes antibodies, and antigen-binding fragments thereof, which are derived from any of the amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s) of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"), and having weak or no detectable binding to a CD3 antigen. Several such exemplary antibodies that recognize CD3 are described in Tables 12 and 18 herein.

[0136] Furthermore, the antibodies of the present invention may contain any combination of two or more germline mutations within the framework and/or CDR regions, e.g., wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antibodies and antigen-binding fragments that contain one or more germline mutations can be tested for one or more desired properties such as, improved binding specificity, weak or reduced binding affinity, improved or enhanced pharmacokinetic properties, reduced immunogenicity, etc. Antibodies and antigen-binding fragments obtained in this general manner given the guidance of the present disclosure are encompassed within the present invention.

[0137] The present invention also includes anti-CD3 antibodies comprising variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes anti-CD3 antibodies having HCVR, LCVR, and/or CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences set forth in Tables 1, 9, 11, 12, 15, and 17 herein. The antibodies and bispecific antigen-binding molecules of the present invention comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and

light chain variable domains as compared to the corresponding germline sequences from which the individual antigen-binding domains were derived, while maintaining or improving the desired weak-to-no detectable binding to CD3 antigen. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein, *i.e.* the amino acid substitution maintains or improves the desired weak to no detectable binding affinity in the case of anti-CD3 binding molecules. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet *et al.* (1992) Science 256: 1443-1445. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0138] The present invention also includes antigen-binding molecules comprising an antigen-binding domain with an HCVR and/or CDR amino acid sequence that is substantially identical to any of the HCVR and/or CDR amino acid sequences disclosed herein, while maintaining or improving the desired weak affinity to CD3 antigen. The term "substantial identity" or "substantially identical," when referring to an amino acid sequence means that two amino acid sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) Methods Mol. Biol. 24: 307-331.

[0139] Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to

determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) *supra*). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410 and Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-402.

[0140] Once obtained, antigen-binding domains that contain one or more germline mutations were tested for decreased binding affinity utilizing one or more *in vitro* assays. Although antibodies that recognize a particular antigen are typically screened for their purpose by testing for high (*i.e.* strong) binding affinity to the antigen, the antibodies of the present invention exhibit weak binding or no detectable binding. Bispecific antigen-binding molecules comprising one or more antigen-binding domains obtained in this general manner are also encompassed within the present invention and were found to be advantageous as avidity-driven tumor therapies.

[0141] Unexpected benefits, for example, improved pharmacokinetic properties and low toxicity to the patient may be realized from the methods described herein.

Binding Properties of the Antibodies

[0142] As used herein, the term "binding" in the context of the binding of an antibody, immunoglobulin, antibody-binding fragment, or Fc-containing protein to either, e.g., a predetermined antigen, such as a cell surface protein or fragment thereof, typically refers to an interaction or association between a minimum of two entities or molecular structures, such as an antibody-antigen interaction.

[0143] For instance, binding affinity typically corresponds to a K_D value of about 10^{-7} M or less, such as about 10^{-8} M or less, such as about 10^{-9} M or less when determined by, for instance, surface plasmon resonance (SPR) technology in a BIAcore 3000 instrument using the antigen as the ligand and the antibody, Ig, antibody-binding fragment, or Fc-containing protein as the analyte (or antiligand). Cell-based binding strategies, such as fluorescent-activated cell sorting (FACS) binding assays, are also routinely used, and FACS data correlates well with other methods such as radioligand competition binding and SPR (Benedict, CA, *J Immunol Methods.* 1997, 201(2):223-31; Geuijen, CA, *et al. J Immunol Methods.* 2005, 302(1-2):68-77).

[0144] Accordingly, the antibody or antigen-binding protein of the invention binds to the predetermined antigen or cell surface molecule (receptor) having an affinity corresponding to a K_D value that is at least ten-fold lower than its affinity for binding to a non-specific antigen (e.g., BSA, casein). According to the present invention, the affinity of an antibody corresponding to a K_D value that is equal to or less than ten-fold lower than a non-specific antigen may be considered non-detectable binding, however such an antibody may be paired with a second antigen binding arm for the production of a bispecific antibody of the invention.

[0145] The term " K_D " (M) refers to the dissociation equilibrium constant of a particular antibody-antigen interaction, or the dissociation equilibrium constant of an antibody or antibody-binding fragment binding to an antigen. There is an inverse relationship between K_D and binding affinity, therefore the smaller the K_D value, the higher, *i.e.* stronger, the affinity. Thus, the terms "higher affinity" or "stronger affinity" relate to a higher ability to form an interaction and therefore a smaller K_D value, and conversely the terms "lower affinity" or "weaker affinity" relate to a lower ability to form an interaction and therefore a larger K_D value. In some circumstances, a higher binding affinity (or K_D) of a particular molecule (e.g. antibody) to its interactive partner molecule (e.g. antigen X) compared to the binding affinity of the molecule (e.g. antibody) to another interactive partner molecule (e.g. antigen Y) may be expressed as a binding ratio determined by dividing the larger K_D value (lower, or weaker, affinity) by the smaller K_D (higher, or stronger, affinity), for example expressed as 5-fold or 10-fold greater binding affinity, as the case may be.

[0146] The term " k_d " (sec⁻¹ or 1/s) refers to the dissociation rate constant of a particular antibody-antigen interaction, or the dissociation rate constant of an antibody or antibody-binding fragment. Said value is also referred to as the k_{off} value.

[0147] The term " k_a " (M⁻¹ x sec⁻¹ or 1/M) refers to the association rate constant of a particular antibody-antigen interaction, or the association rate constant of an antibody or antibody-binding fragment.

[0148] The term " K_A " (M⁻¹ or 1/M) refers to the association equilibrium constant of a particular antibody-antigen interaction, or the association equilibrium constant of an antibody or antibody-binding fragment. The association equilibrium constant is obtained by dividing the k_a by the k_d .

[0149] The term "EC50" or "EC₅₀" refers to the half maximal effective concentration, which includes the concentration of an antibody which induces a response halfway between the baseline and maximum after a specified exposure time. The EC₅₀ essentially represents the concentration of an antibody where 50% of its maximal effect is observed. In certain embodiments, the EC₅₀ value equals the concentration of an antibody of the invention that gives half-maximal binding to cells expressing CD3 or tumor-associated antigen, as determined by e.g. a FACS binding assay. Thus,

reduced or weaker binding is observed with an increased EC_{50} , or half maximal effective concentration value.

[0150] In one embodiment, decreased binding can be defined as an increased EC_{50} antibody concentration which enables binding to the half-maximal amount of target cells.

[0151] In another embodiment, the EC_{50} value represents the concentration of an antibody of the invention that elicits half-maximal depletion of target cells by T cell cytotoxic activity. Thus, increased cytotoxic activity (e.g. T cell-mediated tumor cell killing) is observed with a decreased EC_{50} , or half maximal effective concentration value.

Bispecific Antigen-Binding Molecules

[0152] The antibodies of the present invention may be monospecific, bi-specific, or multispecific. Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, e.g., Tutt et al., 1991, J. Immunol. 147:60-69; Kufer *et al.*, 2004, Trends Biotechnol. 22:238-244. The anti-STEAP2 monospecific antibodies or anti-STEAP2/anti-CD3 bispecific antibodies of the present invention can be linked to or co-expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multispecific antibody with a second or additional binding specificity.

[0153] Use of the expression "anti-CD3 antibody" or "anti-STEAP2 antibody" herein is intended to include both monospecific anti-CD3 or anti-STEAP2 antibodies as well as bispecific antibodies comprising a CD3-binding arm and a STEAP2-binding arm. Thus, the present invention includes bispecific antibodies wherein one arm of an immunoglobulin binds human CD3, and the other arm of the immunoglobulin is specific for human STEAP2. The CD3-binding arm can comprise any of the HCVR/LCVR or CDR amino acid sequences as set forth in Tables 1, 9, 11, 12, 15, and 17 herein.

[0154] In certain embodiments, the CD3-binding arm binds to human CD3 and induces human T cell activation. In certain embodiments, the CD3-binding arm binds weakly to human CD3 and induces human T cell activation. In other embodiments, the CD3-binding arm binds weakly to human CD3 and induces tumor-associated antigen-expressing cell killing in the context of a bispecific or multispecific antibody. In other embodiments, the CD3-binding arm binds or associated weakly with human and cynomolgus (monkey) CD3, yet the binding interaction is not detectable by *in vitro* assays known in the art. The STEAP2-binding arm can comprise any of the HCVR/LCVR or CDR amino acid sequences as set forth in Table 1 herein.

[0155] According to certain exemplary embodiments, the present invention includes bispecific antigen-binding molecules that specifically bind CD3 and STEAP2. Such molecules may be referred to herein as, e.g., "anti-CD3/anti-STEAP2," or "anti-CD3xSTEAP2" or "CD3xSTEAP2" bispecific molecules, or other similar terminology (e.g., anti-STEAP2/anti-CD3).

[0156] The term "STEAP2," as used herein, refers to the human STEAP2 protein unless specified as being from a non-human species (e.g., "mouse STEAP2," "monkey STEAP2," etc.). The human STEAP2 protein has the amino acid sequence shown in SEQ ID NO:1899.

[0157] The aforementioned bispecific antigen-binding molecules that specifically bind CD3 and STEAP2 may comprise an anti-CD3 antigen-binding molecule which binds to CD3 with a weak binding affinity such as exhibiting a K_D of greater than about 40 nM, as measured by an *in vitro* affinity binding assay. In some cases, the CD3 binding arm binds CD3 with a K_D or EC_{50} greater than about 100 nM, greater than about 200 nM, greater than about 300 nM, greater than about 400 nM, greater than about 500 nM, or greater than about 1 μ M (e.g., as measures in a surface plasmon resonance assay). In some cases, the first antigen-binding domain specifically binds CD3 (e.g., either or both of human CD3 and cynomolgus CD3 with weak or no measurable affinity).

[0158] As used herein, the expression "antigen-binding molecule" means a protein, polypeptide or molecular complex comprising or consisting of at least one complementarity determining region (CDR) that alone, or in combination with one or more additional CDRs and/or framework regions (FRs), specifically binds to a particular antigen. In certain embodiments, an antigen-binding molecule is an antibody or a fragment of an antibody, as those terms are defined elsewhere herein.

[0159] As used herein, the expression "bispecific antigen-binding molecule" means a protein, polypeptide or molecular complex comprising at least a first antigen-binding domain and a second antigen-binding domain. Each antigen-binding domain within the bispecific antigen-binding molecule comprises at least one CDR that alone, or in combination with one or more additional CDRs and/or FRs, specifically binds to a particular antigen. In the context of the present invention, the first antigen-binding domain specifically binds a first antigen (e.g., CD3), and the second antigen-binding domain specifically binds a second, distinct antigen (e.g., STEAP2).

[0160] In certain exemplary embodiments of the present invention, the bispecific antigen-binding molecule is a bispecific antibody. Each antigen-binding domain of a bispecific antibody comprises a heavy chain variable domain (HCVR) and a light chain variable domain (LCVR). In the context of a bispecific antigen-binding molecule comprising a first and a second antigen-binding domain (e.g., a bispecific antibody), the CDRs of the first antigen-binding domain may be designated with the prefix "A1" and the CDRs of the second antigen-binding domain may be designated with the prefix "A2". Thus, the CDRs of the first antigen-binding domain may be referred to herein as A1-HCDR1, A1-

HCDR2, and A1-HCDR3; and the CDRs of the second antigen-binding domain may be referred to herein as A2-HCDR1, A2-HCDR2, and A2-HCDR3.

[0161] The first antigen-binding domain and the second antigen-binding domain may be directly or indirectly connected to one another to form a bispecific antigen-binding molecule of the present invention. Alternatively, the first antigen-binding domain and the second antigen-binding domain may each be connected to a separate multimerizing domain. The association of one multimerizing domain with another multimerizing domain facilitates the association between the two antigen-binding domains, thereby forming a bispecific antigen-binding molecule. As used herein, a "multimerizing domain" is any macromolecule, protein, polypeptide, peptide, or amino acid that has the ability to associate with a second multimerizing domain of the same or similar structure or constitution. For example, a multimerizing domain may be a polypeptide comprising an immunoglobulin C_H3 domain. A non-limiting example of a multimerizing component is an Fc portion of an immunoglobulin (comprising a C_H2-C_H3 domain), *e.g.*, an Fc domain of an IgG selected from the isotypes IgG1, IgG2, IgG3, and IgG4, as well as any allotype within each isotype group.

[0162] Bispecific antigen-binding molecules of the present invention will typically comprise two multimerizing domains, *e.g.*, two Fc domains that are each individually part of a separate antibody heavy chain. The first and second multimerizing domains may be of the same IgG isotype such as, *e.g.*, IgG1/IgG1, IgG2/IgG2, IgG4/IgG4. Alternatively, the first and second multimerizing domains may be of different IgG isotypes such as, *e.g.*, IgG1/IgG2, IgG1/IgG4, IgG2/IgG4, etc.

[0163] In certain embodiments, the multimerizing domain is an Fc fragment or an amino acid sequence of from 1 to about 200 amino acids in length containing at least one cysteine residue. In other embodiments, the multimerizing domain is a cysteine residue, or a short cysteine-containing peptide. Other multimerizing domains include peptides or polypeptides comprising or consisting of a leucine zipper, a helix-loop motif, or a coiled-coil motif.

[0164] Any bispecific antibody format or technology may be used to make the bispecific antigen-binding molecules of the present invention. For example, an antibody or fragment thereof having a first antigen binding specificity can be functionally linked (*e.g.*, by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment having a second antigen-binding specificity to produce a bispecific antigen-binding molecule. Specific exemplary bispecific formats that can be used in the context of the present invention include, without limitation, *e.g.*, scFv-based or diabody bispecific formats, IgG-scFv fusions, dual variable domain (DVD)-Ig, Quadroma, knobs-into-holes, common light chain (*e.g.*, common light chain with knobs-into-holes, etc.), CrossMab, CrossFab, (SEED)body, leucine zipper, Duobody, IgG1/IgG2, dual acting Fab (DAF)-IgG, and Mab² bispecific formats (*see, e.g.*,

Klein *et al.* 2012, mAbs 4:6, 1-11, and references cited therein, for a review of the foregoing formats).

[0165] In the context of bispecific antigen-binding molecules of the present invention, the multimerizing domains, *e.g.*, Fc domains, may comprise one or more amino acid changes (*e.g.*, insertions, deletions or substitutions) as compared to the wild-type, naturally occurring version of the Fc domain. For example, the invention includes bispecific antigen-binding molecules comprising one or more modifications in the Fc domain that results in a modified Fc domain having a modified binding interaction (*e.g.*, enhanced or diminished) between Fc and FcRn. In one embodiment, the bispecific antigen-binding molecule comprises a modification in a C_H2 or a C_H3 region, wherein the modification increases the affinity of the Fc domain to FcRn in an acidic environment (*e.g.*, in an endosome where pH ranges from about 5.5 to about 6.0). Non-limiting examples of such Fc modifications include, *e.g.*, a modification at position 250 (*e.g.*, E or Q); 250 and 428 (*e.g.*, L or F); 252 (*e.g.*, L/Y/F/W or T), 254 (*e.g.*, S or T), and 256 (*e.g.*, S/R/Q/E/D or T); or a modification at position 428 and/or 433 (*e.g.*, L/R/S/P/Q or K) and/or 434 (*e.g.*, H/F or Y); or a modification at position 250 and/or 428; or a modification at position 307 or 308 (*e.g.*, 308F, V308F), and 434. In one embodiment, the modification comprises a 428L (*e.g.*, M428L) and 434S (*e.g.*, N434S) modification; a 428L, 259I (*e.g.*, V259I), and 308F (*e.g.*, V308F) modification; a 433K (*e.g.*, H433K) and a 434 (*e.g.*, 434Y) modification; a 252, 254, and 256 (*e.g.*, 252Y, 254T, and 256E) modification; a 250Q and 428L modification (*e.g.*, T250Q and M428L); and a 307 and/or 308 modification (*e.g.*, 308F or 308P).

[0166] The present invention also includes bispecific antigen-binding molecules comprising a first C_H3 domain and a second Ig C_H3 domain, wherein the first and second Ig C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces binding of the bispecific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig C_H3 domain binds Protein A and the second Ig C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise a Y96F modification (by IMGT; Y436F by EU). See, for example, US Patent No. 8,586,713. Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 antibodies; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 antibodies.

[0167] In certain embodiments, the Fc domain may be chimeric, combining Fc sequences derived from more than one immunoglobulin isotype. For example, a chimeric Fc domain can comprise part or all of a C_H2 sequence derived from a human IgG1, human IgG2 or human IgG4 C_H2 region, and part or all of a C_H3 sequence derived from a human IgG1, human IgG2 or human IgG4. A chimeric Fc domain can also contain a chimeric hinge region. For example, a chimeric hinge may comprise an "upper hinge" sequence, derived from a human IgG1, a human IgG2 or a human IgG4 hinge region, combined with a "lower hinge" sequence, derived from a human IgG1, a human IgG2 or a human IgG4 hinge region. A particular example of a chimeric Fc domain that can be included in any of the antigen-binding molecules set forth herein comprises, from N- to C-terminus: [IgG4 C_H1] - [IgG4 upper hinge] - [IgG2 lower hinge] - [IgG4 CH2] - [IgG4 CH3]. Another example of a chimeric Fc domain that can be included in any of the antigen-binding molecules set forth herein comprises, from N- to C-terminus: [IgG1 C_H1] - [IgG1 upper hinge] - [IgG2 lower hinge] - [IgG4 CH2] - [IgG1 CH3]. These and other examples of chimeric Fc domains that can be included in any of the antigen-binding molecules of the present invention are described in US Publication 2014/0243504, published August 28, 2014, which is herein incorporated in its entirety. Chimeric Fc domains having these general structural arrangements, and variants thereof, can have altered Fc receptor binding, which in turn affects Fc effector function.

[0168] In certain embodiments, the invention provides an antibody heavy chain wherein the heavy chain constant region (CH) region comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of SEQ ID NO: 1911, SEQ ID NO: 1912, SEQ ID NO: 1913, SEQ ID NO: 1914, SEQ ID NO: 1915, SEQ ID NO: 1916, SEQ ID NO: 1917, SEQ ID NO: 1918, SEQ ID NO: 1919 or SEQ ID NO: 1920. In some embodiments, the heavy chain constant region (CH) region comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1911, SEQ ID NO: 1912, SEQ ID NO: 1913, SEQ ID NO: 1914, SEQ ID NO: 1915, SEQ ID NO: 1916, SEQ ID NO: 1917, SEQ ID NO: 1918, SEQ ID NO: 1919 and SEQ ID NO: 1920.

[0169] In other embodiments, the invention provides an antibody heavy chain wherein the Fc domain comprises an amino acid sequence at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of SEQ ID NO: 1921, SEQ ID NO: 1922, SEQ ID NO: 1923 SEQ ID NO: 1924 SEQ ID NO: 1925, SEQ ID NO: 1926, SEQ ID NO: 1927, SEQ ID NO: 1928, SEQ ID NO: 1929 or SEQ ID NO: 1930. In some embodiments, the Fc domain comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1921, SEQ ID NO: 1922, SEQ ID NO: 1923 SEQ ID NO: 1924 SEQ ID NO: 1925, SEQ ID NO: 1926, SEQ ID NO: 1927, SEQ ID NO: 1928, SEQ ID NO: 1929 and SEQ ID NO: 1930.

Sequence Variants

[0170] The antibodies and bispecific antigen-binding molecules of the present invention may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences from which the individual antigen-binding domains were derived. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The antigen-binding molecules of the present invention may comprise antigen-binding domains which are derived from any of the exemplary amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s) of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the residues found in the original germline sequence from which the antigen-binding domain was originally derived. In other embodiments, only certain residues are mutated back to the original germline sequence, *e.g.*, only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. In other embodiments, one or more of the framework and/or CDR residue(s) are mutated to the corresponding residue(s) of a different germline sequence (*i.e.*, a germline sequence that is different from the germline sequence from which the antigen-binding domain was originally derived). Furthermore, the antigen-binding domains may contain any combination of two or more germline mutations within the framework and/or CDR regions, *e.g.*, wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antigen-binding domains that contain one or more germline mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity, etc. Bispecific antigen-binding molecules comprising one or more antigen-binding domains obtained in this general manner are encompassed within the present invention.

[0171] The present invention also includes antigen-binding molecules wherein one or both antigen-binding domains comprise variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes antigen-binding molecules comprising an antigen-binding domain having HCVR, LCVR, and/or CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet *et al.* (1992) Science 256: 1443-1445, herein incorporated by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0172] The present invention also includes antigen-binding molecules comprising an antigen-binding domain with an HCVR, LCVR, and/or CDR amino acid sequence that is substantially identical to any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein. The term "substantial identity" or "substantially identical," when referring to an amino acid sequence means that two amino acid sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) Methods Mol. Biol. 24: 307-331, herein incorporated by reference.

[0173] Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar

sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) *supra*). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410 and Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-402, each herein incorporated by reference.

pH-Dependent Binding

[0174] The present invention includes anti-STEAP2 antibodies, and anti-CD3/anti-STEAP2 bispecific antigen-binding molecules, with pH-dependent binding characteristics. For example, an anti-STEAP2 antibody of the present invention may exhibit reduced binding to STEAP2 at acidic pH as compared to neutral pH. Alternatively, anti-STEAP2 antibodies of the invention may exhibit enhanced binding to STEAP2 at acidic pH as compared to neutral pH. The expression "acidic pH" includes pH values less than about 6.2, e.g., about 6.0, 5.95, 5.9, 5.85, 5.8, 5.75, 5.7, 5.65, 5.6, 5.55, 5.5, 5.45, 5.4, 5.35, 5.3, 5.25, 5.2, 5.15, 5.1, 5.05, 5.0, or less. As used herein, the expression "neutral pH" means a pH of about 7.0 to about 7.4. The expression "neutral pH" includes pH values of about 7.0, 7.05, 7.1, 7.15, 7.2, 7.25, 7.3, 7.35, and 7.4.

[0175] In certain instances, "reduced binding ... at acidic pH as compared to neutral pH" is expressed in terms of a ratio of the K_D value of the antibody binding to its antigen at acidic pH to the K_D value of the antibody binding to its antigen at neutral pH (or vice versa). For example, an antibody or antigen-binding fragment thereof may be regarded as exhibiting "reduced binding to STEAP2 at acidic pH as compared to neutral pH" for purposes of the present invention if the antibody or antigen-binding fragment thereof exhibits an acidic/neutral K_D ratio of about 3.0 or greater. In certain exemplary embodiments, the acidic/neutral K_D ratio for an antibody or antigen-binding fragment of the present invention can be about 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11.0, 11.5, 12.0, 12.5, 13.0, 13.5, 14.0, 14.5, 15.0, 20.0, 25.0, 30.0, 40.0, 50.0, 60.0, 70.0, 100.0 or greater.

[0176] Antibodies with pH-dependent binding characteristics may be obtained, *e.g.*, by screening a population of antibodies for reduced (or enhanced) binding to a particular antigen at acidic pH as compared to neutral pH. Additionally, modifications of the antigen-binding domain at the amino acid level may yield antibodies with pH-dependent characteristics. For example, by substituting one or more amino acids of an antigen-binding domain (*e.g.*, within a CDR) with a histidine residue, an antibody with reduced antigen-binding at acidic pH relative to neutral pH may be obtained.

Antibodies Comprising Fc Variants

[0177] According to certain embodiments of the present invention, anti-STEAP2 antibodies, and anti-CD3/anti-STEAP2 bispecific antigen-binding molecules, are provided comprising an Fc domain comprising one or more mutations which enhance or diminish antibody binding to the FcRn receptor, *e.g.*, at acidic pH as compared to neutral pH. For example, the present invention includes antibodies comprising a mutation in the C_H2 or a C_H3 region of the Fc domain, wherein the mutation(s) increases the affinity of the Fc domain to FcRn in an acidic environment (*e.g.*, in an endosome where pH ranges from about 5.5 to about 6.0). Such mutations may result in an increase in serum half-life of the antibody when administered to an animal. Non-limiting examples of such Fc modifications include, *e.g.*, a modification at position 250 (*e.g.*, E or Q); 250 and 428 (*e.g.*, L or F); 252 (*e.g.*, L/Y/F/W or T), 254 (*e.g.*, S or T), and 256 (*e.g.*, S/R/Q/E/D or T); or a modification at position 428 and/or 433 (*e.g.*, H/L/R/S/P/Q or K) and/or 434 (*e.g.*, H/F or Y); or a modification at position 250 and/or 428; or a modification at position 307 or 308 (*e.g.*, 308F, V308F), and 434. In one embodiment, the modification comprises a 428L (*e.g.*, M428L) and 434S (*e.g.*, N434S) modification; a 428L, 259I (*e.g.*, V259I), and 308F (*e.g.*, V308F) modification; a 433K (*e.g.*, H433K) and a 434 (*e.g.*, 434Y) modification; a 252, 254, and 256 (*e.g.*, 252Y, 254T, and 256E) modification; a 250Q and 428L modification (*e.g.*, T250Q and M428L); and a 307 and/or 308 modification (*e.g.*, 308F or 308P).

[0178] For example, the present invention includes anti-STEAP2 antibodies, and anti-CD3/anti-STEAP2 bispecific antigen-binding molecules, comprising an Fc domain comprising one or more pairs or groups of mutations selected from the group consisting of: 250Q and 248L (*e.g.*, T250Q and M248L); 252Y, 254T and 256E (*e.g.*, M252Y, S254T and T256E); 428L and 434S (*e.g.*, M428L and N434S); and 433K and 434F (*e.g.*, H433K and N434F). All possible combinations of the foregoing Fc domain mutations, and other mutations within the antibody variable domains disclosed herein, are contemplated within the scope of the present invention.

Biological Characteristics of the Antibodies and Bispecific Antigen-Binding Molecules

[0179] The present invention includes antibodies and antigen-binding fragments thereof that bind human STEAP2 with high affinity (e.g., sub-nanomolar K_D values).

[0180] The present invention also includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules which inhibit tumor growth in immunocompromised mice bearing human prostate cancer xenografts. (see, e.g., Example 5).

[0181] The present invention includes antibodies and antigen-binding fragments thereof that bind human CD3 with high affinity. The present invention also includes antibodies and antigen-binding fragments thereof that bind human CD3 with medium or low affinity, depending on the therapeutic context and particular targeting properties that are desired. For example, in the context of a bispecific antigen-binding molecule, wherein one arm binds CD3 and another arm binds a target antigen (e.g., STEAP2), it may be desirable for the target antigen-binding arm to bind the target antigen with high affinity while the anti-CD3 arm binds CD3 with only moderate or low affinity. In this manner, preferential targeting of the antigen-binding molecule to cells expressing the target antigen may be achieved while avoiding general/untargeted CD3 binding and the consequent adverse side effects associated therewith.

[0182] The present invention includes bispecific antigen-binding molecules (e.g., bispecific antibodies) which are capable of simultaneously binding to human CD3 and a human STEAP2. The binding arm that interacts with cells that express CD3 may have weak to no detectable binding as measured in a suitable *in vitro* binding assay. The extent to which a bispecific antigen-binding molecule binds cells that express CD3 and/or STEAP2 can be assessed by fluorescence activated cell sorting (FACS).

[0183] The present invention also includes antibodies, antigen-binding fragments, and bispecific antibodies thereof which bind to STEAP2-expressing cells and cell lines (e.g., CA-2 cells), with an EC_{50} value of between about 1 nM and 50 nM, as determined using a FACS binding assay as set forth in Example 2 or a substantially similar assay. In certain embodiments, the antibodies, antigen-binding fragments, and bispecific antibodies thereof which bind to STEAP2-expressing cells and cell lines (e.g., CA-2 cells), with an EC_{50} value of about 50 nM, of about 40 nM, of about 30 nM, of about 20 nM, of about of less than about 15 nM, of about 10nM, of about 5 nM, of about 4nM, of about 3nM, or of about 2nM, of about 1nM, as determined using a FACS binding assay as set forth in Example 2 or a substantially similar assay.

[0184] The present invention includes antibodies, antigen-binding fragments, and bispecific antibodies thereof that bind human CD3 with weak (*i.e.* low) or even no detectable affinity. According to certain embodiments, the present invention includes antibodies and antigen-binding fragments of antibodies that bind human CD3 (e.g., at 37°C) with a K_D of greater than about 11 nM

as measured by surface plasmon resonance. In certain embodiments, the antibodies or antigen-binding fragments of the present invention bind CD3 with a K_D of greater than about 15 nM, greater than about 20 nM, greater than about 25 nM, greater than about 30 nM, greater than about 35 nM, greater than about 40 nM, greater than about 45 nM, greater than about 50 nM, greater than about 55 nM, greater than about 60 nM, greater than about 65 nM, greater than about 70 nM, greater than about 75 nM, at least 80 nM, greater than about 90 nM, greater than about 100 nM, greater than about 110 nM, at least 120 nM, greater than about 130 nM, greater than about 140 nM, greater than about 150 nM, at least 160 nM, greater than about 170 nM, greater than about 180 nM, greater than about 190 nM, greater than about 200 nM, greater than about 250 nM, greater than about 300 nM, greater than about 400 nM, greater than about 500 nM, or greater than about 1 μ M, or with no detectable affinity, as measured by surface plasmon resonance (e.g., mAb-capture or antigen-capture format), or a substantially similar assay.

[0185] The present invention includes antibodies, antigen-binding fragments, and bispecific antibodies thereof that bind monkey (*i.e.* cynomolgus) CD3 with weak (*i.e.* low) or even no detectable affinity.

[0186] The present invention includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules which bind to and are internalized by human STEAP2 expressing cells (e.g., CA-2 cells), as measured by an assay format as defined by Example 3 herein or a substantially similar assay. The present invention includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules which are specific for binding to human STEAP2. In certain embodiments, the anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the present invention bind human STEAP-2 transiently expressed in HEK293 cells, as measured by an assay format as defined by Example 3 herein or a substantially similar assay. In certain embodiments, the anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the present invention do not bind human STEAP1, human STEAP2, or human STEAP4 transiently expressed in HEK293 cells, as measured by an assay format as defined by Example 3 herein or a substantially similar assay.

[0187] The present invention includes anti-CD3/anti-STEAP2 bispecific antigen-binding molecules which are capable of inhibiting C4-2 tumor growth (see, e.g., Example 5). For example, according to certain embodiments, anti-CD3/anti-STEAP2 bispecific antigen-binding molecules are provided, wherein a single administration e.g., at a dose of about 0.1 mg/kg or about 0.01 mg/kg) causes a reduction in the tumor size compared to animals administered a isotype control bispecific antibody, when measured 46 days post-tumor implantation, as detected in a subject using standard caliper measurement methods, e.g., as set forth in Example 5, herein..

[0188] The present invention also includes anti-STEAP2 antibody drug conjugates which inhibit tumor growth in in vivo STEAP2 positive prostate cancer xenograft models (see, e.g., Example 7, or

in a substantially similar assay). In certain embodiments, anti- STEAP2 antibody drug conjugates with **Compound 7** are provided, wherein one dose at 10, 20, or 40 mg/kg administered on day 13 after tumor implantation, inhibit C4-2 tumor growth in in vivo STEAP2 positive prostate cancer xenograft models. In certain embodiments, anti- STEAP2 antibody drug conjugates with **Compound 7** are provided wherein one dose at 5 or 20 mg/kg administered on day 14 after implantation, inhibit C4-2 tumor growth in in vivo STEAP2 positive prostate cancer xenograft models. In certain embodiments, anti- STEAP2 antibody drug conjugates with **Compound 7** are provided wherein one dose at 150 µg/kg administered on day 17 after implantation, inhibit C4-2 tumor growth in in vivo STEAP2 positive prostate cancer xenograft models. In other embodiments, anti- STEAP2 antibody drug conjugates with **Compound 60** are provided wherein one dose of at least 2.5 mg/kg administered on day 29 after implantation, inhibits C4-2 tumor growth in *in vivo* STEAP2 positive prostate cancer xenograft models.

Epitope Mapping and Related Technologies

[0189] The epitope on CD3 and/or STEAP2 to which the antigen-binding molecules of the present invention bind may consist of a single contiguous sequence of 3 or more (e.g., 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) amino acids of a CD3 or STEAP2 protein.

Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) of CD3 or STEAP2. The antibodies of the invention may interact with amino acids contained within a single CD3 chain (e.g., CD3-epsilon, CD3-delta or CD3-gamma), or may interact with amino acids on two or more different CD3 chains. The term "epitope," as used herein, refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstances, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

[0190] Various techniques known to persons of ordinary skill in the art can be used to determine whether an antigen-binding domain of an antibody "interacts with one or more amino acids" within a polypeptide or protein. Exemplary techniques include, e.g., routine cross-blocking assay such as that described Antibodies, Harlow and Lane (Cold Spring Harbor Press, Cold Spring Harb., NY), alanine scanning mutational analysis, peptide blots analysis (Reineke, 2004, *Methods Mol Biol* 248:443-463), and peptide cleavage analysis. In addition, methods such as epitope excision,

epitope extraction and chemical modification of antigens can be employed (Tomer, 2000, *Protein Science* 9:487-496). Another method that can be used to identify the amino acids within a polypeptide with which an antigen-binding domain of an antibody interacts is hydrogen/deuterium exchange detected by mass spectrometry. In general terms, the hydrogen/deuterium exchange method involves deuterium-labeling the protein of interest, followed by binding the antibody to the deuterium-labeled protein. Next, the protein/antibody complex is transferred to water to allow hydrogen-deuterium exchange to occur at all residues except for the residues protected by the antibody (which remain deuterium-labeled). After dissociation of the antibody, the target protein is subjected to protease cleavage and mass spectrometry analysis, thereby revealing the deuterium-labeled residues which correspond to the specific amino acids with which the antibody interacts. See, e.g., Ehrling (1999) *Analytical Biochemistry* 267(2):252-259; Engen and Smith (2001) *Anal. Chem.* 73:256A-265A. X-ray crystallography of the antigen/antibody complex may also be used for epitope mapping purposes.

[0191] The present invention further includes anti-STEAP2 antibodies that bind to the same epitope as any of the specific exemplary antibodies described herein (e.g. antibodies comprising any of the amino acid sequences as set forth in Table 1 herein). Likewise, the present invention also includes anti-STEAP2 antibodies that compete for binding to STEAP2 with any of the specific exemplary antibodies described herein (e.g. antibodies comprising any of the amino acid sequences as set forth in Table 1 herein).

[0192] The present invention also includes bispecific antigen-binding molecules comprising a first antigen-binding domain that specifically binds human CD3 and/or cynomolgus CD3 with low or detectable binding affinity, and a second antigen binding domain that specifically binds human STEAP2, wherein the first antigen-binding domain binds to the same epitope on CD3 as any of the specific exemplary CD3-specific antigen-binding domains described herein, and/or wherein the second antigen-binding domain binds to the same epitope on STEAP2 as any of the specific exemplary STEAP2-specific antigen-binding domains described herein.

[0193] Likewise, the present invention also includes bispecific antigen-binding molecules comprising a first antigen-binding domain that specifically binds human CD3, and a second antigen binding domain that specifically binds human STEAP2, wherein the first antigen-binding domain competes for binding to CD3 with any of the specific exemplary CD3-specific antigen-binding domains described herein, and/or wherein the second antigen-binding domain competes for binding to STEAP2 with any of the specific exemplary STEAP2-specific antigen-binding domains described herein.

[0194] One can easily determine whether a particular antigen-binding molecule (e.g., antibody) or antigen-binding domain thereof binds to the same epitope as, or competes for binding with, a

reference antigen-binding molecule of the present invention by using routine methods known in the art. For example, to determine if a test antibody binds to the same epitope on STEAP2 (or CD3) as a reference bispecific antigen-binding molecule of the present invention, the reference bispecific molecule is first allowed to bind to a STEAP2 protein (or CD3 protein). Next, the ability of a test antibody to bind to the STEAP2 (or CD3) molecule is assessed. If the test antibody is able to bind to STEAP2 (or CD3) following saturation binding with the reference bispecific antigen-binding molecule, it can be concluded that the test antibody binds to a different epitope of STEAP2 (or CD3) than the reference bispecific antigen-binding molecule. On the other hand, if the test antibody is not able to bind to the STEAP2 (or CD3) molecule following saturation binding with the reference bispecific antigen-binding molecule, then the test antibody may bind to the same epitope of STEAP2 (or CD3) as the epitope bound by the reference bispecific antigen-binding molecule of the invention. Additional routine experimentation (*e.g.*, peptide mutation and binding analyses) can then be carried out to confirm whether the observed lack of binding of the test antibody is in fact due to binding to the same epitope as the reference bispecific antigen-binding molecule or if steric blocking (or another phenomenon) is responsible for the lack of observed binding. Experiments of this sort can be performed using ELISA, RIA, Biacore, flow cytometry or any other quantitative or qualitative antibody-binding assay available in the art. In accordance with certain embodiments of the present invention, two antigen-binding proteins bind to the same (or overlapping) epitope if, *e.g.*, a 1-, 5-, 10-, 20- or 100-fold excess of one antigen-binding protein inhibits binding of the other by at least 50% but preferably 75%, 90% or even 99% as measured in a competitive binding assay (see, *e.g.*, Junghans et al., Cancer Res. 1990:50:1495-1502). Alternatively, two antigen-binding proteins are deemed to bind to the same epitope if essentially all amino acid mutations in the antigen that reduce or eliminate binding of one antigen-binding protein reduce or eliminate binding of the other. Two antigen-binding proteins are deemed to have "overlapping epitopes" if only a subset of the amino acid mutations that reduce or eliminate binding of one antigen-binding protein reduce or eliminate binding of the other.

[0195] To determine if an antibody or antigen-binding domain thereof competes for binding with a reference antigen-binding molecule, the above-described binding methodology is performed in two orientations: In a first orientation, the reference antigen-binding molecule is allowed to bind to a STEAP2 protein (or CD3 protein) under saturating conditions followed by assessment of binding of the test antibody to the STEAP2 (or CD3) molecule. In a second orientation, the test antibody is allowed to bind to a STEAP2 (or CD3) molecule under saturating conditions followed by assessment of binding of the reference antigen-binding molecule to the STEAP2 (or CD3) molecule. If, in both orientations, only the first (saturating) antigen-binding molecule is capable of binding to the STEAP2 (or CD3) molecule, then it is concluded that the test antibody and the

reference antigen-binding molecule compete for binding to STEAP2 (or CD3). As will be appreciated by a person of ordinary skill in the art, an antibody that competes for binding with a reference antigen-binding molecule may not necessarily bind to the same epitope as the reference antibody, but may sterically block binding of the reference antibody by binding an overlapping or adjacent epitope.

Preparation of Antigen-Binding Domains and Construction of Bispecific Molecules

[0196] Antigen-binding domains specific for particular antigens can be prepared by any antibody generating technology known in the art. Once obtained, two different antigen-binding domains, specific for two different antigens (*e.g.*, CD3 and STEAP2), can be appropriately arranged relative to one another to produce a bispecific antigen-binding molecule of the present invention using routine methods. (A discussion of exemplary bispecific antibody formats that can be used to construct the bispecific antigen-binding molecules of the present invention is provided elsewhere herein). In certain embodiments, one or more of the individual components (*e.g.*, heavy and light chains) of the multispecific antigen-binding molecules of the invention are derived from chimeric, humanized or fully human antibodies. Methods for making such antibodies are well known in the art. For example, one or more of the heavy and/or light chains of the bispecific antigen-binding molecules of the present invention can be prepared using VELOCIMMUNE™ technology. Using VELOCIMMUNE™ technology (or any other human antibody generating technology), high affinity chimeric antibodies to a particular antigen (*e.g.*, CD3 or STEAP2) are initially isolated having a human variable region and a mouse constant region. The antibodies are characterized and selected for desirable characteristics, including affinity, selectivity, epitope, etc. The mouse constant regions are replaced with a desired human constant region to generate fully human heavy and/or light chains that can be incorporated into the bispecific antigen-binding molecules of the present invention.

[0197] Genetically engineered animals may be used to make human bispecific antigen-binding molecules. For example, a genetically modified mouse can be used which is incapable of rearranging and expressing an endogenous mouse immunoglobulin light chain variable sequence, wherein the mouse expresses only one or two human light chain variable domains encoded by human immunoglobulin sequences operably linked to the mouse kappa constant gene at the endogenous mouse kappa locus. Such genetically modified mice can be used to produce fully human bispecific antigen-binding molecules comprising two different heavy chains that associate with an identical light chain that comprises a variable domain derived from one of two different human light chain variable region gene segments. (See, *e.g.*, US 2011/0195454). Fully human refers to an antibody, or antigen-binding fragment or immunoglobulin domain thereof, comprising an

amino acid sequence encoded by a DNA derived from a human sequence over the entire length of each polypeptide of the antibody or antigen-binding fragment or immunoglobulin domain thereof. In some instances, the fully human sequence is derived from a protein endogenous to a human. In other instances, the fully human protein or protein sequence comprises a chimeric sequence wherein each component sequence is derived from human sequence. While not being bound by any one theory, chimeric proteins or chimeric sequences are generally designed to minimize the creation of immunogenic epitopes in the junctions of component sequences, *e.g.* compared to any wild-type human immunoglobulin regions or domains.

Bioequivalents

[0198] The present invention encompasses antigen-binding molecules having amino acid sequences that vary from those of the exemplary molecules disclosed herein but that retain the ability to bind CD3 and/or STEAP2. Such variant molecules may comprise one or more additions, deletions, or substitutions of amino acids when compared to parent sequence, but exhibit biological activity that is essentially equivalent to that of the described bispecific antigen-binding molecules.

[0199] The present invention includes antigen-binding molecules that are bioequivalent to any of the exemplary antigen-binding molecules set forth herein. Two antigen-binding proteins, or antibodies, are considered bioequivalent if, for example, they are pharmaceutical equivalents or pharmaceutical alternatives whose rate and extent of absorption do not show a significant difference when administered at the same molar dose under similar experimental conditions, either single dose or multiple dose. Some antigen-binding proteins will be considered equivalents or pharmaceutical alternatives if they are equivalent in the extent of their absorption but not in their rate of absorption and yet may be considered bioequivalent because such differences in the rate of absorption are intentional and are reflected in the labeling, are not essential to the attainment of effective body drug concentrations on, *e.g.*, chronic use, and are considered medically insignificant for the particular drug product studied.

[0200] In one embodiment, two antigen-binding proteins are bioequivalent if there are no clinically meaningful differences in their safety, purity, and potency.

[0201] In one embodiment, two antigen-binding proteins are bioequivalent if a patient can be switched one or more times between the reference product and the biological product without an expected increase in the risk of adverse effects, including a clinically significant change in immunogenicity, or diminished effectiveness, as compared to continued therapy without such switching.

[0202] In one embodiment, two antigen-binding proteins are bioequivalent if they both act by a common mechanism or mechanisms of action for the condition or conditions of use, to the extent that such mechanisms are known.

[0203] Bioequivalence may be demonstrated by in vivo and in vitro methods. Bioequivalence measures include, e.g., (a) an in vivo test in humans or other mammals, in which the concentration of the antibody or its metabolites is measured in blood, plasma, serum, or other biological fluid as a function of time; (b) an in vitro test that has been correlated with and is reasonably predictive of human in vivo bioavailability data; (c) an in vivo test in humans or other mammals in which the appropriate acute pharmacological effect of the antibody (or its target) is measured as a function of time; and (d) in a well-controlled clinical trial that establishes safety, efficacy, or bioavailability or bioequivalence of an antigen-binding protein.

[0204] Bioequivalent variants of the exemplary bispecific antigen-binding molecules set forth herein may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine residues not essential for biological activity can be deleted or replaced with other amino acids to prevent formation of unnecessary or incorrect intramolecular disulfide bridges upon renaturation. In other contexts, bioequivalent antigen-binding proteins may include variants of the exemplary bispecific antigen-binding molecules set forth herein comprising amino acid changes which modify the glycosylation characteristics of the molecules, e.g., mutations which eliminate or remove glycosylation.

Species Selectivity and Species Cross-Reactivity

[0205] According to certain embodiments of the invention, antigen-binding molecules are provided which bind to human CD3 but not to CD3 from other species. Also provided are antigen-binding molecules which bind to human STEAP2 but not to STEAP2 from other species. The present invention also includes antigen-binding molecules that bind to human CD3 and to CD3 from one or more non-human species; and/or antigen-binding molecules that bind to human STEAP2 and to STEAP2 from one or more non-human species.

[0206] According to certain exemplary embodiments of the invention, antigen-binding molecules are provided which bind to human CD3 and/or human STEAP2 and may bind or not bind, as the case may be, to one or more of mouse, rat, guinea pig, hamster, gerbil, pig, cat, dog, rabbit, goat, sheep, cow, horse, camel, cynomolgus, marmoset, rhesus or chimpanzee CD3 and/or STEAP2. For example, in a particular exemplary embodiment of the present invention bispecific antigen-binding molecules are provided comprising a first antigen-binding domain that binds human CD3

and cynomolgus CD3, and a second antigen-binding domain that specifically binds human STEAP2.

Antibody-Drug Conjugates (ADCs)

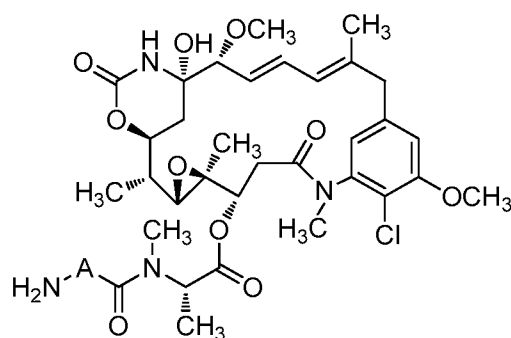
[0207] The present invention provides antibody-drug conjugates (ADCs) comprising an anti-STEAP2 antibody or antigen-binding fragment thereof conjugated to a therapeutic moiety such as a cytotoxic agent, a chemotherapeutic drug, immunosuppressant or a radioisotope. In general terms, the ADCs comprise: $A - [L - P]_y$, in which A is an antigen-binding molecule, *e.g.* an anti-STEAP2 antibody, or a fragment thereof (*e.g.*, a fragment comprising at least a HCDR3 selected from any of the HCDR3 amino acid sequences listed in Table 1), L is a linker, P is the payload or therapeutic moiety (*e.g.*, cytotoxic agent), and y is an integer from 1 to 30. In various embodiments, the ADC comprises an anti-STEAP2 antibody or antigen-binding fragment thereof that comprises the CDRs of a HCVR and a LCVR having the amino acid sequences of the SEQ ID NOs (*e.g.*, SEQ ID NOs: 2 and 10) set forth in Table 1, or specific HCVR/LCVR pairs (*e.g.*, SEQ ID NOs: 2/10). In some cases, the anti-STEAP2 antibody or fragment comprises CDRs with the amino acid sequences of the SEQ ID NOs (*e.g.*, SEQ ID NOs: 4-6-8-12-14-16) set forth in Table 1. In some cases, the anti-STEAP2 antibody or fragment comprises a HCVR and a LCVR having the amino acid sequences of the SEQ ID NOs (*e.g.*, SEQ ID NOs: 2 and 10) set forth in Table 1, or specific amino acid sequence pairs (*e.g.*, SEQ ID NOs: 2/10).

[0208] Cytotoxic agents include any agent that is detrimental to the growth, viability or propagation of cells. The antigen-binding molecules or antibodies of the invention deliver these cytotoxic agents, referred to herein as “payloads”, to the target cells. Examples of suitable cytotoxic agents and chemotherapeutic agents for forming ADCs are known in the art.

[0209] Examples of suitable cytotoxic agents and chemotherapeutic agents that can be conjugated to anti-STEAP2 antibodies in accordance with this aspect of the invention include, *e.g.*, 1-(2chloroethyl)-1,2-dimethanesulfonyl hydrazide, 1,8-dihydroxy-bicyclo[7.3.1]trideca-4,9-diene-2,6-diyne-13-one, 1-dehydrotestosterone, 5-fluorouracil, 6-mercaptopurine, 6-thioguanine, 9-amino camptothecin, actinomycin D, amanitins, aminopterin, anguidine, anthracycline, anthramycin (AMC), auristatins (monomethyl auristatin E or monomethyl auristatin F), bleomycin, busulfan, butyric acid, calicheamicins, camptothecin, carminomycins, carmustine, cedadotins, cisplatin, colchicin, combretastatins, cyclophosphamide, cytarabine, cytochalasin B, dactinomycin, daunorubicin, decarbazine, diacetoxypentylidoxorubicin, dibromomannitol, dihydroxy anthracin dione, disorazoles, dolastatin, doxorubicin, duocarmycin, echinomycins, eleutherobins, emetine, epothilones, esperamicin, estramustines, ethidium bromide, etoposide, fluorouracils, geldanamycins, gramicidin D, glucocorticoids, irinotecans, leptomycins, leurosines, lidocaine,

lomustine (CCNU), maytansinoids, mechlorethamine, melphalan, mercaptopurines, methopterin, methotrexate, mithramycin, mitomycin, mitoxantrone, N8-acetyl spermidine, podophyllotoxins, procaine, propranolol, pteridines, puromycin, rhizoxins, streptozotocin, tallysomycins, taxol, tenoposide, tetracaine, thioepa chlorambucil, tomaymycins, topotecans, tubulysin, vinblastine, vincristine, vindesine, vinorelbines, and derivatives of any of the foregoing.

[0210] According to certain embodiments, the cytotoxic agent that is conjugated to an anti-STEAP2 antibody is an auristatin such as monomethyl auristatin E (MMAE) or monomethyl auristatin F (MMAF), a tubulysin such as TUB-OH or TUB-OMOM, a tomaymycin derivative, a dolastatin derivative, or a maytansinoid such as DM1 or DM4. In some embodiments, the cytotoxic agent is a maytansinoid having the structure of Formula (I), including stereoisomers of the compounds of Formula (I):



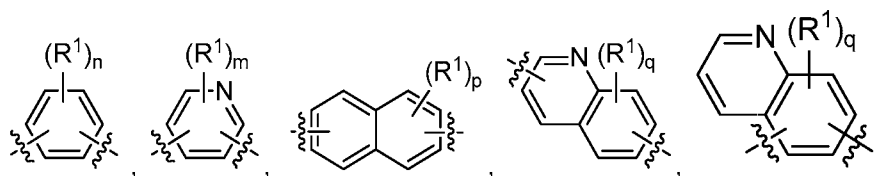
(Formula I)

wherein A is arylene or heteroarylene.

[0211] In some embodiments, A is a divalent radical of benzene, of pyridine, of naphthalene, or of quinolone, which are optionally substituted.

[0212] In some embodiments, A is arylene.

[0213] In some embodiments, A is:



wherein:

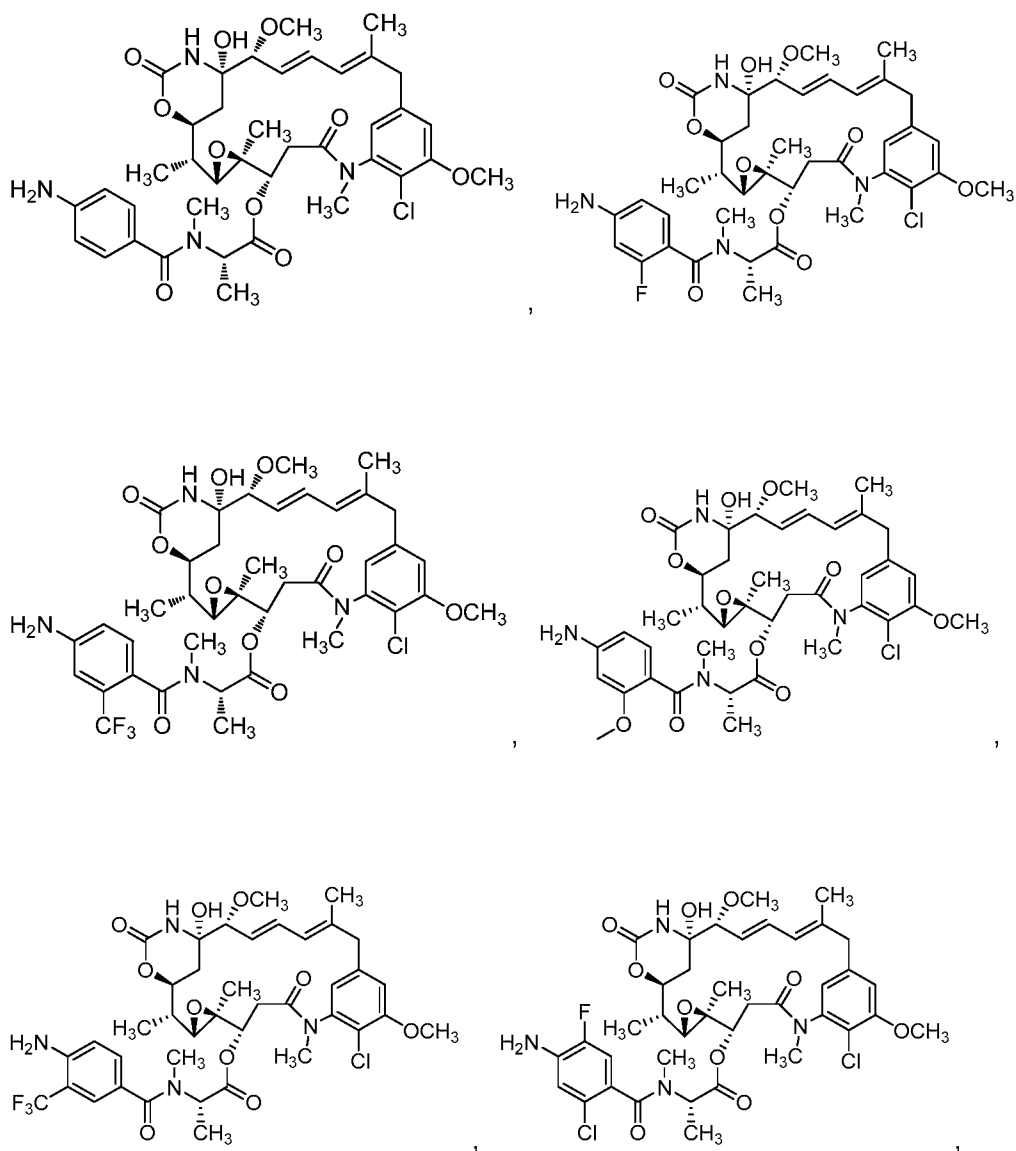
R^1 is, independently at each occurrence, alkyl, alkenyl, alkynyl, aryl, alkaryl, aralkyl, halo,

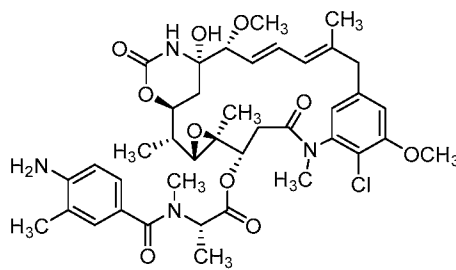
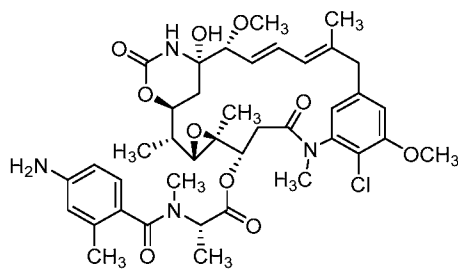
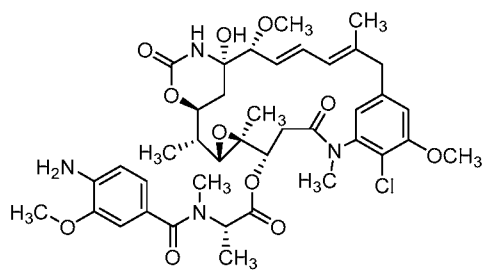
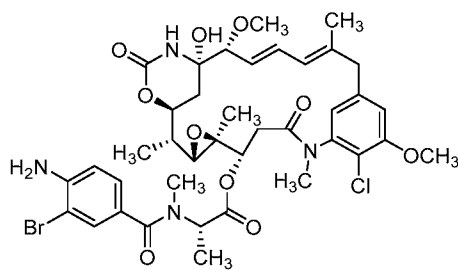
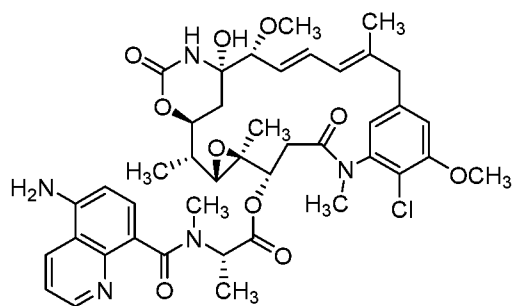
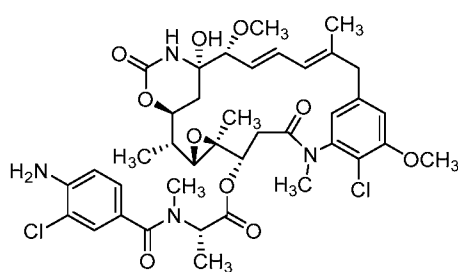
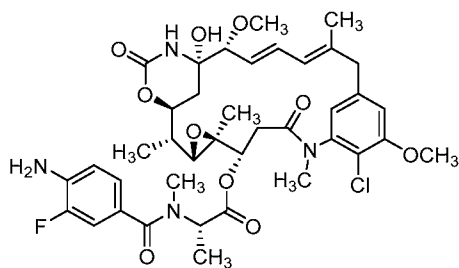
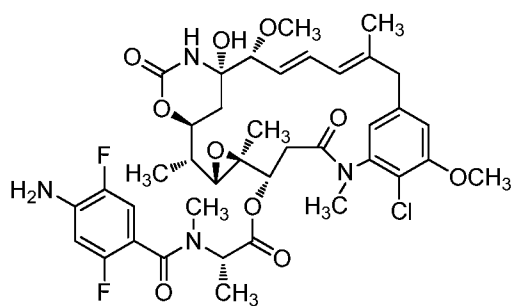
heteroaryl, heterocycloalkyl, hydroxyl, cyano, nitro, $-\text{OR}^A$, $-\text{SO}_2\text{R}^A$, $-\text{C}(=\text{O})\text{R}^A$, or azido,

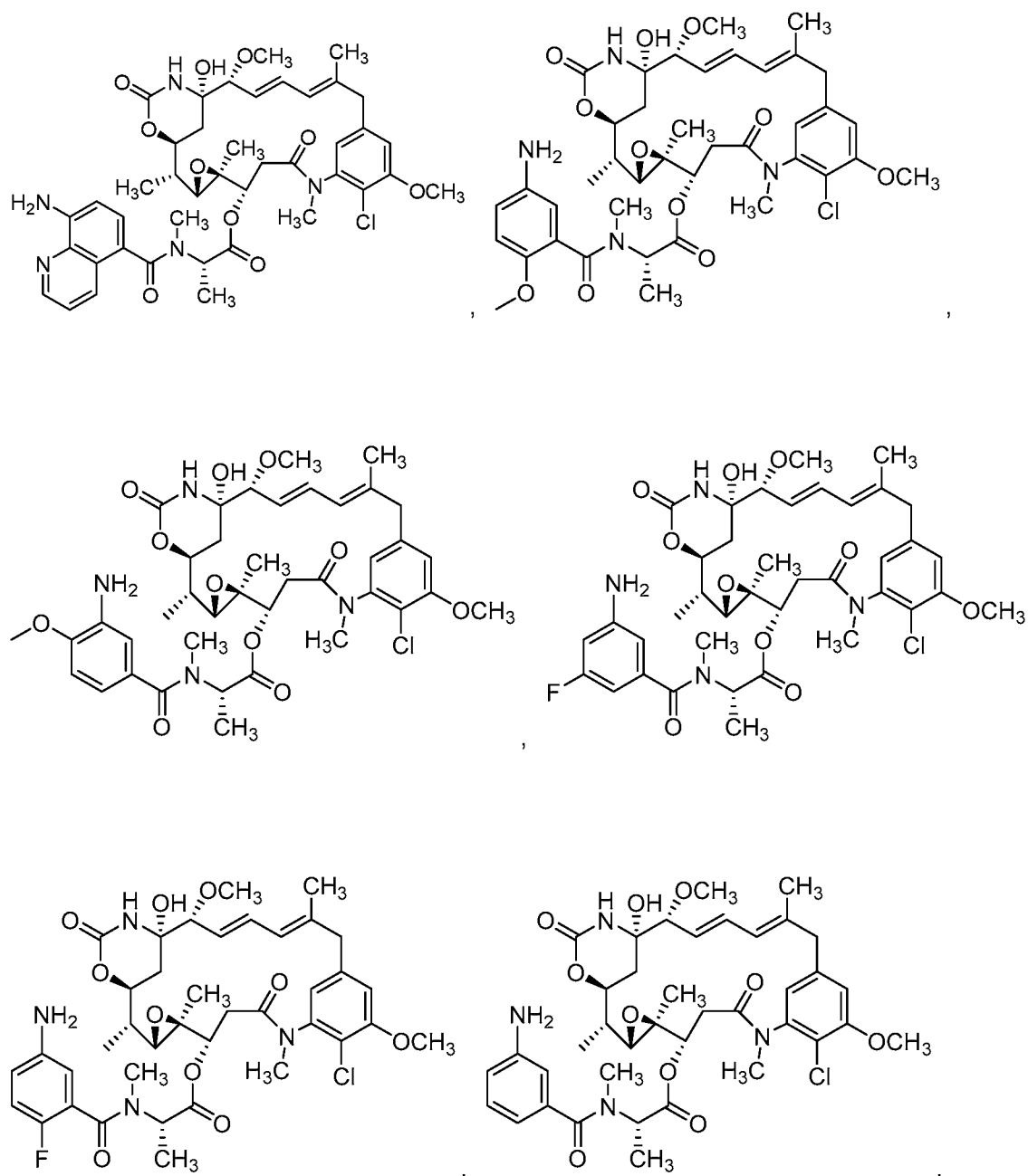
wherein R^A is alkyl or heteroalkyl;

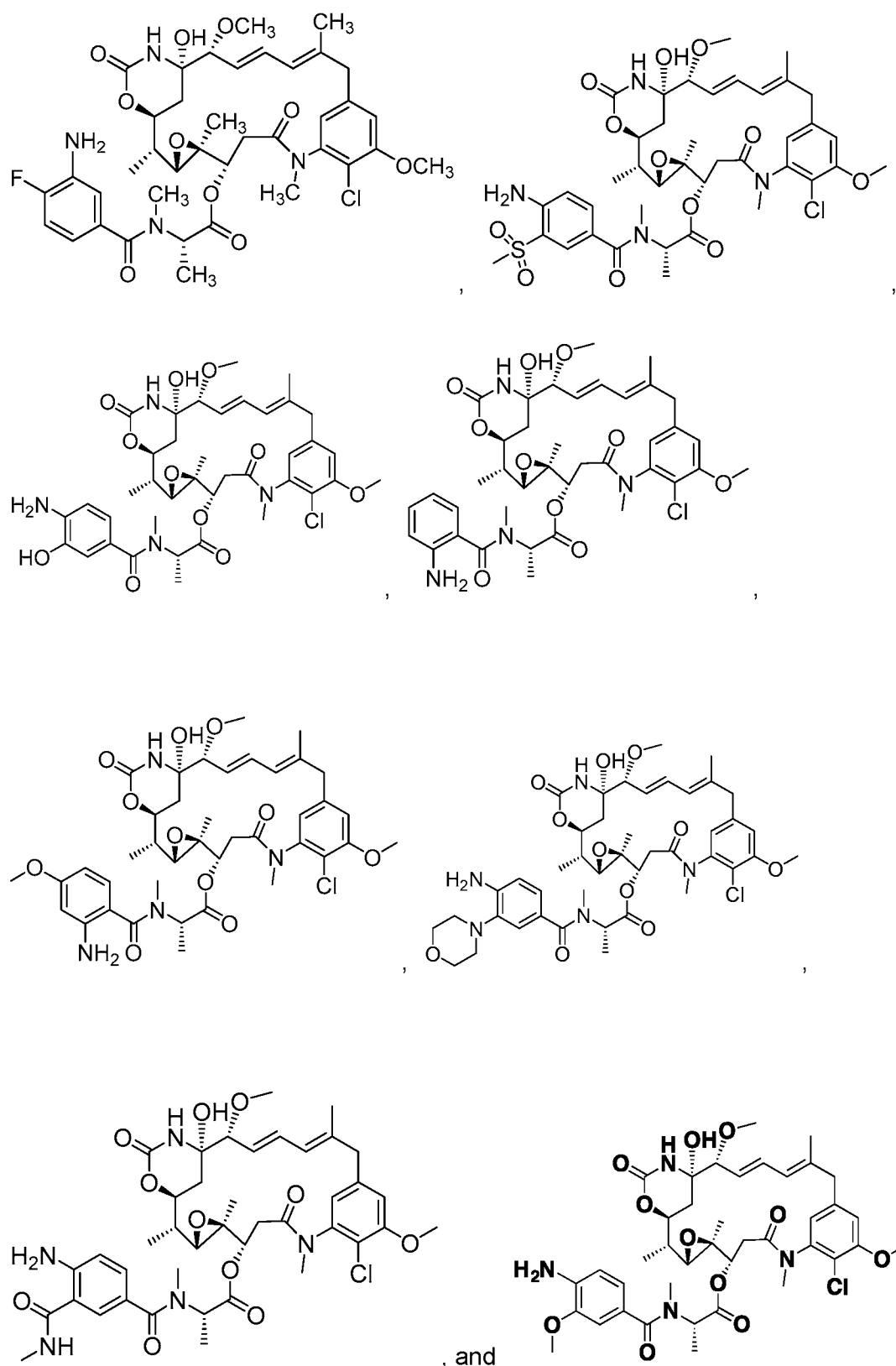
n is an integer from 0 to 4;
 m is an integer from 0 to 3;
 p is an integer from 0 to 6; and
 q is an integer from 0 to 5.

[0214] In some embodiments, the compound of Formula I is selected from the group consisting of:

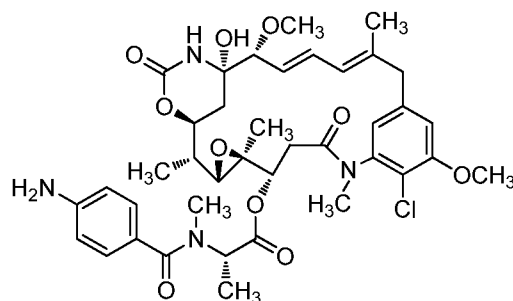




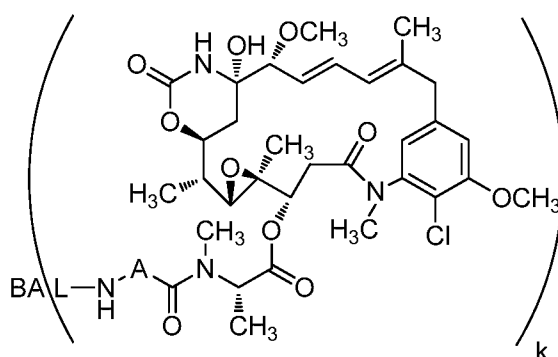




[0215] In one embodiment, the compound of Formula (I) is:



[0216] In some embodiments, the maytansinoid of Formula (I) is conjugated to an anti-STEAP2 antibody or antigen-binding fragment thereof via a linker, as shown in Formula (IA), below:



(Formula IA)

wherein:

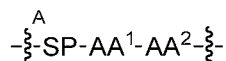
A is arylene or heteroarylene, as discussed above in connection with Formula (I);

L is a linker;

BA is an anti-STEAP2 antibody or antigen-binding fragment thereof; and

k is an integer from 1 to 30.

[0217] In various embodiments, L is:



wherein:

SP is a spacer;

$-\overset{A}{\underset{\sim}{\text{SP}}}-$ is one or more bonds to the anti-STEAP2 antibody or fragment thereof;

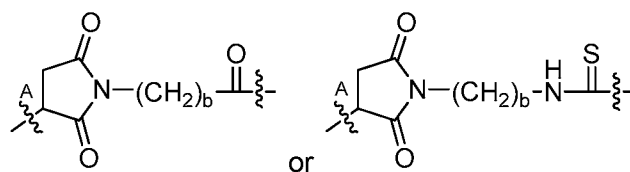
AA¹ is an amino acid; and

AA² is an amino acid.

[0218] In some embodiments, AA¹-AA² is: valine-citrulline, citrulline-valine, lysine-phenylalanine, phenylalanine-lysine, valine-asparagine, asparagine-valine, threonine-asparagine, asparagine-

threonine, serine-asparagine, asparagine-serine, phenylalanine-asparagine, asparagine-phenylalanine, leucine-asparagine, asparagine-leucine, isoleucine-asparagine, asparagine-isoleucine, glycine-asparagine, asparagine-glycine, glutamic acid-asparagine, asparagine-glutamic acid, citrulline-asparagine, asparagine-citrulline, alanine-asparagine, or asparagine-alanine.

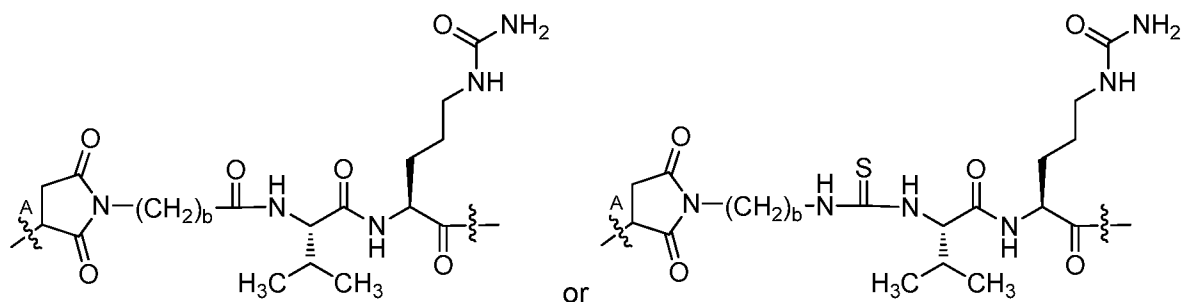
[0219] In some embodiments, SP is:



wherein:

 is a bond to the anti-STEAP2 antibody or fragment thereof; and
b is an integer from 2 to 8.

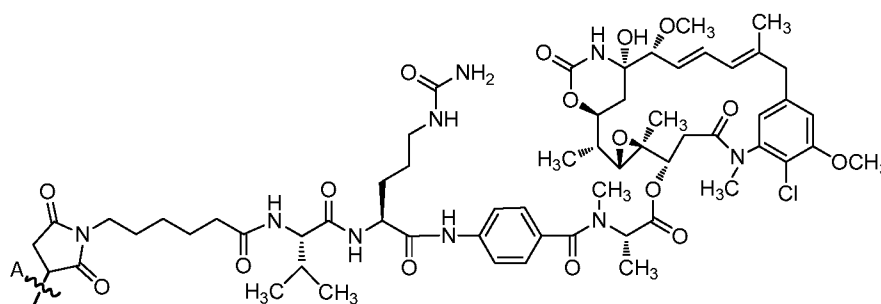
In other embodiments, L is:



wherein:

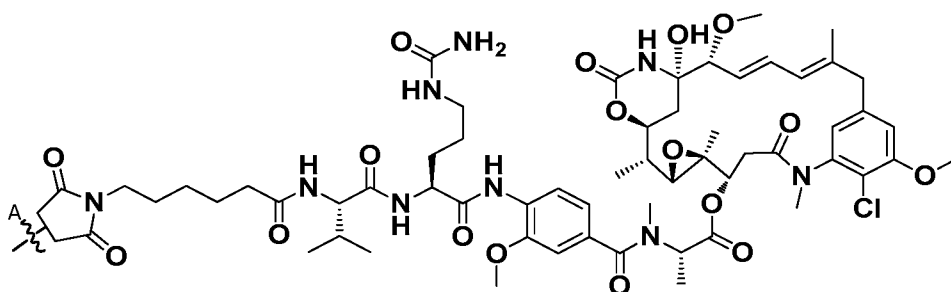
 is a bond to the anti-STEAP2 antibody or fragment thereof; and
b is an integer from 2 to 8.

[0220] In one embodiment, the compound of Formula (IA), including the linker, that is bound to the anti-STEAP2 antibody or antigen-binding fragment thereof is:



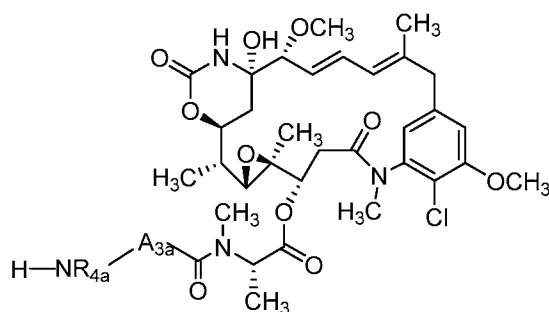
wherein $\overset{\text{A}}{\sim}$ is a bond to the anti-STEAP2 antibody or fragment thereof. In some instances, this moiety is referred to as "Compound 10."

[0221] In one embodiment, the compound of Formula (IA), including the linker, that is bound to the anti-STEAP2 antibody or antigen-binding fragment thereof is:



wherein $\overset{\text{A}}{\sim}$ is a bond to the anti-STEAP2 antibody or fragment thereof. In some instances, this moiety is referred to as "Compound 60."

[0222] In some embodiments, the cytotoxic agent is a maytansinoid having the structure of Formula (II), including stereoisomers of the compounds of Formula (II):



(Formula II)

wherein:

A_{3a} is an amino acid, a peptide having 2-20 amino acids, an alkyl, an alkynyl, an alkenyl, a cycloalkyl, an aryl, a heteroaryl, a heterocyclyl, $-CR_5R_6-$, $-O-$, $-C(=O)-$, $-O-C(=O)-$, $-C(=O)-O-$, $-O-C(=O)-O-$, $-C(=O)-(CH_2)_{p1}-$, $-C(=O)-O-(CH_2)_{p1}-$, $-(CH_2)_{p1}-C(=O)-$, $-(CH_2)_{p1}-C(=O)-O-$, $-(O-(CH_2)_{p2})_{p3}-$, $-((CH_2)_{p2}-O)_{p3}-$, $-C(=S)-$, $-C(=S)-S-$, $-C(=S)-NH-$, $-S-C(=S)-$, $-S-C(=S)-S-$, $-S-$, $-SO-$, $-SO_2-$, $-NR_4-$, $-N(R_4)-C(=O)-N(R_8)-$, $-N(R_4)-C(=O)O-$, $-N(R_4)-C(=O)-$, $-C(=O)-N(R_4)-$, $-C(=O)-N(R_4)-C(=O)-$, or $-O-C(=O)-NR_4-$, wherein alkyl, alkynyl, alkenyl, cycloalkyl, aryl, heteroaryl, and heterocyclyl are optionally substituted; and

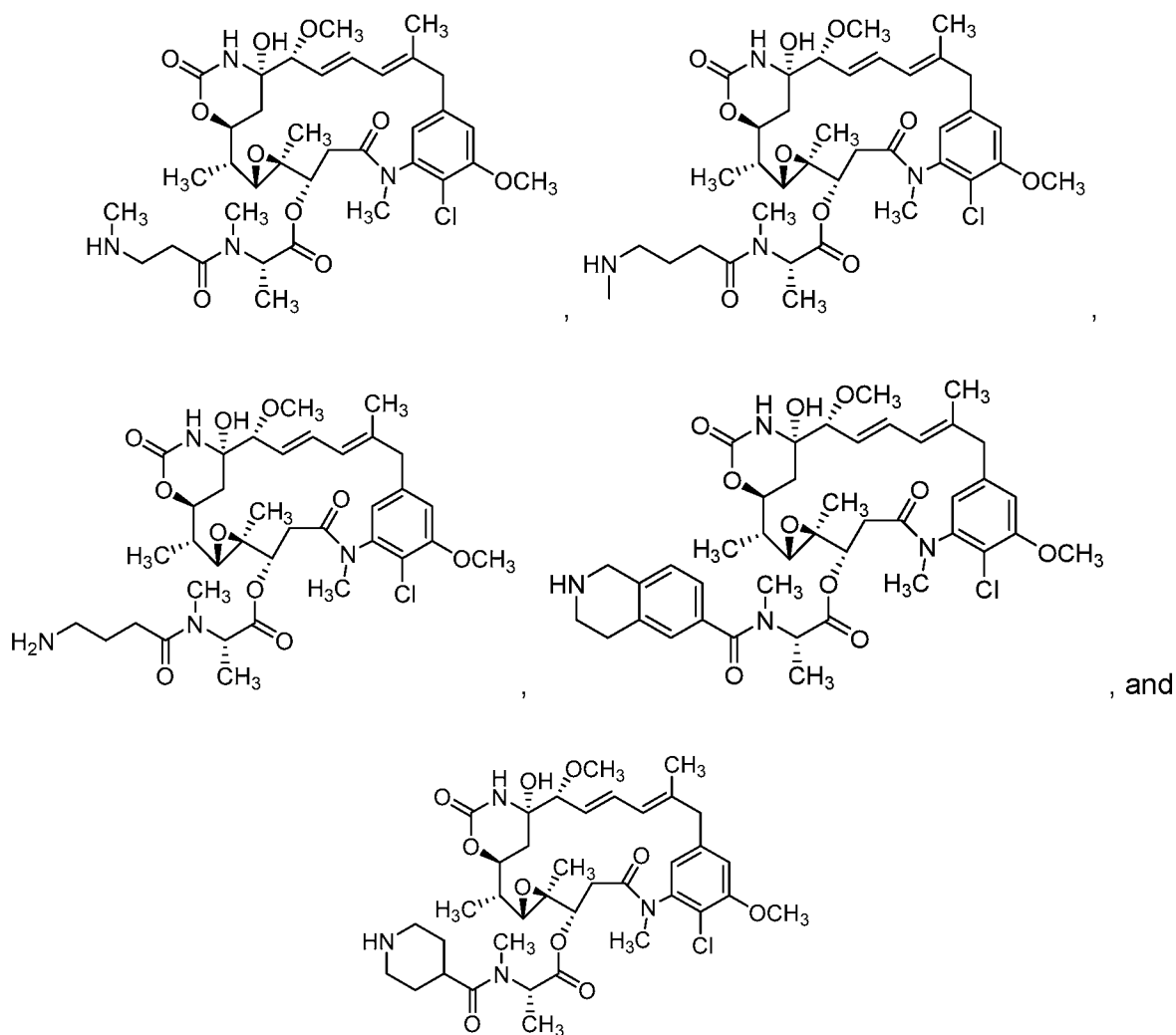
p1, p2 and p3 are each independently 0, or an integer from 1 to 100;

x is 0, 1 or 2;

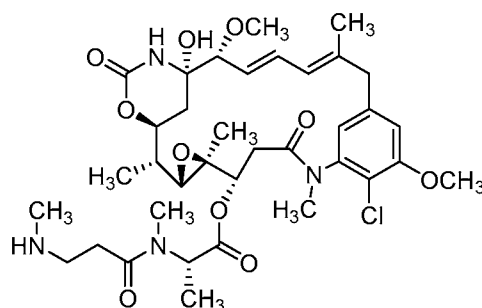
R₄, R₅, R₆ and R₈ are each independently H, or a substituted or unsubstituted: alkyl, alkenyl, alkynyl, aryl, heteroaryl, or heterocyclyl; and

R_{4a} is a substituted or unsubstituted: alkyl, alkenyl, alkynyl, aryl, heteroaryl, or heterocyclyl.

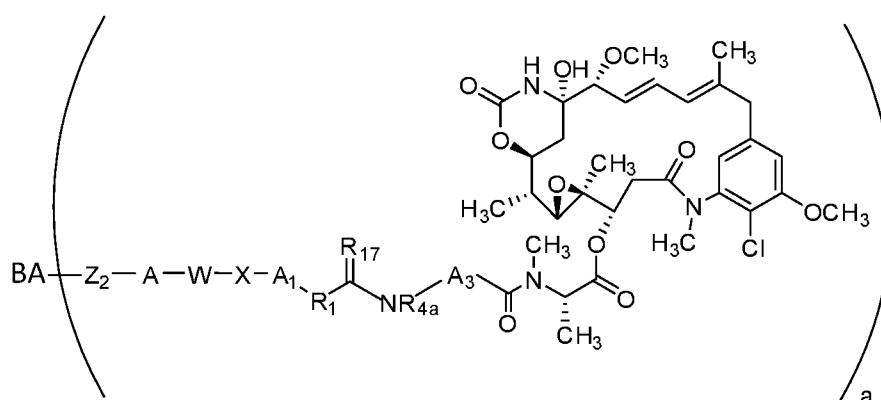
[0223] In some embodiments, the compound of Formula (II) is selected from the group consisting of:



[0224] In one embodiment, the compound of Formula (II) is:



[0225] In some embodiments, the maytansinoid of Formula (II) is conjugated to an anti-STEAP2 antibody or antigen-binding fragment thereof via a linker, as shown in Formula (IIA), below:



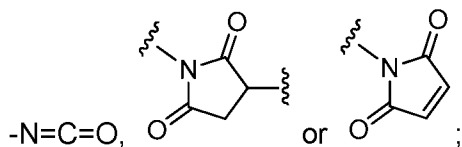
(Formula IIA)

wherein:

BA is an anti-STEAP2 antibody or antigen-binding fragment thereof;

a is an integer from 1 to 30;

Z_2 is represented by the following structural formula: $-Z_{2A}-Z_{2B}-Z_{2C}-Z_{2D}$, wherein Z_{2A} , Z_{2B} , Z_{2C} and Z_{2D} are each independently absent, an amino acid, a peptide having 2-20 amino acids, an alkyl, an alkynyl, an alkenyl, a cycloalkyl, an aryl, a heteroaryl, a heterocyclyl, $-CR_5R_6-$, $-O-$, $-C(=O)-$, $-O-C(=O)-$, $-C(=O)-O-$, $-O-C(=O)-O-$, $-C(=O)-(CH_x)_{p1}$, $-C(=O)-O-(CH_x)_{p1}$, $-(CH_x)_{p1}-C(=O)-$, $-(CH_x)_{p1}-C(=O)-O-$, $-(O-(CH_2)_{p2})_{p3}-$, $-((CH_2)_{p2}-O)_{p3}-$, $-C(=S)-$, $-C(=S)-S-$, $-C(=S)-NH-$, $-S-C(=S)-$, $-S-C(=S)-S-$, $-S-$, $-SO-$, $-SO_2-$, $-NR_4-$, $-N(R_4)-C(=O)-N(R_8)-$, $-N(R_4)-C(=O)O-$, $-N(R_4)-C(=O)-$, $-C(=O)-N(R_4)-$, $-C(=O)-N(R_4)-C(=O)-$, $-O-C(=O)-N(R_4)-$, $-O-C(=S)-N(R_4)-$, $-C(=S)-N(R_4)-$, $-N=C=S$,



A is a natural or non-natural amino acid, or a peptide comprising 2-20 amino acids;

W is -O-, -S-, -CR₅R₆-, or -NR₄-;

X is aryl, heteroaryl, cycloalkyl, or heterocyclyl, wherein aryl, heteroaryl, cycloalkyl, and heterocyclyl are optionally substituted;

wherein A₁, A₃, and R₁ are each independently an amino acid, a peptide having 2-20 amino acids, an alkyl, an alkynyl, an alkenyl, a cycloalkyl, an aryl, a heteroaryl, a heterocyclyl, -CR₅R₆-, -O-, -C(=O)-, -O-C(=O)-, -C(=O)-O-, -O-C(=O)-O-, -C(=O)-(CH_x)_{p1}-, -C(=O)-O-(CH_x)_{p1}-, -(CH_x)_{p1}-C(=O)-, -(CH_x)_{p1}-C(=O)-O-, -(O-(CH₂)_{p2})_{p3}-, -((CH₂)_{p2}-O)_{p3}-, -C(=S)-, -C(=S)-S-, -S-C(=S)-, -C(=S)-NH-, -S-C(=S)-S-, -S-, -SO-, -SO₂-, -NR₄-, -N(R₄)-C(=O)-N(R₈)-, -N(R₄)-C(=O)O-, -N(R₄)-C(=O)-, -C(=O)-N(R₄)-, -C(=O)-N(R₄)-C(=O)-, or -O-C(=O)-NR₄-, wherein alkyl, alkynyl, alkenyl, cycloalkyl, aryl, heteroaryl, and heterocyclyl are optionally substituted;

R₁₇ is selected from the group consisting of O, S, NR₁₈, and CR₅R₆;

R₁₈ is selected from the group consisting of H, alkyl, alkynyl, alkenyl, cycloalkyl, aryl, heteroaryl, heterocyclyl, and acyl, wherein alkyl, alkynyl, alkenyl, cycloalkyl, aryl, heteroaryl, heterocyclyl, and acyl are optionally substituted;

R₄, R₅, R₆ and R₈ are each independently H, or a substituted or unsubstituted: alkyl, alkenyl, alkynyl, aryl, heteroaryl, or heterocyclyl;

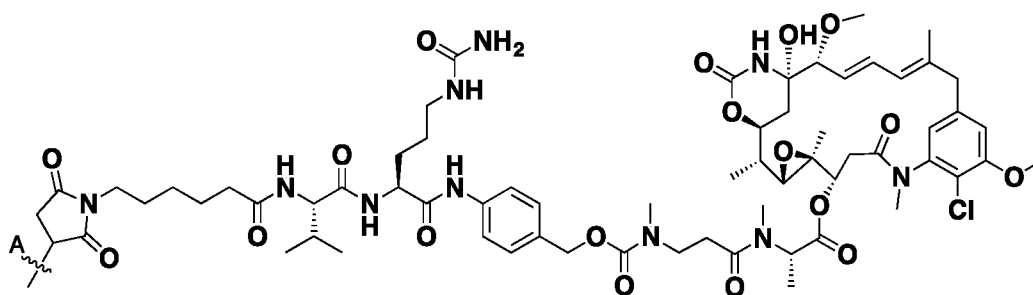
R_{4a} is a substituted or unsubstituted: alkyl, alkenyl, alkynyl, aryl, heteroaryl, or heterocyclyl;

p₁, p₂ and p₃ are each independently 0, or an integer from 1 to 100; and

x is 0, 1 or 2.

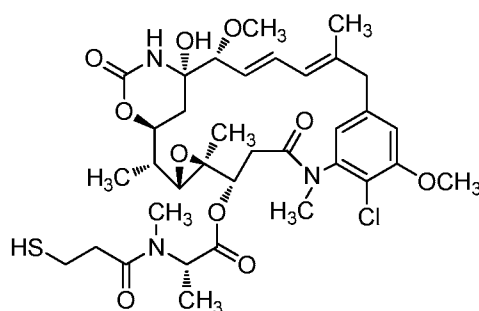
[0226] In some embodiments of Formula (IIA), A is a peptide selected from the group consisting of valine-citrulline, citrulline-valine, lysine-phenylalanine, phenylalanine-lysine, valine-asparagine, asparagine-valine, threonine-asparagine, asparagine-threonine, serine-asparagine, asparagine-serine, phenylalanine-asparagine, asparagine-phenylalanine, leucine-asparagine, asparagine-leucine, isoleucine-asparagine, asparagine-isoleucine, glycine-asparagine, asparagine-glycine, glutamic acid-asparagine, asparagine-glutamic acid, citrulline-asparagine, asparagine-citrulline, alanine-asparagine, and asparagine-alanine.

[0227] In one embodiment, the compound of Formula (IIA) that is bound to the anti-STEAP2 antibody or antigen-binding fragment thereof is:



wherein $\text{---}\overset{\text{A}}{\underset{\text{---}}{\text{C}}}$ is a bond to the anti-STEAP2 antibody or fragment thereof. In some instances, this moiety is referred to as "Compound 7."

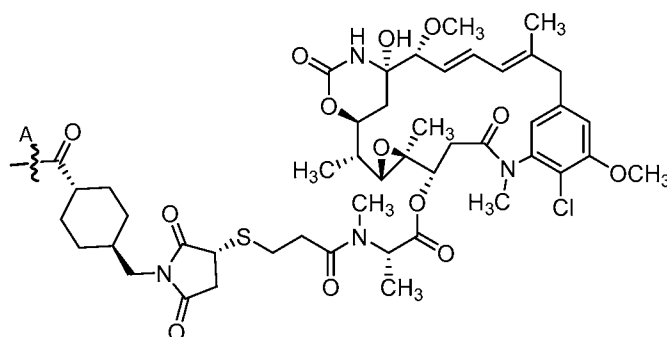
[0228] In some embodiments, the cytotoxic agent that is conjugated to an anti-STEAP2 antibody or fragment thereof is a pure, or substantially pure, diastereomer of DM1:



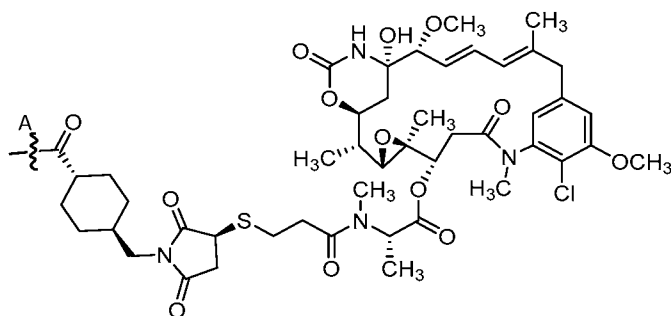
(DM1)

and y is an integer 1 to 0.

[0229] In another embodiment, the ADC comprises a "A – [L – P]_y" structure in which A is an anti-STEAP2 antibody or antigen-binding fragment thereof, and [L – P] is:



, or



, or

a mixture thereof, and

wherein y is an integer 1 to 30, and

$\text{---}\overset{\text{A}}{\underset{\text{B}}{\text{C}}}\text{---}$ is a bond to the anti-STEAP2 antibody or fragment thereof.

[0230] Other maytansinoid derivatives are discussed in WO 2014/145090, WO2016/160615, and WO 2015/031396, each of which is hereby incorporated by reference in its entirety.

[0231] In some embodiments, the cytotoxic agent that is conjugated to an anti-STEAP2 antibody or fragment thereof is MMAE or MMAF.

[0232] Other cytotoxic agents known in the art are contemplated within the scope of the present invention, including, e.g., protein toxins such as ricin, *C. difficile* toxin, pseudomonas exotoxin, diphtheria toxin, botulinum toxin, bryodin, saporin, pokeweed toxins (*i.e.*, phytolaccatoxin and phytolaccigenin), and others such as those set forth in Sapra *et al.*, *Pharmacol. & Therapeutics*, 2013, 138:452-469.

[0233] Cytotoxic agents ("payloads") can be tethered to an anti-STEAP2 antigen-binding molecule or antibody of the invention via a chemical linker that covalently binds the payload compound to the protein molecule (*i.e.* antibody). Exemplary embodiments of specific linkers are discussed above. More generally, and as used herein, the term "linker" refers to any divalent group or moiety that links, connects, or bonds a binding agent (e.g., an antibody or an antigen-binding fragment thereof) with a payload compound set forth herein. Generally, suitable binding agent linkers for the antibody conjugates described herein are those that are sufficiently stable to exploit the circulating half-life of the antibody and, at the same time, capable of releasing its payload after antigen-mediated internalization of the conjugate. Linkers can be cleavable or non-cleavable. Cleavable linkers are linkers that are cleaved by intracellular metabolism following internalization, e.g., cleavage via hydrolysis, reduction, or enzymatic reaction. Non-cleavable linkers are linkers that release an attached payload via lysosomal degradation of the antibody following internalization. Suitable linkers include, but are not limited to, acid-labile linkers, hydrolysis-labile

linkers, enzymatically cleavable linkers, reduction labile linkers, self-immolative linkers, and non-cleavable linkers. Suitable linkers also include, but are not limited to, those that are or comprise peptides, glucuronides, succinimide-thioethers, polyethylene glycol (PEG) units, hydrazones, mal-caproyl units, dipeptide units, valine-citrulline units, and para-aminobenzyl (PAB) units. In some cases, the linker is capable of bonding to the antibody or antigen-binding fragment through a lysine residue or a cysteine residue (e.g., via cleavage of a disulfide group of the antibody or fragment, or via a cysteine residue engineered into the antibody or fragment). In some cases, the linker is capable of bonding to the antibody or fragment through a glutamine residue, including those derived via transglutaminase-mediated conjugation.

[0234] Exemplary linkers that can be used in the context of the present invention include linkers that comprise or consist of e.g., MC (6-maleimidocaproyl), MCC (maleimidomethyl cyclohexane-1-carboxylate), MP (maleimidopropanoyl), val-cit (valine-citrulline), val-ala (valine-alanine), ala-phe (alanine-phenylalanine), phe-lys (phenylalanine-lysine), dipeptide site in protease-cleavable linker, PAB (p-aminobenzyloxycarbonyl), SPP (N-Succinimidyl 4-(2-pyridylthio) pentanoate), SMCC (N-Succinimidyl 4-(N-maleimidomethyl)cyclohexane-1 carboxylate), SIAB (N-Succinimidyl (4-iodoacetyl)aminobenzoate), and variants and combinations thereof. Additional examples of linkers that can be used in the context of the present invention are disclosed in, e.g., US Pat. No. 7,754,681 and in Ducry, *Bioconjugate Chem.*, 2010, 21:5-13, and the references cited therein, the contents of which are incorporated by reference herein in their entireties. In some cases, the linker is or contains a self-immolative spacer, such as those discussed in Jin, *et al.*, *Bioorganic & Medicinal Chemistry*, 2012, 20:3465-3469, and Wu, *et al.*, *Bioorganic & Medicinal Chemistry*, 2016, 24:2697-2706.

[0235] Payloads may be linked to the anti-STEAP2 antibody or antigen-binding fragment via an attachment at a particular amino acid within the antibody or antigen-binding molecule. Exemplary amino acid attachments that can be used in the context of this aspect of the invention include, e.g., lysine (see, e.g., U.S. Pat. No. 5,208,020; US 2010/0129314; Hollander *et al.*, *Bioconjugate Chem.*, 2008, 19:358-361; WO 2005/089808; U.S. Pat. No. 5,714,586; US 2013/0101546; and US 2012/0585592), cysteine (see, e.g., US 2007/0258987; WO 2013/055993; WO 2013/055990; WO 2013/053873; WO 2013/053872; WO 2011/130598; US 2013/0101546; and U.S. Pat. No. 7,750,116), selenocysteine (see, e.g., WO 2008/122039; and Hofer *et al.*, *Proc. Natl. Acad. Sci., USA*, 2008, 105:12451-12456), formyl glycine (see, e.g., Carrico *et al.*, *Nat. Chem. Biol.*, 2007, 3:321-322; Agarwal *et al.*, *Proc. Natl. Acad. Sci., USA*, 2013, 110:46-51, and Rabuka *et al.*, *Nat. Protocols*, 2012, 10:1052-1067), non-natural amino acids (see, e.g., WO 2013/068874, and WO 2012/166559), and acidic amino acids (see, e.g., WO 2012/05982). Linkers can also be conjugated to an antigen-binding protein via attachment to carbohydrates (see, e.g., US 2008/0305497, and

Ryan et al., Food & Agriculture Immunol., 2001, 13:127-130) and disulfide linkers (see, e.g., WO 2013/085925, WO 2010/010324, WO 2011/018611, and Shaunak et al., Nat. Chem. Biol., 2006, 2:312-313).

[0236] Drug-to-antibody ratio (DAR) is the average number of drugs conjugated to the antibody or antigen-binding fragment, which has an important effect on the efficacy, potency and pharmacokinetics of the ADC. In various embodiments, the DAR is from 1, 2, 3, 4, 5, 6, 7, or 8 drug molecules per antibody. In some embodiments, the DAR is from 1 to 4. In certain embodiments, the DAR is from 2 to 4. In some cases, the DAR is from 2 to 3. In certain cases, the DAR is from 3 to 4. In some embodiments, the DAR is from 1 to 10, 1 to 20 or 1 to 30 (*i.e.*, from 1 to 30 drug molecules per antibody or antigen-binding fragment thereof).

Therapeutic Formulation and Administration

[0237] The present invention provides pharmaceutical compositions comprising the antigen-binding molecules of the present invention. The pharmaceutical compositions of the invention are formulated with suitable carriers, excipients, and other agents that provide improved transfer, delivery, tolerance, and the like. A multitude of appropriate formulations can be found in the formulary known to all pharmaceutical chemists: Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, PA. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as LIPOFECTIN™, Life Technologies, Carlsbad, CA), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. See also Powell et al. "Compendium of excipients for parenteral formulations" PDA (1998) J Pharm Sci Technol 52:238-311.

[0238] The dose of antigen-binding molecule administered to a patient may vary depending upon the age and the size of the patient, target disease, conditions, route of administration, and the like. The preferred dose is typically calculated according to body weight or body surface area. When a bispecific antigen-binding molecule of the present invention is used for therapeutic purposes in an adult patient, it may be advantageous to intravenously administer the bispecific antigen-binding molecule of the present invention normally at a single dose of about 0.01 to about 20 mg/kg body weight, more preferably about 0.02 to about 7, about 0.03 to about 5, or about 0.05 to about 3 mg/kg body weight. Depending on the severity of the condition, the frequency and the duration of the treatment can be adjusted. Effective dosages and schedules for administering a bispecific antigen-binding molecule may be determined empirically; for example, patient progress can be monitored by periodic assessment, and the dose adjusted accordingly. Moreover, interspecies

scaling of dosages can be performed using well-known methods in the art (e.g., Mordenti *et al.*, 1991, *Pharmaceut. Res.* 8:1351).

[0239] Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu et al., 1987, *J. Biol. Chem.* 262:4429-4432). Methods of introduction include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The composition may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local.

[0240] A pharmaceutical composition of the present invention can be delivered subcutaneously or intravenously with a standard needle and syringe. In addition, with respect to subcutaneous delivery, a pen delivery device readily has applications in delivering a pharmaceutical composition of the present invention. Such a pen delivery device can be reusable or disposable. A reusable pen delivery device generally utilizes a replaceable cartridge that contains a pharmaceutical composition. Once all of the pharmaceutical composition within the cartridge has been administered and the cartridge is empty, the empty cartridge can readily be discarded and replaced with a new cartridge that contains the pharmaceutical composition. The pen delivery device can then be reused. In a disposable pen delivery device, there is no replaceable cartridge. Rather, the disposable pen delivery device comes prefilled with the pharmaceutical composition held in a reservoir within the device. Once the reservoir is emptied of the pharmaceutical composition, the entire device is discarded.

[0241] Numerous reusable pen and autoinjector delivery devices have applications in the subcutaneous delivery of a pharmaceutical composition of the present invention. Examples include, but are not limited to AUTOPEN™ (Owen Mumford, Inc., Woodstock, UK), DISETRONIC™ pen (Disetronic Medical Systems, Bergdorf, Switzerland), HUMALOG MIX 75/25™ pen, HUMALOG™ pen, HUMALIN 70/30™ pen (Eli Lilly and Co., Indianapolis, IN), NOVOPEN™ I, II and III (Novo Nordisk, Copenhagen, Denmark), NOVOPEN JUNIOR™ (Novo Nordisk, Copenhagen, Denmark), BD™ pen (Becton Dickinson, Franklin Lakes, NJ), OPTIPEN™, OPTIPEN PRO™, OPTIPEN STARLET™, and OPTICLIK™ (sanofi-aventis, Frankfurt, Germany), to name only a few. Examples of disposable pen delivery devices having applications in subcutaneous delivery of a pharmaceutical composition of the present invention include, but are not limited to the SOLOSTAR™ pen (sanofi-aventis), the FLEXPEN™ (Novo Nordisk), and the KWIKPEN™ (Eli Lilly), the SURECLICK™ Autoinjector (Amgen, Thousand Oaks, CA), the PENLET™ (Haselmeier,

Stuttgart, Germany), the EPIPEN (Dey, L.P.), and the HUMIRA™ Pen (Abbott Labs, Abbott Park IL), to name only a few.

[0242] In certain situations, the pharmaceutical composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201). In another embodiment, polymeric materials can be used; see, Medical Applications of Controlled Release, Langer and Wise (eds.), 1974, CRC Pres., Boca Raton, Florida. In yet another embodiment, a controlled release system can be placed in proximity of the composition's target, thus requiring only a fraction of the systemic dose (see, *e.g.*, Goodson, 1984, in Medical Applications of Controlled Release, *supra*, vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer, 1990, Science 249:1527-1533.

[0243] The injectable preparations may include dosage forms for intravenous, subcutaneous, intracutaneous and intramuscular injections, drip infusions, etc. These injectable preparations may be prepared by methods publicly known. For example, the injectable preparations may be prepared, *e.g.*, by dissolving, suspending or emulsifying the antibody or its salt described above in a sterile aqueous medium or an oily medium conventionally used for injections. As the aqueous medium for injections, there are, for example, physiological saline, an isotonic solution containing glucose and other auxiliary agents, etc., which may be used in combination with an appropriate solubilizing agent such as an alcohol (*e.g.*, ethanol), a polyalcohol (*e.g.*, propylene glycol, polyethylene glycol), a nonionic surfactant [*e.g.*, polysorbate 80, HCO-50 (polyoxyethylene (50 mol) adduct of hydrogenated castor oil)], etc. As the oily medium, there are employed, *e.g.*, sesame oil, soybean oil, etc., which may be used in combination with a solubilizing agent such as benzyl benzoate, benzyl alcohol, etc. The injection thus prepared is preferably filled in an appropriate ampoule.

[0244] Advantageously, the pharmaceutical compositions for oral or parenteral use described above are prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc. The amount of the aforesaid antibody contained is generally about 5 to about 500 mg per dosage form in a unit dose; especially in the form of injection, it is preferred that the aforesaid antibody is contained in about 5 to about 100 mg and in about 10 to about 250 mg for the other dosage forms.

Therapeutic Uses of the Antigen-Binding Molecules

[0245] The present invention includes methods comprising administering to a subject in need thereof a therapeutic composition comprising an anti-STEAP2 antibody or antigen-binding fragment thereof, or a bispecific antigen-binding molecule that specifically binds CD3 and

STEAP2. The therapeutic composition can comprise any of the antibodies or bispecific antigen-binding molecules as disclosed herein and a pharmaceutically acceptable carrier or diluent. As used herein, the expression "a subject in need thereof" means a human or non-human animal that exhibits one or more symptoms or indicia of cancer (e.g., a subject expressing a tumor or suffering from any of the cancers mentioned herein below), or who otherwise would benefit from an inhibition or reduction in STEAP2 activity or a depletion of STEAP2+ cells (e.g., prostate cancer cells).

[0246] The antibodies and bispecific antigen-binding molecules of the invention (and therapeutic compositions comprising the same) are useful, *inter alia*, for treating any disease or disorder in which stimulation, activation and/or targeting of an immune response would be beneficial. In particular, the anti-STEAP2 antibodies or the anti-CD3/anti-STEAP2 bispecific antigen-binding molecules of the present invention may be used for the treatment, prevention and/or amelioration of any disease or disorder associated with or mediated by STEAP2 expression or activity or the proliferation of STEAP2+ cells. The mechanism of action by which the therapeutic methods of the invention are achieved include killing of the cells expressing STEAP2 in the presence of effector cells, for example, by CDC, apoptosis, ADCC, phagocytosis, or by a combination of two or more of these mechanisms. Cells expressing STEAP2 which can be inhibited or killed using the bispecific antigen-binding molecules of the invention include, for example, prostate tumor cells.

[0247] The antigen-binding molecules of the present invention may be used to treat, e.g., primary and/or metastatic tumors arising in the prostate, bladder, cervix, lung, colon, kidney, breast, pancreas, stomach, uterus, and/or ovary. In certain embodiments, the bispecific antigen-binding molecules of the invention are used to treat one or more of the following cancers: prostate cancer, bladder cancer, cervical cancer, lung cancer, colon cancer, kidney cancer, breast cancer, pancreatic cancer, stomach cancer, uterine cancer, and ovarian cancer. According to certain embodiments of the present invention, the anti-STEAP2 antibodies or anti-STEAP2/anti-CD3 bispecific antibodies are useful for treating a patient afflicted with a castrate-resistant prostate cancer. According to other related embodiments of the invention, methods are provided comprising administering an anti-STEAP2 antibody or an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule as disclosed herein to a patient who is afflicted with a castrate-resistant prostate cancer. Analytic/diagnostic methods known in the art, such as tumor scanning, etc., may be used to ascertain whether a patient harbors a tumor that is castrate-resistant.

[0248] The present invention also includes methods for treating residual cancer in a subject. As used herein, the term "residual cancer" means the existence or persistence of one or more cancerous cells in a subject following treatment with an anti-cancer therapy.

[0249] According to certain aspects, the present invention provides methods for treating a disease or disorder associated with STEAP2 expression (e.g., prostate cancer) comprising

administering one or more of the anti-STEAP2 or bispecific antigen-binding molecules described elsewhere herein to a subject after the subject has been determined to have prostate cancer (e.g., castrate-resistant prostate cancer). For example, the present invention includes methods for treating prostate cancer comprising administering an anti-STEAP2 antibody or an anti-CD3/anti-STEAP2 bispecific antigen-binding molecule to a patient 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks or 4 weeks, 2 months, 4 months, 6 months, 8 months, 1 year, or more after the subject has received hormone therapy (e.g., anti-androgen therapy).

Combination Therapies and Formulations

[0250] The present invention provides methods which comprise administering a pharmaceutical composition comprising any of the exemplary antibodies and bispecific antigen-binding molecules described herein in combination with one or more additional therapeutic agents. Exemplary additional therapeutic agents that may be combined with or administered in combination with an antigen-binding molecule of the present invention include, e.g., an EGFR antagonist (e.g., an anti-EGFR antibody [e.g., cetuximab or panitumumab] or small molecule inhibitor of EGFR [e.g., gefitinib or erlotinib]), an antagonist of another EGFR family member such as Her2/ErbB2, ErbB3 or ErbB4 (e.g., anti-ErbB2, anti-ErbB3 or anti-ErbB4 antibody or small molecule inhibitor of ErbB2, ErbB3 or ErbB4 activity), an antagonist of EGFRvIII (e.g., an antibody that specifically binds EGFRvIII), a cMET antagonist (e.g., an anti-cMET antibody), an IGF1R antagonist (e.g., an anti-IGF1R antibody), a B-raf inhibitor (e.g., vemurafenib, sorafenib, GDC-0879, PLX-4720), a PDGFR- α inhibitor (e.g., an anti-PDGFR- α antibody), a PDGFR- β inhibitor (e.g., an anti-PDGFR- β antibody), a VEGF antagonist (e.g., a VEGF-Trap, see, e.g., US 7,087,411 (also referred to herein as a "VEGF-inhibiting fusion protein"), anti-VEGF antibody (e.g., bevacizumab), a small molecule kinase inhibitor of VEGF receptor (e.g., sunitinib, sorafenib or pazopanib), a DLL4 antagonist (e.g., an anti-DLL4 antibody disclosed in US 2009/0142354 such as REGN421), an Ang2 antagonist (e.g., an anti-Ang2 antibody disclosed in US 2011/0027286 such as H1H685P), a FOLH1 (PSMA) antagonist, a PRLR antagonist (e.g., an anti-PRLR antibody), a STEAP1 or STEAP2 antagonist (e.g., an anti-STEAP1 antibody or an anti-STEAP2 antibody), a TMPRSS2 antagonist (e.g., an anti-TMPRSS2 antibody), a MSLN antagonist (e.g., an anti-MSLN antibody), a CA9 antagonist (e.g., an anti-CA9 antibody), a uroplakin antagonist (e.g., an anti-uroplakin antibody), etc. Other agents that may be beneficially administered in combination with the antigen-binding molecules of the invention include cytokine inhibitors, including small-molecule cytokine inhibitors and antibodies that bind to cytokines such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-11, IL-12, IL-13, IL-17, IL-18, or to their respective receptors. The pharmaceutical compositions of the present invention (e.g., pharmaceutical compositions comprising an anti-CD3/anti-STEAP2 bispecific antigen-binding

molecule as disclosed herein) may also be administered as part of a therapeutic regimen comprising one or more therapeutic combinations selected from "ICE": ifosfamide (e.g., Ifex®), carboplatin (e.g., Paraplatin®), etoposide (e.g., Etopophos®, Toposar®, VePesid®, VP-16); "DHAP": dexamethasone (e.g., Decadron®), cytarabine (e.g., Cytosar-U®, cytosine arabinoside, ara-C), cisplatin (e.g., Platinol®-AQ); and "ESHAP": etoposide (e.g., Etopophos®, Toposar®, VePesid®, VP-16), methylprednisolone (e.g., Medrol®), high-dose cytarabine, cisplatin (e.g., Platinol®-AQ).

[0251] The present invention also includes therapeutic combinations comprising any of the antigen-binding molecules mentioned herein and an inhibitor of one or more of VEGF, Ang2, DLL4, EGFR, ErbB2, ErbB3, ErbB4, EGFRvIII, cMet, IGF1R, B-raf, PDGFR- α , PDGFR- β , FOLH1 (PSMA), PRLR, STEAP1, STEAP2, Tmprss2, MSLN, CA9, uroplakin, or any of the aforementioned cytokines, wherein the inhibitor is an aptamer, an antisense molecule, a ribozyme, an siRNA, a peptibody, a nanobody or an antibody fragment (e.g., Fab fragment; F(ab')₂ fragment; Fd fragment; Fv fragment; scFv; dAb fragment; or other engineered molecules, such as diabodies, triabodies, tetrabodies, minibodies and minimal recognition units). The antigen-binding molecules of the invention may also be administered and/or co-formulated in combination with antivirals, antibiotics, analgesics, corticosteroids and/or NSAIDs. The antigen-binding molecules of the invention may also be administered as part of a treatment regimen that also includes radiation treatment and/or conventional chemotherapy.

[0252] The additional therapeutically active component(s) may be administered just prior to, concurrent with, or shortly after the administration of an antigen-binding molecule of the present invention; (for purposes of the present disclosure, such administration regimens are considered the administration of an antigen-binding molecule "in combination with" an additional therapeutically active component).

[0253] The present invention includes pharmaceutical compositions in which an antigen-binding molecule of the present invention is co-formulated with one or more of the additional therapeutically active component(s) as described elsewhere herein.

Administration Regimens

[0254] According to certain embodiments of the present invention, multiple doses of an antigen-binding molecule (e.g., an anti-STEAP2 antibody or a bispecific antigen-binding molecule that specifically binds STEAP2 and CD3) may be administered to a subject over a defined time course. The methods according to this aspect of the invention comprise sequentially administering to a subject multiple doses of an antigen-binding molecule of the invention. As used herein, "sequentially administering" means that each dose of an antigen-binding molecule is administered

to the subject at a different point in time, e.g., on different days separated by a predetermined interval (e.g., hours, days, weeks or months). The present invention includes methods which comprise sequentially administering to the patient a single initial dose of an antigen-binding molecule, followed by one or more secondary doses of the antigen-binding molecule, and optionally followed by one or more tertiary doses of the antigen-binding molecule.

[0255] The terms "initial dose," "secondary doses," and "tertiary doses," refer to the temporal sequence of administration of the antigen-binding molecule of the invention. Thus, the "initial dose" is the dose which is administered at the beginning of the treatment regimen (also referred to as the "baseline dose"); the "secondary doses" are the doses which are administered after the initial dose; and the "tertiary doses" are the doses which are administered after the secondary doses. The initial, secondary, and tertiary doses may all contain the same amount of the antigen-binding molecule, but generally may differ from one another in terms of frequency of administration. In certain embodiments, however, the amount of an antigen-binding molecule contained in the initial, secondary and/or tertiary doses varies from one another (e.g., adjusted up or down as appropriate) during the course of treatment. In certain embodiments, two or more (e.g., 2, 3, 4, or 5) doses are administered at the beginning of the treatment regimen as "loading doses" followed by subsequent doses that are administered on a less frequent basis (e.g., "maintenance doses").

[0256] In one exemplary embodiment of the present invention, each secondary and/or tertiary dose is administered 1 to 26 (e.g., 1, 1½, 2, 2½, 3, 3½, 4, 4½, 5, 5½, 6, 6½, 7, 7½, 8, 8½, 9, 9½, 10, 10½, 11, 11½, 12, 12½, 13, 13½, 14, 14½, 15, 15½, 16, 16½, 17, 17½, 18, 18½, 19, 19½, 20, 20½, 21, 21½, 22, 22½, 23, 23½, 24, 24½, 25, 25½, 26, 26½, or more) weeks after the immediately preceding dose. The phrase "the immediately preceding dose," as used herein, means, in a sequence of multiple administrations, the dose of antigen-binding molecule which is administered to a patient prior to the administration of the very next dose in the sequence with no intervening doses.

[0257] The methods according to this aspect of the invention may comprise administering to a patient any number of secondary and/or tertiary doses of an antigen-binding molecule (e.g., an anti-STEAP2 antibody or a bispecific antigen-binding molecule that specifically binds STEAP2 and CD3). For example, in certain embodiments, only a single secondary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) secondary doses are administered to the patient. Likewise, in certain embodiments, only a single tertiary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) tertiary doses are administered to the patient.

[0258] In embodiments involving multiple secondary doses, each secondary dose may be administered at the same frequency as the other secondary doses. For example, each secondary dose may be administered to the patient 1 to 2 weeks after the immediately preceding dose.

Similarly, in embodiments involving multiple tertiary doses, each tertiary dose may be administered at the same frequency as the other tertiary doses. For example, each tertiary dose may be administered to the patient 2 to 4 weeks after the immediately preceding dose. Alternatively, the frequency at which the secondary and/or tertiary doses are administered to a patient can vary over the course of the treatment regimen. The frequency of administration may also be adjusted during the course of treatment by a physician depending on the needs of the individual patient following clinical examination.

Diagnostic Uses of the Antibodies

[0259] The anti-STEAP2 antibodies of the present invention may also be used to detect and/or measure STEAP2, or STEAP2-expressing cells in a sample, *e.g.*, for diagnostic purposes. For example, an anti-STEAP2 antibody, or fragment thereof, may be used to diagnose a condition or disease characterized by aberrant expression (*e.g.*, over-expression, under-expression, lack of expression, etc.) of STEAP2. Exemplary diagnostic assays for STEAP2 may comprise, *e.g.*, contacting a sample, obtained from a patient, with an anti-STEAP2 antibody of the invention, wherein the anti-STEAP2 antibody is labeled with a detectable label or reporter molecule. Alternatively, an unlabeled anti-STEAP2 antibody can be used in diagnostic applications in combination with a secondary antibody which is itself detectably labeled. The detectable label or reporter molecule can be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I ; a fluorescent or chemiluminescent moiety such as fluorescein isothiocyanate, or rhodamine; or an enzyme such as alkaline phosphatase, beta-galactosidase, horseradish peroxidase, or luciferase. Another exemplary diagnostic use of the anti-STEAP2 antibodies of the invention includes ^{89}Zr -labeled, such as ^{89}Zr -desferrioxamine-labeled, antibody for the purpose of noninvasive identification and tracking of tumor cells in a subject (*e.g.* positron emission tomography (PET) imaging). (See, *e.g.*, Tavaré, R. et al. *Cancer Res.* 2016 Jan 1;76(1):73-82; and Azad, BB. et al. *Oncotarget.* 2016 Mar 15;7(11):12344-58.) Specific exemplary assays that can be used to detect or measure STEAP2 in a sample include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence-activated cell sorting (FACS).

[0260] Samples that can be used in STEAP2 diagnostic assays according to the present invention include any tissue or fluid sample obtainable from a patient which contains detectable quantities of STEAP2 protein, or fragments thereof, under normal or pathological conditions. Generally, levels of STEAP2 in a particular sample obtained from a healthy patient (*e.g.*, a patient not afflicted with a disease or condition associated with abnormal STEAP2 levels or activity) will be measured to initially establish a baseline, or standard, level of STEAP2. This baseline level of STEAP2 can then be compared against the levels of STEAP2 measured in samples obtained from

individuals suspected of having a STEAP2 related disease (e.g., a tumor containing STEAP2-expressing cells) or condition.

EXAMPLES

[0261] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1: Generation of Anti-STEAP2 Antibodies

[0262] Anti-STEAP2 antibodies were obtained by immunizing a genetically modified mouse with a human STEAP2 antigen or by immunizing an engineered mouse comprising DNA encoding human immunoglobulin heavy and kappa light chain variable regions with a human STEAP2 antigen.

[0263] Genetically modified mice were immunized with hSTEAP2 antigen (SEQ ID:1899). Following immunization, splenocytes were harvested from each mouse and either (1) fused with mouse myeloma cells to preserve their viability and form hybridoma cells and screened for STEAP2 specificity, or (2) B-cell sorted (as described in US 2007/0280945A1) using a human STEAP2 fragment as the sorting reagent that binds and identifies reactive antibodies (antigen-positive B cells).

[0264] Chimeric antibodies to STEAP2 were initially isolated having a human variable region and a mouse constant region. The antibodies were characterized and selected for desirable characteristics, including affinity, selectivity, etc. If necessary, mouse constant regions were replaced with a desired human constant region, for example wild-type or modified IgG1 or IgG4 constant region, to generate a fully human anti-STEAP2 antibody. While the constant region selected may vary according to specific use, high affinity antigen-binding and target specificity characteristics reside in the variable region. The antibody name designations such as H1H11243N and H1M7804N denote fully human antibodies "H1H" or chimeric human variable/mouse constant region antibodies "H1M". Antibodies identified by the hybridoma method are indicated with antibody ID numbers ending with "N" or "N2"; Antibodies identified by the B-cell sorting method are indicated with antibody ID numbers ending with "P" or "P2".

[0265] Certain biological properties of the exemplary anti-STEAP2 antibodies generated in accordance with the methods of this Example are described in detail in the Examples set forth below.

Heavy and Light Chain Variable Region Amino Acid and Nucleic Acid Sequences of anti-STEAP2 antibodies

[0266] Table 1 sets forth the amino acid sequence identifiers of the heavy and light chain variable regions and CDRs of selected anti-STEAP2 antibodies of the invention. The corresponding nucleic acid sequence identifiers are set forth in Table 2.

Table 1: Amino Acid Sequence Identifiers

Antibody Designation	SEQ ID NOs:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H11243N	2	4	6	8	10	12	14	16
H1H11878P	18	20	22	24	26	28	30	32
H1H11880P	34	36	38	40	42	44	46	48
H1H11888P2	50	52	54	56	58	60	62	64
H1H11892P2	66	68	70	72	58	60	62	64
H1H11893P2	74	76	78	80	58	60	62	64
H1H11894P2	82	84	86	88	58	60	62	64
H1H11895P2	90	92	94	96	58	60	62	64
H1H11896P2	98	100	102	104	58	60	62	64
H1H11897P2	106	108	110	112	114	116	118	120
H1H7968P	122	124	126	128	130	132	134	136
H1H7969P	138	140	142	144	146	148	150	152
H1H7970P	154	156	158	160	162	164	166	168
H1H7971P	170	172	174	176	178	180	182	184
H1H7972P	186	188	190	192	194	196	198	200
H1M7804N	202	204	206	208	210	212	214	216
H1M7814N	218	220	222	224	226	228	230	232
H1M7832N	234	236	238	240	242	244	246	248
H2M11162N	250	252	254	256	258	260	262	264
H2M11163N	266	268	270	272	274	276	278	280
H2M11164N	282	284	286	288	290	292	294	296
H2M7806N	298	300	302	304	306	308	310	312
H2M7807N	314	316	318	320	322	324	326	328
H2M7809N	330	332	334	336	338	340	342	344
H2M7810N	346	348	350	352	354	356	358	360
H2M7811N	362	364	366	368	370	372	374	376
H2M7812N	378	380	382	384	386	388	390	392

Table 2: Nucleic Acid Sequence Identifiers

Antibody Designation	SEQ ID NOs:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H11243N	1	3	5	7	9	11	13	15
H1H11878P	17	19	21	23	25	27	29	31
H1H11880P	33	35	37	39	41	43	45	47
H1H11888P2	49	51	53	55	57	59	61	63
H1H11892P2	65	67	69	71	57	59	61	63
H1H11893P2	73	75	77	79	57	59	61	63
H1H11894P2	81	83	85	87	57	59	61	63
H1H11895P2	89	91	93	95	57	59	61	63
H1H11896P2	97	99	101	103	57	59	61	63
H1H11897P2	105	107	109	111	113	115	117	119
H1H7968P	121	123	125	127	129	131	133	135
H1H7969P	137	139	141	143	145	147	149	151
H1H7970P	153	155	157	159	161	163	165	167
H1H7971P	169	171	173	175	177	179	181	183
H1H7972P	185	187	189	191	193	195	197	199
H1M7804N	201	203	205	207	209	211	213	215
H1M7814N	217	219	221	223	225	227	229	231
H1M7832N	233	235	237	239	241	243	245	247
H2M11162N	249	251	253	255	257	259	261	263
H2M11163N	265	267	269	271	273	275	277	279
H2M11164N	281	283	285	287	289	291	293	295
H2M7806N	297	299	301	303	305	307	309	311
H2M7807N	313	315	317	319	321	323	325	327
H2M7809N	329	331	333	335	337	339	341	343
H2M7810N	345	347	349	351	353	355	357	359
H2M7811N	361	363	365	367	369	371	373	375

Example 2: Anti-human STEAP2 Antibodies Selectively Bind to STEAP2 Expressing Cell Lines via FACS

[0267] The ability of anti-STEAP2 antibodies to selectively bind to human six-transmembrane epithelial antigen of prostate 2 (STEAP2) endogenously expressing cell lines was determined via FACS analysis.

[0268] Briefly, 1×10^5 cells were incubated with 10 $\mu\text{g/ml}$ of anti STEAP2 antibodies, or isotype control antibodies for 30 min on ice in antibody dilution buffer. Following one wash with antibody dilution buffer, cells were incubated with 10 $\mu\text{g/ml}$ of PE conjugated anti-human or anti mouse Fc secondary antibodies for 30 min on ice. Following one additional wash, samples were incubated with Cytofix (1% formaldehyde) for 20 minutes. After one final wash, samples were filtered through

a Pall 96 well filtration block, run on a Hypercyt® cytometer and analyzed in ForeCyt™ (IntelliCyt, Albuquerque, NM). Mean fluorescence intensities (MFI) were expressed as fold change above unstained levels (background). The average fold above background at antibody concentrations of 100 - 300 nM were determined. For cell binding EC₅₀ determinations, mAb concentrations ranged from 300 nM to 5pM and EC₅₀ values were determined from a four-parameter logistic equation over a 12-point response curve (GraphPad Prism).

Tables 3A and 3B: FACS Binding Properties of Anti-STEAP2 Antibodies to STEAP2-expressing and STEAP2 negative cell lines

Table 3A: Binding Properties of Selected Human-Fc Anti-STEAP2 Antibodies

		<i>STEAP2 Expressing</i>		<i>STEAP2 Negative</i>		
Cell line	HEK293	C4-2		FADU	SKBR3	Raji
Antibody	Avg <i>F.A.B</i>	Avg <i>F.A.B</i>	Avg EC₅₀ (nM)	Avg <i>F.A.B</i>	Avg <i>F.A.B</i>	Avg <i>F.A.B</i>
H1H7809N	31	89	>50	21	37	3
H1H7810N	3	26	ND	3	3	2
H1H7811N	5	65	>50	3	5	4
H1H7814N	2	96	4	2	2	2
H1H7972P	4	119	9	2	3	59
H1H11162N	10	104	1	3	3	2
H1H11163N	6	90	3	2	3	2
H1H11164N	10	117	2	3	2	2
H1H11243N	3	41	ND	2	3	2
H1H11878P	5	27	>50	ND	ND	ND
H1H11880P	7	6	5	ND	ND	ND
H1H11888P2	9	6	3	ND	ND	ND
H1H11892P2	3	4	ND	ND	ND	ND
H1H11893P2	3	9	21	ND	ND	ND
H1H11894P2	4	7	ND	ND	ND	ND
H1H11895P2	4	6	16	ND	ND	ND
H1H11896P2	7	6	21	ND	ND	ND
H1H11897P2	16	29	>50	ND	ND	ND

hlgG1 Isotype Control –I	1	2	ND	1	2	4
hlgG1 Isotype Control –II	1.7 ± 0.5	2	ND	3	2	ND
anti-human PE	1.1 ± 0.1	1	ND	1	2	1
Unstained	1 ± 0	1	ND	1	1	ND

F.A.B.: Fold Above Background; ND: Not Detected

Table 3B: Binding Properties of Anti-STEAP2 Hybridoma-generated Antibodies

		STEAP2 Expressing		STEAP2 Negative		
Cell line	HEK293	C4-2		FADU	SKBR3	Raji
Antibody	Avg <i>F.A.B</i>	Avg <i>F.A.B</i>	Avg EC ₅₀ (nM)	Avg <i>F.A.B</i>	Avg <i>F.A.B</i>	Avg <i>F.A.B</i>
H1M11243N	ND	116	23	ND	ND	ND
H1M11249N	ND	11	ND	ND	ND	ND
H2M11160N	ND	8	ND	ND	ND	ND
H2M11162N	ND	365	4.9	ND	ND	ND
H2M11163N	ND	256	13	ND	ND	ND
H2M11164N	ND	360	3.7	ND	ND	ND
H2M11166N	ND	12	ND	ND	ND	ND
H2M11168N	ND	9	ND	ND	ND	ND
H2M11245N	ND	18	ND	ND	ND	ND
H2M11246N	ND	11	ND	ND	ND	ND
H2M11247N	ND	482	18	ND	ND	ND
H2M11248N	ND	50	>50	ND	ND	ND
H3M11161N	ND	5	ND	ND	ND	ND
H3M11165N	ND	13	ND	ND	ND	ND
H3M11167N	ND	14	ND	ND	ND	ND
H3M11244N	ND	2	ND	ND	ND	ND
mIgG1 Isotype Control	ND	2	ND	ND	ND	ND
mIgG2 Isotype Control	ND	3	ND	ND	ND	ND

mlgG3 Isotype Control	ND	4	ND	ND	ND	ND
anti-human PE	1.1 ± 0.1	1	ND	1	2	1
Unstained	1 ± 0	1	ND	1	1	ND

F.A.B.: Fold Above Background; ND: Not Detected

[0269] As the results in Tables 3A and 3B demonstrate, several anti-STEAP2 antibodies specifically bound to high-STEAP2 expressing C4-2 prostate adenocarcinoma cell lines at levels greater than 50-fold above background, with low nM EC50s, via FACS. Some anti-STEAP2 antibodies also bound weakly to low-STEAP2- expressing HEK293 cells. Negligible binding was observed for most anti-STEAP2 antibodies on STEAP2-negative FADU, SK-BR-3, and Raji cells. This example illustrates the ability of several anti-STEAP2 antibodies of this invention to specifically and selectively bind to high-expressing STEAP2 cell lines.

Example 3: Anti-human STEAP2 Antibodies Show Potent Internalization and Specificity for Human-STEAP2

[0270] The ability of the anti-STEAP2 antibodies of this invention to selectively bind to STEAP2-expressing cell lines has been described (see Example 2 – FACS binding). Next, the internalization properties of the anti-STEAP2 antibodies of this invention were also assessed.

[0271] Briefly, 20,000 C4-2 cells were seeded in PDL coated 96 well plates. The next day, cells were incubated with anti-human STEAP2 antibodies (10 µg/ml) for 30 min on ice followed by two PBS washes. Cells were then incubated with alexa488-conjugated anti-hFc Fab secondary antibody for 30 minutes on ice, followed by two additional PBS washes. Antibodies were allowed to internalize for 1h at 37°C in internalization buffer (PBS + 2% FBS) or were maintained at 4°C. Cells were fixed in 4% formaldehyde, nuclei were stained with DRAQ5 (Cell signaling), and images were acquired on the ImageXpress micro XL (Molecular Devices).

[0272] A qualitative visual assessment of the total binding intensity and the intensity of antibodies that had internalized into vesicles was performed and scored according to the following criteria: - (no internalization or binding), + (weak internalization or binding), ++ (moderate internalization or binding) and +++ (robust internalization or binding).

[0273] As the results in Table 4 illustrate, several antibodies showed robust internalization capabilities on the C4-2 cell line. In general, robust internalization correlated with the highest levels of total binding intensity.

[0274] Selected STEAP2 antibodies were then tested for binding to other human (h) STEAP family members (STEAP1, STEAP3, and STEAP4). To assess anti STEAP2 antibody specificity, plasmid constructs expressing hSTEAP1, hSTEAP2, hSTEAP3 or hSTEAP4 fused to Green Fluorescent Protein (GFP) were transiently introduced into HEK293 cells via lipofectamine 2000 based methodology. After 48 h, transiently transfected cells were stained with anti STEAP2 antibodies and imaged as described above for the internalization assay. Wells with GFP positive cells that bound anti STEAP2 antibodies were scored as positive (+) and those that did not bind anti STEAP2 antibodies were scored as negative (-). All tested antibodies bound hSTEAP2-GFP positive cells but did not bind STEAP1-GFP, STEAP3-GFP, or STEAP4-GFP positive cells, confirming specificity of binding to human STEAP2. The results are summarized in Table 5.

[0275] In summary, several anti-STEAP2 antibodies of this invention demonstrate potent internalization ability and are specific binders to human STEAP2.

Table 4. Qualitative assessment of internalization and total binding properties of Anti-STEAP2 antibodies on high-STEAP2 expressing C4-2 cell line

	Internalization (37°C, 1h)	Total Binding (4°C)
Antibody	Qualitative Score	Qualitative Score
H1H7814N	+	+
H1H11162N	+++	+++
H1H11163N	++	++
H1H11164N	+++	+++
H1H11878P	+	+
H1H11880P	+	+
H1H11888P2	+	+
H1H11892P2	+/-	+/-
H1H11893P2	+/-	+/-
H1H11894P2	+/-	+
H1H11895P2	+	+
H1H11896P2	+	+
H1H11897P2	-	-
H1H7972P	+	+
H1M11243N	+	+
H2M11162N	+++	+++
H2M11163N	++	++
H2M11164N	+++	+++
H2M11247N	+++	+++

higG1 Isotype Control (Ab to irrelevant antigen)	-	-

Table 5. Specificity of anti-STEAP2 Antibodies: Assessment of Binding to hSTEAP1, hSTEAP2, hSTEAP3 or hSTEAP4 fused to GFP

	HEK293 Cells Transfected with STEAP/GFP fusion Plasmids			
Antibodies	hSTEAP1	hSTEAP2	hSTEAP3	hSTEAP4
H2M7807	-	+	-	-
H2M7810	-	+	-	-
H2M7811	-	+	-	-
H1M7814	-	+	-	-
H1H7972	-	+	-	-

Example 4: Generation of Bispecific Antibodies that Bind STEAP2 and CD3

[0276] The present invention provides bispecific antigen-binding molecules that bind CD3 and STEAP2; such bispecific antigen-binding molecules are also referred to herein as “anti-STEAP2/anti-CD3 or anti-STEAP2xCD3 bispecific molecules”. The anti-STEAP2 portion of the anti-STEAP2/anti-CD3 bispecific molecule is useful for targeting tumor cells that express six-transmembrane epithelial antigen of prostate 2 (STEAP2) (STEAP2), and the anti-CD3 portion of the bispecific molecule is useful for activating T-cells. The simultaneous binding of STEAP2 on a tumor cell and CD3 on a T-cell facilitates directed killing (cell lysis) of the targeted tumor cell by the activated T-cell.

[0277] Bispecific antibodies comprising an anti-STEAP2-specific binding domain and an anti-CD3-specific binding domain were recombinantly constructed by standard molecular cloning methodologies and expressed in CHO cells, wherein the anti-STEAP2 antigen binding domain and the anti-CD3 antigen binding domain each comprise different, distinct HCVRs paired with a common LCVR. In exemplified bispecific antibodies, the molecules were constructed utilizing a heavy chain from an anti-CD3 antibody, a heavy chain from an anti-STEAP2 antibody and a common light chain from the anti-STEAP2 antibody, and expressed in CHO cells. In some instances, the bispecific antibodies may be constructed utilizing a heavy chain from an anti-CD3 antibody, a heavy chain from an anti-STEAP2 antibody and a light chain from an anti-CD3 antibody

or an antibody light chain known to be promiscuous or pair effectively with a variety of heavy chain arms, such as Vk1-39JK5 or Vk3-20JK1.

[0278] The bispecific antibodies described in the following examples consist of anti-CD3 binding arms having varying binding affinities to human soluble heterodimeric hCD3 ϵ/δ protein (as described in Example 12 herein); and human STEAP2 (see Examples 1-2 above). Exemplified bispecific antibodies were manufactured having a modified (chimeric) IgG4 Fc domain as set forth in US Patent Application Publication No. US20140243504A1, published on August 28, 2014.

[0279] A summary of the component parts of the antigen-binding domains of the various anti-STEAP2xCD3 bispecific antibodies constructed is set forth in Table 6.

Table 6: Construction of STEAP2xCD3 Bispecific Antibodies

Bispecific Antibody Identifier	Anti-STEAP2 Antigen-Binding Domain	Anti-CD3 Antigen-Binding Domain	Common Light Chain Variable Region
	<i>Heavy Chain Variable Region</i>	<i>Heavy Chain Variable Region</i>	
BSSTEAP2/CD3-001	H2M11162N (SEQ ID NO:250)	CD3-VH-G (SEQ ID NO: 1730)	H2M11162N (SEQ ID NO:258)
BSSTEAP2/CD3-002		CD3-VH-G5 (SEQ ID NO: 1762)	
BSSTEAP2/CD3-003		CD3-VH-G20 (SEQ ID NO:1866)	
BSSTEAP2/CD3-004	H1H7814N (SEQ ID NO:218)	H1H7251P (SEQ ID NO:1570)	H1H7814N (SEQ ID NO:226)
BSSTEAP2/CD3-005	H1H11162 (SEQ ID NO:250)	H1H7208P (SEQ ID NO:1490)	H1H11162 (SEQ ID NO:258)
BSSTEAP2/CD3-006		CD3-VH-P (SEQ ID NO:1882)	
BSSTEAP2/CD3-007		H1H7195P (SEQ ID NO:1450)	
BSSTEAP2/CD3-008	H1H11163 (SEQ ID NO:266)	H1H7208P (SEQ ID NO:1490)	H1H11163 (SEQ ID NO:274)
BSSTEAP2/CD3-009	H1H11164 (SEQ ID NO:282)	H1H7208P (SEQ ID NO:1490)	H1H11164 (SEQ ID NO:290)
BSSTEAP2/CD3-010	H1H7809N (SEQ ID NO:330)	H1H7198P (SEQ ID NO:1466)	H1H7809N (SEQ ID NO:339)
BSSTEAP2/CD3-011		H1H7203P (SEQ ID NO:1474)	

[0280] The light chains listed in Table 6 were common to both the CD3 and STEAP2 targeting arms of the bispecific antibodies. Tables 1 and 2 set out amino acid and nucleic acid sequence

identifiers, respectively, for the various heavy chain variable regions, and their corresponding CDRs, of the anti-STEAP2 arms (*i.e.* HCVR and LCVR are derived from H2M11162N) to construct the bispecific antibodies of this Example. Table 15 and 16 set out amino acid and nucleic acid sequence identifiers, respectively, for the various heavy chain variable regions, and their corresponding CDRs, of the anti-CD3 arms of the bispecific antibodies of this Example.

Example 5: Anti-STEAP2/anti-CD3 Bispecific Antibodies Display Potent Anti-Tumor Efficacy *in vivo*

[0281] To determine the efficacy of exemplary anti-STEAP2/anti-CD3 bispecific antibodies *in vivo*, studies were performed in immune-compromised mice bearing prostate cancer xenografts.

Efficacy of anti-STEAP2/anti-CD3 bispecific antibodies in human tumor xenograft models

[0282] To assess the *in vivo* efficacy of the anti-STEAP2/anti-CD3 bispecifics in human tumor xenograft studies, NOD *scid* gamma (NSG) mice (Jackson Laboratories, Bar Harbor, Maine) were co-implanted with human peripheral blood mononuclear cells (PBMCs; ReachBio LLC., Seattle, WA) along with human prostate cancer C4-2 cells (MD Anderson Cancer Center, Houston TX) which endogenously express STEAP2.

[0283] Briefly, 5.0×10^6 C4-2 cells were co-implanted subcutaneously (*s.c.*) with 1.25×10^6 human PBMCs in a 50:50 mix of matrigel matrix (BD Biosciences, San Jose, CA) into the right flank of male NSG mice. Mice were treated intraperitoneally (*i.p.*) on the day of implantation (immediate treatment model) with anti-STEAP2/anti-CD3 bispecifics BSSTEAP2/CD3-001, BSSTEAP2/CD3-002 or BSSTEAP2/CD3-003, or an isotype control, at a dose of 0.1 or 0.01 mg/kg (N=5 mice/group).

[0284] Tumor size was measured 2x/week using calipers and tumor volume calculated as $\text{Volume} = (\text{length} \times \text{width}^2) / 2$. Data is shown as tumor size (mm^3) at study endpoint, 46d post-tumor implantation (Table 7).

Table 7: Efficacy of anti-STEAP2/anti-CD3 Bispecific Antibodies in Immune-Compromised Xenograft Model: Immediate Dosing

Tumor Model / Mouse Strain	Bispecific Antibody Identifier	Dose (mg/kg)	N	Tumor Size (mm^3) 46 d post-tumor implantation (mean $\pm$ SD)
C4-2 / NSG	BSSTEAP2/CD3-001	0.1	5	18.0 $\pm$ 14.0

	BSSTEAP2/CD3-002	0.01	5	23.0 ± 220
		0.1	5	15.0 ± 12.0
		0.01	5	17.0 ± 8.0
	BSSTEAP2/CD3-003	0.1	5	19.0 ± 12.0
		0.01	5	25.0 ± 21.0
	Control Bispecific	0.1	5	1020.0 ± 922.0

[0285] As the results in Table 7 show, BSSTEAP2/CD3-001, BSSTEAP2/CD3-002 and BSSTEAP2/CD3-003 significantly suppressed tumor growth compared to an isotype control when tumor sizes were measured at study endpoint. Importantly, the anti-STEAP2/anti-CD3 bispecific antibodies were efficacious in inhibiting C4-2 tumor growth even at the lowest dose of 0.1 mg/kg.

Example 6: Conjugate Preparation and Characterization

[0286] All the monoclonal antibodies were expressed in CHO cells and purified by Protein A. An isotype control was also prepared in a similar fashion. The non-binding isotype control antibody was derived from an immunological antigen having no relation to oncology.

[0287] The antibody (10 mg/ml) in 50 mM HEPES, 150 mM NaCl, pH 7.5, was treated with 1 mM dithiothreitol at 37 °C for 30 min. After gel filtration (G-25, pH 4.5 sodium acetate), the maleimido linker payload derivative **Compound 7** (1.2 equivalents/SH group) in DMSO (10 mg/ml) was added to the reduced antibody and the mixture adjusted to pH 7.0 with 1 M HEPES (pH 7.4). **Compound 7**, and methods of making the compound, is described in PCT Publication No. WO2014/145090, published on September 18, 2014, which is entirely incorporated herein by reference. After 1 h the reaction was quenched with excess N-ethyl maleimide. The conjugates were purified by size exclusion chromatography and sterile filtered. Protein and linker payload concentrations were determined by UV spectral analysis. Size-exclusion HPLC established that all conjugates used were >95% monomeric, and RP-HPLC established that there was <0.5% unconjugated linker payload. Yields are reported in Table 8 based on protein titer determination. All conjugated antibodies were analyzed by UV for linker payload loading values according to Hamblett et al, Cancer Res 2004 10 7063. The results are summarized in Table 8.

[0288] A conjugate comprising **Compound 60** can be prepared using a similar method. **Compound 60**, and methods of making the compound, is described in PCT Publication No. WO2016/160615 (Example 20), published on October 6, 2016, which is entirely incorporated herein

by reference. Compound **60** is *Maytansin-N-methyl-L-alanine-(3-methoxy-4-amino)benzamido-Cit-Val-Cap-Mal*.

Table 8: Summary of Payload (Chemotoxic Drug) and Antibody-Drug-Conjugate Parameters

Compound	$\epsilon_{252 \text{ nm}} (\text{cm}^{-1} \text{ M}^{-1})$	$\epsilon_{280 \text{ nm}} (\text{cm}^{-1} \text{ M}^{-1})$
7 <i>[Maytansin-3-N-methyl-L-(S)-alanine-propanamidyl-3-N-methyl-N-[4-(amino-citrulline-valine-hexanamide-6-maleimidy)benzyl]carbamate]</i>	50600	8100
Antibody	$\epsilon_{252 \text{ nm}} (\text{cm}^{-1} \text{ M}^{-1})$	$\epsilon_{280 \text{ nm}} (\text{cm}^{-1} \text{ M}^{-1})$
H1H7814N	110440	212400
Isotype Control	75113	218360
Antibody Conjugate	Payload:Antibody (UV)	Yield %
H1H7814N-7	2.7	48
Isotype Control-7	3.0	48

Example 7: Anti-STEAP2 antibody drug conjugates (ADCs) are potent inhibitors of tumor growth in *in vivo* STEAP2 positive prostate cancer xenograft models

[0289] A. To determine the *in vivo* efficacy of anti-STEAP2 antibodies conjugated to **Compound 7**, studies were performed in immune-compromised mice bearing STEAP2 positive prostate cancer xenografts.

[0290] For these studies, Male SCID mice (Taconic, Hudson NY) were implanted with C4-2 cells endogenously expressing STEAP2. Once tumors had reached an average volume of 200-250 mm³ (~Day 13-17), mice were randomized into treatment groups, and dosed with either anti-STEAP2 conjugated antibodies, a non-binding conjugated antibody or vehicle. In these *in vivo* studies, antibodies were dosed once and tumors were then monitored until an average tumor size of approximately 1500-2000 mm³ was attained in the cohort dosed with vehicle alone (~40 – 50 days). Treatment groups showing efficacy were maintained for a longer period of time (80 – 110 days).

[0291] In an initial study, an exemplary anti-STEAP2 antibody conjugated to **Compound 7** was examined for efficacy in reducing C4-2 tumor volume. Mice received a single dose of anti-STEAP2

and control ADCs at 10, 20 or 40 mg/kg on day 13 after implantation. As summarized in Fig. 1, H1H7841N-7 (DAR 2.92) potently inhibited tumor growth at all doses tested. At the highest dose (40 mg/kg), H1H784N-7 efficiently reduced tumor size, although the non-binding control antibody (40 mg/kg) also showed an effect on tumor volume. Across all the doses investigated, H1H784N-7 reduced tumor size more potently than the control conjugated antibody.

[0292] In a second study, anti-STEAP2 ADC was administered at 5 and 20 mg/kg and the control antibody at 20 mg/kg on day 14 after implantation. As summarized in Fig. 2, H1H7841N-7 (DAR 2.92) potently inhibited tumor growth at the 20 mg/kg dose as in the previous experiment, but showed reduced efficacy at the 5 mg/kg dose. The control antibody at the 20 mg/kg dose showed no difference to vehicle control.

[0293] In a further study, H1H7841N-7 (DAR 2.7) and the control antibody were dosed at $\mu\text{g/kg}$ drug equivalents based on ADC drug:antibody ratios ("DAR"). The dose was 150 $\mu\text{g/kg}$ administered on day 17 after implantation (Fig. 3). H1H7841N-7 potently inhibited tumor growth at the 150 $\mu\text{g/kg}$ dose showing tumor regression up to 42 days post implantation and 25 days after injection. At this point, tumor growth began to rebound. Tumor growth with the control antibody at this dose was no different from vehicle control.

[0294] B. In analogous studies, Male SCID mice (Taconic, Hudson NY) were implanted with C4-2 cells endogenously expressing STEAP2. An exemplary anti-STEAP2 (H1H7814N) antibody conjugated to **Compound 60** was examined for efficacy in C4-2 tumor regression. Mice received a single dose of anti-STEAP2 ADC, isotype control ADC (binds to irrelevant antigen), or vehicle (PBS) at 2.5 mg/kg on day 29 after implantation. Tumor volume and body weight was recorded at day 0 (day of injection), and at day 4, 6, 8, 12, 14, and day 20 following the injection. As summarized in Fig. 4, H1H7814N-60 (DAR 3.6) potently inhibited tumor growth at the dose tested, showing tumor regression up to 20 days after injection (49 days post implantation). Percent change in body weight for the test ADC was no more than -2.01% through day 14 (following injection of H1H7814N-60) compared to mice treated with the Control Ab-ADC for which body weight percent change was observed from -4.02% to -11.55% through day 14.

Example 8: Generation of Anti-CD3 Antibodies

[0295] Anti-CD3 antibodies were obtained by immunizing an engineered mouse comprising DNA encoding human Immunoglobulin heavy and kappa light chain variable regions with cells expressing CD3 or with DNA encoding CD3. The antibody immune response was monitored by a CD3-specific immunoassay. When a desired immune response was achieved, splenocytes were harvested and fused with mouse myeloma cells to preserve their viability and form hybridoma cell lines. The hybridoma cell lines were screened and selected to identify cell lines that produce CD3-

specific antibodies. Using this technique several anti-CD3 chimeric antibodies (*i.e.*, antibodies possessing human variable domains and mouse constant domains) were obtained. In addition, several fully human anti-CD3 antibodies were isolated directly from antigen-positive B cells without fusion to myeloma cells, as described in US 2007/0280945A1.

[0296] Certain biological properties of the exemplary anti-CD3 antibodies generated in accordance with the methods of this Example are described in detail in the Examples herein.

Example 9: Heavy and Light Chain Variable Region Amino Acid and Nucleic Acid Sequences

[0297] Table 9 sets forth the amino acid sequence identifiers of the heavy and light chain variable regions and CDRs of selected anti-CD3 antibodies of the invention. The corresponding nucleic acid sequence identifiers are set forth in Table 10. Methods of making the anti-CD3 antibodies disclosed herein can also be found in US publication 2014/0088295 published March 27, 2014.

Table 9: Amino Acid Sequence Identifiers

Antibody Designation	SEQ ID NOs:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR11	LCDR2	LCDR3
H1H2712N	402	404	406	408	410	412	414	416
H1M2692N	418	420	422	424	426	428	430	432
H1M3542N	434	436	438	440	442	444	446	448
H1M3544N	450	452	454	456	458	460	462	464
H1M3549N	466	468	470	472	474	476	478	480
H1M3613N	482	484	486	488	490	492	494	496
H2M2689N	498	500	502	504	506	508	510	512
H2M2690N	514	516	518	520	522	524	526	528
H2M2691N	530	532	534	536	538	540	542	544
H2M2704N	546	548	550	552	554	556	558	560
H2M2705N	562	564	566	568	570	572	574	576
H2M2706N	578	580	582	584	586	588	590	592
H2M2707N	594	596	598	600	602	604	606	608
H2M2708N	610	612	614	616	618	620	622	624
H2M2709N	626	628	630	632	634	636	638	640
H2M2710N	642	644	646	648	650	652	654	656
H2M2711N	658	660	662	664	666	668	670	672
H2M2774N	674	676	678	680	682	684	686	688
H2M2775N	690	692	694	696	698	700	702	704
H2M2776N	706	708	710	712	714	716	718	720
H2M2777N	722	724	726	728	730	732	734	736

H2M2778N	738	740	742	744	746	748	750	752
H2M2779N	754	756	758	760	762	764	766	768
H2M2789N	770	772	774	776	778	780	782	784
H2M2862N	786	788	790	792	794	796	798	800
H2M2885N	802	804	806	808	810	812	814	816
H2M2886N	818	820	822	824	826	828	830	832
H2M3540N	834	836	838	840	842	844	846	848
H2M3541N	850	852	854	856	858	860	862	864
H2M3543N	866	868	870	872	874	876	878	880
H2M3547N	882	884	886	888	890	892	894	896
H2M3548N	898	900	902	904	906	908	910	912
H2M3563N	914	916	918	920	922	924	926	928
H1H5751P	930	932	934	936	938	940	942	944
H1H5752P	946	948	950	952	954	956	958	960
H1H5753B	962	964	966	968	970	972	974	976
H1H5754B	978	980	982	984	986	988	990	992
H1H5755B	994	996	998	1000	1002	1004	1006	1008
H1H5756B	1010	1012	1014	1016	1018	1020	1022	1024
H1H5757B	1026	1028	1030	1032	1034	1036	1038	1040
H1H5758B	1042	1044	1046	1048	1050	1052	1054	1056
H1H5761P	1058	1060	1062	1064	1066	1068	1070	1072
H1H5763P	1074	1076	1078	1080	1082	1084	1086	1088
H1H5764P	1090	1092	1094	1096	1098	1100	1102	1104
H1H5769P	1106	1108	1110	1112	1114	1116	1118	1120
H1H5771P	1122	1124	1126	1128	1130	1132	1134	1136
H1H5772P	1138	1140	1142	1144	1146	1148	1150	1152
H1H5777P	1154	1156	1158	1160	1162	1164	1166	1168
H1H5778P	1170	1172	1174	1176	1178	1180	1182	1184
H1H5780P	1186	1188	1190	1192	1194	1196	1198	1200
H1H5781P	1202	1204	1206	1208	1210	1212	1214	1216
H1H5782P	1218	1220	1222	1224	1226	1228	1230	1232
H1H5785B	1234	1236	1238	1240	1242	1244	1246	1248
H1H5786B	1250	1252	1254	1256	1258	1260	1262	1264
H1H5788P	1266	1268	1270	1272	1274	1276	1278	1280
H1H5790B	1282	1284	1286	1288	1290	1292	1294	1296
H1H5791B	1298	1300	1302	1304	1306	1308	1310	1312
H1H5792B	1314	1316	1318	1320	1322	1324	1326	1328
H1H5793B	1330	1332	1334	1336	1338	1340	1342	1344

H1H5795B	1346	1348	1350	1352	1354	1356	1358	1360
H1H5796B	1362	1364	1366	1368	1370	1372	1374	1376
H1H5797B	1378	1380	1382	1384	1386	1388	1390	1392
H1H5798B	1394	1396	1398	1400	1402	1404	1406	1408
H1H5799P	1410	1412	1414	1416	1418	1420	1422	1424
H1H5801B	1426	1428	1430	1432	1434	1436	1438	1440
H1H7194B	1442	1444	1446	1448	1634	1636	1638	1640
H1H7195B	1450	1452	1454	1456	1634	1636	1638	1640
H1H7196B	1458	1460	1462	1464	1634	1636	1638	1640
H1H7198B	1466	1468	1470	1472	1634	1636	1638	1640
H1H7203B	1474	1476	1478	1480	1634	1636	1638	1640
H1H7204B	1482	1484	1486	1488	1634	1636	1638	1640
H1H7208B	1490	1492	1494	1496	1634	1636	1638	1640
H1H7211B	1498	1500	1502	1504	1634	1636	1638	1640
H1H7221B	1506	1508	1510	1512	1634	1636	1638	1640
H1H7223B	1514	1516	1518	1520	1634	1636	1638	1640
H1H7226B	1522	1524	1526	1528	1634	1636	1638	1640
H1H7232B	1530	1532	1534	1536	1634	1636	1638	1640
H1H7233B	1538	1540	1542	1544	1634	1636	1638	1640
H1H7241B	1546	1548	1550	1552	1634	1636	1638	1640
H1H7242B	1554	1556	1558	1560	1634	1636	1638	1640
H1H7250B	1562	1564	1566	1568	1634	1636	1638	1640
H1H7251B	1570	1572	1574	1576	1634	1636	1638	1640
H1H7254B	1578	1580	1582	1584	1634	1636	1638	1640
H1H7258B	1586	1588	1590	1592	1634	1636	1638	1640
H1H7269B	1594	1596	1598	1600	1634	1636	1638	1640
H1H7279B	1602	1604	1606	1608	1634	1636	1638	1640
H1xH7221G	1610	1612	1614	1616	1634	1636	1638	1640
H1xH7221G3	1618	1620	1622	1624	1634	1636	1638	1640
H1xH7221G5	1626	1628	1630	1632	1634	1636	1638	1640

Table 10: Nucleic Acid Sequence Identifiers

Antibody Designation	SEQ ID NOs:							
	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H2712N	401	403	405	407	409	411	413	415
H1M2692N	417	419	421	423	425	427	429	431
H1M3542N	433	435	437	439	441	443	445	447
H1M3544N	449	451	453	455	457	459	461	463
H1M3549N	465	467	469	471	473	475	477	479
H1M3613N	481	483	485	487	489	491	493	495

H2M2689N	497	499	501	503	505	507	509	511
H2M2690N	513	515	517	519	521	523	525	527
H2M2691N	529	531	533	535	537	539	541	543
H2M2704N	545	547	549	551	553	555	557	559
H2M2705N	561	563	565	567	569	571	573	575
H2M2706N	577	579	581	583	585	587	589	591
H2M2707N	593	595	597	599	601	603	605	607
H2M2708N	609	611	613	615	617	619	621	623
H2M2709N	625	627	629	631	633	635	637	639
H2M2710N	641	643	645	647	649	651	653	655
H2M2711N	657	659	661	663	665	667	669	671
H2M2774N	673	675	677	679	681	683	685	687
H2M2775N	689	691	693	695	697	699	701	703
H2M2776N	705	707	709	711	713	715	717	719
H2M2777N	721	723	725	727	729	731	733	735
H2M2778N	737	739	741	743	745	747	749	751
H2M2779N	753	755	757	759	761	763	765	767
H2M2789N	769	771	773	775	777	779	781	783
H2M2862N	785	787	789	791	793	795	797	799
H2M2885N	801	803	805	807	809	811	813	815
H2M2886N	817	819	821	823	825	827	829	831
H2M3540N	833	835	837	839	841	843	845	847
H2M3541N	849	851	853	855	857	859	861	863
H2M3543N	865	867	869	871	873	875	877	879
H2M3547N	881	883	885	887	889	891	893	895
H2M3548N	897	899	901	903	905	907	909	911
H2M3563N	913	915	917	919	921	923	925	927
H1H5751P	929	931	933	935	937	939	941	943
H1H5752P	945	947	949	951	953	955	957	959
H1H5753B	961	963	965	967	969	971	973	975
H1H5754B	977	979	981	983	985	987	989	991
H1H5755B	993	995	997	999	1001	1003	1005	1007
H1H5756B	1009	1011	1013	1015	1017	1019	1021	1023
H1H5757B	1025	1027	1029	1031	1033	1035	1037	1039
H1H5758B	1041	1043	1045	1047	1049	1051	1053	1055
H1H5761P	1057	1059	1061	1063	1065	1067	1069	1071
H1H5763P	1073	1075	1077	1079	1081	1083	1085	1087
H1H5764P	1089	1091	1093	1095	1097	1099	1101	1103
H1H5769P	1105	1107	1109	1111	1113	1115	1117	1119
H1H5771P	1121	1123	1125	1127	1129	1131	1133	1135
H1H5772P	1137	1139	1141	1143	1145	1147	1149	1151
H1H5777P	1153	1155	1157	1159	1161	1163	1165	1167
H1H5778P	1169	1171	1173	1175	1177	1179	1181	1183
H1H5780P	1185	1187	1189	1191	1193	1195	1197	1199
H1H5781P	1201	1203	1205	1207	1209	1211	1213	1215
H1H5782P	1217	1219	1221	1223	1225	1227	1229	1231

H1H5785B	1233	1235	1237	1239	1241	1243	1245	1247
H1H5786B	1249	1251	1253	1255	1257	1259	1261	1263
H1H5788P	1265	1267	1269	1271	1273	1275	1277	1279
H1H5790B	1281	1283	1285	1287	1289	1291	1293	1295
H1H5791B	1297	1299	1301	1303	1305	1307	1309	1311
H1H5792B	1313	1315	1317	1319	1321	1323	1325	1327
H1H5793B	1329	1331	1333	1335	1337	1339	1341	1343
H1H5795B	1345	1347	1349	1351	1353	1355	1357	1359
H1H5796B	1361	1363	1365	1367	1369	1371	1373	1375
H1H5797B	1377	1379	1381	1383	1385	1387	1389	1391
H1H5798B	1393	1395	1397	1399	1401	1403	1405	1407
H1H5799P	1409	1411	1413	1415	1417	1419	1421	1423
H1H5801B	1425	1427	1429	1431	1433	1435	1437	1439
H1H7194B	1441	1443	1445	1447	1633	1635	1637	1639
H1H7195B	1449	1451	1453	1455	1633	1635	1637	1639
H1H7196B	1457	1459	1461	1463	1633	1635	1637	1639
H1H7198B	1465	1467	1469	1471	1633	1635	1637	1639
H1H7203B	1473	1475	1477	1479	1633	1635	1637	1639
H1H7204B	1481	1483	1485	1487	1633	1635	1637	1639
H1H7208B	1489	1491	1493	1495	1633	1635	1637	1639
H1H7211B	1497	1499	1501	1503	1633	1635	1637	1639
H1H7221B	1505	1507	1509	1511	1633	1635	1637	1639
H1H7223B	1513	1515	1517	1519	1633	1635	1637	1639
H1H7226B	1521	1523	1525	1527	1633	1635	1637	1639
H1H7232B	1529	1531	1533	1535	1633	1635	1637	1639
H1H7233B	1537	1539	1541	1543	1633	1635	1637	1639
H1H7241B	1545	1547	1549	1551	1633	1635	1637	1639
H1H7242B	1553	1555	1557	1559	1633	1635	1637	1639
H1H7250B	1561	1563	1565	1567	1633	1635	1637	1639
H1H7251B	1569	1571	1573	1575	1633	1635	1637	1639
H1H7254B	1577	1579	1581	1583	1633	1635	1637	1639
H1H7258B	1585	1587	1589	1591	1633	1635	1637	1639
H1H7269B	1593	1595	1597	1599	1633	1635	1637	1639
H1H7279B	1601	1603	1605	1607	1633	1635	1637	1639
H1xH7221G	1609	1611	1613	1615	1633	1635	1637	1639
H1xH7221G3	1617	1619	1621	1623	1633	1635	1637	1639
H1xH7221G5	1625	1627	1629	1631	1633	1635	1637	1639

[0298] Antibodies are typically referred to herein according to the following nomenclature: Fc prefix (e.g. "H1H," "H1M," "H2M," etc.), followed by a numerical identifier (e.g. "2712," "2692," etc., as shown in Table 1), followed by a "P," "N," or "B" suffix. Thus, according to this nomenclature, an antibody may be referred to herein as, e.g., "H1H2712N," "H1M2692N," "H2M2689N," etc. The H1H, H1M and H2M prefixes on the antibody designations used herein indicate the particular Fc region isotype of the antibody. For example, an "H1H" antibody has a human IgG1 Fc, an "H1M"

antibody has a mouse IgG1 Fc, and an "H2M" antibody has a mouse IgG2 Fc, (all variable regions are fully human as denoted by the first 'H' in the antibody designation). As will be appreciated by a person of ordinary skill in the art, an antibody having a particular Fc isotype can be converted to an antibody with a different Fc isotype (e.g., an antibody with a mouse IgG1 Fc can be converted to an antibody with a human IgG4, etc.), but in any event, the variable domains (including the CDRs) – which are indicated by the numerical identifiers shown in Table 1 – will remain the same, and the binding properties are expected to be identical or substantially similar regardless of the nature of the Fc domain.

[0299] Tables 11 and 12 set out the amino acid sequence identifiers for heavy chain variable regions (Table 13) and light chain variable regions (Table 14), and their corresponding CDRs, of additional anti-CD3 HCVRs and LCVRs useful in anti-STEAP2 x anti-CD3 bispecific antibodies of the invention.

Table 11 (Heavy Chain Variable Region Amino Acid Sequences)

Heavy Chain Identifier	SEQ ID NOs			
	HCVR	HCDR1	HCDR2	HCDR3
CD3-VH-AA	1642	1644	1646	1648
CD3-VH-B	1658	1660	1662	1664
CD3-VH-C	1674	1676	1678	1680
CD3-VH-D	1690	1692	1694	1696
CD3-VH-E	1706	1708	1710	1712
CD3-VH-F [#]	1721	1722	1723	1724

Table 12 (Light Chain Variable Region Amino Acid Sequences)

Light Chain Identifier	SEQ ID NOs			
	LCVR	LCDR1	LCDR2	LCDR3
CD3-VL-AA	1650	1652	1654	1656
CD3-VL-B	1666	1668	1670	1672
CD3-VL-C	1682	1684	1686	1688
CD3-VL-D	1698	1700	1702	1704
CD3-VL-E	1714	1716	1718	1720
CD3-VL-F [#]	1725	1726	1727	1728

[0300] The heavy and light chain variable regions of CD3-VH-F and CD3-VL-F were derived from the anti-CD3 antibody designated "L2K" as set forth in WO2004/106380.

[0301] In addition, Tables 13 and 14 set out the sequence identifiers for the nucleotide sequences encoding the heavy chain variable regions (Table 13) and light chain variable regions (Table 14),

and their corresponding CDRs, of additional anti-CD3 HCVRs and LCVRs useful in anti-STEAP2 x anti-CD3 bispecific antibodies of the invention.

Table 13 (Nucleotide Sequences Encoding Heavy Chain Variable Region Sequences)

Heavy Chain Identifier	SEQ ID NOs			
	HCVR	HCDR1	HCDR2	HCDR3
CD3-VH-AA	1641	1643	1645	1647
CD3-VH-B	1657	1659	1661	1663
CD3-VH-C	1673	1675	1677	1679
CD3-VH-D	1689	1691	1693	1695
CD3-VH-E	1705	1707	1709	1711

Table 14 (Nucleotide Sequences Encoding Light Chain Variable Region Sequences)

Light Chain Identifier	SEQ ID NOs			
	LCVR	LCDR1	LCDR2	LCDR3
CD3-VL-AA	1649	1651	1653	1655
CD3-VL-B	1665	1667	1669	1671
CD3-VL-C	1681	1683	1685	1687
CD3-VL-D	1697	1699	1701	1703
CD3-VL-E	1713	1715	1717	1719

Control Constructs Used in the Following Examples

[0302] Various control constructs (anti-CD3 antibodies) were included in the following experiments for comparative purposes: "OKT-3," a mouse monoclonal antibody against human T-cell surface antigens available from the American Type Culture Collection (ATCC) under catalog no. CRL-8001; and "SP34," a commercially available mouse monoclonal antibody obtained, e.g., from Biolegend, San Diego, CA (Cat. No. 302914) or BD Pharmagen, Cat. 55052, reactive against the epsilon chain of the T3 complex on human T lymphocyte cells.

Example 10: Generation of Additional Anti-CD3 Antibodies

[0303] The following procedures were aimed at identifying antibodies that specifically recognized CD3 (T cell co-receptor) as an antigen.

[0304] A pool of anti-CD3 antibodies were derived from a genetically modified mouse. Briefly, mice were immunized with a CD3 antigen and generated B cells that comprised a diversity of human VH rearrangements in order to express a diverse repertoire of high-affinity antigen-specific antibodies. Antibodies described in Tables 15-18 have the same light chain sequence of VK1-39JK5 (LCVR set forth in SEQ ID NO: 1890).

[0305] Generated antibodies were tested for affinity to human and cynomolgus monkey CD3 antigen in an *in vitro* binding assay, and e.g. one CD3 antibody: designated CD3-VH-P (HCVR set

forth in SEQ ID NO: 1882) was identified, amongst a few others, that were found to bind to both human and cynomolgus CD3 having an EC_{50} between 1 and 40 nM affinity, as determined in a FACS titration of Jurkat cells and cynomolgus T cells, respectively. See, e.g. FACS binding experiments outlined in Example 12 and in PCT/US2016/044732 filed July 29, 2016.

[0306] The germline amino acid residues of CD3-VH-P were subsequently identified and an antibody designated “CD3-VH-G” was engineered to contain only germline frameworks. Other antibody derivatives were engineered by well-known molecular cloning techniques to replace amino acid residues in a stepwise manner based on differences between the germline sequence and the CD3-VH-P sequence. Each antibody derivative is given a “CD3-VH-G” number designation. See Table 15.

[0307] While CD3-VH-G and some other engineered antibodies retained their binding affinity as seen in the FACS assays, several anti-CD3 antibodies in a bispecific format bound to human or cynomolgus CD3 *in vitro* with weak to no measurable binding affinity, such greater than 100 nM EC_{50} . Binding affinities, binding kinetics, and other biological properties to elucidate toxicity and pharmacokinetic (pK) profiles were subsequently investigated further as bispecific antibodies comprising the exemplary anti-CD3 antibodies, and were generated in accordance with the methods of this Example.

Example 11: Heavy and Light Chain Variable Regions (Amino Acid and Nucleic Acid Sequences of the CDRs)

[0308] Table 15 sets forth the amino acid sequence identifiers of the heavy chain variable regions and CDRs of selected anti-CD3 antibodies of the invention. The corresponding nucleic acid sequence identifiers are set forth in Table 16.

[0309] Amino acid and nucleic acid sequences were determined for each antibody heavy chain sequence. Each antibody heavy chain derived from the germline sequence (SEQ ID NO: 1910) was assigned a “G” number designation for consistent nomenclature. Table 15 sets forth the amino acid sequence identifiers of the heavy chain variable regions and CDRs of engineered anti-CD3 antibodies of the invention. The corresponding nucleic acid sequence identifiers are set forth in Table 16. The amino acid and nucleic acid sequence identifiers of the light chain variable region and CDRs are also identified below in Tables 17 and 18, respectively.

Table 15: Heavy Chain Amino Acid Sequence Identifiers

Antibody CD3-VH Designation	SEQ ID NOs:

	HCVR	CDR1	CDR2	CDR3
CD3-VH-G	1730	1732	1734	1736
CD3-VH-G2	1738	1740	1742	1744
CD3-VH-G3	1746	1748	1750	1752
CD3-VH-G4	1754	1756	1758	1760
CD3-VH-G5	1762	1764	1766	1768
CD3-VH-G8	1770	1772	1774	1776
CD3-VH-G9	1778	1780	1782	1784
CD3-VH-G10	1786	1788	1790	1792
CD3-VH-G11	1794	1796	1798	1800
CD3-VH-G12	1802	1804	1806	1808
CD3-VH-G13	1810	1812	1814	1816
CD3-VH-G14	1818	1820	1822	1824
CD3-VH-G15	1826	1828	1830	1832
CD3-VH-G16	1834	1836	1838	1840
CD3-VH-G17	1842	1844	1846	1848
CD3-VH-G18	1850	1852	1854	1856
CD3-VH-G19	1858	1860	1862	1864
CD3-VH-G20	1866	1868	1870	1872
CD3-VH-G21	1874	1876	1878	1880
CD3-VH-P	1882	1884	1886	1888

Table 16: Heavy Chain Nucleic Acid Sequence Identifiers

Antibody CD3-VH Designation	SEQ ID NOs:			
	HCVR	CDR1	CDR2	CDR3
CD3-VH-G	1729	1731	1733	1735
CD3-VH-G2	1737	1739	1741	1743
CD3-VH-G3	1745	1747	1749	1751
CD3-VH-G4	1753	1755	1757	1759
CD3-VH-G5	1761	1763	1765	1767
CD3-VH-G8	1769	1771	1773	1775
CD3-VH-G9	1777	1779	1781	1783
CD3-VH-G10	1785	1787	1789	1791
CD3-VH-G11	1793	1795	1797	1799
CD3-VH-G12	1801	1803	1805	1807

CD3-VH-G13	1809	1811	1813	1815
CD3-VH-G14	1817	1819	1821	1823
CD3-VH-G15	1825	1827	1829	1831
CD3-VH-G16	1833	1835	1837	1839
CD3-VH-G17	1841	1843	1845	1847
CD3-VH-G18	1849	1851	1853	1855
CD3-VH-G19	1857	1859	1861	1863
CD3-VH-G20	1865	1867	1869	1871
CD3-VH-G21	1873	1875	1877	1879
CD3-VH-P	1881	1883	1885	1887

Table 17: Light Chain Amino Acid Sequence Identifiers

Antibody Designation	SEQ ID NOs:			
	LCVR	CDR1	CDR2	CDR3
VK1-39JK5	1890	1892	1894	1896

Table 18: Light Chain Nucleic Acid Sequence Identifiers

Antibody Designation	SEQ ID NOs:			
	LCVR	CDR1	CDR2	CDR3
VK1-39JK5	1889	1891	1893	1895

[0310] Control 1 antibody designated "CD3-L2K" was constructed based on a known anti-CD3 antibody (*i.e.*, the anti-CD3 antibody "L2K" as set forth in WO2004/106380).

[0311] Isotype Control Antibody, referred to in the Examples herein, is an isotype matched (modified IgG4) antibody that interacts with an irrelevant antigen, *i.e.* FeID1 antigen.

Example 12: In vitro and in vivo studies on Human Monoclonal Anti-CD3 Antibodies

[0312] In vivo and in vitro studies on human monoclonal anti-CD3 antibodies were done as described in US publication 2014/0088295 published March 27, 2014, and PCT/US2016/044732 filed July 29, 2016, which are hereby incorporated by reference.

[0313] Some human monoclonal anti-CD3 antibodies of the present invention bind soluble heterodimeric CD3 protein, in either antibody-capture or antigen-capture formats, with high affinity. Soluble heterodimeric CD3 protein (hCD3-epsilon/hCD3-delta; SEQ ID NOs:1900/1901) was prepared with either a human Fc tag (hFcΔAdp/hFc; SEQ ID NOs:1931/1932) or a mouse Fc tag

(mFcΔAdp/mFc; SEQ ID NOs:1933/1934). Heterodimeric CD3 protein was purified using the method described in Davis *et al.* (US2010/0331527).

[0314] Some human monoclonal anti-CD3 antibodies of the invention bound human T-cells and induced T-cell proliferation. Some human monoclonal anti-CD3 antibodies of the invention bound CD2+CD4+ monkey T-cells and induced their proliferation. Some human monoclonal anti-CD3 antibodies supported redirected T-cell mediated killing via Fc/FcR interaction in a calcein based U937 killing assay. The observed killing, believed to be dependent on the antibody's Fc engagement with the Fc Receptor on U937 cells leading to clustering of CD3 on adjacent T-cells, was squelched by addition of non-specific human IgG (data not shown).

Example 13: In vitro studies on Human STEAP2xCD3 Bispecific Antibodies

[0315] *FACS Binding Titration on Jurkat Cells, PC3_STEAP2/1 Cells and cynomolgus T Cells:* Flow cytometric analysis was utilized to determine binding of STEAP2xCD3 bispecific antibodies to Jurkat, PC3_STEAP2/1 chimeric and cynomolgus T cells, followed by detection with a phycoerythrin (PE)-labeled anti-human IgG antibody. Briefly, 2x 10⁵ cells/well were incubated for 30 minutes at 4°C with a serial dilution of STEAP2xCD3 bispecific antibodies or cocontrol antibody (a human IgG1 antibody that binds a feline antigen with no cross-reactivity to STEAP2 or human or cynomolgus CD3) ranging from 66.6nM to 0.001nM. After incubation, the cells were washed twice with cold PBS containing 1% filtered FBS and a PE-conjugated anti-human secondary antibody was added to the cells and incubated for an additional 30 minutes. Wells containing no antibody or secondary antibody only were used as a control. After incubation, cells were washed, re-suspended in 200 µL cold PBS containing 1% filtered FBS and analyzed by flow cytometry on a BD FACS Canto II.

Table 19: FACS Binding of selected STEAP2xCD3 Bispecific Antibodies to Jurkat, PC3_STEAP2/1 and cynomolgus T cells

Bispecific Antibody Designation	FACS Jurkat EC50 [M]	FACS PC3_STEAP2/1 EC50 [M]	Cynomolgus T cells EC50 [M]
BSSTEAP2/CD3-0010	1.36E-08	No Binding	Very Weak
BSSTEAP2/CD3-004	6.88E-10	7.91E-08	1.99E-09
BSSTEAP2/CD3-0011	8.63E-09	No Binding	No Binding
BSSTEAP2/CD3-005	1.41E-08	3.18E-08	No Binding
BSSTEAP2/CD3-001	7.19E-09	3.44E-09	7.27E-09
BSSTEAP2/CD3-006	3.98E-09	1.22E-08	7.99E-09
BSSTEAP2/CD3-007	6.15E-10	5.37E-09	1.73E-08

BSSTEAP2/CD3-008	1.52E-09	6.88E-08	1.66E-08
BSSTEAP2/CD3-009	4.14E-09	4.21E-08	No Binding

[0316] Jurkat cells are derived from a T cell lymphoblastic cell line that expresses human CD3. All bispecific antibodies tested (Table 19 and Figure 5) bound to Jurkat cells with EC₅₀ ranging from 1.41E-08 M to 6.15E-10 M. PC3 cells, a human prostate cancer cell line, was engineered to express a STEAP2/1 chimeric construct. Several bispecific antibodies bound to PC3_STEAP2/1 cells, with EC₅₀ ranging from 7.91E-08 M to 3.44E-09 M (Table 19 and Figure 6).

[0317] Binding of STEAP2xCD3 bispecific antibodies to the surface of purified Cynomolgus T cells was also tested. Several bispecific antibodies bound EC₅₀ ranging from 1.73E-08 M to 7.27E-09 M. Control antibodies did not bind to either cell line. See Table 19 and Figures 7 and 8.

[0318] *T Cell Proliferation Assay:* Thawed human or freshly isolated monkey PBMCs (50,000 cells/well) were incubated with 3-fold (human, concentration range: 5E-10M to 2.82E-15M; cynomolgus, concentration range: 1E-09M to 4.57E-13M) serial dilutions of STEAP2xCD3 bispecifics or isotype control in complete medium (RPMI supplemented with 10% FBS, 100 U/mL penicillin, 100 µg/mL streptomycin, 292 µg/mL L-glutamine) and a fixed concentration (human: 200 ng/mL, cyno: 500 ng/mL) of a commercial anti-CD28 antibody (Biolegend, Catalog#302914) in white flat bottom 96-well plates for 72 hours at 37°C. Isolated monkey PBMCs were from two donors (identified as mk8781M or mk9381M). Following incubation, CellTiter Glo® (Promega, Cat#7573) was added and luminescence, as readout for cell viability, was measured using a VICTOR X5 multi-label plate reader. Cell titer was calculated by dividing the luminescence of stimulated cells by the baseline luminescence of unstimulated cells.

[0319] All αSTEAP2xαCD3 bispecific antibodies induce human PBMC proliferation in the presence of a co-stimulatory anti-CD28 antibody (See Table 20 and Figure 9). PBMCs were incubated with a serial dilution of bispecific antibodies or the control antibody and a fixed concentration of anti-CD28 for 72 hours, and cell viability was measured in a luminescence assay to detect live cells. Proliferation was determined by comparing luminescence of bispecific antibodies-stimulated cells to cells without antibody. EC₅₀ values (defined as the concentration of antibody required to generate half maximal proliferation) ranged from 3.68E-13M to 1.60E-10M. In contrast, Control antibody exhibited no activity under the same conditions.

**Table 20: T-cell activation proliferation induced by selected
STEAP2xCD3 Bispecific Antibodies**

Bispecific Antibody Designation	hPBMC Proliferation [M]	Cyno PBMC Proliferation [M] (donor)

BSSTEAP2/CD3-0010	6.55E-12	7.034E-13 (mk8781M)
BSSTEAP2/ CD3-004	7.10E-13	[++] (mk8781M) [-] (mk9381M)
BSSTEAP2/ CD3-011	8.62E-12	3.597E-12 (mk8781M)
BSSTEAP2/ CD3-005	2.76E-12	[-] (mk9381M) (mk8781M)
BSSTEAP2/ CD3-001	1.60E-10	4.592E-12 (mk9381M) [+] (mk8781M)
BSSTEAP2/ CD3-006	8.14E-13	1.532E-11 (mk9381M) [+] (mk8781M)
BSSTEAP2/ CD3-007	8.26E-11	[+/-] (mk9381M) [+] (mk8781M)
BSSTEAP2/ CD3-008	7.76E-12	[+/-] (mk9381M) [+] (mk8781M)
BSSTEAP2/ CD3-009	3.68E-13	[-] (mk9381M) (mk8781M)

[0320] Bispecific antibodies BSSTEAP2/ CD3-0010 and BSSTEAP2/ CD3-011 also induced cynomolgus PBMC proliferation (with donor mk8781M) exhibiting EC₅₀s of 7E-13 and 3.6E-12, respectively. BSSTEAP2/ CD3-004 activity was donor dependent. Two additional bispecific antibodies, BSSTEAP2/ CD3-001 and BSSTEAP2/ CD3-006, induced robust cynomolgus PBMC proliferation in all donors tested. EC₅₀ values using donor mk9381M were 4.6E-12M and 1.53E-11M, respectively (See Table 20 and Figure 10).

[0321] BSSTEAP2/ CD3-007 and BSSTEAP2/ CD3-008 activity was donor dependent. In contrast, BSSTEAP2/ CD3-005, BSSTEAP2/ CD3-009 and isotype control exhibited no activity.

[0322] *Cytotoxicity assay targeting C4-2 cells in the presence of anti-STEAP2xCD3 bispecific antibodies and human T cells:* In order to monitor the specific killing of STEAP2-bearing target cells by flow cytometry, C4-2 cells were labeled with 1μM of the fluorescent tracking dye Violet Cell Tracker (Life Technologies kit, #C34557). After labeling, cells were plated overnight at 37°C. Separately, human PBMCs were plated in supplemented RPMI media at 1x10⁶ cells/mL and incubated overnight at 37°C in order to enrich for lymphocytes by depleting adherent macrophages, dendritic cells, and some monocytes. The next day, target cells were co-incubated with adherent cell-depleted naïve PBMC (Effector/Target cell 4:1 ratio) and a serial dilution of STEAP2xCD3 bispecific antibodies or an IgG1 control antibody (does not bind to STEAP2) (concentration range:

66.7nM to 0.25pM) for 48 hours at 37°C. Cells were removed from cell culture plates using an enzyme-free cell dissociation buffer, and analyzed by FACS. For FACS analysis, cells were stained with a dead/live far red cell tracker (Invitrogen). 5×10^5 counting beads were added to each well immediately before FACS analysis. 1×10^5 beads were collected for each sample. For the assessment of specificity of killing, cells were gated on live Violet labeled populations. Percent of live population was recorded and used for the calculation of normalized survival.

[0323] T cell activation was assessed by incubating cells with directly conjugated antibodies to CD2 and CD69, and by reporting the percent of activated (CD69+) T cells out of total T cells (CD2+). Several anti_STEAP2xCD3 bispecific antibodies were tested on their ability to induce naïve T cells to kill target cells expressing human STEAP2 (See Table 21 and Figure 11). All antibodies tested activated and directed human T cells to deplete C4-2 cells (human prostate adenocarcinoma sub line derived from LnCap cells). Target cell killing was only observed in the presence of the bispecific antibodies, with C4-2 cells depleted in a dose-dependent manner with pM EC50s. Additionally, the observed target-cell lysis was associated with upregulation of CD69 cells on CD2+ T cells, with pM EC50s (See Table 21 and Figure 12).

Table 21: Cytotoxicity and T-cell activation properties of selected STEAP2xCD3 Bispecific Antibodies

Bispecific Antibody Designation	C4-2 cells depletion EC50 [M]	T cells activation EC50 [M]
BSSTEAP2/ CD3-004	3.11E-12	9.40E-13
BSSTEAP2/ CD3-005	7.29E-12	+++
BSSTEAP2/ CD3-001	4.68E-12	1.61E-12
BSSTEAP2/ CD3-006	3.93E-12	+++
BSSTEAP2/ CD3-007	8.11E-12	+++
BSSTEAP2/ CD3-008	4.11E-12	+++
BSSTEAP2/ CD3-009	2.73E-12	+++

[0324] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are intended to fall within the scope of the appended claims.

[0325] In the claims which follow and in the preceding description of the invention, except where the context requires otherwise due to express language or necessary implication, the word

“comprise” or variations such as “comprises” or “comprising” is used in an inclusive sense, i.e. to specify the presence of the stated features but not to preclude the presence or addition of further features in various embodiments of the invention.

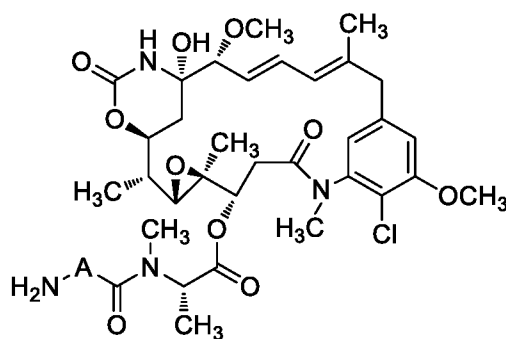
What is claimed is:

1. An antibody-drug conjugate (ADC) comprising an antibody or antigen-binding fragment thereof that specifically binds to human six-transmembrane epithelial antigen of prostate 2 (STEAP2), and a cytotoxic agent, wherein the antibody or antigen-binding fragment thereof and the cytotoxic agent are covalently attached via a linker, and wherein the antibody or antigen-binding fragment thereof comprises complementarity determining regions HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 comprising the amino acid sequences of: SEQ ID NOs: 220-222-224-228-230-232, respectively.

2. The ADC of claim 1, wherein the antibody or antigen-binding fragment thereof comprises a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 218, and a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 226.

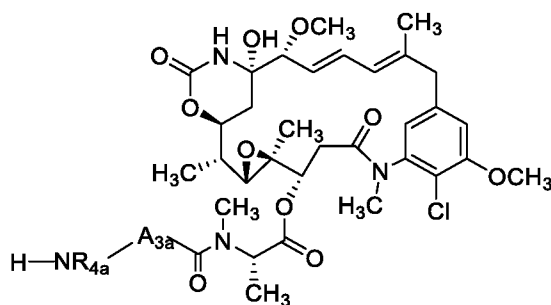
3. The ADC of any one of claim 1 or 2, wherein the cytotoxic agent is:

- (a) selected from an auristatin, a maytansinoid, a tubulysin, a tomaymycin, or a dolastatin;
- (b) an auristatin selected from MMAE or MMAF, or a maytansinoid selected from DM1 or DM4; or
- (c) a maytansinoid having the structure of:



(Formula I)

wherein A is arylene or heteroarylene, or



(Formula II)

wherein:

A_{3a} is an amino acid, a peptide having 2-20 amino acids, an alkyl, an alkynyl, an alkenyl, a cycloalkyl, an aryl, a heteroaryl, a heterocyclyl, -CR₅R₆-, -O-, -C(=O)-, -O-C(=O)-, -C(=O)-O-, -O-C(=O)-O-, -C(=O)-(CH_x)_{p1}-, -C(=O)-O-(CH_x)_{p1}-, -(CH_x)_{p1}-C(=O)-, -(CH_x)_{p1}-C(=O)-O-, -(O-(CH₂)_{p2})_{p3}-, -((CH₂)_{p2}-O)_{p3}-, -C(=S)-, -C(=S)-S-, -C(=S)-NH-, -S-C(=S)-, -S-C(=S)-S-, -S-, -SO-, -SO₂-, -NR₄-, -N(R₄)-C(=O)-N(R₈)-, -N(R₄)-C(=O)O-, -N(R₄)-C(=O)-, -C(=O)-N(R₄)-, -C(=O)-N(R₄)-C(=O)-, or -O-C(=O)-NR₄-; and

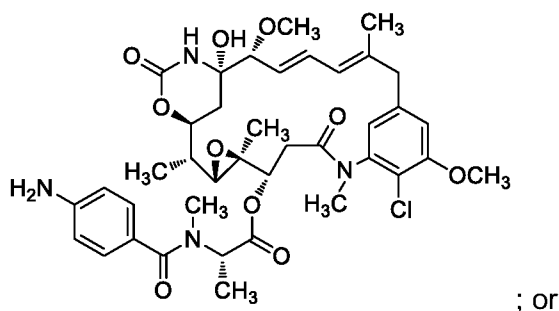
p₁, p₂ and p₃ are each independently 0, or an integer from 1 to 100;

x is 0, 1 or 2;

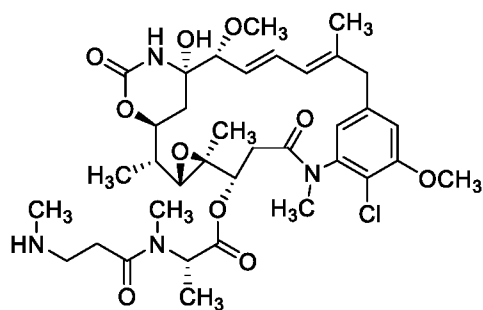
R₄, R₅, R₆ and R₈ are each independently H, or a substituted or unsubstituted: alkyl, alkenyl, alkynyl, aryl, heteroaryl, or heterocyclyl; and

R_{4a} is a substituted or unsubstituted: alkyl, alkenyl, alkynyl, aryl, heteroaryl, or heterocyclyl.

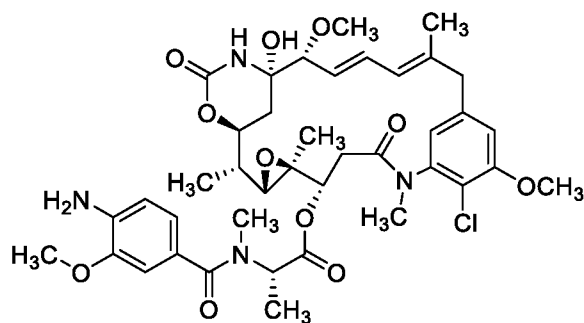
4. The ADC of claim 3, wherein the maytansinoid is:



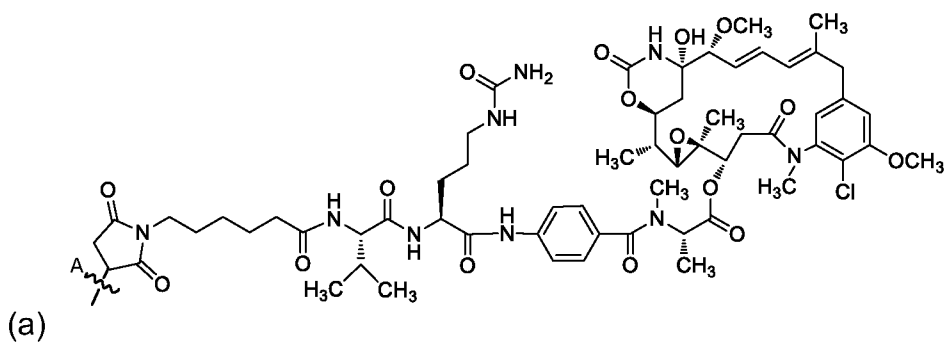
; or



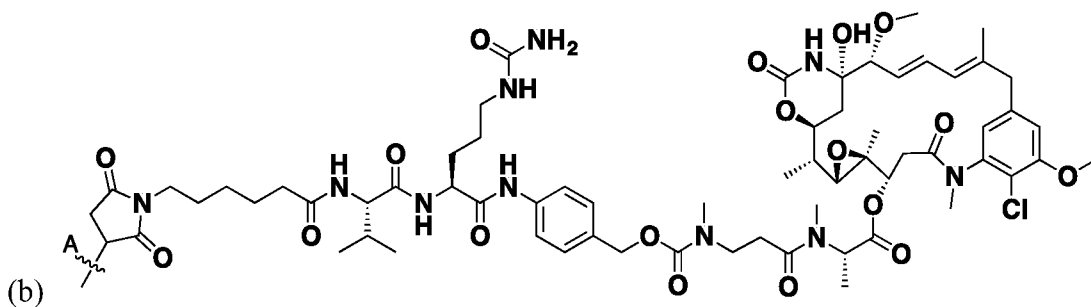
; or



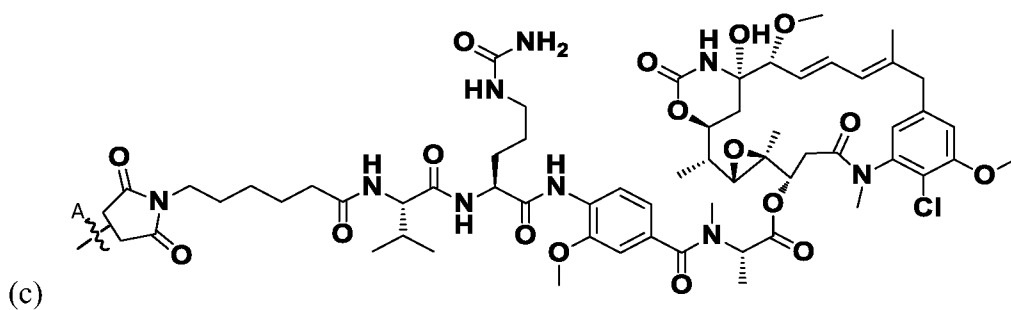
5. The ADC of claim 1 or 2, comprising the antibody or antigen-binding fragment thereof, and:



wherein $\text{---}\overset{\text{A}}{\text{~}}\text{---}$ is a bond to the anti-STEAP2 antibody or fragment thereof; or



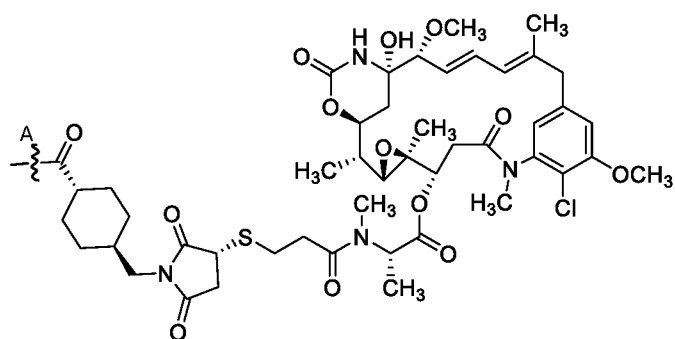
wherein $\text{---}\overset{\text{A}}{\text{~}}\text{---}$ is a bond to the anti-STEAP2 antibody or fragment thereof; or



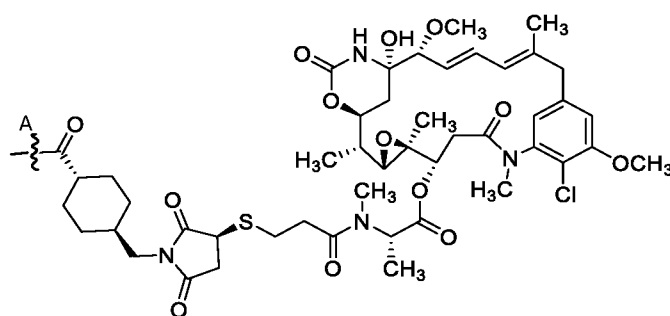
wherein $\text{---}\overset{\text{A}}{\underset{\text{A}}{\text{---}}}$ is a bond to the anti-STEAP2 antibody or fragment thereof.

6. The ADC of claim 5, wherein bond contacts the antibody or fragment thereof via a sulfur constituent of a cysteine residue.

7. The ADC of claim 1 or 2, comprising the antibody or antigen-binding fragment thereof, and



, or



, or

a mixture thereof,

wherein $\text{---}\overset{\text{A}}{\underset{\text{A}}{\text{---}}}$ is a bond to the antibody or antigen-binding fragment thereof.

8. The ADC of claim 7, wherein the bond contacts the antibody or antigen-binding fragment thereof via a nitrogen constituent of a lysine residue.

9. The ADC of any one of claims 1-8, wherein the ADC comprises 1 to 4 cytotoxic agents per antibody or antigen-binding fragment thereof.

10. An antibody or antigen-binding fragment thereof that specifically binds human six-transmembrane epithelial antigen of prostate 2 (STEAP2)-expressing cells, wherein the antibody or antigen-binding fragment thereof a heavy chain variable region (HCVR) comprising complementarity determining regions HCDR1, HCDR2, and HCDR3 comprising the amino acid sequences of SEQ ID NOs: 220, 222, and 224, respectively, and a light chain variable region (LCVR) comprising complementarity determining regions LCDR1, LCDR2, and LCDR3 comprising the amino acid sequences of SEQ ID NOs: 228, 230, and 232, respectively.

11. The antibody or antigen-binding fragment thereof of claim 10, wherein the HCVR comprises the amino acid sequence of SEQ ID NO: 218 and the LCVR comprises the amino acid sequence of SEQ ID NO: 226.

12. The ADC of any one of claims 1-9 or the antibody or antigen-binding fragment thereof of claim 10 or 11 that is internalized by human STEAP2-expressing cells.

13. The ADC or the antibody or antigen-binding fragment thereof of any one of claims 1-12, wherein the antibody or antigen-binding fragment thereof is fully human.

14. The antibody or antigen-binding fragment thereof of any one of claims 10-13 that is bispecific.

15. A nucleic acid molecule comprising a nucleotide sequence encoding an antibody or antigen-binding fragment thereof of claim 10 or 11, or a pair of nucleic acid molecules comprising nucleotide sequences, respectively, encoding the HCVR of the antibody or antigen-binding fragment thereof, and the LCVR of the antibody or antigen-binding fragment thereof of claim 10 or 11.

16. An expression vector comprising the nucleic acid molecule of claim 15, or a pair of expression vectors comprising, respectively, the pair of nucleic acid molecules of claim 15.

17. An isolated host cell comprising the antibody or antigen-binding fragment thereof of claim 10 or 11, the nucleic acid molecule or pair of nucleic acid molecules of claim 15, or the expression vector or pair of expression vectors of claim 16.

18. A method of producing an anti-STEAP2 antibody or antigen-binding fragment

thereof, comprising culturing the host cell of claim 17 under conditions permitting production of the antibody or antigen-binding fragment, and recovering the antibody or antigen-binding fragment so produced.

19. The method of claim 18, wherein the host cell is a Chinese hamster ovary cell.

20. A pharmaceutical composition comprising the ADC or the antibody or antigen-binding fragment thereof of any one of claims 1-14, and a pharmaceutically acceptable carrier or diluent.

21. A method of treating a STEAP2-expressing cancer, the method comprising administering the ADC or the antibody or antigen-binding fragment thereof of any one of claims 1-14, or the pharmaceutical composition of claim 20.

22. Use of the ADC or the antibody or antigen-binding fragment thereof of any one of claims 1-14 or the pharmaceutical composition of claim 20 in the manufacture of a medicament for treating a STEAP2-expressing cancer.

23. The method of claim 21 or use of claim 22, wherein the STEAP2-expressing cancer is selected from the group consisting of prostate cancer, bladder cancer, cervical cancer, lung cancer, colon cancer, kidney cancer, breast cancer, pancreatic cancer, stomach cancer, uterine cancer, and ovarian cancer.

24. The method or use of claim 23, wherein the cancer is prostate cancer.

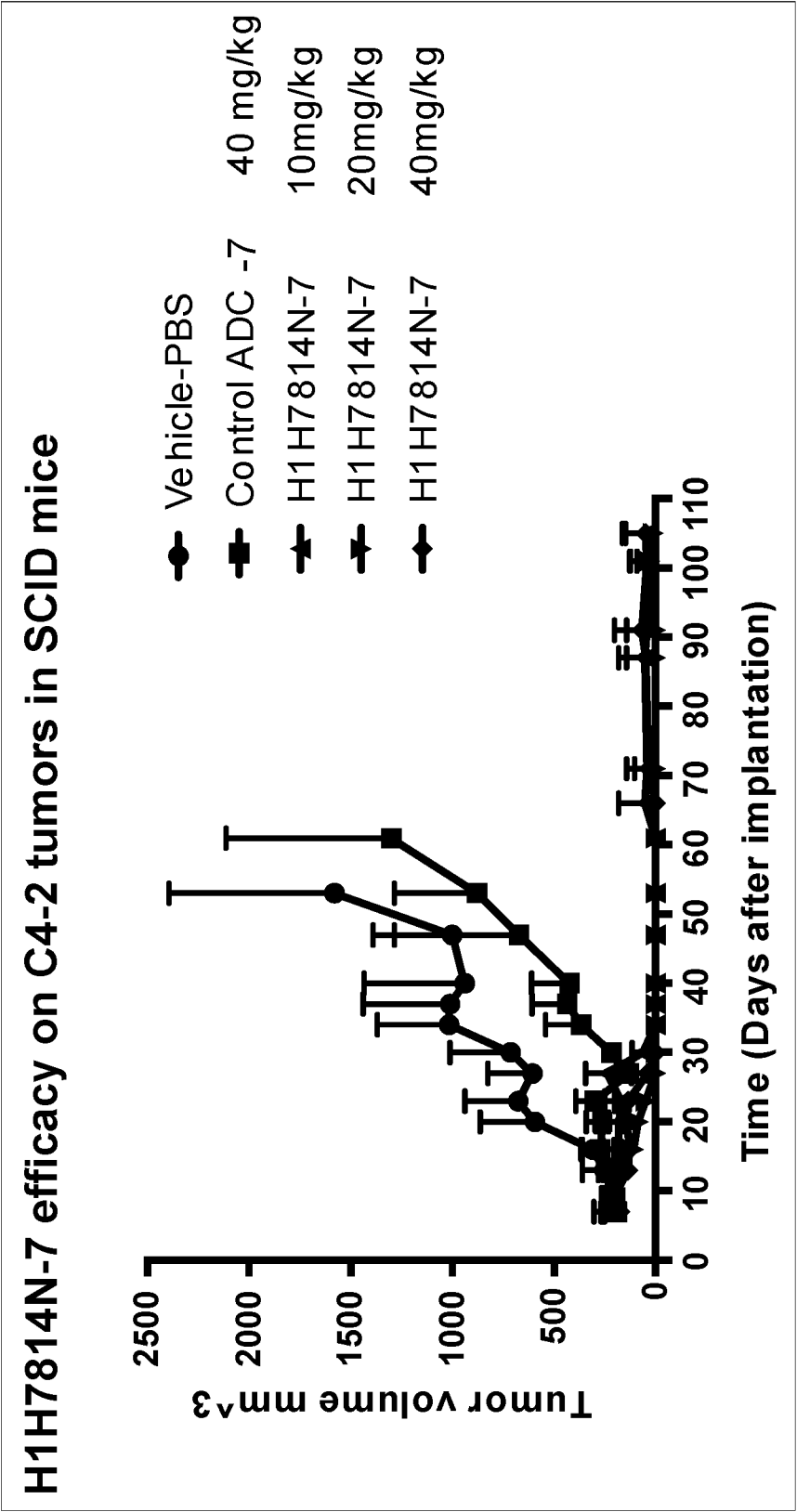


FIG. 1

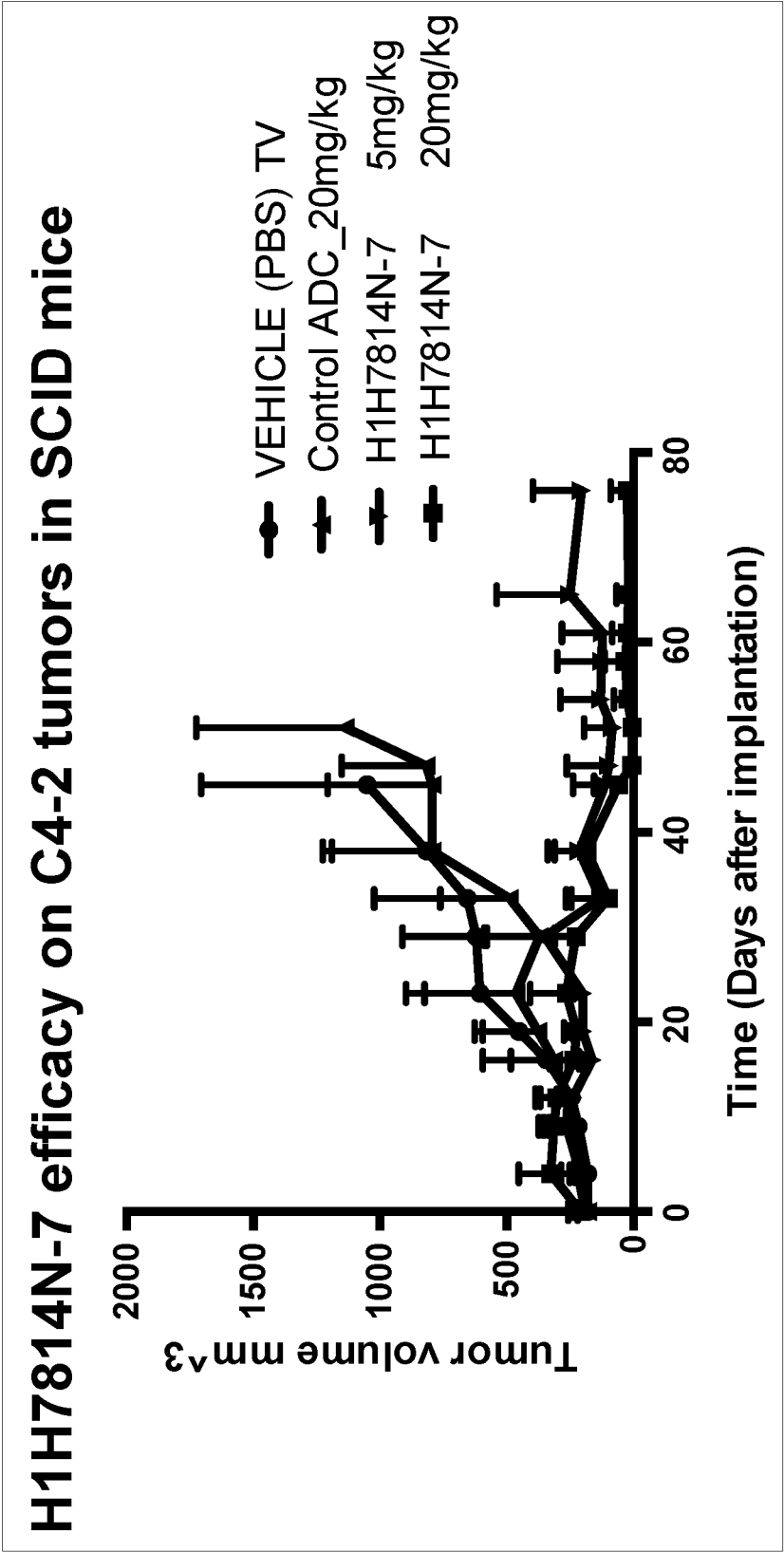


FIG. 2

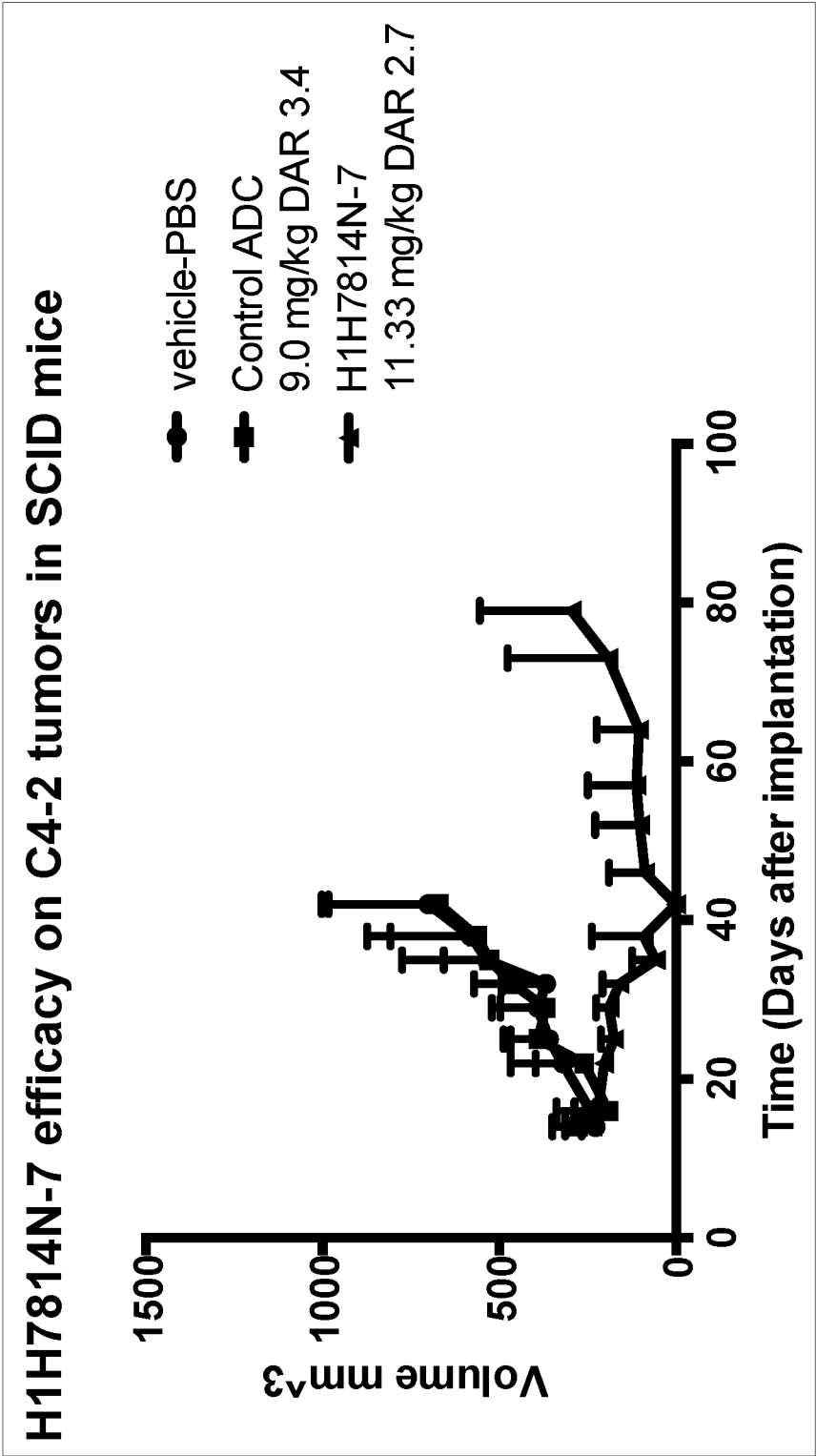


FIG. 3

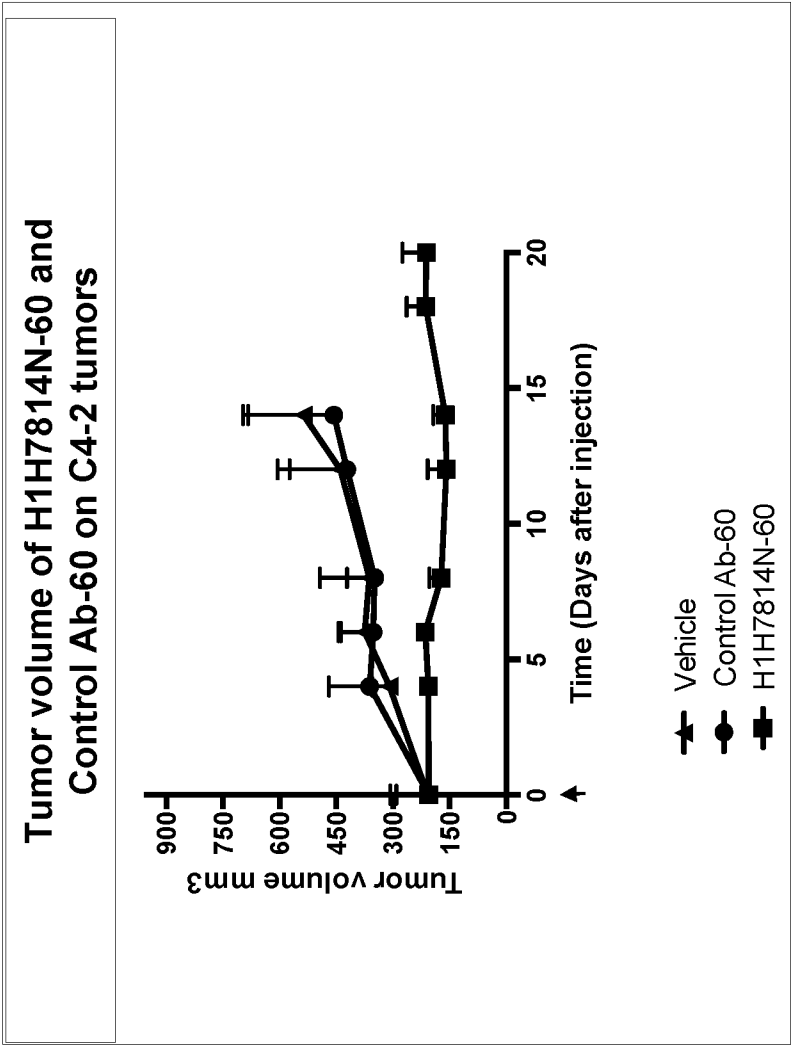


FIG. 4

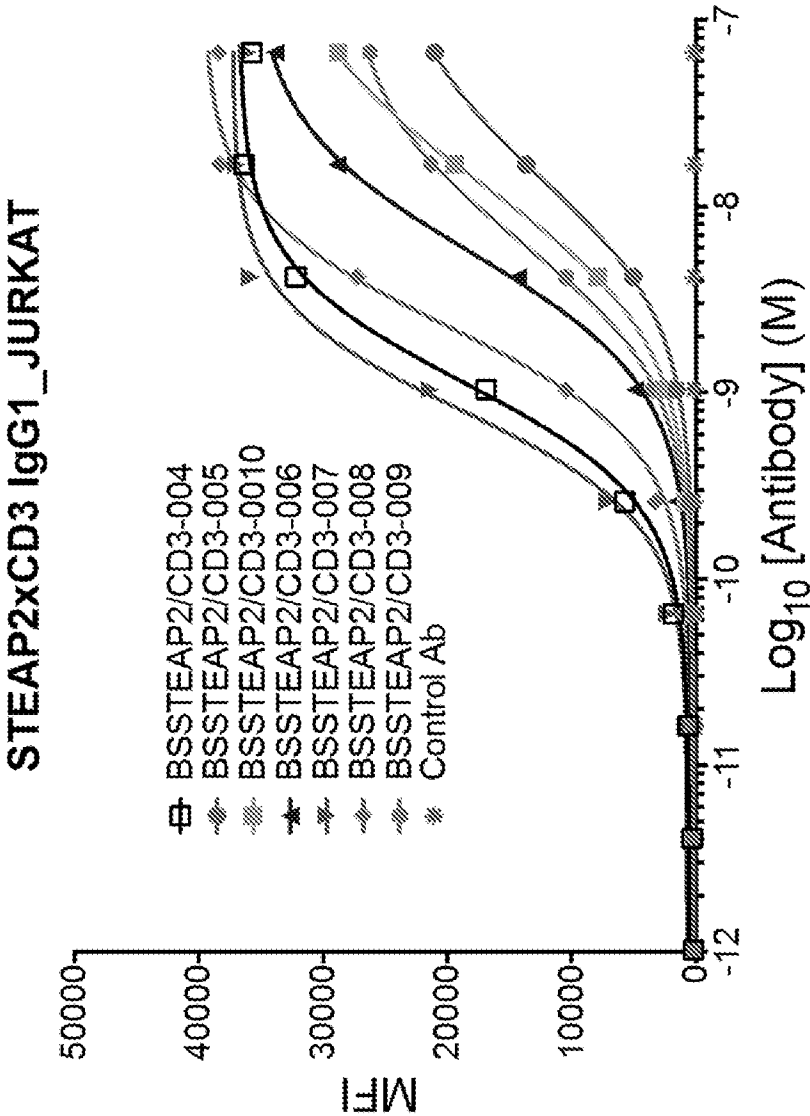


FIG. 5

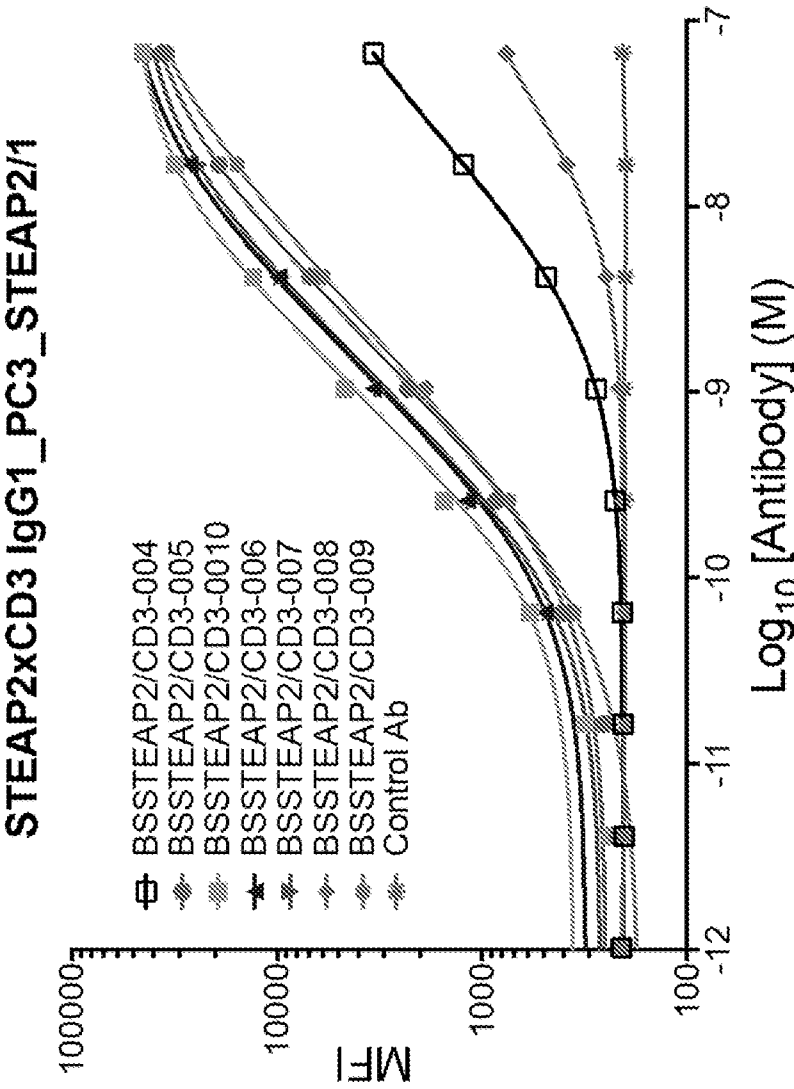


FIG. 6

STEAP2xCD3 - Cynomolgus T cells

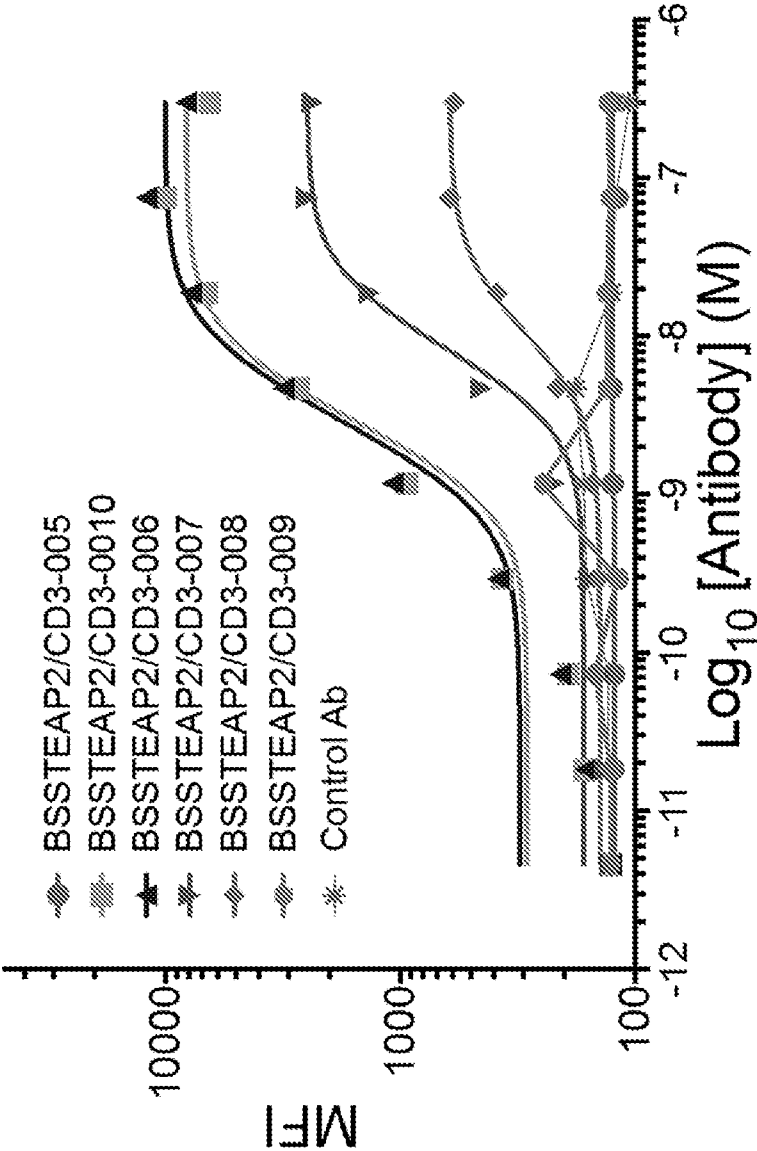


FIG. 7

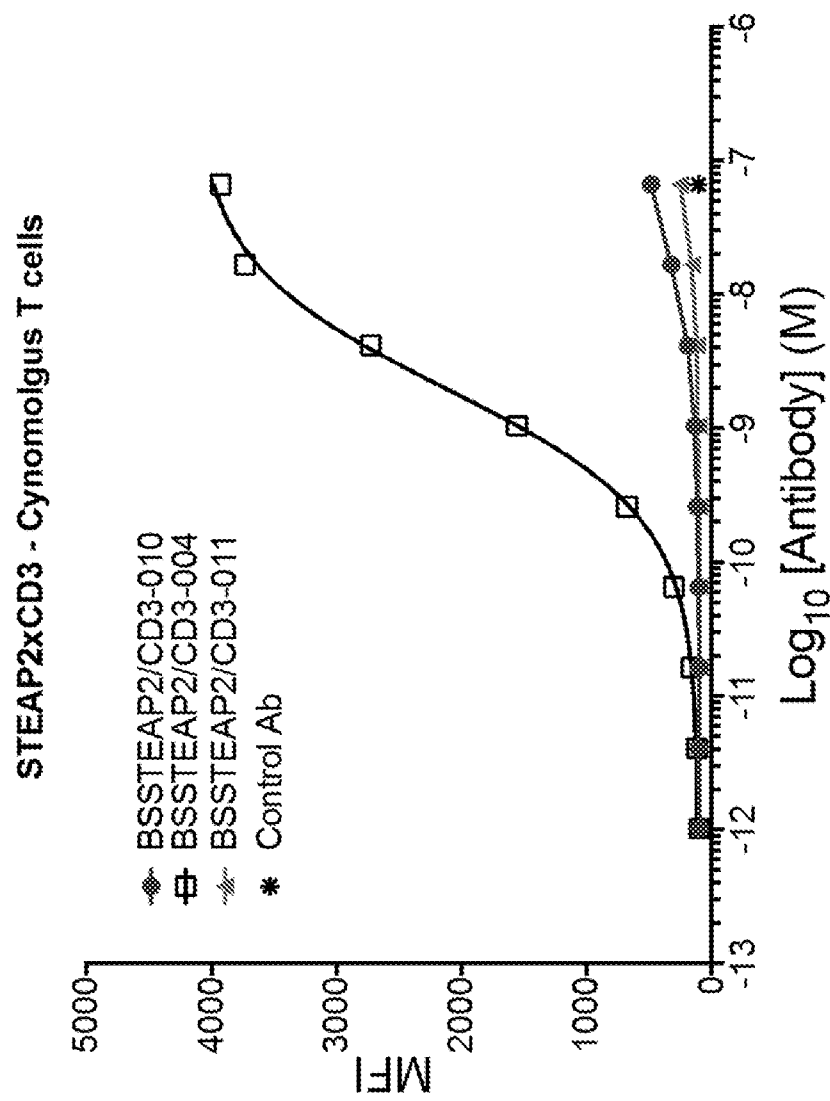


FIG. 8

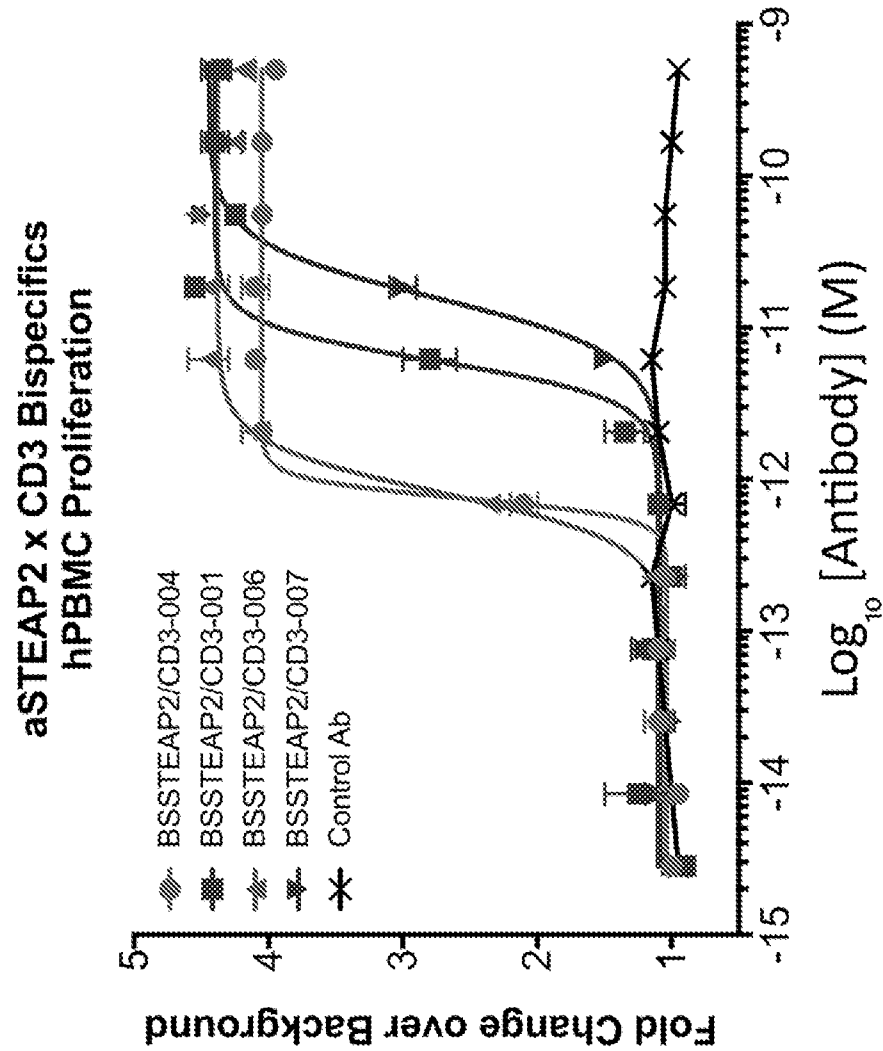


FIG. 9

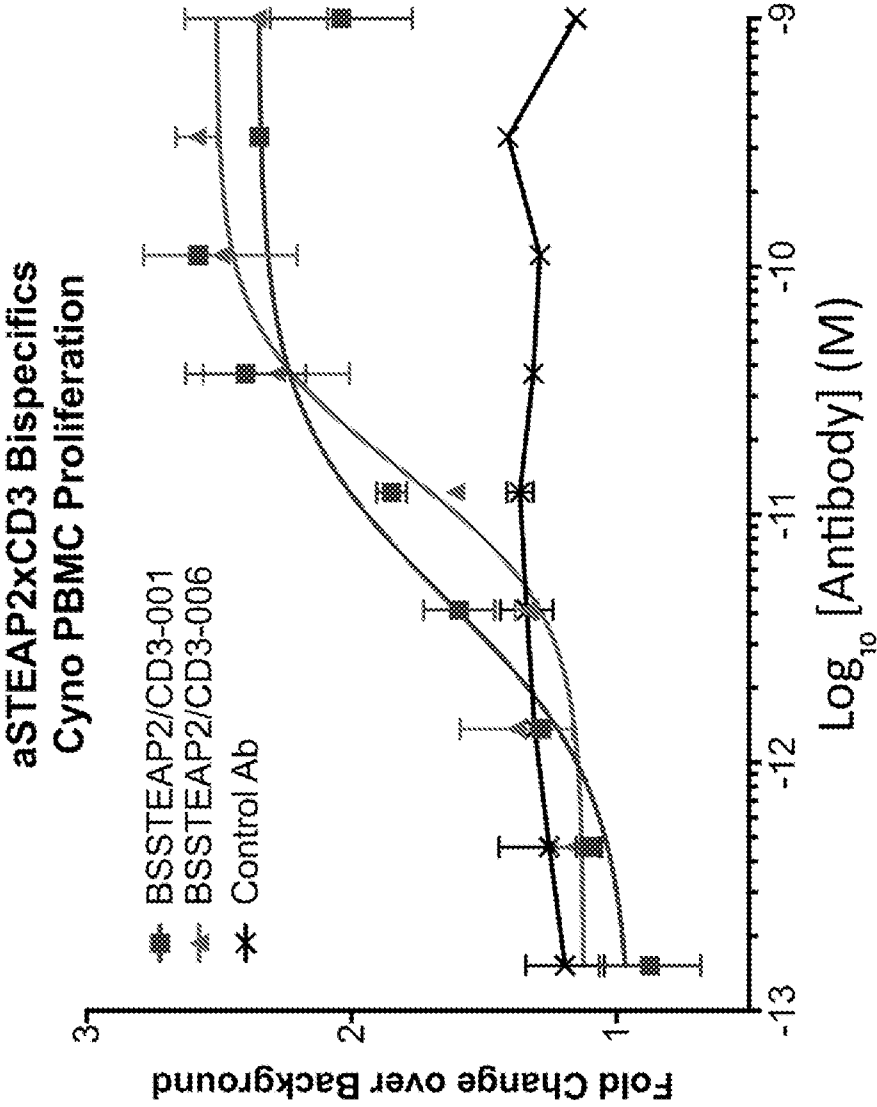


FIG. 10

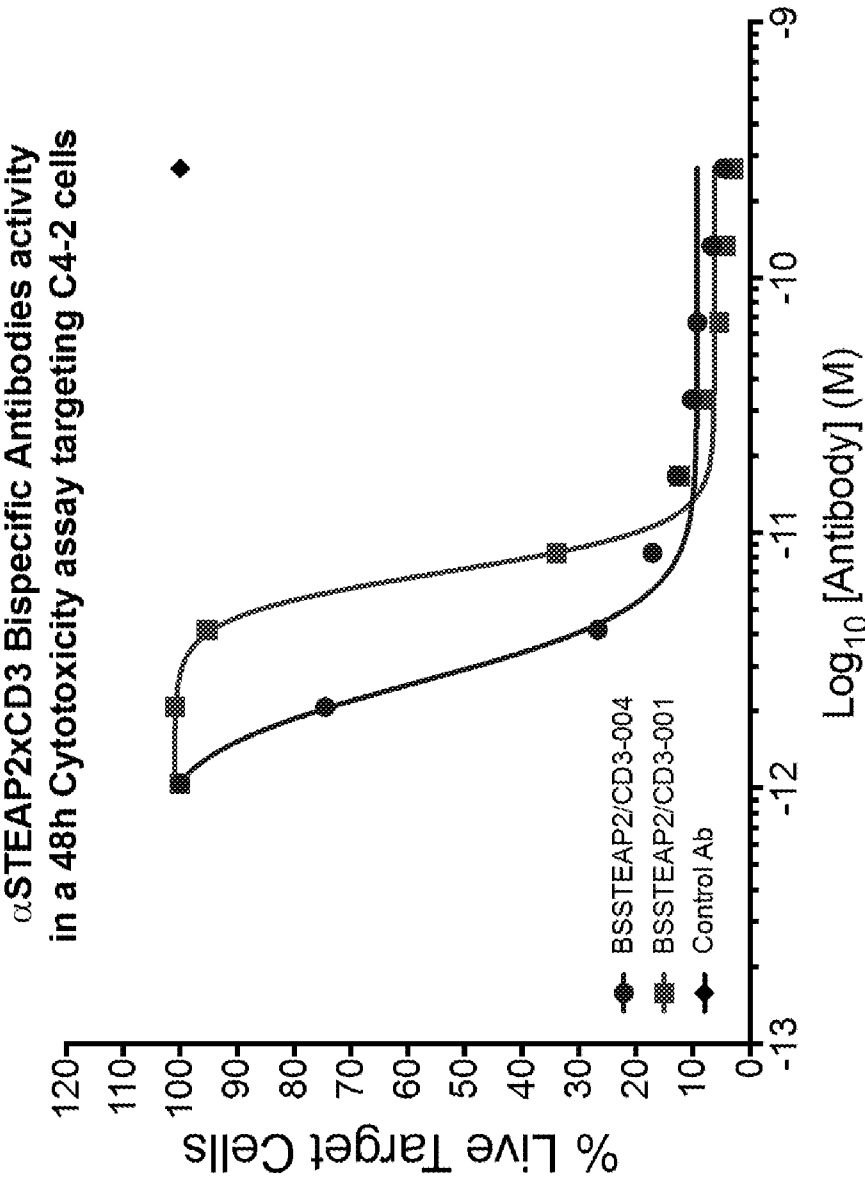


FIG. 11

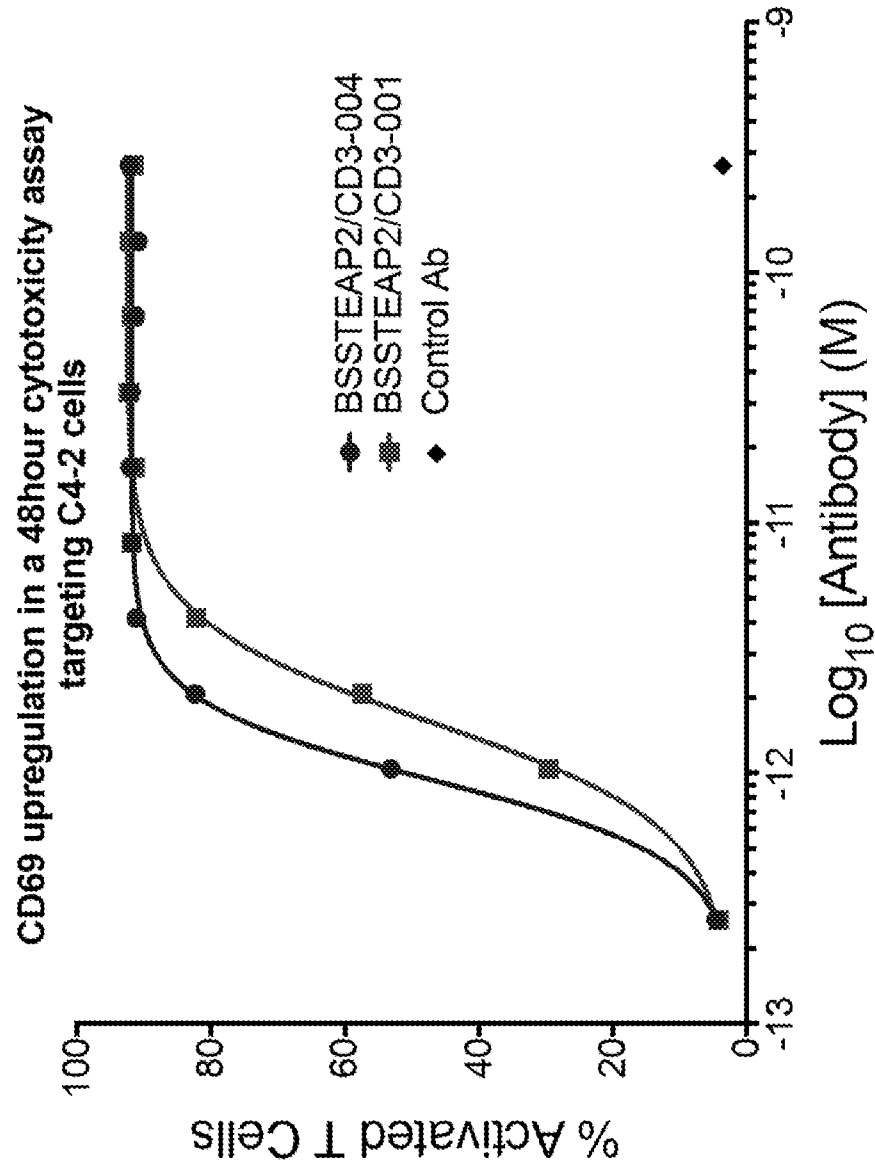


FIG. 12

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<151> 2016-09-23

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Gly Tyr Thr Phe Thr Gly Tyr Asp
 1 5

<210> 21
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<220>
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<400> 21
 atcaacccta acagtgggtgg caca 24

<210> 22
 <211> 8
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<400> 22

Ile Asn Pro Asn Ser Gly Gly Thr
1 5

<210> 23

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 23

gcgagaattg ggatggtagt atcaggtgct aattactact actactacgg tatggacgtc 60

<210> 24

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 24

Ala Arg Ile Gly Met Val Val Ser Gly Ala Asn Tyr Tyr Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 25

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 25

gccatccaga tgaccagtc tccatcctcc ctgtctgcat atgtaggaga cagagtcac 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120

10296W001-Sequence.txt

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca      180
aggttcagcg gcagtagatc tggcacagtt ttcactctca ccatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtctgcaa gattacaatt acccgtggac gttcggccaa      300
gggaccaagg tggaatcaa a                                                  321

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<210> 26
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 26

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Tyr Val Gly
 1 5 10 15

Asp Arg Val Ile Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Arg Ser Gly Thr Val Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 27
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 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 27

cagggcatta gaaatgat

18

<210> 28

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 28

Gln Gly Ile Arg Asn Asp

1 5

<210> 29

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 29

gctgcatcc

9

<210> 30

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 30

Ala Ala Ser

1

<210> 31

<211> 27

<212> DNA

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<400> 31

ctgcaagatt acaattaccc gtggacg

27

<210> 32

<211> 9

<212> PRT

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<220>

<223> Synthetic

<400> 32

Leu Gln Asp Tyr Asn Tyr Pro Trp Thr

1 5

<210> 33

<211> 360

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<213> Artificial Sequence

<220>

<223> Synthetic

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tcctgtgcag cctctggatt caccttcagt acctatgcta tgactgggt ccgccaggct 120

ccagggaagg gactgcaaca tgtttcaact attagtacta atgggggttaa cacatattat 180

gcagactctg tgaagggcag attcaccatc tccagagaca attccaagag cacgctgtat 240

cttcaaatgg gcagcctgag agctgaggac atggctgtat attactgtgc gagagataaa 300

gatttttggg gtgggttattt tgactactgg ggccaggga ccctgggtcac cgtctcctca 360

<210> 34

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

10296W001-Sequence.txt

<400> 34

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

Ser Thr Ile Ser Thr Asn Gly Val Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 35

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35

ggattcacct tcagtaccta tgct

24

<210> 36

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 36

Gly Phe Thr Phe Ser Thr Tyr Ala
1 5

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 37

attagtacta atgggggttaa caca

24

<210> 38

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 38

Ile Ser Thr Asn Gly Val Asn Thr
1 5

<210> 39

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 39

gcgagagata aagatTTTTg gAgTggttat tttgactac

39

<210> 40

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 40

Ala Arg Asp Lys Asp Phe Trp Ser Gly Tyr Phe Asp Tyr
 1 5 10

<210> 41

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 41

gaaattgtga tgacgcagtc tccaggcacc ctgtctgtgt ctccagggga aagagccacc 60
 ctctcctgta gggccagtca gagggttagt agcaacttag cctggtacca ccagaaacct 120
 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tttcccagcc 180
 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtcg 240
 gaagattttg cagcttatta ctgtcagcag tataataatt ggcccatcac cttcggccaa 300
 gggacacgac tggagattaa a 321

<210> 42

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 42

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30

Leu Ala Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

10296W001-Sequence.txt

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Phe Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
cagagtgtta gtagcaac

18

<210> 44
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 44

Gln Ser Val Ser Ser Asn
1 5

<210> 45
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 45
ggtgcatcc

9

<210> 46
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 46

Gly Ala Ser
 1

<210> 47
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 47
 cagcagtata ataattggcc catcacc

27

<210> 48
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 48

Gln Gln Tyr Asn Asn Trp Pro Ile Thr
 1 5

<210> 49
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 49
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60

10296W001-Sequence.txt

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acctgcactg tctctgggta ctccatcaac agtgggtggc atttctggag ctggatccgc      120
cagcaccag  ggaagggcct ggagtggatt ggggacatct attacagtgg gaacacctac      180
tccattccgt ccctcaagcg tcgaatttcc atgtcagtag acacgtctaa gaaccacttc      240
tccctgaaac tgatctctgt gacggccgcg gacacggcca tttattactg tgcgagaaat      300
agtgggggct atcttgatgc ttttgatatc tggggccaag ggacaatggc caccgtctct      360
tca                                                                    363

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<210> 50
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 50

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Asn Ser Gly
 20 25 30

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

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

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

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

Cys Ala Arg Asn Ser Gly Gly Tyr Leu Asp Ala Phe Asp Ile Trp Gly
 100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 51
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 51
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30

<210> 52
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 52

Gly Tyr Ser Ile Asn Ser Gly Gly His Phe
 1 5 10

<210> 53
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 53
 atctattaca gtgggaacac c

21

<210> 54
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 54

10296W001-Sequence.txt

Ile Tyr Tyr Ser Gly Asn Thr
1 5

<210> 55
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55
gcgagaaata gtgggggcta tcttgatgct tttgatatc 39

<210> 56
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56

Ala Arg Asn Ser Gly Gly Tyr Leu Asp Ala Phe Asp Ile
1 5 10

<210> 57
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgctca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

10296W001-Sequence.txt

<210> 58
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 58

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
 85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 59
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 59

cagagcatta gcagctat

18

<210> 60
 <211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60

Gln Ser Ile Ser Ser Tyr
1 5

<210> 61
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61
gctgcatcc

9

<210> 62
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62

Ala Ala Ser
1

<210> 63
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63
caacagagtt acagtacccc tccgatcacc

30

<210> 64
<211> 10

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 64

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
 1 5 10

<210> 65
 <211> 387
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 65
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 tcctgtgcaa cctctggatt caccttcagt aactacgact tccactgggt ccgccaaatt 120
 agaggacaag gtctggagtg ggtctctact attgacactg ctggtgacac atacttttca 180
 ggctccgtga agggccgctt caccatctcc agagacactg ccaaaacctc cttgtatctt 240
 caaatgaaca gcctgagagc cggggacacg gctgtgtatt actgtgcaag agcccctcgt 300
 tatgatagta ctggtaacta ctacaattac tattcctatt tcggcctgga cgtctggggc 360
 caagggacca cggtcaccgt ctcctca 387

<210> 66
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 66

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

Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

10296W001-Sequence.txt

Asp Phe His Trp Val Arg Gln Ile Arg Gly Gln Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asp Thr Ala Gly Asp Thr Tyr Phe Ser Gly Ser Val Lys
 50 55 60

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

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

Arg Ala Pro Arg Tyr Asp Ser Thr Gly Asn Tyr Tyr Asn Tyr Tyr Ser
 100 105 110

Tyr Phe Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser

<210> 67
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 67
 ggattcacct tcagtaacta cgac

24

<210> 68
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 68

Gly Phe Thr Phe Ser Asn Tyr Asp
 1 5

<210> 69
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 69
 attgacactg ctggtgacac a 21

<210> 70
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 70

Ile Asp Thr Ala Gly Asp Thr
 1 5

<210> 71
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 71
 gcaagagccc ctcgttatga tagtactggt aactactaca attactattc ctatttcggc 60

ctggacgtc 69

<210> 72
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

10296W001-Sequence.txt

<400> 72

Ala Arg Ala Pro Arg Tyr Asp Ser Thr Gly Asn Tyr Tyr Asn Tyr Tyr
1 5 10 15

Ser Tyr Phe Gly Leu Asp Val
20

<210> 73

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 73

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tcctgcaagg tttccggata caccctcact gaattatcca tgcactgggt gcgacaggct 120
cctggaaaag ggcttgagtg gatgggaagt tttgatcctg aagatgatga aacaatctac 180
gcacagaagt tccagggcag agtcaccatg accgaggaca catctacaga cacagcctac 240
atggacctga gcagcctaag atctgaggac acggccgtgt attactgttc aatagaggaa 300
gttcgttggc ggggatcgga ctactactac gttatggacg tctggggcca agggaccacg 360
gtcaccgtct cctca 375

<210> 74

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 74

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

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

10296W001-Sequence.txt

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

Gly Ser Phe Asp Pro Glu Asp Asp Glu Thr Ile Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr
 65 70 75 80

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

Ser Ile Glu Glu Val Arg Trp Arg Gly Ser Asp Tyr Tyr Tyr Val Met
 100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 75
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 75
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24

<210> 76
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 76

Gly Tyr Thr Leu Thr Glu Leu Ser
 1 5

<210> 77
 <211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 77

tttgatcctg aagatgatga aaca

24

<210> 78

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 78

Phe Asp Pro Glu Asp Asp Glu Thr

1 5

<210> 79

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 79

tcaatagagg aagttcggtg gcggggatcg gactactact acgttatgga cgtc

54

<210> 80

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 80

Ser Ile Glu Glu Val Arg Trp Arg Gly Ser Asp Tyr Tyr Tyr Val Met

1 5 10 15

Asp Val

10296W001-Sequence.txt

<210> 81
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 81
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 tcctgcaggg cttctggagg caccttcagc agatttgcta tcggctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttggtac agcaagctac 180
 gcacagaagt tccagggcag agtcacgatt accacggacg aatccacgag cacagcctac 240
 atggagttgc gaagcctgag atctgaggac acggccgtat attactgtac gagagaaggt 300
 ataactggtc gaggctacta ctactacggt atggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 82
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 82

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

Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Thr Phe Ser Arg Phe
 20 25 30

Ala Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Ser Tyr Ala Gln Lys Phe
 50 55 60

10296W001-Sequence.txt

Gln Gly Arg Val Thr Ile Thr Thr Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Thr Arg Glu Gly Ile Thr Gly Arg Gly Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 83
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83
ggaggcacct tcagcagatt tgct

24

<210> 84
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84

Gly Gly Thr Phe Ser Arg Phe Ala
1 5

<210> 85
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85
atcatcccta tctttgtac agca

24

<210> 86
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 86

Ile Ile Pro Ile Phe Gly Thr Ala
 1 5

<210> 87
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 87

acgagagaag gtataactgg tcgaggctac tactactacg gstatggacgt c 51

<210> 88
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 88

Thr Arg Glu Gly Ile Thr Gly Arg Gly Tyr Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 89
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>

10296W001-Sequence.txt

<223> Synthetic

<400> 89

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ccaggggaagg gactggagtg gattgggaat atctttttaca gtgggagcac caactacaac      180
ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaatca gttttccctg      240
aagttgagct ctgtgaccgc tgcggacacg gccgtgtatt actgtgagag agagagactg      300
gggcgttacg atgcttttga taattggggc caagggacaa tggtcaccgt ctcttca      357
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<210> 90

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 90

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

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ile Tyr
          20           25           30
```

```
Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
          35           40           45
```

```
Gly Asn Ile Phe Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
          50           55           60
```

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

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

```
Arg Glu Arg Leu Gly Arg Tyr Asp Ala Phe Asp Asn Trp Gly Gln Gly
          100          105          110
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Thr Met Val Thr Val Ser Ser
115

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 91
ggtggctcca tcagtattta ctac

24

<210> 92
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92

Gly Gly Ser Ile Ser Ile Tyr Tyr
1 5

<210> 93
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93
atcttttaca gtgggagcac c

21

<210> 94
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 94

Ile Phe Tyr Ser Gly Ser Thr
 1 5

<210> 95

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 95

gcgagagaga gactggggcg ttacgatgct tttgataat

39

<210> 96

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 96

Ala Arg Glu Arg Leu Gly Arg Tyr Asp Ala Phe Asp Asn
 1 5 10

<210> 97

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 97

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctagatt cacctttagt agctatgcca tgagttgggt ccgccaggct 120

ccaggggaagg ggctggagtg ggtctcactt attagtggta gtggtggtag gacatggtag 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgag agccgaggac acggccgtct attactgtgc gaaagaaggg 300

gggatttttg gagtggttac cttctttgac tactggggcc agggaaccct ggtcaccgtc 360

tcctca

<210> 98
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 98

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Arg Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Leu Ile Ser Gly Ser Gly Gly Arg Thr Trp Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Glu Gly Gly Ile Phe Gly Val Val Thr Phe Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 99

agattcacct ttagtagcta tgcc

24

<210> 100

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 100

Arg Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 101

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 101

attagtggtgta gtggtggtgtag gaca

24

<210> 102

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 102

Ile Ser Gly Ser Gly Gly Arg Thr
1 5

<210> 103

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 103

gcgaaagaag gggggatttt tggagtgggtt accttctttg actac

45

<210> 104

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 104

Ala	Lys	Glu	Gly	Gly	Ile	Phe	Gly	Val	Val	Thr	Phe	Phe	Asp	Tyr
1				5				10					15	

<210> 105

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 105

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tcctgtgcag tctctggatt caccttttagc agctatgcca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtgattt cacataccac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagtc cacgctgtat 240

ctgcaattga acagcctgag agccgaggac acggccgtat attactgtgc gaaaaagggc 300

ttacgatatt ttgactggta cgactactgg ggccaggga ccctgggtcac cgtctcctca 360

<210> 106

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 106

10296W001-Sequence.txt

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Val Ile Ser Gly Ser Gly Asp Phe Thr Tyr His Ala Asp Ser Val
50 55 60

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

Leu Gln Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Lys Gly Leu Arg Tyr Phe Asp Trp Tyr Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 107
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107
ggattcacct ttagcagcta tgcc

24

<210> 108
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 109

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 109

attagtggta gtggtgattt caca

24

<210> 110

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 110

Ile Ser Gly Ser Gly Asp Phe Thr
1 5

<210> 111

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 111

gcgaaaaagg gcttacgata ttttgactgg tacgactac

39

<210> 112

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 112

Ala Lys Lys Gly Leu Arg Tyr Phe Asp Trp Tyr Asp Tyr
 1 5 10

<210> 113

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 113

gaaatagttt tgacacagag tcccggcaca ctgtcactct ctcccgggga aagagccacc 60
 ttgtcatgta gagcaagtca gtcagtctct agctcttata tcgcctggta ccagcagaag 120
 ccgggacagg cccctagact gctgatctac ggggcaagtt ccagggccac cggaatcccc 180
 gaccggttca gtggaagcgg aagcgggaacc gattttactt tgacgatttc tagactggag 240
 ccagaggatt tcgccgttta ctattgtcaa cagtacggaa gcagcccgtg gacgtttggc 300
 cagggcacga aggtagaaat caag 324

<210> 114

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 114

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

10296W001-Sequence.txt

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 115
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 115
agagcaagtc agtcagtctc tagctcttat ctcgcc

36

<210> 116
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 117
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117
ggggcaagtt ccagggccac c

21

<210> 118
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 118

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 119
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 119
 caacagtacg gaagcagccc gtggacg

27

<210> 120
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 120

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1 5

<210> 121
 <211> 375
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 121
 caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60

acctgcactg tctctggtgg ctccatcagt agttactact ggacctggat ccggcagacc 120

10296W001-Sequence.txt

ccaggaagg gactggagt gattgggtat atttattaca gtgggagcac caactacaac 180
 ccctccctca agagtcgagt caccatatca gtagacacgt ccaagaacca gttctccctg 240
 aagctgaggt ctgtggccgc tgcggacacg gccgtttatt actgtgagag agggacttac 300
 taccgtgata gtagtggaac atatttcaac tggttcgacc cctggggcca gggaaccctg 360
 gtcaccgtct cctca 375

<210> 122
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 122

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30

Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

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

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

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

Arg Gly Thr Tyr Tyr Arg Asp Ser Ser Gly Lys Tyr Phe Asn Trp Phe
 100 105 110

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 123
 ggtggctcca tcagtagtta ctac

24

<210> 124
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 124

Gly Gly Ser Ile Ser Ser Tyr Tyr
 1 5

<210> 125
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 125
 atttattaca gtgggagcac c

21

<210> 126
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 126

Ile Tyr Tyr Ser Gly Ser Thr
 1 5

<210> 127
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 127
gcgagaggga cttactaccg tgatagtagt ggaaaatatt tcaactgggt cgacccc 57

<210> 128
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 128

Ala	Arg	Gly	Thr	Tyr	Tyr	Arg	Asp	Ser	Ser	Gly	Lys	Tyr	Phe	Asn	Trp
1				5					10					15	

Phe Asp Pro

<210> 129
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 129
gacatccaga tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgct gggcgagtca ggatattagc aactgggttag cctgggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatcc 180
aggttcagtg gtagtggatc tgggacagat ttactctct ccatcagcag cctgcagtct 240
gaagattttg caacttacta ttgtcaacag gctaaagggt tccctcggac gttcggccaa 300
gggaccaagg tggaatcaa a 321

10296W001-Sequence.txt

<210> 130
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 130

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Lys Gly Phe Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 131
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 131

caggatatta gcaactgg

18

<210> 132
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 132

Gln Asp Ile Ser Asn Trp
 1 5

<210> 133
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 133
 gctgcatcc

9

<210> 134
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 134

Ala Ala Ser
 1

<210> 135
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 135
 caacaggcta aaggtttccc tcggacg

27

10296W001-Sequence.txt

<210> 136
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 136

Gln Gln Ala Lys Gly Phe Pro Arg Thr
 1 5

<210> 137
 <211> 375
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 137

caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc	60
tcctgtgcag cctctggatt caccttcagt agctttggca tgcactgggt ccgccaggct	120
ccaggcaagg ggctggagtg ggtgtcactt atatcatatg atggtgataa taaatactat	180
gtagactccg tgaagggccg attcaccatc tccagagaca attccgagaa cacgctgtat	240
ctgcaaatga acaacctgcg acctgaggac acggctttct attactgtgc gaaagatgga	300
tttactagtg gctggtacgg ctctacacc ggtttggacg tctggggcca agggaccacg	360
gtcaccgtct cctca	375

<210> 138
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 138

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

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

Ser Leu Ile Ser Tyr Asp Gly Asp Asn Lys Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Arg Pro Glu Asp Thr Ala Phe Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Phe Thr Ser Gly Trp Tyr Gly Ser Tyr Thr Gly Leu
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 139
ggattcacct tcagtagctt tggc

24

<210> 140
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 140

Gly Phe Thr Phe Ser Ser Phe Gly
1 5

10296W001-Sequence.txt

<210> 141
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 141
 atatcatatg atggtgataa taaa

24

<210> 142
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 142

Ile Ser Tyr Asp Gly Asp Asn Lys
 1 5

<210> 143
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 143
 gcgaaagatg gatttactag tggctggtac ggctcctaca ccggtttgga cgtc

54

<210> 144
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 144

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

Asp Val

<210> 145
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 145
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gggcattaga aatgatttag gctggatatca gcagaatcca 120
 gggagagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240
 gaagattttg caacttatta ctgtcttcag tataatagtt accctcggac gttcggccaa 300
 gggaccaagg tggaaatcaa a 321

<210> 146
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 146

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30

Leu Gly Trp Tyr Gln Gln Asn Pro Gly Arg Ala Pro Lys Arg Leu Ile
 35 40 45

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

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asn Ser Tyr Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 147
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 147
cagggcatta gaaatgat

18

<210> 148
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 148

Gln Gly Ile Arg Asn Asp
1 5

<210> 149
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 149
gctgcatcc

9

<210> 150
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 150

Ala Ala Ser
 1

<210> 151
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 151
 cttcagtata atagttaccc tcggacg

27

<210> 152
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 152

Leu Gln Tyr Asn Ser Tyr Pro Arg Thr
 1 5

<210> 153
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 153
 gaggtgcagc tggtggagtc tgggggaggc tgggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacattcagt aacttcgaca tgcactgggt ccgccaagct 120

10296W001-Sequence.txt

gcaggaaaag gtctggagtg ggtctcaatt attgatactg gtggtgacac atactatccg 180
 ggctccgtga agggccgatt caccatatcc agagaagatg ccaagaactc cttctatctt 240
 caaatgaaca gcctgagagc cggggacacg gctatatatt actgtgtaag aggggggtat 300
 accagtggct gggactactt tgactactgg ggccaggga ccctgggtcac cgtctcctca 360

<210> 154
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 154

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Phe
 20 25 30

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

Ser Ile Ile Asp Thr Gly Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Glu Asp Ala Lys Asn Ser Phe Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Ile Tyr Tyr Cys Val
 85 90 95

Arg Gly Gly Tyr Thr Ser Gly Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 155
 ggattcacat tcagtaactt cgac

24

<210> 156
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 156

Gly Phe Thr Phe Ser Asn Phe Asp
 1 5

<210> 157
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 157
 attgatactg gtggtgacac a

21

<210> 158
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 158

Ile Asp Thr Gly Gly Asp Thr
 1 5

10296W001-Sequence.txt

<210> 159
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 159
 gtaagagggg ggtataccag tggctgggac tactttgact ac 42

<210> 160
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 160
 Val Arg Gly Gly Tyr Thr Ser Gly Trp Asp Tyr Phe Asp Tyr
 1 5 10

<210> 161
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 161
 gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtgggaga cagagtcacc 60
 atcacttgct gggccagtca gggcattagc agttatttag cctggtatca gcaaaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca caatccgccg cctgcagcct 240
 gaagattttg caagttatta ctgtcaacag cttaataatt acccgtaac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> 162
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 162

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

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Arg Arg Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Leu Asn Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 163

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 163

cagggcatta gcagttat

18

<210> 164

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 164

Gln Gly Ile Ser Ser Tyr
1 5

<210> 165

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 165

gctgcatcc

9

<210> 166

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 166

Ala Ala Ser
1

<210> 167

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 167

caacagctta ataattaccc gtacact

27

<210> 168

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 168

Gln Gln Leu Asn Asn Tyr Pro Tyr Thr
 1 5

<210> 169

<211> 381

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 169

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag cgtctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatggg 300
 gtctacagta actacggacg atactactac tactacggta tggacgtctg gggccaaggg 360
 accacggtca ccgtctcctc a 381

<210> 170

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 170

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

10296W001-Sequence.txt

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Asp Gly Val Tyr Ser Asn Tyr Gly Arg Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 171
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 171
ggattcacct tcagtagcta tggc

24

<210> 172
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 172

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 173
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 173

atatggtatg atggaagtaa taaa

24

<210> 174

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 174

Ile Trp Tyr Asp Gly Ser Asn Lys

1 5

<210> 175

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 175

gcgagagatg gggctctacag taactacgga cgatactact actactacgg tatggacgtc

60

<210> 176

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 176

Ala Arg Asp Gly Val Tyr Ser Asn Tyr Gly Arg Tyr Tyr Tyr Tyr Tyr

1 5 10 15

Gly Met Asp Val

20

10296W001-Sequence.txt

<210> 177
 <211> 321
 <212> DNA
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<220>
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<400> 177
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 atcacttgcc gggcaagtca gagcatatcgt agcttttttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagttcct aattttctgct gcatccagtt tgcaaagagg ggtcccatct 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaggattctt caacttacta ctgtcaacag agttacagta tcccggtcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 178
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 178

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Phe
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
 35 40 45

Ser Ala Ala Ser Ser Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

10296W001-Sequence.txt

Glu Asp Ser Ser Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Val
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 179
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 179
cagagcatac gtagcttt 18

<210> 180
<211> 6
<212> PRT
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<220>
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<400> 180

Gln Ser Ile Arg Ser Phe
1 5

<210> 181
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 181
gctgcatcc 9

<210> 182
<211> 3
<212> PRT
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<220>

<223> Synthetic

<400> 182

Ala Ala Ser
1

<210> 183

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 183

caacagagtt acagtatccc ggtcact

27

<210> 184

<211> 9

<212> PRT

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<220>

<223> Synthetic

<400> 184

Gln Gln Ser Tyr Ser Ile Pro Val Thr
1 5

<210> 185

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 185

caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60

acctgtgcc a tctccgggga cagtgtctct agcaacagtg ctgcttgga ctggatcagg 120

cagtcccat cgagaggcct tgagtggctg ggaaggacat actacaggtc caagtggat 180

aatgattatg tagtatctgt gaaaagtcga ataatcttca acccagacac atccaagaac 240

cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300

agagtgaggc aggattatag aagtggcccg ttgactact ggggccaggg aaccctggtc 360
accgtctcct ca 372

<210> 186
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 186

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

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Val
50 55 60

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

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Val Arg Gln Asp Tyr Arg Ser Gly Pro Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 187
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 187

ggggacagtg tctctagcaa cagtgctgct

30

<210> 188

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 188

Gly	Asp	Ser	Val	Ser	Ser	Asn	Ser	Ala	Ala
1				5					10

<210> 189

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 189

acatactaca ggtccaagtg gtataat

27

<210> 190

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 190

Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn
1				5				

<210> 191

<211> 42

<212> DNA

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> Synthetic

<400> 191

gcaagagtga ggcaggatta tagaagtggc ccgtttgact ac

42

<210> 192

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 192

Ala Arg Val Arg Gln Asp Tyr Arg Ser Gly Pro Phe Asp Tyr

1

5

10

<210> 193

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 193

gaaatagtga tgacgcagtc tccagtcacc ctgtctgtgt ctccagggga aagagccacc

60

ctctcctgtt gggccagtca gagggttagc agcagcttag cctggtacca gcagaaacct

120

ggccaggctc ccagactcct catctatggt gcatccacca gggccactgg tatcccagcc

180

aggttcagtg gcagtgggtc tgggacaggg ttcactctca ccatcagcag cctgcagtct

240

gaagattttg cagtttatta ctgtcagcag tataataact ggccattcac tttcggccct

300

gggaccaaag tggatatcaa a

321

<210> 194

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

10296W001-Sequence.txt

<400> 194

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

Glu Arg Ala Thr Leu Ser Cys Trp Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 195

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 195

cagagtgtta gcagcagc

18

<210> 196

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 196

Gln Ser Val Ser Ser Ser
1 5

<210> 197
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 197
ggtgcatcc

9

<210> 198
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 198

Gly Ala Ser
1

<210> 199
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 199
cagcagtata ataactggcc attcact

27

<210> 200
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 200

10296W001-Sequence.txt

Gln Gln Tyr Asn Asn Trp Pro Phe Thr
1 5

<210> 201
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 201
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tcctgtgcag cctctggatt caccttttagc agctatgcca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtctcagtt attagtggta gtggtggttag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gaaagagcag 300
tatagccggg gctttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 202
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 202

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Val Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

10296W001-Sequence.txt

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

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

Ala Lys Glu Gln Tyr Ser Arg Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 203
ggattcacct ttagcagcta tgcc

24

<210> 204
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 204

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 205
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 205
attagtggta gtggtggtag caca

24

10296W001-Sequence.txt

<210> 206
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 206

Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 207
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 207
gcgaaagagc agtatagccg gggctttgac tac

33

<210> 208
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 208

Ala Lys Glu Gln Tyr Ser Arg Gly Phe Asp Tyr
1 5 10

<210> 209
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 209
gacatccaga tgaccagtc tccttcacc ctgtctgtat ctgtaggaga cagagtcacc

60

10296W001-Sequence.txt

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atcacttgcc gggccagtca gagtattagt agttggttgg cctggatatca gcagaaacca      120
gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct      240
gatgattttg caacttatta ctgccaacag tataatagtt attggacggt cggccaaggg      300
accaaggtgg aaatcaaa                                                    318

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<210> 210
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 210

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Trp Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 211
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 211
cagagtatta gtagttgg

18

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

<220>
<223> Synthetic

<400> 212

Gln Ser Ile Ser Ser Trp
1 5

<210> 213
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 213
aaggcgtct

9

<210> 214
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 214

Lys Ala Ser
1

<210> 215
<211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 215
 caacagtata atagttattg gacg

24

<210> 216
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 216

Gln Gln Tyr Asn Ser Tyr Trp Thr
 1 5

<210> 217
 <211> 345
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 217
 caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgtag cctctggatt caccatcagt agctatggca tgaactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaggtaa taaatactct 180
 gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa tacgctgtat 240
 ctgcaaataga acagcctgag agctgaggac tcggctgttt attactgtgc gagaggaagg 300
 tacttcgatc tctggggccg tggcaccctg gtcactgtct cctca 345

<210> 218
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 218

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

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ile Ser Ser Tyr
 20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Gly Asn Lys Tyr Ser Val Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 219

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 219

ggattcacca tcagtagcta tggc

24

<210> 220

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 220

Gly Phe Thr Ile Ser Ser Tyr Gly
1 5

<210> 221

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 221

atatcatatg atggaggtaa taaa

24

<210> 222

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 222

Ile Ser Tyr Asp Gly Gly Asn Lys
1 5

<210> 223

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 223

gcgagaggaa ggtacttcga tctc

24

<210> 224

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 224

Ala Arg Gly Arg Tyr Phe Asp Leu
 1 5

<210> 225

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 225

gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
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 gggagagccc ctaacctcct gatctctaag gcgtctagtt taaaaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca ccgtcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacag tattatagtt attcttacac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> 226

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 226

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Asn Leu Leu Ile
 35 40 45

10296W001-Sequence.txt

Ser Lys Ala Ser Ser Leu Lys Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Val Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Ser Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 227
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 227
cagagtatta gtagctgg

18

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 228

Gln Ser Ile Ser Ser Trp
1 5

<210> 229
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 229
aaggcgtct

9

<210> 230
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 230

Lys Ala Ser
1

<210> 231
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 231
caacagtatt atagttattc ttacact

27

<210> 232
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 232

Gln Gln Tyr Tyr Ser Tyr Ser Tyr Thr
1 5

<210> 233
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
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10296W001-Sequence.txt

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acctgcactg tctctggtgg ctccatcagc agtggtggtt actactggag ctggatccgc      120
cagcaccag ggaagggcct ggagtggatt gggtaacatct attacagtgg gagcacctac      180
tacaaccgt ccctcaagag tcgagtcacc atatcagtag acacgtctaa gaaccagttc      240
tccctgaagc tgaactctgt gactgccgcg gacacggccg tgtattactg tgcgaggagc      300
gacggtgact actacggtat ggacgtctgg ggccaaggga ccacggtcac cgtctcctca      360
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<210> 234
<211> 120
<212> PRT
<213> Artificial Sequence
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<220>
<223> Synthetic
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<400> 234

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
      20              25              30

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

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
      50              55              60

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

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

Cys Ala Arg Asp Asp Gly Asp Tyr Tyr Gly Met Asp Val Trp Gly Gln
      100              105              110
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Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 235
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 235
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30

<210> 236
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 236

Gly Gly Ser Ile Ser Ser Gly Gly Tyr Tyr
 1 5 10

<210> 237
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 237
 atctattaca gtgggagcac c

21

<210> 238
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 238

Ile Tyr Tyr Ser Gly Ser Thr
1 5

<210> 239
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 239
gcgaggagacg acgggtgacta ctacggatatg gacgtc 36

<210> 240
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 240

Ala Arg Asp Asp Gly Asp Tyr Tyr Gly Met Asp Val
1 5 10

<210> 241
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 241
gaaatttgtt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gactgttagc agctacttag cctggtacca acagaaacct 120
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggccctccatt cactttcggc 300
cctgggacca aagtggatat caaa 324

10296W001-Sequence.txt

<210> 242
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 242

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 243
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 243

cagactgtta gcagctac

18

<210> 244
 <211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 244

Gln Thr Val Ser Ser Tyr
1 5

<210> 245
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 245
gatgcatcc

9

<210> 246
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 246

Asp Ala Ser
1

<210> 247
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 247
cagcagcgta gcaactggcc tccattcact

30

<210> 248
<211> 10

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 248

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
 1 5 10

<210> 249
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 249
 caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
 acctgtgcc a tctccgggga cagtgtctct agtaatcgtg ctgcttgga ctggatcagg 120
 cagtcccat cgagaggcct tcagtggctg ggaaggacat actataggtc caagtggat 180
 aatgattatg cagtatctct gagaagtcga ataaccatca acccagtcac atccaagaac 240
 caggtcgccc tgcatatgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300
 agggcgggaa ttgttgtagt gccaggtccg gaaactttct actattatga tcacggtttg 360
 gacgtctggg gccaaaggac cacggtcacc gtctcctca 399

<210> 250
 <211> 133
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 250

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

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30

10296W001-Sequence.txt

Arg Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Gln
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

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

Gln Val Ala Leu His Met Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Ala Gly Ile Val Val Val Pro Gly Pro Glu Thr
100 105 110

Phe Tyr Tyr Tyr Asp His Gly Leu Asp Val Trp Gly Gln Gly Thr Thr
115 120 125

Val Thr Val Ser Ser
130

<210> 251
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 251
ggggacagtg tctctagtaa tcgtgctgct

30

<210> 252
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 252

10296W001-Sequence.txt

Gly Asp Ser Val Ser Ser Asn Arg Ala Ala
1 5 10

<210> 253
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 253
acatactata ggtccaagtg gtataat

27

<210> 254
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 254

Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
1 5

<210> 255
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 255
gcaagggcgg gaattgttgt agtgccaggt ccggaaactt tctactatta tgatcacggt

60

ttggacgtc

69

<210> 256
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 256

Ala Arg Ala Gly Ile Val Val Val Pro Gly Pro Glu Thr Phe Tyr Tyr
 1 5 10 15

Tyr Asp His Gly Leu Asp Val
 20

<210> 257

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 257

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gagcattaga agctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctgagctcct gatccatgct gcatccagtt tgcaaagtgg ggtcccttca 180
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg caagttatta ctgtcaacag agttacagtg cccctccgat caccttcggc 300
 caaggacac gactggagat taaa 324

<210> 258

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 258

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
 35 40 45

10296W001-Sequence.txt

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 259
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 259
cagagcatta gaagctat

18

<210> 260
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 260

Gln Ser Ile Arg Ser Tyr
1 5

<210> 261
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 261
gctgcatcc

9

<210> 262
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 262

Ala Ala Ser
1

<210> 263
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 263
caacagagtt acagtgcctt tccgatcacc

30

<210> 264
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 264

Gln Gln Ser Tyr Ser Ala Pro Pro Ile Thr
1 5 10

<210> 265
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

10296W001-Sequence.txt

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<400> 265
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acctgtgcca tctccgggga cagtgtctcc agcaacagtg ctgcttgga ctggatcagg      120
cagtccccct cgagaggcct tgagtggctg ggaaggacat attataggtc caagtggat      180
aatgattatg cagtgtctgt gaaaagtcga ataaccatca acccagacac atccaagaac      240
cacttctccc tgcacctgaa ttctatgact cccgaggaca cggctgtgta ttactgtgca      300
agggcgagaa ttgtagtcgt tccaggtccg gaggtttatt actactacta ctacgatatg      360
gacgtctggg gccaaaggac cacggtcacc gtctcctca      399
```

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<210> 266
<211> 133
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Synthetic
```

```
<400> 266

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

Ala Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
          20           25           30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
          35           40           45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50           55           60

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

His Phe Ser Leu His Leu Asn Ser Met Thr Pro Glu Asp Thr Ala Val
          85           90           95

Tyr Tyr Cys Ala Arg Ala Arg Ile Val Val Val Pro Gly Pro Glu Val
          100          105          110
```

10296W001-Sequence.txt

Tyr Tyr Tyr Tyr Tyr Tyr Asp Met Asp Val Trp Gly Gln Gly Thr Thr
 115 120 125

Val Thr Val Ser Ser
 130

<210> 267
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 267
 ggggacagtg tctccagcaa cagtgtgtgct 30

<210> 268
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 268

Gly Asp Ser Val Ser Ser Asn Ser Ala Ala
 1 5 10

<210> 269
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 269
 acatattata ggtccaagtg gtataat 27

<210> 270
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 270

Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
1 5

<210> 271

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 271

gcaagggcga gaattgtagt cgttcaggt ccggagggtt attactacta ctactacgat 60

atggacgtc 69

<210> 272

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 272

Ala Arg Ala Arg Ile Val Val Val Pro Gly Pro Glu Val Tyr Tyr Tyr
1 5 10 15

Tyr Tyr Tyr Asp Met Asp Val
20

<210> 273

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 273

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

10296W001-Sequence.txt

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atcacttgcc gggcaagtca gagcattaga agctatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta gccctccgat caccttcggc      300
caagggacac gactggagat taaa                                             324

```

<210> 274
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 274

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

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

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Pro
          85           90           95

```

```

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
          100          105

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<210> 275
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 275
cagagcatta gaagctat

18

<210> 276
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 276

Gln Ser Ile Arg Ser Tyr
1 5

<210> 277
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 277
gctgcatcc

9

<210> 278
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 278

Ala Ala Ser
1

<210> 279
<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 279

caacagagtt acagtagccc tccgatcacc

30

<210> 280

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 280

Gln Gln Ser Tyr Ser Ser Pro Pro Ile Thr

1

5

10

<210> 281

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 281

caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60

acctgtgtca tctccgggga cagtgtctct actaatagtg ctgcttgga ctggatcagg 120

cagtccccat cgagaggcct tgagtggctg ggaaggacat attataggtc caagtggat 180

aatgattatg cagtatctgt gagaagtcga ataaccatca acccagtcac atccaagaac 240

caggtcgccc tgcatttgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300

agggcgggaa ttgttggtgt gccaggtccg gaaacttatt actattatta tcacggtttg 360

gacgtctggg gccaaaggac cacggtcacc gtctcctca 399

<210> 282

<211> 133

<212> PRT

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> Synthetic

<400> 282

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

Thr Leu Ser Leu Thr Cys Val Ile Ser Gly Asp Ser Val Ser Thr Asn
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Arg Ser Arg Ile Thr Ile Asn Pro Val Thr Ser Lys Asn
65 70 75 80

Gln Val Ala Leu His Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Ala Gly Ile Val Val Val Pro Gly Pro Glu Thr
100 105 110

Tyr Tyr Tyr Tyr Tyr His Gly Leu Asp Val Trp Gly Gln Gly Thr Thr
115 120 125

Val Thr Val Ser Ser
130

<210> 283

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 283

ggggacagtg tctctactaa tagtgctgct

30

10296W001-Sequence.txt

<210> 284
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 284

Gly Asp Ser Val Ser Thr Asn Ser Ala Ala
 1 5 10

<210> 285
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 285
 acatattata ggtccaagtg gtataat 27

<210> 286
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 286

Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn
 1 5

<210> 287
 <211> 69
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 287
 gcaagggcgg gaattgttgt ggtgccaggt ccggaaactt attactatta ttatcacggt 60

ttggacgtc

69

<210> 288
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 288

Ala Arg Ala Gly Ile Val Val Val Pro Gly Pro Glu Thr Tyr Tyr Tyr
 1 5 10 15

Tyr Tyr His Gly Leu Asp Val
 20

<210> 289
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 289
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggcaagtca gaacattaga agctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatccatggt gcattccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
 cacgggacac gactggaaat taaa 324

<210> 290
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

10296W001-Sequence.txt

<400> 290

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly His Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 291

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 291

cagaacatta gaagctat

18

<210> 292

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 292

Gln Asn Ile Arg Ser Tyr
1 5

<210> 293
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 293
gttgcattcc

9

<210> 294
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 294

Val Ala Ser
1

<210> 295
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 295
caacagagtt acagtacccc tccgatcacc

30

<210> 296
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 296

10296W001-Sequence.txt

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> 297
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 297
cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccctcagc agtaatagtt actactgggg ctggatccgc 120
cagccccag ggaaggggct ggagtggatt gggagtatct attatagtgg gagcacctac 180
tacaaccgt ccctcaagag tcgagtcacc atatccgtag acacgtccca gaaccagttc 240
tccctgaagc tgagctctgt gaccgccgca gacacggctg tgtattactg tgcgagacag 300
aactactttg actactgggg ccaggaacc ctggtcaccg tctcctca 348

<210> 298
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 298

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Leu Ser Ser Asn
20 25 30

Ser Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

10296W001-Sequence.txt

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

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

Cys Ala Arg Gln Asn Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 299
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 299
ggtaggctccc tcagcagtaa tagttactac

30

<210> 300
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 300

Gly Gly Ser Leu Ser Ser Asn Ser Tyr Tyr
1 5 10

<210> 301
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 301
atctattata gtgggagcac c

21

<210> 302
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 302

Ile Tyr Tyr Ser Gly Ser Thr
 1 5

<210> 303
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 303
 gcgagacaga actactttga ctac

24

<210> 304
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 304

Ala Arg Gln Asn Tyr Phe Asp Tyr
 1 5

<210> 305
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 305
 gacatccagt tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc

60

10296W001-Sequence.txt

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atcacttgct gggccagtca gggcattagc aggtatttag cctggatatca gcaaaaacca      120
gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtcaacag cttaatagtt atcctctcac tttcggccct      300
gggaccaaac tggatatcaa a                                              321

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<210> 306
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 306

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

```

```

Asp Arg Val Thr Ile Thr Cys Trp Ala Ser Gln Gly Ile Ser Arg Tyr
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

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

```

```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn Ser Tyr Pro Leu
          85           90           95

```

```

Thr Phe Gly Pro Gly Thr Lys Leu Asp Ile Lys
          100          105

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<210> 307
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 307
cagggcatta gcaggtat

18

<210> 308
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 308

Gln Gly Ile Ser Arg Tyr
1 5

<210> 309
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 309
gctgcatcc

9

<210> 310
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 310

Ala Ala Ser
1

<210> 311
<211> 27

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 311
 caacagctta atagttatcc tctcact

27

<210> 312
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 312

Gln Gln Leu Asn Ser Tyr Pro Leu Thr
 1 5

<210> 313
 <211> 345
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 313
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 tcctgtgcag tctctggatt cacctccagt acctatggca tgaactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180
 gcagactccg tgaagggccg attcaccatc tccagggaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag acctgaggac acggctgtgt attactgtgc gagaggaagg 300
 tacttcgatc tctggggccg tggcaccctg gtcactgtct cctca 345

<210> 314
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 314

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Ser Ser Thr Tyr
 20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 315

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 315

ggattcacct ccagtaccta tggc

24

<210> 316

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 316

Gly Phe Thr Ser Ser Thr Tyr Gly
1 5

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 317

atatcatatg atggaagtaa taaa

24

<210> 318

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 318

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 319

gcgagaggaa ggtacttcga tctc

24

<210> 320

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 320

Ala Arg Gly Arg Tyr Phe Asp Leu

1 5

<210> 321

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 321

gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca aattattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctataag gcgtctagtt tagcaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataaaagtt attcttacac ctttggccag 300

gggaccaacc tggagatcaa a 321

<210> 322

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 322

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ile Ile Ser Ser Trp

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

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Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Tyr Ser Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Asn Leu Glu Ile Lys
100 105

<210> 323
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 323
caaattatta gtagctgg

18

<210> 324
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 324

Gln Ile Ile Ser Ser Trp
1 5

<210> 325
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 325
aaggcgtct

9

<210> 326
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 326

Lys Ala Ser
1

<210> 327
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 327
caacagtata aaagttattc ttacacc

27

<210> 328
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 328

Gln Gln Tyr Lys Ser Tyr Ser Tyr Thr
1 5

<210> 329
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

10296W001-Sequence.txt

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<400> 329
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ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat      180
gtagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagagggg      300
ctacgatttt tggagaatta ctactactac tacggtatgg acgtctgggg ccaagggacc      360
acggtcaccg tctcctca                                          378

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<210> 330
<211> 126
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 330
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1          5          10          15
Ser Leu Gly Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20          25          30
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35          40          45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val
          50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Gly Leu Arg Phe Leu Glu Asn Tyr Tyr Tyr Tyr Tyr Gly
          100          105          110

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Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 331
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 331
 ggattcacct tcagtagcta tggc

24

<210> 332
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 332

Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 333
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 333
 atatggtatg atggaagtaa taaa

24

<210> 334
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 334

Ile Trp Tyr Asp Gly Ser Asn Lys
 1 5

<210> 335

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 335

gcgagagagg ggctacgatt tttggagaat tactactact actacggat ggacgtc 57

<210> 336

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 336

Ala Arg Glu Gly Leu Arg Phe Leu Glu Asn Tyr Tyr Tyr Tyr Tyr Gly
 1 5 10 15

Met Asp Val

<210> 337

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 337

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtattagc agcacctact tagcctggta ccagcagaga 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatcca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

10296W001-Sequence.txt

cctgaagatt ttgcagtgtgta ttactgtcag cagtatggta cctcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 338
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 338

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Thr
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Thr Ser Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 339
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 339
cagagtatta gcagcaccta c

21

<210> 340
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 340

Gln Ser Ile Ser Ser Thr Tyr
1 5

<210> 341
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 341
ggtgcatcc

9

<210> 342
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 342

Gly Ala Ser
1

<210> 343
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 343
cagcagtatg gtacctcacc gtacact 27

<210> 344
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 344

Gln Gln Tyr Gly Thr Ser Pro Tyr Thr
1 5

<210> 345
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 345
cagggtgcagc tgggtggagtc tggggggaggc gtgggtccagc ctgggagggtc cctgagactc 60
tcctgtgcag tctctggatt cacctccagt acctatggca tgaactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagggaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag acctgaggac acggctgtgt attactgtgc gagaggaagg 300
tacttcgatc tctggggccg tggcaccctg gtcactgtct cctca 345

<210> 346
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 346

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

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Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Ser Ser Thr Tyr
20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 347
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 347
ggattcacct ccagtaccta tggc

24

<210> 348
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 348

Gly Phe Thr Ser Ser Thr Tyr Gly
 1 5

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 349
 atatcatatg atggaagtaa taaa

24

<210> 350
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 350

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 351
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 351
 gcgagaggaa ggtacttcga tctc

24

<210> 352
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 352

10296W001-Sequence.txt

Ala Arg Gly Arg Tyr Phe Asp Leu
1 5

<210> 353
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 353
gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggccagtca aattattagt agctggttgg cctggatatca gcagaaacca 120
gggaaagccc ctaaactcct gatctataag gcgtctagtt tagcaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
gatgattttg caacttatta ctgccaacag tataaaagtt attcttacac ctttggccag 300
gggaccaagc tggagatcaa a 321

<210> 354
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 354

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ile Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Tyr Ser Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 355
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 355
caaattatta gtagctgg

18

<210> 356
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 356

Gln Ile Ile Ser Ser Trp
1 5

<210> 357
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 357
aaggcgtct

9

<210> 358
<211> 3

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 358

Lys Ala Ser
 1

<210> 359
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 359
 caacagtata aaagttattc ttacacc

27

<210> 360
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 360

Gln Gln Tyr Lys Ser Tyr Ser Tyr Thr
 1 5

<210> 361
 <211> 345
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 361
 caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag tctctggatt cacctccagt acctatggca tgaactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatttg atggaagtaa taaatactac 180

10296W001-Sequence.txt

gcagactccg tgaagggccg attcaccatc tccagggaca attccaagaa cacgctgtat 240
 ctgcaaata gacgcctgag acctgaggac acggctgtgt attactgtgc gagaggaagg 300
 tacttcgatc tctggggccg tggcaccctg gtcactgtct cctca 345

<210> 362
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 362

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Ser Ser Thr Tyr
 20 25 30

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

Ala Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
 100 105 110

Val Ser Ser
 115

<210> 363
 <211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 363
 ggattcacct ccagtaccta tggc

24

<210> 364
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 364

Gly Phe Thr Ser Ser Thr Tyr Gly
 1 5

<210> 365
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 365
 atatcatttg atggaagtaa taaa

24

<210> 366
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 366

Ile Ser Phe Asp Gly Ser Asn Lys
 1 5

<210> 367
 <211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 367
 gcgagaggaa ggtacttcga tctc

24

<210> 368
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 368

Ala Arg Gly Arg Tyr Phe Asp Leu
 1 5

<210> 369
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 369
 gacaccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc gggccagtca aattattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaaactcct gatctataag gcgtctagtt tagcaagtgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacag tataaaagtt attcttacac ctttggccag 300
 gggaccaacc tggagatcaa a 321

<210> 370
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic

<400> 370

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ile Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Tyr Ser Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Asn Leu Glu Ile Lys
 100 105

<210> 371

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 371

caaattatta gtagctgg

18

<210> 372

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 372

Gln Ile Ile Ser Ser Trp
1 5

<210> 373

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 373

aaggcgtct

9

<210> 374

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 374

Lys Ala Ser
1

<210> 375

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 375

caacagtata aaagttattc ttacacc

27

<210> 376

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 376

Gln Gln Tyr Lys Ser Tyr Ser Tyr Thr
 1 5

<210> 377

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 377

cagggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtgcag tctctggatt cacctccagt acctatggca tgaactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatttg atggaagtaa taaatactac 180
 gcagactccg tgaagggccg attcaccatc tccagggaca attccaagaa cacgctgtat 240
 ctgcaaatga gcagcctgag acctgaggac acggctgtgt attactgtgc gagaggaagg 300
 tacttcgatc tctggggccg tggcaccctg gtcactgtct cctca 345

<210> 378

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 378

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

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Ser Ser Thr Tyr
 20 25 30

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

Ala Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Arg Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 379
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 379
ggattcacct ccagtaccta tggc

24

<210> 380
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 380

Gly Phe Thr Ser Ser Thr Tyr Gly
1 5

<210> 381
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 381
 atatcatttg atggaagtaa taaa

24

<210> 382
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 382

Ile Ser Phe Asp Gly Ser Asn Lys
 1 5

<210> 383
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 383
 gcgagaggaa ggtacttcga tctc

24

<210> 384
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 384

Ala Arg Gly Arg Tyr Phe Asp Leu
 1 5

<210> 385
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

10296W001-Sequence.txt

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<400> 385
gacacccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggccagtca aattattagt agctggttgg cctggatatca gcagaaacca    120
gggaaagccc ctaaactcct gatctataag gcgtctagtt tagcaagtgg ggtcccatca    180
aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct    240
gatgattttg caacttatta ctgccaacag tataaaagtt attcttacac ctttggccag    300
gggaccaacc tggagatcaa a                                              321

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<210> 386
<211> 107
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic

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<400> 386
Asp Thr Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1          5          10          15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ile Ile Ser Ser Trp
          20          25          30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45

Tyr Lys Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Ser Tyr Ser Tyr
          85          90          95

Thr Phe Gly Gln Gly Thr Asn Leu Glu Ile Lys
          100          105

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<210> 387
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<400> 387
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18

<210> 388
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<220>
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<400> 388

Gln Ile Ile Ser Ser Trp
 1 5

<210> 389
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<400> 389
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9

<210> 390
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<220>
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<400> 390

Lys Ala Ser
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<210> 391
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<220>
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<400> 391
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27

<210> 392
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 <212> PRT
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<220>
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<400> 392

Gln Gln Tyr Lys Ser Tyr Ser Tyr Thr
 1 5

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<400> 393
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10296W001-Sequence.txt

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<210> 401
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ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtag cataggctat 180
gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaataa acagtctgag agctgaggac acggccttgt actactgtgc aaaagataat 300
agtggctacg gctattatta ctacggtatg gacgtctggg gccaaaggac cacggtcacc 360
gtctcctca 369

<210> 402
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
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<400> 402

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Asp Asp Phe
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<211> 24
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<220>
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<400> 403
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24

<210> 404
<211> 8
<212> PRT
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<220>
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<400> 404

Gly Phe Thr Phe Asp Asp Phe Thr
1 5

<210> 405
 <211> 24
 <212> DNA
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<220>
 <223> synthetic

<400> 405
 atcagttgga atagtggtag cata

24

<210> 406
 <211> 8
 <212> PRT
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<220>
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<400> 406

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 407
 <211> 48
 <212> DNA
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<220>
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<400> 407
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48

<210> 408
 <211> 16
 <212> PRT
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<400> 408

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
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10296W001-Sequence.txt

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 <212> DNA
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<220>
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<400> 409
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 ctctcctgca gggccagtca cagtgttagc aggaactcag cctggtacca gcagaaacct 120
 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
 aggttcagtg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240
 gaagattttg caatttatta ctgtcagcag tataataatt ggctctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 410
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 410

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser His Ser Val Ser Arg Asn
 20 25 30

Ser Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

10296W001-Sequence.txt

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 411
<211> 18
<212> DNA
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<220>
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<400> 411
cacagtgtta gcaggaac

18

<210> 412
<211> 6
<212> PRT
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<220>
<223> synthetic

<400> 412

His Ser Val Ser Arg Asn
1 5

<210> 413
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 413
ggtgcatcc

9

<210> 414
<211> 3
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 414

Gly Ala Ser

1

<210> 415

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 415

cagcagtata ataattggcc tctcact

27

<210> 416

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 416

Gln Gln Tyr Asn Asn Trp Pro Leu Thr

1

5

<210> 417

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 417

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tcctgtgcag cctctggatt ctcctttgat gattatacca tgcactgggt ccggcaacct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

10296W001-Sequence.txt

ctgcaaatga acagtctgag agctggggac acggccttgt actactgtgc aaaagataat 300
 agtggctacg gctattacta ctactacggt atggacgtct ggggcccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 418
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 418

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 419
 <211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 419
 ggattctcct ttgatgatta tacc

24

<210> 420
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 420

Gly Phe Ser Phe Asp Asp Tyr Thr
 1 5

<210> 421
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 421
 attagttgga atagtggtag cata

24

<210> 422
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 422

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 423
 <211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 423

gcaaaagata atagtggcta cggctattac tactactacg gtatggacgt c

51

<210> 424

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 424

Ala	Lys	Asp	Asn	Ser	Gly	Tyr	Gly	Tyr	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5				10					15		

Val

<210> 425

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 425

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ctctcctgca gggccagtca gagtgtttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccagactcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240

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gggaccaagg tggagatcaa a 321

<210> 426

<211> 107

<212> PRT
 <213> Artificial Sequence

<220>
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<400> 426

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Trp Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 427
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 427
 cagagtgtta gcagcaac

18

<210> 428
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 428

Gln Ser Val Ser Ser Asn
1 5

<210> 429

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 429

ggtgcatcc

9

<210> 430

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 430

Gly Ala Ser
1

<210> 431

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 431

cagcagtatt ataactggcc tctcact

27

<210> 432

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 432

Gln Gln Tyr Tyr Asn Trp Pro Leu Thr

1 5

<210> 433

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 433

gaagtacagc tggtggagtc tgggggaggc ttggtacagc ctggcaggctc cctgagactc 60

tcctgtgtag cctctggatt cccctttgct gattatacca tgcactgggt ccggcaagct 120

ccaggggaagg gcctggagtg ggtctcagat attagttgga atagtggtag caaaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttct attactgtgc aaaagatatg 300

agtggctacg cccactactt ctactacggt atggacgtct ggggccaagg gaccacggctc 360

accgtctcct ca 372

<210> 434

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 434

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Pro Phe Ala Asp Tyr

20 25 30

10296W001-Sequence.txt

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

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

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Phe Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 435
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 435
ggattcccct ttgctgatta tacc

24

<210> 436
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 436

Gly Phe Pro Phe Ala Asp Tyr Thr
1 5

<210> 437
<211> 24

<212> DNA
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<220>
 <223> synthetic

<400> 437
 attagttgga atagtggtag caaa

24

<210> 438
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 438

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 439
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 439
 gcaaaagata tgagtggcta cgcccactac ttctactacg gtatggacgt c

51

<210> 440
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 440

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Phe Tyr Tyr Gly Met Asp
 1 5 10 15

Val

10296W001-Sequence.txt

<210> 441
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 441
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 atcacttgcc ggccaagtca gagcattagc agctatttaa attggtttca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
 caagggacac gactggagat taaa 324

<210> 442
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 442

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

Asp Arg Val Thr Ile Thr Cys Arg Pro Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

10296W001-Sequence.txt

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 443
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 443
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18

<210> 444
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 444

Gln Ser Ile Ser Ser Tyr
1 5

<210> 445
<211> 9
<212> DNA
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<220>
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<400> 445
gctgcatcc

9

<210> 446
<211> 3
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<220>

<223> synthetic

<400> 446

Ala Ala Ser

1

<210> 447

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 447

caacagagtt acagtacccc tccgatacc

30

<210> 448

<211> 10

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<400> 448

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr

1

5

10

<210> 449

<211> 372

<212> DNA

<213> Artificial Sequence

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<400> 449

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tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagtt 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggcag cttggcctac 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ttccctgtat 240

10296W001-Sequence.txt

ctgcaaatga acagtcttca ccctgaggac acggccctct attactgtgt aaaagatggg 300
 agtggctacg gccactactc ctactacggt ttggacgtct ggggccaggg gaccacggtc 360
 accgtctcct ca 372

<210> 450
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 450

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu His Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly His Tyr Ser Tyr Tyr Gly Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 451
 <211> 24

<212> DNA
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<220>
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<400> 451
 ggattcacct ttgatgatta tacc

24

<210> 452
 <211> 8
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<220>
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<400> 452

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 453
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 <212> DNA
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<220>
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<400> 453
 attagttgga atagtggcag cttg

24

<210> 454
 <211> 8
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<220>
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<400> 454

Ile Ser Trp Asn Ser Gly Ser Leu
 1 5

<210> 455
 <211> 51

<212> DNA

<213> Artificial Sequence

<220>

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<400> 455

gtaaaagatg gtagtggcta cggccactac tcctactacg gtttggacgt c

51

<210> 456

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 456

Val	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	His	Tyr	Ser	Tyr	Tyr	Gly	Leu	Asp
1				5				10					15		

Val

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<211> 324

<212> DNA

<213> Artificial Sequence

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<400> 457

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gttcaccttg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> 458

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 458

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 459

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 459

cagagtgtta gcagcagcta c

21

<210> 460

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 460

Gln Ser Val Ser Ser Ser Tyr
1 5

<210> 461

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 461

ggtgcatcc

9

<210> 462

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 462

Gly Ala Ser
1

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 463

cagcagtatg gtagttcacc ttggacg

27

<210> 464

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 464

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 1 5

<210> 465

<211> 372

<212> DNA

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<220>

<223> synthetic

<400> 465

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ccaggggaagg gcctggagtg ggtctcagat attagttgga atagtggtag cataggctat      180
gcggactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtat      240
ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatatg      300
agtggctacg cccactactt ctactacggt atggacgtct ggggccaagg gaccacggctc      360
accgtctcct ca                                                                372

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<210> 466

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 466

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

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Pro Phe Ala Asp Tyr
 20 25 30

10296W001-Sequence.txt

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Phe Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 467
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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24

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<220>
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<400> 468

Gly Phe Pro Phe Ala Asp Tyr Thr
1 5

<210> 469
<211> 24

<212> DNA
 <213> Artificial Sequence

<220>
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<400> 469
 attagttgga atagtggtag cata

24

<210> 470
 <211> 8
 <212> PRT
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<220>
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<400> 470

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 471
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 471
 gcaaaagata tgagtggcta cgcccactac ttctactacg gtatggacgt c

51

<210> 472
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 472

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Phe Tyr Tyr Gly Met Asp
 1 5 10 15

Val

10296W001-Sequence.txt

<210> 473
 <211> 324
 <212> DNA
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<220>
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<400> 473
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 atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
 caagggacac gactggagat taaa 324

<210> 474
 <211> 108
 <212> PRT
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<220>
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<400> 474
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Phe Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

10296W001-Sequence.txt

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 475
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<400> 475
cagagcatta gcagctat

18

<210> 476
<211> 6
<212> PRT
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<220>
<223> synthetic

<400> 476

Gln Ser Ile Ser Ser Tyr
1 5

<210> 477
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 477
gctgcatcc

9

<210> 478
<211> 3
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<220>

<223> synthetic

<400> 478

Ala Ala Ser

1

<210> 479

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 479

caacagagtt acagtacccc tccgatcacc

30

<210> 480

<211> 10

<212> PRT

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<223> synthetic

<400> 480

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr

1

5

10

<210> 481

<211> 372

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 481

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tcctgtacag cctctggatt cacctttgct gattatacca tgcactgggt ccgacaaggt 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag taaaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

10296W001-Sequence.txt

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatatg 300
 agtggctacg cccactacta ctactacgct ttggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 482
 <211> 124
 <212> PRT
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<400> 482

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

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

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Tyr Tyr Tyr Ala Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 483
 <211> 24

<212> DNA
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<220>
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<400> 483
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24

<210> 484
 <211> 8
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<220>
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<400> 484

Gly Phe Thr Phe Ala Asp Tyr Thr
 1 5

<210> 485
 <211> 24
 <212> DNA
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<220>
 <223> synthetic

<400> 485
 attagttgga atagtggtag taaa

24

<210> 486
 <211> 8
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<220>
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<400> 486

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 487
 <211> 51

10296W001-Sequence.txt

<212> DNA

<213> Artificial Sequence

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<400> 487

gcaaaagata tgagtggcta cgcccactac tactactacg ctttggacgt c 51

<210> 488

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<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 488

Ala	Lys	Asp	Met	Ser	Gly	Tyr	Ala	His	Tyr	Tyr	Tyr	Tyr	Ala	Leu	Asp
1				5					10					15	

Val

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<211> 324

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 489

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta acccccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> 490

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 490

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Asn Pro Pro
 85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 491

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 491

cagagcatta gcaactat

18

<210> 492

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 492

Gln Ser Ile Ser Asn Tyr
1 5

<210> 493

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 493

gctgcatcc

9

<210> 494

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 494

Ala Ala Ser
1

<210> 495

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 495

caacagagtt acagtaaccc cccgatcacc

30

<210> 496

<211> 10

<212> PRT

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 496

Gln Gln Ser Tyr Ser Asn Pro Pro Ile Thr
1 5 10

<210> 497

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 497

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tcctgtgcag cctctggatt caccttcagt agaaaaggca tgcactgggt ccgccaggct	120
ccagtcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgac agctgaggac acggctgtgt attactgtgc gaaagaaggg	300
gggcatgact atggtggtac ctttgactac tggggccagg gaaccctggt caccgtctcc	360
tca	363

<210> 498

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 498

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Lys
20 25 30

10296W001-Sequence.txt

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Glu Gly Gly His Asp Tyr Gly Gly Thr Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 499
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 499
 ggattcacct tcagtagaaa aggc

24

<210> 500
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 500

Gly Phe Thr Phe Ser Arg Lys Gly
 1 5

<210> 501
 <211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 501
 atatcatatg atggaagtaa taaa

24

<210> 502
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 502

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 503
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 503
 gcgaaagaag gggggcatga ctatggtggt acctttgact ac

42

<210> 504
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 504

Ala Lys Glu Gly Gly His Asp Tyr Gly Gly Thr Phe Asp Tyr
 1 5 10

<210> 505
 <211> 321

10296W001-Sequence.txt

<212> DNA

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<220>

<223> synthetic

<400> 505

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atcacttgcc aggcgagtca ggacattaac aactatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagttcct gatctacgat gcatccaatt tggaaacagg ggtcccatca      180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct      240
gaagatattg caacatatta ctgtcaacag tatgatgata tccattcac tttcggcctt      300
gggaccaaag tggatatcaa a                                     321

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<210> 506

<211> 107

<212> PRT

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<220>

<223> synthetic

<400> 506

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

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

```

```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
          35           40           45

```

```

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50           55           60

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

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Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asp Leu Pro Phe
          85           90           95

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Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 507
<211> 18
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<220>
<223> synthetic

<400> 507
caggacatta acaactat

18

<210> 508
<211> 6
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<220>
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<400> 508

Gln Asp Ile Asn Asn Tyr
1 5

<210> 509
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 509
gatgcatcc

9

<210> 510
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 510

Asp Ala Ser
1

<210> 511

<211> 27

<212> DNA

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<220>

<223> synthetic

<400> 511

caacagtatg atgatctccc attcact

27

<210> 512

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 512

Gln Gln Tyr Asp Asp Leu Pro Phe Thr
1 5

<210> 513

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 513

gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggctc cctgagactc 60

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ccaggggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180

gctggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300

agtggctacg gtcactacta ctacggaatg gacgtctggg gcccaaggac cacggtcacc 360

gtcgcctca

<210> 514
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 514

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
 115 120

<210> 515
 <211> 24
 <212> DNA
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<220>

<223> synthetic

<400> 515
ggattcacct ttgatgatta tacc

24

<210> 516
<211> 8
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<220>
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<400> 516

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 517
<211> 24
<212> DNA
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<400> 517
attagttgga atagtggtag tata

24

<210> 518
<211> 8
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<400> 518

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 519
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<400> 519

gcaaaagata atagtggcta cggtcactac tactacggaa tggacgtc

48

<210> 520

<211> 16

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<213> Artificial Sequence

<220>

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<400> 520

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<211> 321

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<400> 521

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcac tatattaact ggctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

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<212> PRT

<213> Artificial Sequence

<220>

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10296W001-Sequence.txt

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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18

<210> 524
<211> 6
<212> PRT
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<220>
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<400> 524

Gln Ser Val Ser Ser Asn
1 5

<210> 525
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<220>
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<400> 525
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9

<210> 526
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 <213> Artificial Sequence

<220>
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<400> 526

Gly Ala Ser
 1

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 <211> 27
 <212> DNA
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 cagcactata ttaactggcc tctcact

27

<210> 528
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<400> 528

Gln His Tyr Ile Asn Trp Pro Leu Thr
 1 5

10296W001-Sequence.txt

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 ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300
 agtggctacg gtcactacta ctacggaatg gacgtctggg gccaaaggac cacggtcacc 360
 gtcgcctca 369

<210> 530
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 <213> Artificial Sequence

<220>
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<400> 530
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 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
115 120

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<400> 531
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24

<210> 532
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<400> 532

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 533
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attagttgga atagtggtag tata

24

<210> 534
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<400> 534

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 535
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 <212> DNA
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<220>
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<400> 535
 gcaaaagata atagtggcta cggtcactac tactacggaa tggacgtc 48

<210> 536
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<220>
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<400> 536

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
 1 5 10 15

<210> 537
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 537
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10296W001-Sequence.txt

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ctctcctgca gggccagtca gagggttagc agcaacttag cctggtacca gcaaaaacct      120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct      240
gaagattttg cagtttatta ctgtcagcac tatattaact ggcctctcac tttcggcgga      300
gggaccaagg tggagatcaa a                                              321

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<210> 538
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 <212> PRT
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<220>
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<400> 538

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

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<400> 539
cagagtgtta gcagcaac

18

<210> 540
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<220>
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<400> 540

Gln Ser Val Ser Ser Asn
1 5

<210> 541
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<400> 541
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9

<210> 542
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<400> 542

Gly Ala Ser
1

<210> 543
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<212> DNA
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<400> 543
 cagcactata ttaactggcc tctcact

27

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<400> 544

Gln His Tyr Ile Asn Trp Pro Leu Thr
 1 5

<210> 545
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 ccaggcaggg ggctggagtg ggtggcaatg atatattatg atggaaataa taaatactat 180
 gcagactccg tgagggggccg attcaccgtt tccagagaca attccaagaa caccctgtat 240
 ctgcaaata ga gcagcctgag agccgaggac acggctctat atttctgtgc gcgagggcct 300
 gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 546
 <211> 118
 <212> PRT
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<400> 546

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

Ser Leu Arg Leu Ser Cys Gly Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Thr Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Ala Met Ile Tyr Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Arg Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 547

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 547

ggattcacct tcagaagtta tggc

24

<210> 548

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 548

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> 549

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 549

atatattatg atggaaataa taaa

24

<210> 550

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 550

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> 551

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 551

gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 552

<211> 11

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<223> synthetic

<400> 552

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 553

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 553

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct      240
gaagattttg cagtttatta ctgtcagcag tataataacc ggcctctcac tttcggcgga      300
gggaccgagg tggagatcaa a      321
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<210> 554

<211> 107

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<400> 554

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1 5 10 15

10296W001-Sequence.txt

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Xaa Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 555
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 555
cagagtatta gcaggaac

18

<210> 556
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 556

Gln Ser Ile Ser Arg Asn
1 5

<210> 557
<211> 9

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 557
ggtgcatcc

9

<210> 558
<211> 3
<212> PRT
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<220>
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<400> 558

Gly Ala Ser
1

<210> 559
<211> 27
<212> DNA
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<220>
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<400> 559
cagcagtata ataaccggcc tctcact

27

<210> 560
<211> 9
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<213> Artificial Sequence

<220>
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<400> 560

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> 561
<211> 354

10296W001-Sequence.txt

<212> DNA

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<220>

<223> synthetic

<400> 561

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ccaggcaagg gactgcagtg ggtggcaatg atttactatg atggttaagaa taaatattat      180
gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacactgtat      240
ctgcaaatga acaatctgag agtcgaggac acggctatgt atttctgtgc gcgagggcct      300
gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcaactgtttc ctca          354
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<210> 562

<211> 118

<212> PRT

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<220>

<223> synthetic

<400> 562

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1              5              10              15
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Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
                20              25              30
```

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

```
Ala Met Ile Tyr Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
                50              55              60
```

```
Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65              70              75              80
```

```
Leu Gln Met Asn Asn Leu Arg Val Glu Asp Thr Ala Met Tyr Phe Cys
                85              90              95
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10296W001-Sequence.txt

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 563
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<213> Artificial Sequence

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<400> 563
ggattcacct tcagaagtta tggc

24

<210> 564
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 564

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> 565
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 565
atttactatg atggttaagaa taaa

24

<210> 566
<211> 8
<212> PRT
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<220>

<223> synthetic

<400> 566

Ile Tyr Tyr Asp Gly Lys Asn Lys
 1 5

<210> 567

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 567

gcgcgagggc ctgggtacaa ttggctcgac ccc

33

<210> 568

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 568

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
 1 5 10

<210> 569

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 569

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ctctcctgca gggccagtca gagaattagc agcaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

10296W001-Sequence.txt

gaggatgttg cagtttatta ctgtcagcaa catcataact ggcctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 570
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<400> 570

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ser Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His His Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 571
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 571
cagagaatta gcagcaac

18

<210> 572
<211> 6
<212> PRT
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<220>
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<400> 572

Gln Arg Ile Ser Ser Asn
1 5

<210> 573
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 573
ggtgcatcc

9

<210> 574
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 574

Gly Ala Ser
1

<210> 575
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 575
cagcaacatc ataactggcc tctcact 27

<210> 576
<211> 9
<212> PRT
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<220>
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<400> 576

Gln Gln His His Asn Trp Pro Leu Thr
1 5

<210> 577
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<400> 577
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ccaggcaagg ggctggagtg ggtggcaatg gtatactatg atggaaataa tcaatactat 180
gcagactccg tgagggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300
gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 578
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
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<400> 578

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

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

Ala Met Val Tyr Tyr Asp Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 579
<211> 24
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<220>
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<400> 579
ggatttacct tcagaagtta tgcc

24

<210> 580
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 580

Gly Phe Thr Phe Arg Ser Tyr Ala
 1 5

<210> 581
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 581
 gtatactatg atggaaataa tcaa

24

<210> 582
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 582

Val Tyr Tyr Asp Gly Asn Asn Gln
 1 5

<210> 583
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 583
 gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 584
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<220>
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<400> 584

10296W001-Sequence.txt

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 585
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 585
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ctctcctgca gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccggcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcagcag tataataact ggctctcac tttcggcgga 300
gggaccaagg tggatgatcaa a 321

<210> 586
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<400> 586

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

10296W001-Sequence.txt

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Val Ile Lys
100 105

<210> 587
<211> 18
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<213> Artificial Sequence

<220>
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<400> 587
cagagtgtta gcaggaac

18

<210> 588
<211> 6
<212> PRT
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<220>
<223> synthetic

<400> 588

Gln Ser Val Ser Arg Asn
1 5

<210> 589
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 589
ggtgcatcc

9

<210> 590
<211> 3

<212> PRT
 <213> Artificial Sequence

<220>
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<400> 590

Gly Ala Ser
 1

<210> 591
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 591
 cagcagtata ataactggcc tctcact

27

<210> 592
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 592

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
 1 5

<210> 593
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 593
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 tcctgtattg cgtctggatt taccttcaga agttatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcaatg atatattatg atggaaacaa taaatactat 180

10296W001-Sequence.txt

gcagactccg tgaggggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300
 ggggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 594
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 594

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

Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

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

Ala Met Ile Tyr Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 595
 <211> 24

<212> DNA
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<400> 595
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24

<210> 596
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 596

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> 597
<211> 24
<212> DNA
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<220>
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<400> 597
atatattatg atggaaacaa taaa

24

<210> 598
<211> 8
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<220>
<223> synthetic

<400> 598

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> 599
<211> 33

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<400> 599

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33

<210> 600

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<400> 600

Ala	Arg	Gly	Pro	Gly	Tyr	Asn	Trp	Leu	Asp	Pro
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<210> 601

<211> 321

<212> DNA

<213> Artificial Sequence

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<400> 601

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataaca ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 602

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 602

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 603

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 603

cagagtgtta gcagcaac

18

<210> 604

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 604

Gln Ser Val Ser Ser Asn
1 5

<210> 605

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 605

ggtgcatcc

9

<210> 606

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 606

Gly Ala Ser
1

<210> 607

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 607

cagcagtata ataacaggcc tctcact

27

<210> 608

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 608

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

<210> 609

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 609

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ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat	180
gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat	240
ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct	300
gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca	354

<210> 610

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 610

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
 20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

10296W001-Sequence.txt

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 611
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 611
ggattcacct tcagaagttt tggc

24

<210> 612
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 612

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> 613
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 613
atatattttg atggaaaaaa taaa

24

<210> 614
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 614

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> 615
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 615
gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 616
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 616

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 617
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

10296W001-Sequence.txt

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ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240
gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300
gggaccgagg tggagatcaa a 321

<210> 618
<211> 107
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<220>
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<400> 618
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1 5 10 15
Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80
Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 619
 <211> 18
 <212> DNA
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<220>
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 cagagtatta gcaggaac

18

<210> 620
 <211> 6
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<220>
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<400> 620

Gln Ser Ile Ser Arg Asn
 1 5

<210> 621
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<220>
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<400> 621
 ggtgcatcc

9

<210> 622
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<220>
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<400> 622

Gly Ala Ser
 1

<210> 623
 <211> 27
 <212> DNA
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<220>
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<400> 623
 cagcagtata ataataggcc tctcact

27

<210> 624
 <211> 9
 <212> PRT
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<400> 624

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

<210> 625
 <211> 354
 <212> DNA
 <213> Artificial Sequence

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 tcctgtgctg cgtctggatt caccttcaga agttttggca tgactgggt cgcaggct 120
 ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180
 gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240
 ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300
 ggggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 626
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10296W001-Sequence.txt

<220>

<223> synthetic

<400> 626

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 627

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 627

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24

<210> 628

<211> 8

<212> PRT
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<220>
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<400> 628

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> 629
<211> 24
<212> DNA
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<220>
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<400> 629
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24

<210> 630
<211> 8
<212> PRT
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<400> 630

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> 631
<211> 33
<212> DNA
<213> Artificial Sequence

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<400> 631
gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 632
<211> 11

<212> PRT
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<220>
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<400> 632

Ala	Arg	Gly	Pro	Gly	Tyr	Asn	Trp	Leu	Asp	Pro
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<210> 633
 <211> 321
 <212> DNA
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<220>
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<400> 633
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 ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcaraaacct 120
 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180
 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240
 gaagattttg cagtttttca ctgtcagcag tataataata ggctctcac tttcggcgga 300
 gggaccgagg tggagatcaa a 321

<210> 634
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 <212> PRT
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<220>
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 <222> (38)..(38)
 <223> Xaa = Any Amino Acid

<400> 634

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

10296W001-Sequence.txt

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

Leu Ala Trp Tyr Gln Xaa Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 635
<211> 18
<212> DNA
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<220>
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<400> 635
cagagtatta gcaggaac

18

<210> 636
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 636

Gln Ser Ile Ser Arg Asn
1 5

<210> 637
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 637
 ggtgcatcc

9

<210> 638
 <211> 3
 <212> PRT
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<220>
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<400> 638

Gly Ala Ser
 1

<210> 639
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 639
 cagcagtata ataataggcc tctcact

27

<210> 640
 <211> 9
 <212> PRT
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<220>
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<400> 640

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

10296W001-Sequence.txt

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<400> 641
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 tcctgtgctg cgtctggatt caccttcaga agttttggca tgcactgggt ccgccaggct 120
 ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180
 gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240
 ctggaaatga gcagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300
 ggggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 642
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 642

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
 20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

10296W001-Sequence.txt

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 643
<211> 24
<212> DNA
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<220>
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<400> 643
ggattcacct tcagaagttt tggc

24

<210> 644
<211> 8
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<400> 644

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> 645
<211> 24
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<220>
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<400> 645
atatattttg atggaaaaaa taaa

24

<210> 646
<211> 8

<212> PRT
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<220>
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<400> 646

Ile Tyr Phe Asp Gly Lys Asn Lys
 1 5

<210> 647
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 <212> DNA
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<400> 647
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33

<210> 648
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 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 648

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
 1 5 10

<210> 649
 <211> 321
 <212> DNA
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<220>
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<400> 649
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 ctctcctgta gggccagtca gagtgtttagc aggaacttgg cctggtacca gcaaaaacct 120
 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

10296W001-Sequence.txt

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240
gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300
gggaccgagg tggagatcaa a 321

<210> 650
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<400> 650

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 651
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 651
cagagtgtta gcaggaac

18

<210> 652
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 652

Gln Ser Val Ser Arg Asn
1 5

<210> 653
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 653
ggtgcatcc

9

<210> 654
<211> 3
<212> PRT
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<220>
<223> synthetic

<400> 654

Gly Ala Ser
1

<210> 655
<211> 27
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<220>

<223> synthetic

<400> 655

cagcagtata ataataggcc tctcact

27

<210> 656

<211> 9

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<400> 656

Gln Gln Tyr Asn Asn Arg Pro Leu Thr

1

5

<210> 657

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 657

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tcctgtgctg cgtctggatt caccttcaga agttttggca tgacttgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gcagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

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<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 658

10296W001-Sequence.txt

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 659
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 659
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24

<210> 660
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 660

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> 661

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 661

atatattttg atggaaaaaa taaa

24

<210> 662

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 662

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> 663

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 663

gcgcgagggc ctgggtacaa ttggctcgac ccc

33

<210> 664

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 664

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
 1 5 10

<210> 665

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 665

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 ctctcctgta gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120
 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180
 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240
 gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300
 gggaccgagg tggagatcaa a 321

<210> 666

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 666

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
 50 55 60

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 667
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 667
cagagtgtta gcaggaac

18

<210> 668
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 668

Gln Ser Val Ser Arg Asn
1 5

<210> 669
<211> 9
<212> DNA
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<220>
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<400> 669
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9

<210> 670
 <211> 3
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 <213> Artificial Sequence

<220>
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<400> 670

Gly Ala Ser
 1

<210> 671
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 671
 cagcagtata ataataggcc tctcact

27

<210> 672
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 <212> PRT
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<220>
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<400> 672

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

<210> 673
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 673
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tcctgtgttg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct 120

10296W001-Sequence.txt

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ccaggcaagg gactgcagtg ggtggcaatg atttactatg atggtaagaa taaatattat      180
gcagactccg tgagggggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaataga acagtctgag agccgaagac acggctatgt atttctgtgc gcgagggcct      300
gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcactgtctc ctca              354
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<210> 674
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 674

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

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

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

Ala Met Ile Tyr Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 675
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 675
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24

<210> 676
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 676

Gly Phe Thr Phe Arg Ser Tyr Gly
 1 5

<210> 677
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 677
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24

<210> 678
 <211> 8
 <212> PRT
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<220>
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<400> 678

Ile Tyr Tyr Asp Gly Lys Asn Lys
 1 5

10296W001-Sequence.txt

<210> 679
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 679
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33

<210> 680
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 680

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 681
<211> 321
<212> DNA
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<220>
<223> synthetic

<400> 681
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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
gaagatgttg cagtttatta ctgtcagcaa cataataact ggcctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 682
<211> 107
<212> PRT
<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 682

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ser Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 683

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 683

cagagaatta gcagcaac

18

<210> 684

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 684

Gln Arg Ile Ser Ser Asn
1 5

<210> 685

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 685

ggtgcatcc

9

<210> 686

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 686

Gly Ala Ser
1

<210> 687

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 687

cagcaacata ataactggcc tctcact

27

<210> 688

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 688

Gln Gln His Asn Asn Trp Pro Leu Thr
1 5

<210> 689

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 689

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ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat	180
gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat	240
ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct	300
gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca	354

<210> 690

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 690

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe	
20 25 30	

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

10296W001-Sequence.txt

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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24

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Gly Phe Thr Phe Arg Ser Phe Gly
1 5

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24

<210> 694
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<400> 694

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> 695
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33

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<400> 696

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
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<210> 697
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10296W001-Sequence.txt

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<400> 697

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ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180
aggttcagtg gcagtggggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240
gaagattttg cagtttttta ctgtcagcag tataataata ggctctcac tttcggcgga 300
gggaccgagg tggagatcaa a 321

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<211> 107

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<223> synthetic

<400> 698

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

```

```

Glu Arg Val Ile Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
          35           40           45

```

```

Tyr Gly Ala Thr Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
          50           55           60

```

```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65           70           75           80

```

```

Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
          85           90           95

```

```

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
          100          105

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18

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Gln Ser Ile Ser Arg Asn
 1 5

<210> 701
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<400> 701
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9

<210> 702
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<220>
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<400> 702

Gly Ala Thr
 1

<210> 703
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<400> 703
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27

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Gln Gln Tyr Asn Asn Arg Pro Leu Thr
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 ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180
 gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240
 ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300
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 <211> 118

10296W001-Sequence.txt

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<400> 706

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 707
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<210> 708
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<400> 708

Gly Phe Thr Phe Arg Ser Phe Gly
 1 5

<210> 709
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<400> 709
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24

<210> 710
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<400> 710

Ile Tyr Phe Asp Gly Lys Asn Lys
 1 5

<210> 711
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33

10296W001-Sequence.txt

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<400> 712

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1				5					10	

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<400> 713

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ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc	180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct	240
gaagattttg cagtttttta ctgtcagcag tataataata ggcctctcac tttcggcgga	300
gggaccgagg tggagatcaa a	321

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10296W001-Sequence.txt

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1 5 10 15

Glu Arg Val Ile Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Xaa Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 715
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18

<210> 716
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<400> 716

Gln Ser Ile Ser Arg Asn
1 5

<210> 717
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<400> 717
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9

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Gly Ala Thr
 1

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27

<210> 720
 <211> 9
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<400> 720

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

10296W001-Sequence.txt

<210> 721
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 ccaggcaagg ggctggagtg ggtggcaatg atatattatg atggaaacaa taaatactat 180
 gcagactccg tgagggggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300
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<210> 722
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 722
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 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Met Ile Tyr Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

10296W001-Sequence.txt

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 723
<211> 24
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<400> 723
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24

<210> 724
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<400> 724

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> 725
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<400> 725
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24

<210> 726
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<220>
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<400> 726

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> 727
<211> 33
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gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 728
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<400> 728

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 729
<211> 321
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<220>
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<400> 729

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60

ctctcctgca gggccagtca gagtgttagc agcaacttgg cctggtacca gcagaaacct

120

10296W001-Sequence.txt

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc      180
aggttcagtg gcagtggggtc tgggacagag ttcactctca ccatcagcag cctgcagtct      240
gaagattttg cagtttatta ctgtcagcag tataataaca ggcctctcac tttcggcgga      300
gggaccaagg tggagatcaa a                                              321
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<400> 730

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
          20           25           30
```

```
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
          35           40           45
```

```
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
          50           55           60
```

```
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65           70           75           80
```

```
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
          85           90           95
```

```
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105
```

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18

<210> 732

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<220>

<223> synthetic

<400> 732

Gln Ser Val Ser Ser Asn

1 5

<210> 733

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<212> DNA

<213> Artificial Sequence

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<400> 733

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9

<210> 734

<211> 3

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27

<210> 736

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<400> 736

Gln Gln Tyr Asn Asn Arg Pro Leu Thr

1

5

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<211> 372

<212> DNA

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ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtcgtag catagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagataat 300

agtggctatg gccgctatta ctactacggg atggacgtct ggggccaagg gaccacggtc 360

tccgtctcct ca 372

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<211> 124

<212> PRT

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<400> 738

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Arg Ser Ile Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Val Lys Asp Asn Ser Gly Tyr Gly Arg Tyr Tyr Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Ser Val Ser Ser
 115 120

<210> 739

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 739

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24

<210> 740

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 740

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 741

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 741

attagttgga atagtcgtag cata

24

<210> 742

<211> 8

<212> PRT

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<220>

<223> synthetic

<400> 742

Ile Ser Trp Asn Ser Arg Ser Ile
1 5

<210> 743

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 743

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<223> synthetic

<400> 744

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1				5					10					15	

Val

<210> 745

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 745

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ggccaggctc	ccaggctcct	catctatggt	gcatccacca	gggccactag	tatcccagcc	180
aggttcagtg	gcagtgggtc	tgggacagag	ttcactctca	ccatcagcag	cctgcagtct	240
gaagattttg	cagtttattt	ctgtcagcac	tattataact	ggcctctcac	tttcggcgga	300
gggaccaagg	tggagatcag	a				321

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<212> PRT

<213> Artificial Sequence

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<400> 746

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

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Gly	Asn
			20					25					30		

10296W001-Sequence.txt

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Ser Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Tyr Phe Cys Gln His Tyr Tyr Asn Trp Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
 100 105

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18

<210> 748
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 748

Gln Ser Val Ser Gly Asn
 1 5

<210> 749
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 749

ggtgcatcc

9

<210> 750

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

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<400> 750

Gly Ala Ser

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<210> 751

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 751

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27

<210> 752

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<212> PRT

<213> Artificial Sequence

<220>

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<400> 752

Gln His Tyr Tyr Asn Trp Pro Leu Thr

1

5

<210> 753

<211> 369

<212> DNA

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

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<400> 753

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ccaggaagg	gcctggagtg	ggtctcaggt	atcagttgga	atagtggtag	cataggctat	180
gtggactctg	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	ctccctgtat	240
ctgcaaatga	acagtctgag	agctgaggac	acggccttgt	actactgtgc	aaaagataat	300
agtggctacg	gctattatta	ctacggtatg	gacgtctggg	gccaagggac	cacggtcacc	360
gtctcctca						369

<210> 754

<211> 123

<212> PRT

<213> Artificial Sequence

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<400> 754

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

10296W001-Sequence.txt

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 755
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 755
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24

<210> 756
<211> 8
<212> PRT
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<220>
<223> synthetic

<400> 756

Gly Phe Thr Phe Asp Asp Phe Thr
1 5

<210> 757
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 757
atcagttgga atagtggtag cata

24

<210> 758
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 758

Ile Ser Trp Asn Ser Gly Ser Ile

1 5

<210> 759

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 759

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<210> 760

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 760

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val

1 5 10 15

<210> 761

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 761

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tggtaccagc agaaaccagg acagcctcct aagctgctca ttctactgggc atctaccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

ccgtacactt ttggccaggg gaccaagctg gagatcaaa 339

<210> 762
 <211> 113
 <212> PRT
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<400> 762

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

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

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
 100 105 110

Lys

<210> 763
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 763

cagagtgttt tatacagctc caacaataag aactac

36

<210> 764

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 764

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 765

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 765

tgggcatct

9

<210> 766

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

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<400> 766

Trp Ala Ser
1

<210> 767

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 767

cagcaatatt atagtactcc gtacact

27

<210> 768

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 768

Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr

1 5

<210> 769

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

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acctgcacct tctctggggtt ctactcagc actagtggaa tgtgtgtgag ctggatccgt 120

cagccccag ggaaggccct ggagtggctt gcacgcattg attgggatga tgataaatac 180

tacagcacat ctctgaagac caggctcacc atctccaagg acacctcaa aaaccaggtg 240

gtccttacia tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggatg 300

gatatagtgg gagctagagg ggggtgggtc gacccttggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> 770

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 770

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Cys Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Arg Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Met Asp Ile Val Gly Ala Arg Gly Gly Trp Phe Asp Pro
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 771

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 771

gggttctcac tcagcactag tggaatgtgt

30

<210> 772

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 772

Gly	Phe	Ser	Leu	Ser	Thr	Ser	Gly	Met	Cys
1				5					10

<210> 773

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 773

attgattggg atgatgataa a

21

<210> 774

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 774

Ile	Asp	Trp	Asp	Asp	Asp	Lys
1				5		

<210> 775

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 775

gcacggatgg atatagtggg agctagaggg ggggtggttcg acccc

45

<210> 776

<211> 15

<212> PRT

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 776

Ala	Arg	Met	Asp	Ile	Val	Gly	Ala	Arg	Gly	Gly	Trp	Phe	Asp	Pro
1				5					10					15

<210> 777

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 777

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gggaaagccc	ctaagtcct	gatctatgct	gcatccagtt	tgcaaagtgg	ggtcccatca	180
aagttcagcg	gcagtggatc	tgggacagat	ttcactctca	ccatcagcag	cctgcagcct	240
gaagattttg	caacttatta	ctgccaacag	tataatagtt	acccgctcac	tttcggcgga	300
gggaccaagg	tggagatcaa	a				321

<210> 778

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 778

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Asn	Tyr
			20					25					30		

Leu	Ala	Trp	Phe	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Ser	Leu	Ile
			35				40					45			

10296W001-Sequence.txt

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 779
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 779
cagggcatta gcaattat

18

<210> 780
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 780

Gln Gly Ile Ser Asn Tyr
1 5

<210> 781
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 781
gctgcatcc

9

<210> 782
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 782

Ala Ala Ser
1

<210> 783
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 783
caacagtata atagttaccc gtcact

27

<210> 784
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 784

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 785
<211> 404
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

10296W001-Sequence.txt

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tcctgtgctg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct      120
ccaggcaagg ggctggagtg ggtggcaatg atatattatg atggaaataa taaaaagtat      180
gcagactccg tgagggggccg attcaccatt tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agtcgaggac acggctgtgt atttctgtgc gcgagggcct      300
gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctcagccaaa      360
acaacagccc caccggttta tccactggcc cctggaagct tggg                        404
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<210> 786
<211> 134
<212> PRT
<213> Artificial Sequence
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<220>
<223> synthetic
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<400> 786

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
          20             25             30

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

Ala Met Ile Tyr Tyr Asp Gly Asn Asn Lys Lys Tyr Ala Asp Ser Val
          50             55             60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
          100            105            110
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10296W001-Sequence.txt

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

Leu Ala Pro Gly Ser Leu
 130

<210> 787
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 787
 ggattcacct tcagaagtta tggc

24

<210> 788
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 788

Gly Phe Thr Phe Arg Ser Tyr Gly
 1 5

<210> 789
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 789
 atatattatg atggaaataa taaa

24

<210> 790
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 790

Ile Tyr Tyr Asp Gly Asn Asn Lys

1 5

<210> 791

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 791

gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 792

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 792

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro

1 5 10

<210> 793

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 793

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ctctcctgca gggccagtca gagggttagc aggaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactga tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcattctca acatcagcag cctgcagtct 240

10296W001-Sequence.txt

gaagattttg cactttatta ctgtcaacaa tatagtaact ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> 794
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 794

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Ile Leu Asn Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Leu Tyr Tyr Cys Gln Gln Tyr Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 795
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 795
cagagtgtta gcaggaac

18

<210> 796
<211> 6
<212> PRT
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<220>
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<400> 796

Gln Ser Val Ser Arg Asn
1 5

<210> 797
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 797
ggtgcatcc

9

<210> 798
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 798

Gly Ala Ser
1

<210> 799
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 799
caacaatata gtaactggcc tctcact 27

<210> 800
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 800

Gln Gln Tyr Ser Asn Trp Pro Leu Thr
1 5

<210> 801
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 801
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tcctgtgctg cgtctggttt caccttcaga agttttggca tgcactgggt ccgccaggct 120
ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180
gcagactccg tgagggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240
ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300
gggtacaact ggctcgacct ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 802
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
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<400> 802

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
 20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 803
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 803
 ggtttcacct tcagaagttt tggc

24

<210> 804
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 804

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> 805
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 805
atatattttg atggaaaaa taaa

24

<210> 806
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 806

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> 807
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 807
gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 808
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 808

10296W001-Sequence.txt

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 809
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
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<400> 809
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ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcagaaacct 120
ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180
aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240
gaagattttg cagtttttta ctgtcagcag tataataata ggctctcac tttcggcgga 300
gggaccgagg tggagatcaa a 321

<210> 810
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<400> 810

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

Glu Arg Val Ile Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
50 55 60

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
100 105

<210> 811
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 811
cagagtatta gcaggaac

18

<210> 812
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 812

Gln Ser Ile Ser Arg Asn
1 5

<210> 813
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 813
ggtgcaacc

9

<210> 814
<211> 3

<212> PRT
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<220>
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<400> 814

Gly Ala Thr
 1

<210> 815
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 815
 cagcagtata ataataggcc tctcact

27

<210> 816
 <211> 9
 <212> PRT
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<220>
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<400> 816

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

<210> 817
 <211> 354
 <212> DNA
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<220>
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<400> 817
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 tcctgtgctg cgtctggttt caccttcaga agttttggca tgcactgggt ccgccaggct 120
 ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

10296W001-Sequence.txt

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240
 ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300
 ggggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 818
 <211> 118
 <212> PRT
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<220>
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<400> 818

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
 20 25 30

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

Ala Met Ile Tyr Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 819
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
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<400> 819
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24

<210> 820
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 820

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> 821
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 821
atatattttg atggaaaaaa taaa

24

<210> 822
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 822

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> 823
<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 823

gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 824

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<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 824

Ala	Arg	Gly	Pro	Gly	Tyr	Asn	Trp	Leu	Asp	Pro
1				5					10	

<210> 825

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 825

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ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttta ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> 826

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 826

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

Glu Arg Val Ile Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Thr Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Phe Tyr Cys Gln Gln Tyr Asn Asn Arg Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Glu Val Glu Ile Lys
 100 105

<210> 827

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 827

cagagtatta gcaggaac

18

<210> 828

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 828

Gln Ser Ile Ser Arg Asn
1 5

<210> 829

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 829

ggtgcaacc

9

<210> 830

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 830

Gly Ala Thr
1

<210> 831

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 831

cagcagtata ataataggcc tctcact

27

<210> 832

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 832

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
 1 5

<210> 833

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 833

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 tcctgttcag cgtctggttt caccttcagt agttatgcca tgactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaactaa taaatattat 180
 ttagattccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240
 ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagagatcgg 300
 ggaagtataa taaccactg gggccaggga accctgggtca ccgtctcctc a 351

<210> 834

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 834

Gln Val His Leu Glu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

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

10296W001-Sequence.txt

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

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

Ala Arg Asp Arg Gly Ser Ile Ile Thr His Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 835
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 835
ggtttcacct tcagtagtta tgcc

24

<210> 836
<211> 8
<212> PRT
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<220>
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<400> 836

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

<210> 837
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 837
atatggtatg atggaactaa taaa

24

<210> 838
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 838

Ile Trp Tyr Asp Gly Thr Asn Lys
1 5

<210> 839
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 839
gcgagagatc ggggaagtat aataaccac

30

<210> 840
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 840

Ala Arg Asp Arg Gly Ser Ile Ile Thr His
1 5 10

<210> 841
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

10296W001-Sequence.txt

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctataggaga cagagtcacc      60
atcacttgcc gggcaagtca gaacattagc agctatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag acttacagta cccctccgat caccttcggc      300
caagggacac gactggagat taaa                                             324
```

```
<210> 842
<211> 108
<212> PRT
<213> Artificial Sequence
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```
<220>
<223> synthetic
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<400> 842

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Thr Pro Pro
          85           90           95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
          100          105
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<210> 843
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 843
 cagaacatta gcagctat

18

<210> 844
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 844

Gln Asn Ile Ser Ser Tyr
 1 5

<210> 845
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 845
 gctgcatcc

9

<210> 846
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 846

Ala Ala Ser
 1

10296W001-Sequence.txt

<210> 847
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 847
 caacagactt acagtacccc tccgatcacc

30

<210> 848
 <211> 10
 <212> PRT
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<220>
 <223> synthetic

<400> 848

Gln Gln Thr Tyr Ser Thr Pro Pro Ile Thr
 1 5 10

<210> 849
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 849
 gaagtacagc tggtggagtc tgggggaggc ttggtacggc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccgccaagct 120
 ccagggaagg gcctggagtg ggtctcagat attagtggga atagtgggac cataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag acctgaggac acggccttgt attactgtgc aaaagatatg 300
 agtggctacg cccactacta ctactacggt atggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 850
 <211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 850

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Tyr Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 851

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 851

ggattcacct ttgatgatta tacc

<210> 852
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 852

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 853
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 853
 attagttgga atagtgggac cata

24

<210> 854
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 854

Ile Ser Trp Asn Ser Gly Thr Ile
 1 5

<210> 855
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 855
 gcaaaagata tgagtggcta cgcccactac tactactacg gtatggacgt c

51

10296W001-Sequence.txt

<210> 856
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 856

Ala	Lys	Asp	Met	Ser	Gly	Tyr	Ala	His	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 857
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 857

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc	300
caagggacac gactggagat taaa	324

<210> 858
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 858

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

10296W001-Sequence.txt

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 859
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 859
cagagcatta gcagctat

18

<210> 860
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 860

Gln Ser Ile Ser Ser Tyr
1 5

<210> 861
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 861
 gctgcatcc

9

<210> 862
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 862

Ala Ala Ser
 1

<210> 863
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 863
 caacagagtt acagtacccc tccgatcacc

30

<210> 864
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 864

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
 1 5 10

10296W001-Sequence.txt

<210> 865
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 865
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 tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctccgat attagttgga atagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccgtc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaataa acagtctgag aggtgaggac acggccctgt attactgtgc aaaagatatg 300
 agtggctacg cccactacgg ctactacggt atggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 866
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 866
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Asp Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

10296W001-Sequence.txt

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Gly Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 867
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 867
 ggattcacct ttgatgatta tacc

24

<210> 868
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 868

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 869
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 869
 attagttgga atagtggtag cata

24

<210> 870
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 870

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 871
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 871
 gcaaaagata tgagtggcta cgcccactac ggctactacg gtatggacgt c

51

<210> 872
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 872

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Gly Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 873
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

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<400> 873
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atcacttgcc gggcaagtca gagcattagg aactatttaa attggtatca gcagaaacca      120
gggaaagtcc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta accctccgat caccttcggc      300
caagggacac gactggagat taaa                                             324

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<210> 874
<211> 108
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 874
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
          35           40           45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Asn Pro Pro
          85           90           95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
          100          105

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<210> 875
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 875
cagagcatta ggaactat

18

<210> 876
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 876

Gln Ser Ile Arg Asn Tyr
1 5

<210> 877
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 877
gctgcatcc

9

<210> 878
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 878

Ala Ala Ser
1

10296W001-Sequence.txt

<210> 879
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic

 <400> 879
 caacagagtt acagtaaccc tccgatcacc 30

<210> 880
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 880

Gln Gln Ser Tyr Ser Asn Pro Pro Ile Thr
 1 5 10

<210> 881
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 881
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 tcctgtacaa cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg gatctctgat attagttaga atggtggaac caaaggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgcaaaaaa ctccctgtat 240
 ctgcaaatgg acagtctgag aggtgaggac acggccttat attactgtgt aaaagataaa 300
 agtggctacg ggcacttcta cttcggtttg gacgtctggg gccaaaggac cacggtcacc 360
 gtctcctca 369

<210> 882
 <211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 882

Glu Ala Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

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

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

Ser Asp Ile Ser Trp Asn Gly Gly Thr Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Arg Gly Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Phe Gly Leu Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 883

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 883

ggattcacct ttgatgatta tacc

<210> 884
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 884

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 885
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 885
 attagttgga atggtggaac caaa

24

<210> 886
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 886

Ile Ser Trp Asn Gly Gly Thr Lys
 1 5

<210> 887
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 887
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48

10296W001-Sequence.txt

<210> 888
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 888

Val	Lys	Asp	Lys	Ser	Gly	Tyr	Gly	His	Phe	Tyr	Phe	Gly	Leu	Asp	Val
1				5					10					15	

<210> 889
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 889

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ttcacttgcc	gggcaagtca	gagcattagc	aggcatttaa	gttggtatca	gcagaaacca	120
gggaaagccc	ctaagctcct	gatctatgct	gcatccagtt	tggaaagtgg	ggtccttca	180
aggttcagt	gcagtggatc	tgggacagat	ttcactctca	ccatcagcag	tctgcaccct	240
gaagattttg	caacttacta	ctgtcaacag	agctacagta	accctccgat	caccttcggc	300
caagggacac	gactggagat	taaa				324

<210> 890
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 890

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

Asp	Arg	Val	Thr	Phe	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Arg	His
			20					25					30		

10296W001-Sequence.txt

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu His Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Asn Pro Pro
 85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 891
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 891
 cagagcatta gcaggcat

18

<210> 892
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 892

Gln Ser Ile Ser Arg His
 1 5

<210> 893
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 893

gctgcatcc

9

<210> 894

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 894

Ala Ala Ser

1

<210> 895

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 895

caacagagct acagtaaccc tccgatcacc

30

<210> 896

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 896

Gln Gln Ser Tyr Ser Asn Pro Pro Ile Thr

1

5

10

<210> 897

<211> 369

<212> DNA

<213> Artificial Sequence

10296W001-Sequence.txt

 $\langle 220 \rangle$

<223> synthetic

<400> 897

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tcctgtgcag cctctggatt caagtttgct gattatgcc a tgcactgggt ccggcaagct 120

ccaggggaagg gcctggagtg ggtctcagag attagttagg atagtggtag cataggttat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagataaa 300

agtggctacg ggcactacta tatcggtatg gacgtctggg gccaaagggac cacgggtcatc 360

gtctcctcc 369

<210> 898

$\langle 211 \rangle$ 123

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> synthetic

<400> 898

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ala Asp Tyr
20 25 30

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

Ser Glu Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

10296W001-Sequence.txt

Val Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Ile Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Ile Val Ser Ser
 115 120

<210> 899
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 899
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24

<210> 900
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 900

Gly Phe Lys Phe Ala Asp Tyr Ala
 1 5

<210> 901
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 901
 attagttgga atagtggttag cata

24

<210> 902
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 902

Ile Ser Trp Asn Ser Gly Ser Ile

1 5

<210> 903

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 903

gtaaaagata aaagtggcta cgggcactac tatatcggta tggacgtc 48

<210> 904

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 904

Val Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Ile Gly Met Asp Val

1 5 10 15

<210> 905

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 905

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagtattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

10296W001-Sequence.txt

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300
caagggacac gactggagat taaa 324

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<211> 108
<212> PRT
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<400> 906

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

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18

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<400> 908

Gln Ser Ile Ser Ser Tyr
1 5

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9

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Ala Ala Ser
1

<210> 911
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<400> 911
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<210> 912
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<400> 912

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
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<210> 913
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tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctccgat attagttgga atagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccgtc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag aggtgaggac acggccttgt attactgtgc aaaagatatg 300
agtggctacg gccactacgg caagtacggt atggacgtct ggggccaagg gaccacggtc 360
accgtctcct ca 372

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10296W001-Sequence.txt

Glu Val His Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Met Ser Gly Tyr Gly His Tyr Gly Lys Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 915
<211> 24
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<400> 915
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24

<210> 916
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<212> PRT
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<220>
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<400> 916

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 917

<211> 24

<212> DNA

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<220>

<223> synthetic

<400> 917

attagttgga atagtggtag cata

24

<210> 918

<211> 8

<212> PRT

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<223> synthetic

<400> 918

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 919

<211> 51

<212> DNA

<213> Artificial Sequence

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<400> 919

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<212> PRT

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10296W001-Sequence.txt

<400> 920

Ala Lys Asp Met Ser Gly Tyr Gly His Tyr Gly Lys Tyr Gly Met Asp
1 5 10 15

Val

<210> 921

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 921

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gggaaagtcc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagtg gcagtggatc tgggacagat ttactctca ccatcaacag tctgcaacct	240
gacgattttg caacttacta ctgtcaacag acttacagta accctccgat caccttcggc	300
caaggacac gactggagat taaa	324

<210> 922

<211> 108

<212> PRT

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<220>

<223> synthetic

<400> 922

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

10296W001-Sequence.txt

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Asn Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

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<400> 923
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18

<210> 924
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<212> PRT
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<400> 924

Gln Ser Ile Arg Ser Tyr
1 5

<210> 925
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 925
gctgcatcc

9

<210> 926
<211> 3
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<400> 926

Ala Ala Ser
1

<210> 927
<211> 30
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<400> 927
caacagactt acagtaaccc tccgatacc

30

<210> 928
<211> 10
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<220>
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<400> 928

Gln Gln Thr Tyr Ser Asn Pro Pro Ile Thr
1 5 10

<210> 929
<211> 372
<212> DNA
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<220>
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10296W001-Sequence.txt

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ccagggaagg gcctggagtg ggtctcaatt attagttgga atggtaatac cattgactat      180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240
cttcaaatac acagtctgag agctgaggac acggccttgt attactgtgc aaaagataag      300
agtggctacg gacacttcta ctattacgtt ttggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                                372

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<210> 930
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<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 930

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg
1           5           10           15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Val Leu Asp
          100          105          110

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Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 931
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 931
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24

<210> 932
<211> 8
<212> PRT
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<220>
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<400> 932

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 933
<211> 24
<212> DNA
<213> Artificial Sequence

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<400> 933
attagttgga atggaatac catt

24

<210> 934
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 934

Ile Ser Trp Asn Gly Asn Thr Ile
 1 5

<210> 935

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

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<400> 935

gcaaaagata agagtggcta cggacacttc tactattacg ttttggacgt c 51

<210> 936

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 936

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Val Leu Asp
 1 5 10 15

Val

<210> 937

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 937

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgct gcttccagtt tgcaaagtgg ggtcccgta 180

aggttcagtg gcagtggttc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

10296W001-Sequence.txt

gaagattttg caacttacta ctctcaacag agttacagtt tcccgtaggac gttcggccaa 300
gggaccaagg tggaaatcaa a 321

<210> 938
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<400> 938

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Ser Gln Gln Ser Tyr Ser Phe Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 939
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 939
cagagcatta acaactat

18

<210> 940
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<212> PRT
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<220>
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<400> 940

Gln Ser Ile Asn Asn Tyr
1 5

<210> 941
<211> 9
<212> DNA
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<220>
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<400> 941
gctgcttcc

9

<210> 942
<211> 3
<212> PRT
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<220>
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<400> 942

Ala Ala Ser
1

<210> 943
<211> 27
<212> DNA
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<400> 943
caacagagtt acagtttccc gtggacg 27

<210> 944
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<400> 944

Gln Gln Ser Tyr Ser Phe Pro Trp Thr
1 5

<210> 945
<211> 363
<212> DNA
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<220>
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<400> 945
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ccaggtaagg gactagagtg gatggcacac atatgggtata atggaaagaa taaatattat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctatat 240
ctgcaaatga acagcctgag acccgaggac acggctgtat attattgtgc gagagatgggt 300
gtatcagcac gtggtactcc atttgactac tggggccagg gaaccctggt caccgtctcc 360
tca 363

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<212> PRT
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<400> 946

10296W001-Sequence.txt

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

Ser Leu Arg Pro Ser Cys Ala Ala Ser Gly Phe Ser Phe Arg Asp Tyr
20 25 30

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

Ala His Ile Trp Tyr Asn Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Val Ser Ala Arg Gly Thr Pro Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 947
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 947
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24

<210> 948
<211> 8
<212> PRT
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<400> 948

Gly Phe Ser Phe Arg Asp Tyr Gly
1 5

<210> 949

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

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<400> 949

atatggtata atggaaagaa taaa

24

<210> 950

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<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 950

Ile Trp Tyr Asn Gly Lys Asn Lys
1 5

<210> 951

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 951

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<210> 952

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<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 952

Ala Arg Asp Gly Val Ser Ala Arg Gly Thr Pro Phe Asp Tyr
 1 5 10

<210> 953

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 953

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 ggagaaactg ctattttcat tattcaagaa gcttctactc tcgttcctgg aatctcacct 180
 cgattcagtg gcagcgggta tggaacacat tttaccctca caattaataa catagattct 240
 gaggatgctg cattttactt ctgtctccaa catgataatt tcccgtacac ttttggccag 300
 gggaccaagc tggagatcaa a 321

<210> 954

<211> 107

<212> PRT

<213> Artificial Sequence

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<400> 954

Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Ala Pro Gly
 1 5 10 15

Asp Lys Val Ser Ile Ser Cys Ile Ala Ser Gln Tyr Ile Asp Asp Asp
 20 25 30

Val Asn Trp Tyr Gln Gln Lys Pro Gly Glu Thr Ala Ile Phe Ile Ile
 35 40 45

Gln Glu Ala Ser Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly
 50 55 60

10296W001-Sequence.txt

Ser Gly Tyr Gly Thr His Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser
65 70 75 80

Glu Asp Ala Ala Phe Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 955
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<212> DNA
<213> Artificial Sequence

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<400> 955
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18

<210> 956
<211> 6
<212> PRT
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<400> 956

Gln Tyr Ile Asp Asp Asp
1 5

<210> 957
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<400> 957
gaagcttct

9

<210> 958
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<400> 958

Glu Ala Ser
 1

<210> 959
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 <212> DNA
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<220>
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<400> 959
 ctccaacatg ataatttccc gtacact

27

<210> 960
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<400> 960

Leu Gln His Asp Asn Phe Pro Tyr Thr
 1 5

<210> 961
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 <213> Artificial Sequence

<220>
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<400> 961
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tcctgtgcag cctcttattt caccttttagc agttttgccca tgaactgggt ccgccaggct 120

10296W001-Sequence.txt

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ccagggcagg gcctggagtg ggtctcagct attagtggta gggctctcagc tattagtgggt      180
agtgggtggta tcacatacta cgcagactcc gtgaagggcc ggttcatcat ctccagagac      240
aattccaaga acacgctgta tctgcaaattg agcggcctga gagccgagga cacggccgta      300
tattactgtg cgaaaggccc ctatttgact acagtcaccc cctttgacta ctggggccag      360
ggaaccctgg tcaccgtctc ctca      384
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 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 962

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Tyr Phe Thr Phe Ser Ser Phe
 20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Arg Val Ser Ala Ile Ser Gly Ser Gly Gly Ile
 50 55 60

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp
 65 70 75 80

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Ser Gly Leu Arg Ala Glu
 85 90 95

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Pro Tyr Leu Thr Thr Val
 100 105 110

Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 963
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 963
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24

<210> 964
 <211> 8
 <212> PRT
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<220>
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<400> 964

Tyr Phe Thr Phe Ser Ser Phe Ala
 1 5

<210> 965
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<220>
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<400> 965
 attagtggta gtggtggtat caca

24

<210> 966
 <211> 8
 <212> PRT
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<220>
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<400> 966

Ile Ser Gly Ser Gly Gly Ile Thr
 1 5

<210> 967
 <211> 42
 <212> DNA
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<400> 967
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<210> 968
 <211> 14
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<220>
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<400> 968

Ala Lys Gly Pro Tyr Leu Thr Thr Val Thr Pro Phe Asp Tyr
 1 5 10

<210> 969
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 969
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 gggaaagccc ctaaactcct gatctatgct gtatccagtt tgcaaaatgg ggtcccatca 180
 aggttcagcg gcagtggatc tgggacagat ttcaccctca ccatcagcag cctgcagcct 240
 gaagactttg caacttacta ttgtcaacag gctaacagtt tcccattcac tttcggccct 300
 gggaccaagc tggagatcaa acga 324

<210> 970
 <211> 108

<212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 970

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Val Ser Ser Leu Gln Asn Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 971
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 971
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18

<210> 972
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 972

Gln Gly Ile Ser Ser Trp
1 5

<210> 973

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 973

gctgtatcc

9

<210> 974

<211> 3

<212> PRT

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<220>

<223> synthetic

<400> 974

Ala Val Ser
1

<210> 975

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 975

caacaggcta acagtttccc attcact

27

<210> 976

<211> 9

<212> PRT

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<223> synthetic

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Gln Gln Ala Asn Ser Phe Pro Phe Thr

1 5

<210> 977

<211> 369

<212> DNA

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ccaggggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggttat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaata acagtctgag agctgaggac acggccttat attactgtgt aaaagataat 300

agtggctacg catcctacta ctacggtatg gacgtctggg gccaaaggac cacggtcacc 360

gtctcctca 369

<210> 978

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 978

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr

20 25 30

10296W001-Sequence.txt

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Asn Ser Gly Tyr Ala Ser Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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24

<210> 980
<211> 8
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<400> 980

Gly Phe Thr Phe Ala Asp Tyr Ala
1 5

<210> 981
<211> 24

<212> DNA
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attagttgga atagtggtag tata

24

<210> 982
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<212> PRT
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<400> 982

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 983
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 983
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48

<210> 984
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<400> 984

Val Lys Asp Asn Ser Gly Tyr Ala Ser Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 985
<211> 324

10296W001-Sequence.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 985

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca      180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct      240
gaagatattg caacatatta ctgtcaacag tatgataatc tcccattcac tttcggcctt      300
gggaccaaag tggatatcaa acga                                           324

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<210> 986

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 986

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50           55           60

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Phe
          85           90           95

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Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> 987
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<400> 987
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18

<210> 988
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<400> 988

Gln Ser Ile Ser Ser Tyr
1 5

<210> 989
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<220>
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<400> 989
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9

<210> 990
<211> 3
<212> PRT
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<220>
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<400> 990

Asp Ala Ser

1

<210> 991

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 991

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27

<210> 992

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 992

Gln Gln Tyr Asp Asn Leu Pro Phe Thr

1

5

<210> 993

<211> 378

<212> DNA

<213> Artificial Sequence

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<400> 993

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tcctgtgcag cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120

ccaggcaaag ggctggagtg ggtgacagtt atattacatg atggaagtta taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctacat 240

ctgcaaatga acagcctgag aactgaggac acggctgtat attactgtgc gaaagggcct 300

atgtttcggg gagtccctta caaccactac tatggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca

<210> 994
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<400> 994

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

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

Thr Val Ile Leu His Asp Gly Ser Tyr Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Gly Pro Met Phe Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
 100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 995
 <211> 24
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<220>

<223> synthetic

<400> 995

ggattcacct tcagtaacta tggc

24

<210> 996

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<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 996

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

<210> 997

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 997

atattacatg atggaagtta taaa

24

<210> 998

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 998

Ile Leu His Asp Gly Ser Tyr Lys
1 5

<210> 999

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 999

gcgaaagggc ctatgtttcg gggagtcctt tacaaccact actatggtat ggacgtc 57

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<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1000

Ala	Lys	Gly	Pro	Met	Phe	Arg	Gly	Val	Pro	Tyr	Asn	His	Tyr	Tyr	Gly
1				5				10						15	

Met Asp Val

<210> 1001

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1001

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gggaaagccc ctaagcgct gatctatgct gcatccagtt tgcaaagtgg ggtctcatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtagac ttttggccag 300

gggaccaagg tggaatcaa acga 324

<210> 1002

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1002

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Ser Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1003

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1003

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18

<210> 1004

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1004

Gln Gly Ile Arg Asn Asp
1 5

<210> 1005

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1005

gctgcatcc

9

<210> 1006

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<220>

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Ala Ala Ser

1

<210> 1007

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1007

ctacagcata atagttaccc gtacact

27

<210> 1008

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1008

Leu Gln His Asn Ser Tyr Pro Tyr Thr
 1 5

<210> 1009

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1009

gaggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggaggtc cctgagactc 60
 tcctgtacag cgtcagggttt ccccttcagt cgctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggaatg ggtgacattt atatggtatg atggaagtaa taaatactat 180
 gcagactccg cgaagggccg attcaccatc accagagaca attccaagaa cacggtgtat 240
 ctgcaaatgg acagcctgag agccgatgac acggctgttt attattgtgt gagagatcag 300
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<210> 1010

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1010

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

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Pro Phe Ser Arg Tyr
 20 25 30

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

Thr Phe Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Ala
 50 55 60

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Val Tyr
65 70 75 80

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

Val Arg Asp Gln Ala Ala Leu Tyr Tyr Phe Asp Ser Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 1011
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<220>
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<400> 1011
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24

<210> 1012
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1012

Gly Phe Pro Phe Ser Arg Tyr Gly
1 5

<210> 1013
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1013
atatggtatg atggaagtaa taaa

24

<210> 1014
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1014

Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> 1015
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1015
gtgagagatc aggcagctct ctactatctt gactct

36

<210> 1016
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1016

Val Arg Asp Gln Ala Ala Leu Tyr Tyr Phe Asp Ser
1 5 10

<210> 1017
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
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10296W001-Sequence.txt

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gggaaagccc ctaagctcct gatctctgct gcatccagtt tgcaaagtgg agtcccatca      180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcgg cctgcagcct      240
gaagattttg caacttacta ttgtcaaaag gctaacagtt tccctttcac tttcgggcct      300
gggaccaagc tggagatcaa acga                                              324

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<210> 1018
<211> 108
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 1018

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Trp
          20           25           30

```

```

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

Ser Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Lys Ala Asn Ser Phe Pro Phe
          85           90           95

```

```

Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
          100          105

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<210> 1019
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1019
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18

<210> 1020
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1020

Gln Gly Ile Ser Arg Trp
 1 5

<210> 1021
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1021
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9

<210> 1022
 <211> 3
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<220>
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<400> 1022

Ala Ala Ser
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10296W001-Sequence.txt

<210> 1023
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<400> 1023
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27

<210> 1024
<211> 9
<212> PRT
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<220>
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<400> 1024

Gln Lys Ala Asn Ser Phe Pro Phe Thr
1 5

<210> 1025
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1025
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tcctgtgcag cctctggatt caccttcagt agttatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtgacagtt atattacatg atggaagtaa tagatactct 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctttat 240
ctgcaaatga acatcctgag agttgaggac acggctgtgt attactgtac gaaaggggct 300
atggttcggg gagtccctta caatcactac tacggcatgg acgtctgggg ccaagggacc 360
acggtcaccg tctcctca 378

<210> 1026
<211> 126

10296W001-Sequence.txt

<212> PRT
<213> Artificial Sequence

<220>
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<400> 1026

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Thr Val Ile Leu His Asp Gly Ser Asn Arg Tyr Ser Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ile Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 1027
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1027

ggattcacct tcagtagtta tggc

24

<210> 1028
 <211> 8
 <212> PRT
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<220>
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<400> 1028

Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 1029
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1029
 atattacatg atggaagtaa taga

24

<210> 1030
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1030

Ile Leu His Asp Gly Ser Asn Arg
 1 5

<210> 1031
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1031
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57

10296W001-Sequence.txt

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<400> 1032

Thr	Lys	Gly	Ala	Met	Val	Arg	Gly	Val	Pro	Tyr	Asn	His	Tyr	Tyr	Gly
1				5					10					15	

Met Asp Val

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 <211> 324
 <212> DNA
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<220>
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gggaaagccc ctaagcgcct aatctatgct gcatccattt tgcaaagtgg ggtcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct	240
gaagattttg caacttatta ctgtctacag cataatagtt acccgtagac ttttggccag	300
gggaccaagc tggagatcaa acga	324

<210> 1034
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1034

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

10296W001-Sequence.txt

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
 20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
 35 40 45

Tyr Ala Ala Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 1035
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1035
 cagggcatta gaaatgat

18

<210> 1036
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1036

Gln Gly Ile Arg Asn Asp
 1 5

<210> 1037
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1037
 gctgcatcc

9

<210> 1038
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1038

Ala Ala Ser
 1

<210> 1039
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1039
 ctacagcata atagttaccc gtacact

27

<210> 1040
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1040

Leu Gln His Asn Ser Tyr Pro Tyr Thr
 1 5

10296W001-Sequence.txt

<210> 1041
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1041
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 ccaggcaagg ggctggagtg ggtgacagtt atattacatg atggaagtaa tagatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctttat 240
 ctgcaaatac acatcctgag agctgaggac acggctgtgt attactgtac gaaaggggct 300
 atgggttcggg gaggccctta caatcactac tacggcatgg acgtctgggg ccaagggacc 360
 acggtcaccg tctcctca 378

<210> 1042
 <211> 126
 <212> PRT
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<220>
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<400> 1042

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Thr Val Ile Leu His Asp Gly Ser Asn Arg Tyr Tyr Ala Asp Ser Val
 50 55 60

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

10296W001-Sequence.txt

Leu Gln Met Asn Ile Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 1043
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1043
ggattcacct tcagtagcta tggc

24

<210> 1044
<211> 8
<212> PRT
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<220>
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<400> 1044

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> 1045
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1045
atattacatg atggaagtaa taga

24

<210> 1046
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1046

Ile Leu His Asp Gly Ser Asn Arg
 1 5

<210> 1047
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1047
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<210> 1048
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1048

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
 1 5 10 15

Met Asp Val

<210> 1049
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

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gggaaagccc ctaagcgcct gatctatgct gcatccaatt tgcaaagtgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtctacag cataatagtt acccgtagac ttttggccag      300
gggaccaagc tggagatcaa acga                                           324

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<210> 1050
<211> 108
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 1050

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```

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
          20           25           30

```

```

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
          35           40           45

```

```

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60

```

```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
          85           90           95

```

```

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
          100          105

```

<210> 1051
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1051
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18

<210> 1052
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1052

Gln Gly Ile Arg Asn Asp
 1 5

<210> 1053
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1053
 gctgcatcc

9

<210> 1054
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1054

Ala Ala Ser
 1

10296W001-Sequence.txt

<210> 1055
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1055
ctacagcata atagttaccc gtacact

27

<210> 1056
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1056

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> 1057
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1057
caggtgcagc tgggtggagtc tggggggaggc gtggtccagc ctgggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatggca tgcaactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagact attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtgt tttactgtgc gaaaggggct 300
atggttcggg gagtccctta caactactac tacggtatgg acgtctgggg ccaagggacc 360
acggtcaccg tctcctca 378

<210> 1058
<211> 126

10296W001-Sequence.txt

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1058

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 1059
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1059

ggattcacct tcagtagcta tggc

24

<210> 1060
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1060

Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 1061
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1061
 atatcatatg atggaagtaa taaa

24

<210> 1062
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 1062

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 1063
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1063
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57

10296W001-Sequence.txt

<210> 1064
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1064

Ala	Lys	Gly	Ala	Met	Val	Arg	Gly	Val	Pro	Tyr	Asn	Tyr	Tyr	Tyr	Gly
1				5					10					15	

Met Asp Val

<210> 1065
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1065

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atcacttgcc	gggcaagtca	gggcattaga	aatgatttag	gctggtttca	gcagaaacca	120
gggaaagccc	ctaagcgcct	gatctatgct	gcatccagtt	tgcaaagtgg	ggtcccatca	180
aggttcagcg	gcagtggatc	tgggacagaa	ttcactctca	caatcagcag	cctgcagcct	240
gaagattttg	caacttatta	ctgtctacag	cataatagtt	accggtacac	ttttggccag	300
gggaccaagc	tggagatcaa	a				321

<210> 1066
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1066

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

10296W001-Sequence.txt

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1067
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1067
cagggcatta gaaatgat

18

<210> 1068
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1068

Gln Gly Ile Arg Asn Asp
1 5

<210> 1069
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1069
 gctgcatcc

9

<210> 1070
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1070

Ala Ala Ser
 1

<210> 1071
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1071
 ctacagcata atagttaccc gtacact

27

<210> 1072
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1072

Leu Gln His Asn Ser Tyr Pro Tyr Thr
 1 5

10296W001-Sequence.txt

<210> 1073
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1073
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 tcctgtgcag cctctggact caccttcagt agctatggca tgcactgggt ccgccaggct 120
 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
 acagactccg tgaagggccg attcaccatc tccagagaca attctaagaa cacgctgtat 240
 ctgcaaataga acagcctgag agctgaggac acggctgtgt attactgtgc gaaagggggc 300
 atgggttcggg gaggccctta caactactac tacggatatgg acgtctgggg ccaagggacc 360
 acggtcaccg tctcctca 378

<210> 1074
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1074

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Ser Tyr
 20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Thr Asp Ser Val
 50 55 60

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

10296W001-Sequence.txt

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

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
 100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 1075
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1075
 ggactcacct tcagtagcta tggc

24

<210> 1076
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1076

Gly Leu Thr Phe Ser Ser Tyr Gly
 1 5

<210> 1077
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1077
 atatcatatg atggaagtaa taaa

24

<210> 1078
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1078

Ile Ser Tyr Asp Gly Ser Asn Lys
 1 5

<210> 1079
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1079
 gcgaaagggg ccatggttcg gggagtcct tacaactact actacggtat ggacgtc 57

<210> 1080
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1080

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
 1 5 10 15

Met Asp Val

<210> 1081
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

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<400> 1081
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atcacttgcc gggcaagtca gggcattaga aatgatttag gctgggtatca gcagaaacca      120
gggaaagccc ctaagcgcct gatctatgct gcgtccagtt tgcaaagtgg ggtcccatca      180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct      240
gaagattttg caacttatta ctgtctacag cataatagtt acccgtagac ttttggccag      300
gggaccaagc tggagatcaa a                                              321
```

```
<210> 1082
<211> 107
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> synthetic
```

```
<400> 1082
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```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1              5              10              15
```

```
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
          20              25              30
```

```
Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
          35              40              45
```

```
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50              55              60
```

```
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65              70              75              80
```

```
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
          85              90              95
```

```
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100              105
```

<210> 1083
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1083
 cagggcatta gaaatgat

18

<210> 1084
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1084

Gln Gly Ile Arg Asn Asp
 1 5

<210> 1085
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1085
 gctgcgtcc

9

<210> 1086
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1086

Ala Ala Ser
 1

10296W001-Sequence.txt

<210> 1087
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1087
ctacagcata atagttaccc gtacact

27

<210> 1088
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1088

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> 1089
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1089
caggtgcagc tggaggagtc tgggggaggc gtgggtccagc ctgggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagg agctttggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atttcatatg atggaaatta taaatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctgtac attactgtgc gaaaggggct 300
atggttcggg gagtccctta caacttctac tacggtatgg acgtctgggg ccaagggacc 360
acggtcaccg tctcctca 378

<210> 1090
<211> 126

10296W001-Sequence.txt

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1090

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Phe
20 25 30

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

Ala Val Ile Ser Tyr Asp Gly Asn Tyr Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val His Tyr Cys
85 90 95

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Phe Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 1091
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1091

ggattcacct tcaggagctt tggc

24

<210> 1092
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1092

Gly Phe Thr Phe Arg Ser Phe Gly
 1 5

<210> 1093
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1093
 atttcatatg atggaaatta taaa

24

<210> 1094
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1094

Ile Ser Tyr Asp Gly Asn Tyr Lys
 1 5

<210> 1095
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1095
 gcgaaagggg ctatggttcg gggagtcct tacaacttct actacggtat ggacgtc

57

10296W001-Sequence.txt

<210> 1096
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1096

Ala	Lys	Gly	Ala	Met	Val	Arg	Gly	Val	Pro	Tyr	Asn	Phe	Tyr	Tyr	Gly
1				5					10					15	

Met Asp Val

<210> 1097
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1097

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atcacttgcc gggcaagtca ggtcattaga aatgatttag gctggatatca gcagaaacca	120
gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg gatcccatca	180
aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct	240
gaagattttg caacttatta ctgtctacag cataatagtt acccgtagac ttttggccag	300
gggaccaagc tggagatcaa a	321

<210> 1098
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1098

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

10296W001-Sequence.txt

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Val Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1099
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1099
caggtcatta gaaatgat

18

<210> 1100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1100

Gln Val Ile Arg Asn Asp
1 5

<210> 1101
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1101
 gctgcatcc

9

<210> 1102
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1102

Ala Ala Ser
 1

<210> 1103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1103
 ctacagcata atagttaccc gtacact

27

<210> 1104
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1104

Leu Gln His Asn Ser Tyr Pro Tyr Thr
 1 5

10296W001-Sequence.txt

<210> 1105
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1105
 gaggtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagtt 120
 ccaggaaagg gcctggagtg gatctcaggt attagttgga atagtggtag catggactat 180
 gcggactctg tgaagggccg attcaccatc tctagagaca acgccaggaa ctccctgttt 240
 ctgcaaataa acagtgtgag aactgaggac acggccttgt attactgtgc aaaagataag 300
 agtggctacg gctccttcta ctacggtatg gacgtctggg gccaggggac cacggtcacc 360
 gtctcctca 369

<210> 1106
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1106

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

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

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

10296W001-Sequence.txt

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1107
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1107
 ggattcacct ttgatgatta tacc

24

<210> 1108
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1108

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 1109
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1109
 attagttgga atagtggtag catg

24

<210> 1110
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1110

Ile Ser Trp Asn Ser Gly Ser Met
 1 5

<210> 1111
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1111
 gcaaaagata agagtggcta cggctccttc tactacggta tggacgtc 48

<210> 1112
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1112

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
 1 5 10 15

<210> 1113
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1113
 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtgtcagc agcatctact tagcctggta ccagcagaaa 120

10296W001-Sequence.txt

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180
gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagttta ttactgtcag cagcgtgctc actcaccgta cacttttggc 300
caggggacca agctggagat caaa 324

<210> 1114
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1114

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

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ile
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile His Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ala His Ser Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1115

cagagtgatca gcagcatcta c

21

<210> 1116

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1116

Gln Ser Val Ser Ser Ile Tyr

1 5

<210> 1117

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1117

ggtgctcc

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<210> 1118

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1118

Gly Ala Ser

1

<210> 1119

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1119

cagcagcgtg ctcactcacc gtacact

27

<210> 1120

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1120

Gln Gln Arg Ala His Ser Pro Tyr Thr

1 5

<210> 1121

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1121

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggctt cagctttgat aattatgccca tgcactgggt ccggcaagct 120

ccaggacagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca atgccaggaa ctccctgttt 240

ctgcaaatga acagtctgag taatgaggac acggccatgt attactgcgc aaaagataag 300

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gtctcctca 369

<210> 1122

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<212> PRT

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<400> 1122

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Asn Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Asp Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Ser Asn Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

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24

<210> 1124

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1124

Gly Phe Ser Phe Asp Asn Tyr Ala
1 5

<210> 1125

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1125

attagttgga atagtggtag caga

24

<210> 1126

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1126

Ile Ser Trp Asn Ser Gly Ser Arg
1 5

<210> 1127

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1127

gcaaaagata agagtggcta cggctcctac ttctacggta tggacgtc

48

<210> 1128

<211> 16

<212> PRT

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

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<400> 1128

Ala	Lys	Asp	Lys	Ser	Gly	Tyr	Gly	Ser	Tyr	Phe	Tyr	Gly	Met	Asp	Val
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<210> 1129

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1129

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cctggccagg	ctcccaggct	cctcatccat	ggtgcgtcca	ccagggccac	tggcatccca	180
gacaggttca	gtggcagtgg	gtcagggaca	gacttcactc	tcaccatcag	cagactggag	240
cctgaagatt	ttgcagttta	ttactgtcag	cagcgtgtta	gtttaccgta	cacttttggc	300
caggggacca	agctggagat	caaa				324

<210> 1130

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

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<400> 1130

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

Asp	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Arg	Asn	Ile
			20					25					30		

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			

10296W001-Sequence.txt

Ile His Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1131
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1131
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21

<210> 1132
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1132

Gln Ser Ile Arg Asn Ile Tyr
1 5

<210> 1133
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1133
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9

<210> 1134
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1134

Gly Ala Ser
1

<210> 1135
<211> 27
<212> DNA
<213> Artificial Sequence

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<400> 1135
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27

<210> 1136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1136

Gln Gln Arg Val Ser Leu Pro Tyr Thr
1 5

<210> 1137
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

10296W001-Sequence.txt

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ccaggacagg gcctggagtg ggtctcaggt attagttagga atggtagtag cagagactat      180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctccctgttt      240
ctgcaaatga acagtctgtt tactgaggac acggccttgt attactgtgc aaaagataag      300
agtggctacg gctcctactt ctacggtatg gacgtctggg gccaaaggac cacggtcacc      360
gtctcctca                                     369
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<210> 1138
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```
<220>
<223> synthetic
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```
<400> 1138
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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1           5           10           15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asp Asp Tyr
          20           25           30
```

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

```
Ser Gly Ile Ser Trp Asn Gly Gly Ser Arg Asp Tyr Ala Asp Ser Val
          50           55           60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Phe
65           70           75           80
```

```
Leu Gln Met Asn Ser Leu Phe Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95
```

```
Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
          100          105          110
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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1139
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24

<210> 1140
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1140

Gly Phe Ser Phe Asp Asp Tyr Ala
 1 5

<210> 1141
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1141
 attagttgga atggtggttag caga

24

<210> 1142
 <211> 8
 <212> PRT
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<220>
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<400> 1142

Ile Ser Trp Asn Gly Gly Ser Arg
 1 5

<210> 1143

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1143

gcaaaagata agagtggtta cggctcctac ttctacggta tggacgtc 48

<210> 1144

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1144

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
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<210> 1145

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1145

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ctctcctgca gggccagtca gagtattaga aacatctatt tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gttcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 1146
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1146

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

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Asn Ile
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile His Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 1147
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1147

cagagtatta gaaacatcta t

<210> 1148
<211> 7
<212> PRT
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<220>
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<400> 1148

Gln Ser Ile Arg Asn Ile Tyr
1 5

<210> 1149
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 1149
ggtgcgtcc

9

<210> 1150
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1150

Gly Ala Ser
1

<210> 1151
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1151
cagcagcgtg ttagttcacc gtacact

27

10296W001-Sequence.txt

<210> 1152
 <211> 9
 <212> PRT
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<400> 1152

Gln Gln Arg Val Ser Ser Pro Tyr Thr
 1 5

<210> 1153
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1153

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ccaggaaagg gcctggagtg ggtctcaggt attagttagga atagtggtag cagagactat	180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctccctgttt	240
ctgcaaataa acagtctgag tactgaggac acggccttgt attactgtgc aaaagataag	300
agtggctacg gctcctacta ctacggtatg gacgtctggg gccaaaggac cacggtcacc	360
gtctcctca	369

<210> 1154
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1154

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Arg Asp Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Ser Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1155
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 1155
ggattcacct ttgatgatta tgcc

24

<210> 1156
<211> 8
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<400> 1156

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 1157
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<400> 1157
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24

<210> 1158
 <211> 8
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<220>
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<400> 1158

Ile Ser Trp Asn Ser Gly Ser Arg
 1 5

<210> 1159
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1159
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48

<210> 1160
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 <212> PRT
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<220>
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<400> 1160

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Tyr Tyr Gly Met Asp Val
 1 5 10 15

10296W001-Sequence.txt

<210> 1161
 <211> 324
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 cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180
 gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240
 cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gctcaccgta cacttttggc 300
 caggggacca agctggagat caaa 324

<210> 1162
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1162

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

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ile
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile His Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60

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

10296W001-Sequence.txt

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1163
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<212> DNA
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<400> 1163
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21

<210> 1164
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1164

Gln Ser Ile Arg Ser Ile Tyr
1 5

<210> 1165
<211> 9
<212> DNA
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<400> 1165
ggtgcgtcc

9

<210> 1166
<211> 3
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<220>

<223> synthetic

<400> 1166

Gly Ala Ser

1

<210> 1167

<211> 27

<212> DNA

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<400> 1167

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<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1168

Gln Gln Arg Val Ser Ser Pro Tyr Thr

1

5

<210> 1169

<211> 369

<212> DNA

<213> Artificial Sequence

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tcctgtgtag cctctggatt cacctttgct gattttacca tgcactgggt ccggcaagcg 120

ccagggaagg gccttgagtg ggtctcaggt attagttgga atagtaatag tatagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa atccctgttt 240

10296W001-Sequence.txt

ctgcaaatgt ccagtctgag agctgaggac acggccttat attactgtgt caaagacaga 300
agcggatata gcagattcta ctacggtatg gacgtctggg gccaaaggac cacggtcacc 360
gtctcctca 369

<210> 1170
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1170

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

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ala Asp Phe
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Asn Ser Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Val Lys Asp Arg Ser Gly Tyr Ser Arg Phe Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1171
<211> 24

<212> DNA
<213> Artificial Sequence

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<400> 1171
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24

<210> 1172
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1172

Gly Phe Thr Phe Ala Asp Phe Thr
1 5

<210> 1173
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<212> DNA
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<220>
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<400> 1173
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24

<210> 1174
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Ile Ser Trp Asn Ser Asn Ser Ile
1 5

<210> 1175
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<212> DNA

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<213> Artificial Sequence

<220>

<223> synthetic

<400> 1176

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<211> 321

<212> DNA

<213> Artificial Sequence

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<400> 1177

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ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatccgcag cctgcaatct 240

gaagattttg cagtttatta ctgtcaacaa tattataatt ggccgatcac tttcggccac 300

gggacacgac tggagattaa a 321

<210> 1178

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1178

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

Glu Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Asn Ile Asn Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Arg Ser Leu Gln Ser
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Trp Pro Ile
 85 90 95

Thr Phe Gly His Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 1179

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1179

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18

<210> 1180

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1180

Gln Asn Ile Asn Ser Asn
1 5

<210> 1181

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1181

ggtgcatcc

9

<210> 1182

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1182

Gly Ala Ser
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<210> 1183

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1183

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27

<210> 1184

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1184

Gln Gln Tyr Tyr Asn Trp Pro Ile Thr
 1 5

<210> 1185

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1185

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ccaggaaagg gcctggagtg ggtctcaggt attagttgga atggtggtag taaagactat	180
gcggactctg tgaagggccg attcaccatc tccagagaca acaccaggaa ctccctgtct	240
ctgcaaatga acagtctgag aattgaagac acggccttat attactgtgc aaaagataag	300
agtggctacg gtccttcta ctacggtttg gacgtctggg gccaaggac cacggtcacc	360
gtctcctca	369

<210> 1186

<211> 123

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 1186

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
20 25 30	

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

10296W001-Sequence.txt

Ser Gly Ile Ser Trp Asn Gly Gly Ser Lys Asp Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ile Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1187
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1187
ggattcacct ttgatgatta tgcc

24

<210> 1188
<211> 8
<212> PRT
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<400> 1188

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 1189
<211> 24
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<220>

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<400> 1189

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24

<210> 1190

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1190

Ile Ser Trp Asn Gly Gly Ser Lys

1 5

<210> 1191

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1191

gcaaaagata agagtggcta cggctccttc tactacgggtt tggacgtc

48

<210> 1192

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1192

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Leu Asp Val

1 5 10 15

<210> 1193

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

10296W001-Sequence.txt

<223> synthetic

<400> 1193

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gaaatagtgt tgacacagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc      60
ctctcctgca gggccagtca gagtattaga agcatctact tagcctggta ccagcagaaa      120
cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca      180
gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gctcaccgta cacttttggc      300
caggggacca agctggagat caaa                                           324

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<210> 1194

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1194

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

```

```

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ile
          20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45

```

```

Ile His Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
          50           55           60

```

```

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

```

```

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

```

```

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
          100          105

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<210> 1195
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1195
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21

<210> 1196
 <211> 7
 <212> PRT
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<220>
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<400> 1196

Gln Ser Ile Arg Ser Ile Tyr
 1 5

<210> 1197
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 <213> Artificial Sequence

<220>
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<400> 1197
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9

<210> 1198
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1198

Gly Ala Ser
 1

<210> 1199
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1199
 cagcagcgtg ttagctcacc gtacact

27

<210> 1200
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 <212> PRT
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<220>
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<400> 1200

Gln Gln Arg Val Ser Ser Pro Tyr Thr
 1 5

<210> 1201
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1201
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 tcctgtgcag cctctggatt cacctttgat gatttcacca tgcactgggt ccggcaagct 120
 ccaggaaagg gcctggagtg ggtctcagat attagttgga atagtggtag catagactat 180
 gcggactctg tgaagggccg attcaccatt tccagagaca atgccaggaa ctccctgttt 240
 ctacaaatga gcagtctgag aactgaggac acggcctcgt attactgtat aaaagataag 300
 agtggctacg gtcctacaa ctacggtctg gacgtctggg gccaaaggac cacggtcacc 360
 gtctcctca 369

10296W001-Sequence.txt

<210> 1202

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1202

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Phe
20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Ile Asp Tyr Ala Asp Ser Val
50 55 60

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

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

Ile Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Asn Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1203

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1203

ggattcacct ttgatgattt cacc

<210> 1204
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1204

Gly Phe Thr Phe Asp Asp Phe Thr
 1 5

<210> 1205
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1205
 attagttgga atagtggttag cata

24

<210> 1206
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1206

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1207
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1207
 ataaaagata agagtggtgcta cggctcctac aactacggtc tggacgtc

48

10296W001-Sequence.txt

<210> 1208
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1208

Ile	Lys	Asp	Lys	Ser	Gly	Tyr	Gly	Ser	Tyr	Asn	Tyr	Gly	Leu	Asp	Val
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<210> 1209
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1209

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cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca	180
gacaggttca gtggcagtgg gtcggggaca gacttcactc tcaccatcag cagactggag	240
cctgaagatt ttgcacttta ttactgtcac cagcgtgtta gttcaccgta cacttttggc	300
caggggacca agctggagat caaa	324

<210> 1210
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1210

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

10296W001-Sequence.txt

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ile
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile His Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 1211
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1211
cagagtgtta gcagcatcta c

21

<210> 1212
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1212

Gln Ser Val Ser Ser Ile Tyr
1 5

<210> 1213
<211> 9

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1213
ggtgctcc

9

<210> 1214
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1214

Gly Ala Ser
1

<210> 1215
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1215
caccagcgtg ttagttcacc gtacact

27

<210> 1216
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1216

His Gln Arg Val Ser Ser Pro Tyr Thr
1 5

<210> 1217
<211> 369

10296W001-Sequence.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1217

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tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct      120
ccaggaaagg gcctggagtg ggtctcaggt attagttgga atagtggtag taaagactat      180
gcggactctg tgaagggccg attcaccatc tccagagaca acaccaggaa ctccctgttt      240
ctgcaaataa acagtctgag aactgaagac acggccttat attactgtgc aaaagataag      300
agtggctacg gctccttcta ctacggtatg gacgtctggg gccaaaggac cacggtcacc      360
gtctcctca                                     369

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<210> 1218

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1218

```

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
          50           55           60

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

```

10296W001-Sequence.txt

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1219
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1219
ggattcacct ttgatgatta tgcc

24

<210> 1220
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1220

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 1221
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1221
attagttgga atagtggtag taaa

24

<210> 1222
<211> 8

<212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1222

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1223
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1223
 gcaaaagata agagtggcta cggctccttc tactacggta tggacgtc 48

<210> 1224
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1224

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
 1 5 10 15

<210> 1225
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1225
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 atcacttgcc gggccagtc gagtattagt agctggttgg cctgggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180

10296W001-Sequence.txt

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240
 gatgattttg caacttatta ctgccaacag tataatagtt attctccggtt cggccaaggg 300
 accaaggtgg aaatcaaa 318

<210> 1226
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1226

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Ser Pro
 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 1227
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1227
cagagtatta gtagctgg

18

<210> 1228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1228

Gln Ser Ile Ser Ser Trp
1 5

<210> 1229
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1229
aaggcgtct

9

<210> 1230
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1230

Lys Ala Ser
1

<210> 1231
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1231

caacagtata atagttattc tccg

24

<210> 1232

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1232

Gln Gln Tyr Asn Ser Tyr Ser Pro

1

5

<210> 1233

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1233

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggact caccttcagt acctatgtca tgcaactgggt ccgccaggct 120

ccaggcaagg ggctggcgtg ggtggcagtt atagcaaagc atggaagtaa taaatattat 180

gcagactccg tgaagggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240

ctgcaaagta atagcctgag acctgaggac acggctgtgt atttttgtgc gaaagagggg 300

ggtaccagtg ggtcctacta ttactatgga atggacgtct ggggtcaagg gactacggctc 360

accgtctcct ca 372

<210> 1234

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

10296W001-Sequence.txt

<400> 1234

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Thr Tyr
20 25 30

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

Ala Val Ile Ala Asn Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Glu Gly Gly Thr Ser Gly Ser Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1235

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1235

ggactcacct tcagtaccta tgtc

24

<210> 1236

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1236

Gly Leu Thr Phe Ser Thr Tyr Val
1 5

<210> 1237

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1237

atagcaaag atggaagtaa taaa

24

<210> 1238

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1238

Ile Ala Asn Asp Gly Ser Asn Lys
1 5

<210> 1239

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1239

gcgaaagagg ggggtaccag tgggtcctac tattactatg gaatggacgt c

51

<210> 1240

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1240

Ala	Lys	Glu	Gly	Gly	Thr	Ser	Gly	Ser	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 1241

<211> 342

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1241

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atcaactgca	agtccagcca	gagtccttta	ttcaactcca	tcaataagaa	ctacttagct	120
tggtaccagc	agaaaccagg	acagcctcct	aagcttctcc	tttactgggc	atctaccggg	180
gaatccggga	tcctgaccg	attcagtggc	agcgggtctg	ggacagattt	cactctcacc	240
atcaccagcc	tcgaggctga	agatgtggca	ctttattact	gtcagcaata	ttatagtatt	300
ccgtggacgt	tcggccaagg	gaccaaggtg	gaaatcaaac	ga		342

<210> 1242

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1242

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

Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Phe	Asn
			20					25					30		

10296W001-Sequence.txt

Ser Ile Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Leu Tyr Trp Ala Ser Thr Arg Glu Ser Gly Ile
50 55 60

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

Ile Thr Ser Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
85 90 95

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

Lys Arg

<210> 1243
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1243
cagagtcttt tattcaactc catcaataag aactac

36

<210> 1244
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1244

Gln Ser Leu Leu Phe Asn Ser Ile Asn Lys Asn Tyr
1 5 10

<210> 1245
<211> 9

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1245
tgggcatct

9

<210> 1246
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1246

Trp Ala Ser
1

<210> 1247
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1247
cagcaatatt atagtattcc gtggacg

27

<210> 1248
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1248

Gln Gln Tyr Tyr Ser Ile Pro Trp Thr
1 5

<210> 1249
<211> 354

10296W001-Sequence.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1249

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tcctgcaaga cttctggata caccttcacc ggctactata tgcactggat acgacaggcc      120
cctggacaag ggcttgagtg gatgggatgg atcaacccta aaagtgggtgg cacaaattat      180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac      240
atggaactga gcaggctgag atccgacgac atggccgtgt attattgtgc gagaatgggg      300
gacggtgcag tgtttgactt ctggggccag ggaaccctgg tcaccgtctc ctca          354
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<210> 1250

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1250

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

```
Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
              20              25              30
```

```
Tyr Met His Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
              35              40              45
```

```
Gly Trp Ile Asn Pro Lys Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50              55              60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65              70              75              80
```

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


10296W001-Sequence.txt

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 1251
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1251
 ggatacacct tcaccggcta ctat

24

<210> 1252
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1252

Gly Tyr Thr Phe Thr Gly Tyr Tyr
 1 5

<210> 1253
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1253
 atcaacccta aaagtgggtg caca

24

<210> 1254
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1254

Ile Asn Pro Lys Ser Gly Gly Thr

1 5

<210> 1255

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1255

gcgagaatgg gggacggtgc agtgtttgac ttc

33

<210> 1256

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1256

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe

1 5 10

<210> 1257

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1257

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atcacttgcc gggcaagtca gaggattagc agcttttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ctatcagcag tctgcaacct 240

10296W001-Sequence.txt

gaagattttg ctacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300
gggaccaagg tggaaatcaa acga 324

<210> 1258
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1258

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1259
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1259
cagaggatta gcagcttt

18

<210> 1260
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1260

Gln Arg Ile Ser Ser Phe
1 5

<210> 1261
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1261
actgcatcc

9

<210> 1262
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1262

Thr Ala Ser
1

<210> 1263
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1263
caacagagtt acaggacccc gctcact 27

<210> 1264
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Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

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ccagggaagg gcctggagtg ggtctcaggt attagttgga acagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccatt tccagagaca acgccaagaa ctccctgtat 240
ttgcaaatga acagtctgag agctgaggac acggccttgt tttactgtgc aaaagatcaa 300
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10296W001-Sequence.txt

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

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

Ala Lys Asp Gln Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<212> DNA
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24

<210> 1268
<211> 8
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<400> 1268

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 1269

<211> 24

<212> DNA

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<400> 1269

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24

<210> 1270

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<212> PRT

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<223> synthetic

<400> 1270

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

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<211> 48

<212> DNA

<213> Artificial Sequence

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<223> synthetic

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<220>

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<212> DNA

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<400> 1273

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 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactga tatcccagcc 180
 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
 gaagattttg cagtttatca ctgtcagcag tataataact ggccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 1274

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<212> PRT

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<400> 1274

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Ala Arg Phe Ser Gly
 50 55 60

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr His Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1275
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18

<210> 1276
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<400> 1276

Gln Ser Val Ser Ser Asn
1 5

<210> 1277
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<400> 1277
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9

<210> 1278
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<400> 1278

Gly Ala Ser
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<210> 1279
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<400> 1279
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27

<210> 1280
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Gln Gln Tyr Asn Asn Trp Pro Leu Thr
 1 5

<210> 1281
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tcctgtgcag cctctggatt caccttcagt tactatggca tgcactgggt ccgccaggct 120

10296W001-Sequence.txt

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ccaggcaagg ggctggagtg ggtggcagtt atatcatttg atggaaagaa taaatattat 180
gcagactccg tgatgggccg attcaccatc tccagagaca attccaagaa tacactgtat 240
ctgcaaatga acagcctgag agctgaggac tcggctgtgt ttttctgtgc gaggtcttac 300
gacattttga ctggttatgg agccggttac agctaccact acggtatgga cgtctggggc 360
caagggacca cggtcacctgt ctcctca 387
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<400> 1282

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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
 20 25 30

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

Ala Val Ile Ser Phe Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

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

Ala Arg Ser Tyr Asp Ile Leu Thr Gly Tyr Gly Ala Gly Tyr Ser Tyr
 100 105 110

His Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser

<210> 1283
 <211> 24
 <212> DNA
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<220>
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<400> 1283
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24

<210> 1284
 <211> 8
 <212> PRT
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<220>
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<400> 1284

Gly Phe Thr Phe Ser Tyr Tyr Gly
 1 5

<210> 1285
 <211> 24
 <212> DNA
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<220>
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<400> 1285
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24

<210> 1286
 <211> 8
 <212> PRT
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<220>
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<400> 1286

Ile Ser Phe Asp Gly Lys Asn Lys
 1 5

<210> 1287

<211> 66

<212> DNA

<213> Artificial Sequence

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<400> 1287

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gacgtc 66

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<211> 22

<212> PRT

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<400> 1288

Ala Arg Ser Tyr Asp Ile Leu Thr Gly Tyr Gly Ala Gly Tyr Ser Tyr
 1 5 10 15

His Tyr Gly Met Asp Val
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<210> 1289

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1289

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atcacttgcc gggcaagtca gaggattagc agcttttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct aatctatact gcatccaatt tacaaaatgg ggtcccatca 180

10296W001-Sequence.txt

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300
gggaccaagg tggagatcaa acga 324

<210> 1290
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1290

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1291
<211> 18
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<220>

<223> synthetic

<400> 1291
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18

<210> 1292
<211> 6
<212> PRT
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<220>
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<400> 1292

Gln Arg Ile Ser Ser Phe
1 5

<210> 1293
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<212> DNA
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<220>
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<400> 1293
actgcatcc

9

<210> 1294
<211> 3
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<400> 1294

Thr Ala Ser
1

<210> 1295
<211> 27
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<400> 1295

caacagagtt acaggacccc gtcact

27

<210> 1296

<211> 9

<212> PRT

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<220>

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<400> 1296

Gln Gln Ser Tyr Arg Thr Pro Leu Thr

1 5

<210> 1297

<211> 354

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 1297

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cctggacaag ggcttgagt gatgggatgg attaaccta aaagtgggtgt cacaaattat 180

gcacagaagt ttcaggacag agtcgccatg accagggaca cgtccatcag cacagcctac 240

atggaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaatgggg 300

gacggtgcag tgtttgactt ctgggccag ggaaccctgg tcaccgtctc ctca 354

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<212> PRT

<213> Artificial Sequence

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<400> 1298

10296W001-Sequence.txt

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Leu Ser Gly Tyr
20 25 30

Tyr Met His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Lys Ser Gly Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Asp Arg Val Ala Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Ala Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 1299
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1299
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24

<210> 1300
<211> 8
<212> PRT
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<400> 1300

Gly Tyr Thr Leu Ser Gly Tyr Tyr
1 5

<210> 1301

<211> 24

<212> DNA

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<400> 1301

attaacccta aaagtgggtgt caca

24

<210> 1302

<211> 8

<212> PRT

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<220>

<223> synthetic

<400> 1302

Ile Asn Pro Lys Ser Gly Val Thr
1 5

<210> 1303

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1303

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33

<210> 1304

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1304

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
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<210> 1305

<211> 324

<212> DNA

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<400> 1305

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 gggaaagccc ctaagctcct aatctatact gcatccaatt tacaaaatgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300
 gggaccaagc tggagatcaa acga 324

<210> 1306

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1306

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Phe
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1307
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<212> DNA
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18

<210> 1308
<211> 6
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Gln Arg Ile Ser Ser Phe
1 5

<210> 1309
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<400> 1309
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9

<210> 1310
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<220>
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<400> 1310

Thr Ala Ser
 1

<210> 1311
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<400> 1311
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27

<210> 1312
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<400> 1312

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
 1 5

<210> 1313
 <211> 372
 <212> DNA
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<400> 1313
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tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

10296W001-Sequence.txt

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag acctgaggac acggctgtgt attactgtgc gaaagggggg      300
ggtaccagtg ggtcctactt ttactacggt atggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                              372
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 <211> 124
 <212> PRT
 <213> Artificial Sequence

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<400> 1314

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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

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

Ser Thr Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gly Gly Thr Ser Gly Ser Tyr Phe Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1315
 <211> 24
 <212> DNA
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<220>
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<400> 1315
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24

<210> 1316
 <211> 8
 <212> PRT
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<220>
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<400> 1316

Gly Phe Thr Phe Ser Ser Tyr Gly
 1 5

<210> 1317
 <211> 24
 <212> DNA
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<400> 1317
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24

<210> 1318
 <211> 8
 <212> PRT
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<220>
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<400> 1318

Ile Ser Phe Asp Gly Ser Asn Lys
 1 5

<210> 1319
 <211> 51
 <212> DNA
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 <212> PRT
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<220>
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<400> 1320

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Val

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<220>
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<400> 1321
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 gggaaagccc ctaagctcct aatctatact gcatccaatt tacaaaatgg ggtcccatca 180
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300
 gggaccaagc tggagatcaa acga 324

<210> 1322
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1322

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Phe
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 1323
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1323

cagaggatta gcagcttt

<210> 1324
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1324

Gln Arg Ile Ser Ser Phe
 1 5

<210> 1325
 <211> 9
 <212> DNA
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<220>
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<400> 1325
 actgcatcc

9

<210> 1326
 <211> 3
 <212> PRT
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<220>
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<400> 1326

Thr Ala Ser
 1

<210> 1327
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1327
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27

10296W001-Sequence.txt

<210> 1328
 <211> 9
 <212> PRT
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<220>
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<400> 1328

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
 1 5

<210> 1329
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1329

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cctggacaag ggcttgagt gatgggatgg atcaacccta acagtgatgt cacaaagtat	180
gcacagaagt ttcagggcag ggtcaccttg accagggaca cgtccatcag tgcagcctat	240
attgacctga gcaggctgag atctgacgac acggccattt attactgtgc gagaatgggg	300
gacggtgcag tgtttgacta ctggggccag ggaaccctgg tcaccgtctc ctca	354

<210> 1330
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1330

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

Ser Met Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30

10296W001-Sequence.txt

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Asp Val Thr Lys Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Ala Ala Tyr
 65 70 75 80

Ile Asp Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
 85 90 95

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 1331
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<220>
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<400> 1331
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24

<210> 1332
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 1332

Gly Tyr Thr Phe Thr Gly Tyr Tyr
 1 5

<210> 1333
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1333
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24

<210> 1334
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 1334

Ile Asn Pro Asn Ser Asp Val Thr
 1 5

<210> 1335
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1335
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33

<210> 1336
 <211> 11
 <212> PRT
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<220>
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<400> 1336

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr
 1 5 10

10296W001-Sequence.txt

<210> 1337

<211> 324

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 1337

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atcacttgcc gggcaagtca acgcattagc agctatttaa attggtatca acagaaacca 120

gggaaagccc ctaaggtgct gatctctgtt gcatccagtt tacaaagtgg ggtcccatca 180

aggttcagtg gcagtggatt tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaggattctg catcttacta ctgtcaacag agttacaata ccccgctcac tttcggcggc 300

gggaccaagc tggagatcaa acga 324

<210> 1338

<211> 108

<212> PRT

<213> Artificial Sequence

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<400> 1338

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Ser Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

10296W001-Sequence.txt

Glu Asp Ser Ala Ser Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1339
<211> 18
<212> DNA
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<220>
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18

<210> 1340
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<400> 1340

Gln Arg Ile Ser Ser Tyr
1 5

<210> 1341
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<400> 1341
gttgcattcc

9

<210> 1342
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<223> synthetic

<400> 1342

Val Ala Ser
1

<210> 1343

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1343

caacagagtt acaatacccc gctcact

27

<210> 1344

<211> 9

<212> PRT

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<223> synthetic

<400> 1344

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

<210> 1345

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1345

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cctggacaag ggcttgaatg gatgggatgg atcaacccta agagtgggtgt cacaaattat 180

gcacagaggt ttcagggcag ggtcaccatg accagggaca cgtccatcag tactgcctac 240

atggaactga gcaggctgaa atctgacgac acggccgtgt atttctgtgc gagaatgggg 300

gacggtgcag tgtttgactt ctggggccag ggaaccctgg tcaccgtctc ctca

354

<210> 1346
 <211> 118
 <212> PRT
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<220>
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<400> 1346

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Ser Phe Ile Gly Tyr
 20 25 30

Tyr Ile His Trp Met Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Lys Ser Gly Val Thr Asn Tyr Ala Gln Arg Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 1347
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1347

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24

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<211> 8

<212> PRT

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<220>

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<400> 1348

Gly Tyr Ser Phe Ile Gly Tyr Tyr
1 5

<210> 1349

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 1349

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24

<210> 1350

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1350

Ile Asn Pro Lys Ser Gly Val Thr
1 5

<210> 1351

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1351

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33

<210> 1352

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1352

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
1 5 10

<210> 1353

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1353

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gggaaagtcc ctaagctcct gatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcaactggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300

gggaccaaag tggatatcaa acga 324

<210> 1354

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1354

10296W001-Sequence.txt

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

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

Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> 1355
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1355
cagaggatta gcagcttt

18

<210> 1356
<211> 6
<212> PRT
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<220>
<223> synthetic

<400> 1356

Gln Arg Ile Ser Ser Phe
1 5

<210> 1357
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1357
 actgcatcc

9

<210> 1358
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1358

Thr Ala Ser
 1

<210> 1359
 <211> 27
 <212> DNA
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<220>
 <223> synthetic

<400> 1359
 caacagagtt acaggacccc gtcact

27

<210> 1360
 <211> 9
 <212> PRT
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<220>
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<400> 1360

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
 1 5

10296W001-Sequence.txt

<210> 1361
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1361
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 tcctgcaaga cttctggata caccttcacc ggctactata tgcactggat acgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg atcaacccta aaagtgggtg cacaaattat 180
 gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240
 atggaactga gcaggctgag atccgacgac atggccgtgt attattgtgc gagaatgggg 300
 gacggtgcag tgtttgactt ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 1362
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1362

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
 20 25 30

Tyr Met His Trp Ile Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Lys Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

10296W001-Sequence.txt

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 1363
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1363
ggatacacct tcaccggcta ctat

24

<210> 1364
<211> 8
<212> PRT
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<220>
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<400> 1364

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 1365
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1365
atcaacccta aaagtgggtgg caca

24

<210> 1366
 <211> 8
 <212> PRT
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<220>
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<400> 1366

Ile Asn Pro Lys Ser Gly Gly Thr
 1 5

<210> 1367
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1367
 gcgagaatgg gggacggtgc agtgtttgac ttc

33

<210> 1368
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1368

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
 1 5 10

<210> 1369
 <211> 327
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1369
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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

10296W001-Sequence.txt

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgct cactttcggc      300
ggagggacca aagtggatat caaacga                                           327

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<210> 1370
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1370

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

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

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
          85           90           95

```

```

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg
          100          105

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<210> 1371
 <211> 18
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 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1371

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18

<210> 1372

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1372

Gln Ser Ile Ser Ser Tyr

1

5

<210> 1373

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1373

gctgcatcc

9

<210> 1374

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1374

Ala Ala Ser

1

<210> 1375

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1375

caacagagtt acagtacccc tccgctcact

30

<210> 1376

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1376

Gln Gln Ser Tyr Ser Thr Pro Pro Leu Thr

1

5

10

<210> 1377

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1377

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tcctgcaagg cttctggata caccttcacc ggctactata tgactgggt gcgacaggcc 120

cctggacaag ggcttgagt gatgggatgg atcaacccta acagtgatgt cacaactat 180

gcacagaagt ttcagggcag ggacaccttg accagggaca cgtccatcag tacagcctac 240

attgacctga gcaggctgag atctgacgac acggccattt attactgtgc gagaatgggg 300

gacgggtgcag tgtttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 1378

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

10296W001-Sequence.txt

<400> 1378

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Asp Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Leu Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Ile Asp Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 1379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1379

ggatacacct tcaccggcta ctat

24

<210> 1380

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1380

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> 1381

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1381

atcaacccta acagtgatgt caca

24

<210> 1382

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1382

Ile Asn Pro Asn Ser Asp Val Thr
1 5

<210> 1383

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1383

gcgagaatgg gggacggtgc agtgtttgac tac

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<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1384

Ala	Arg	Met	Gly	Asp	Gly	Ala	Val	Phe	Asp	Tyr
1				5					10	

<210> 1385

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1385

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gggaaagccc ctaaggtgct gatctctggt gcatccagtt tgcaaagtgg ggtcccatca	180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccattagtag tctgcaacct	240
gaggattttg catcttacta ctgtcaacag agttacaata ccccgctcac tttcggcgga	300
gggaccaagg tggagatcaa acga	324

<210> 1386

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1386

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Arg	Ile	Ser	Ser	Tyr
			20					25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile
							40					45			

10296W001-Sequence.txt

Ser Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1387
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1387
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18

<210> 1388
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1388

Gln Arg Ile Ser Ser Tyr
1 5

<210> 1389
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1389
gttgcattcc

9

10296W001-Sequence.txt

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<212> PRT
<213> Artificial Sequence

<220>
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<400> 1390

Val Ala Ser
1

<210> 1391
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1391
caacagagtt acaatacccc gtcact

27

<210> 1392
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1392

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

<210> 1393
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1393
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60

10296W001-Sequence.txt

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tcctgtgcag cctctggatt caccttcagt agctatgaca tgagctgggt ccgccaggct      120
ccaggggaagg ggctggagtg ggtttcatac attagtagta gtggtaatac catacattac      180
gcagactctg tgaagggccg attcaccatc tccagagaca attccaagaa ctcactttat      240
ctgcaaatac acagcctgag agccgaggac acggccgtgt attactgtgc gaaagccggt      300
cccgctacgg tgacacggag gtactactac tactacgggt tggacgtctg gggccaaggg      360
accacggtca ccgtctcctc a                                              381

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<210> 1394
 <211> 127
 <212> PRT
 <213> Artificial Sequence

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<400> 1394

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Ser Ser Ser Gly Asn Thr Ile His Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Ala Gly Pro Ala Thr Val Thr Arg Arg Tyr Tyr Tyr Tyr Tyr
 100 105 110

10296W001-Sequence.txt

Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 1395
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1395
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24

<210> 1396
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1396

Gly Phe Thr Phe Ser Ser Tyr Asp
 1 5

<210> 1397
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1397
 attagtagta gtggaatac cata

24

<210> 1398
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 1398

10296W001-Sequence.txt

Ile Ser Ser Ser Gly Asn Thr Ile
1 5

<210> 1399
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1399
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<210> 1400
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1400

Ala Lys Ala Gly Pro Ala Thr Val Thr Arg Arg Tyr Tyr Tyr Tyr Tyr
1 5 10 15

Gly Leu Asp Val
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<210> 1401
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1401
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atcacttgcc gggcaagtca gagaattagc agctatttaa attggtttca gcagaaacca 120
gggaaagccc ctaaggctct gatctatact gcatccagtt tgcaaaatgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagactttg caacttacta ctgtcagcag agttacagga ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acga

<210> 1402
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1402

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1403
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1403
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<210> 1404
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1404

Gln Arg Ile Ser Ser Tyr
 1 5

<210> 1405
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1405
 actgcatcc

9

<210> 1406
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1406

Thr Ala Ser
 1

<210> 1407
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1407
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27

10296W001-Sequence.txt

<210> 1408
 <211> 9
 <212> PRT
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<220>
 <223> synthetic

<400> 1408

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
 1 5

<210> 1409
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1409

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tcctgcaagg cttctggata cacattcatc ggctactata tgcactgggt gcgacaggcc	120
cctggacaag ggcttgagt gatgggatgg atcaacccta aaagtgggtg cacaaactat	180
gcacagaagt ttcagggcag ggtcaccatg accggggaca cgtccatcag cacagcctac	240
atggagctga gcaggctgag atctgacgac acggccgtgt ttactgtgc gagaatgggg	300
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<210> 1410
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<220>
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<400> 1410

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

10296W001-Sequence.txt

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Lys Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Gly Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Met Gly Asp Gly Ala Met Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 1411
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<400> 1411
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24

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<400> 1412

Gly Tyr Thr Phe Ile Gly Tyr Tyr
1 5

<210> 1413
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 <213> Artificial Sequence

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24

<210> 1414
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<400> 1414

Ile Asn Pro Lys Ser Gly Gly Thr
 1 5

<210> 1415
 <211> 33
 <212> DNA
 <213> Artificial Sequence

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<400> 1415
 gcgagaatgg gggacggtgc aatgtttgac tac

33

<210> 1416
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 <212> PRT
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<220>
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<400> 1416

Ala Arg Met Gly Asp Gly Ala Met Phe Asp Tyr
 1 5 10

10296W001-Sequence.txt

<210> 1417
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 atcacttgcc gggcaagtca gagaattagc agctatttaa attggtatca gcagaaagca 120
 gggaaagccc ctaaggtcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180
 cgattcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaacag agttacagta ccccgctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 1418
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 <212> PRT
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<220>
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<400> 1418

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Ala Gly Lys Ala Pro Lys Val Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

10296W001-Sequence.txt

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1419
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<212> DNA
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<220>
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<400> 1419
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18

<210> 1420
<211> 6
<212> PRT
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<220>
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<400> 1420

Gln Arg Ile Ser Ser Tyr
1 5

<210> 1421
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1421
actgcatcc

9

<210> 1422
<211> 3
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<400> 1422

Thr Ala Ser

1

<210> 1423

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

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27

<210> 1424

<211> 9

<212> PRT

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<223> synthetic

<400> 1424

Gln Gln Ser Tyr Ser Thr Pro Leu Thr

1

5

<210> 1425

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1425

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tcctgtgcag cctctggatt cacctttgat gattatgccca tgcactgggt ccgtcaagct 120

ccagggaagg gtctggagtg ggtctctctt attagtgggg atggtggttag cacatactat 180

gcagactctg tgaagggccg attcaccatc tccagagaca acagcaaaaa ctccctgtat 240

10296W001-Sequence.txt

ctgcaaatga acagtctgag aactgaggac accgccttgt attactgtgc aaaagatgat 300
 agcagctcgt cctggtacta ctactactac ggtatggacg tctggggccg agggaccacg 360
 gtcaccgtct cctca 375

<210> 1426
 <211> 125
 <212> PRT
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<220>
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<400> 1426

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Leu Ile Ser Gly Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

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

Asp Val Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 1427
 <211> 24

<212> DNA
 <213> Artificial Sequence

<220>
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<400> 1427
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24

<210> 1428
 <211> 8
 <212> PRT
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<220>
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<400> 1428

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 1429
 <211> 24
 <212> DNA
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<220>
 <223> synthetic

<400> 1429
 attagtgggg atggtggtag caca

24

<210> 1430
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1430

Ile Ser Gly Asp Gly Gly Ser Thr
 1 5

<210> 1431
 <211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1431

gcaaaagatg atagcagctc gtcctggtac tactactact acggtatgga cgtc 54

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<220>

<223> synthetic

<400> 1432

Ala	Lys	Asp	Asp	Ser	Ser	Ser	Ser	Trp	Tyr	Tyr	Tyr	Tyr	Tyr	Gly	Met
1				5					10					15	

Asp Val

<210> 1433

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1433

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gggaaagccc ctaaggtgct gatctctgtt gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaggattttg catcttacta ctgtcaacag agttacaata ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acga 324

<210> 1434

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1434

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

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Arg	Ile	Ser	Ser	Tyr
		20					25					30			

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Val	Leu	Ile
	35					40					45				

Ser	Val	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70					75					80	

Glu	Asp	Phe	Ala	Ser	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Asn	Thr	Pro	Leu
			85					90					95		

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
		100					105				

<210> 1435

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1435

cagcgcatta gcagctat

18

<210> 1436

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1436

Gln Arg Ile Ser Ser Tyr
1 5

<210> 1437

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1437

gttgcattcc

9

<210> 1438

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1438

Val Ala Ser
1

<210> 1439

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1439

caacagagtt acaatacccc gctcact

27

<210> 1440

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1440

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
 1 5

<210> 1441

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1441

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 ccagggaagg gcctggagtg ggtctccgat attagttaga atagtggtag caaagactat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctctat 240
 cttcaaatga acagtctgag aactgaggat acggcctttt attactgtgc aaaagatagt 300
 aggggctacg gtctctacta ccacctcggt ttggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 1442

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1442

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20 25 30

10296W001-Sequence.txt

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

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

Ala Lys Asp Ser Arg Gly Tyr Gly Leu Tyr Tyr His Leu Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1443
ggattcacct ttggtgatta tacc

24

<210> 1444
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1444

Gly Phe Thr Phe Gly Asp Tyr Thr
1 5

<210> 1445
<211> 24

<212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1445
 attagttgga atagtggtag caaa

24

<210> 1446
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1446

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1447
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1447
 gcaaaagata gtaggggcta cggctctctac taccacctcg gtttggacgt c

51

<210> 1448
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1448

Ala Lys Asp Ser Arg Gly Tyr Gly Leu Tyr Tyr His Leu Gly Leu Asp
 1 5 10 15

Val

10296W001-Sequence.txt

<210> 1449
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1449
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 ccaggaagg gcctggagt ggtctcagat attagttgga atagtggtag tatagcctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctctat 240
 cttcaaataa acagtctgag aactgaggac acggcctttt attactgtgc aaaagatagt 300
 aggggctacg gtcactataa gtacctcggg ttggacgtct ggggccaagg gaccacggctc 360
 accgtctcct ca 372

<210> 1450
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1450

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

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

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

Ala Lys Asp Ser Arg Gly Tyr Gly His Tyr Lys Tyr Leu Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1451
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1451
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24

<210> 1452
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1452

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> 1453
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1453
attagttgga atagtggtag tata

24

<210> 1454
 <211> 8
 <212> PRT
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<220>
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<400> 1454

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1455
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1455
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<210> 1456
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1456

Ala Lys Asp Ser Arg Gly Tyr Gly His Tyr Lys Tyr Leu Gly Leu Asp
 1 5 10 15

Val

<210> 1457
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>

10296W001-Sequence.txt

<223> synthetic

<400> 1457

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tcctgtgcag cctctggatt ccccttcaat gattacacca tgcactgggt ccggcaagtc      120
ccagggaggg gcctggagtg ggtctcagat attagttgga atagcggcag taaaggctat      180
gcggactctg tgaagggtcg attcatcatc tccagagaca acgccaagaa ctccctgtac      240
ctgcaaatga acagtctgag agttgaagac acggccttgt attactgtgt aaaagatgga      300
agtggctacg ggaggttcca ttattacgct atggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                              372
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<210> 1458

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1458

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Met Val Gln Pro Gly Arg
1           5           10           15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Asn Asp Tyr
          20           25           30

Thr Met His Trp Val Arg Gln Val Pro Gly Arg Gly Leu Glu Trp Val
          35           40           45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
          50           55           60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95
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10296W001-Sequence.txt

Val Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Tyr Tyr Ala Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1459
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1459
 ggattcccct tcaatgatta cacc

24

<210> 1460
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1460

Gly Phe Pro Phe Asn Asp Tyr Thr
 1 5

<210> 1461
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1461
 attagttgga atagcggcag taaa

24

<210> 1462
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1462

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1463

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1463

gtaaaagatg gaagtggtc cgggaggttc cattattacg ctatggacgt c 51

<210> 1464

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1464

Val Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Tyr Tyr Ala Met Asp
1 5 10 15

Val

<210> 1465

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1465

gaggtgcagc tggtggagtc tggtggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgct gattatacca tgcactgggt ccgccaagtt 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag caaagactat 180

10296W001-Sequence.txt

gcggactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa tttcctgtat 240
 ctgcaaatga acagtctgag agctgaagac acggccttgt attactgtgt aaaatatgga 300
 agtggctacg ggaaattcta cttctacgct atggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 1466
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1466

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
 20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Phe Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Val Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Phe Tyr Ala Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1467
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1467
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24

<210> 1468
 <211> 8
 <212> PRT
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<220>
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<400> 1468

Gly Phe Thr Phe Ala Asp Tyr Thr
 1 5

<210> 1469
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1469
 attagttgga atagtggtag caaa

24

<210> 1470
 <211> 8
 <212> PRT
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<220>
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<400> 1470

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1471

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1471

gtaaaatatg gaagtggtc cgggaaattc tactttctacg ctatggacgt c

51

<210> 1472

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1472

Val	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	Phe	Tyr	Ala	Met	Asp
1				5				10					15		

Val

<210> 1473

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1473

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ccagggaagg gcctggagt ggtctcaggt attagttgga atagtggtag caaagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaatatgga 300

agtggctacg ggagatatct cttctacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

10296W001-Sequence.txt

<210> 1474
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1474

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Arg Tyr Phe Phe Tyr Ala Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1475
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1475
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24

<210> 1476
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1476

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> 1477
<211> 24
<212> DNA
<213> Artificial Sequence

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24

<210> 1478
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<220>
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<400> 1478

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1479
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10296W001-Sequence.txt

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<400> 1480

Ala	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Arg	Tyr	Phe	Phe	Tyr	Ala	Met	Asp
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Val

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<211> 372
<212> DNA
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<400> 1481
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ccagggaagg gcctggagtg ggtctcagat attagttgga atagtaatag taaagactat 180
gcggactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctctat 240
ctacaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagatgga 300
agtggctacg ggaaattttc cctctacgct ttggacgtct ggggccaagg gaccacggctc 360
accgtctcct ca 372

<210> 1482
<211> 124
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<223> synthetic

<400> 1482

Glu Val Gln Leu Val Glu Ser Arg Gly Ala Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Asp Tyr
 20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Asn Ser Lys Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly Lys Phe Ser Leu Tyr Ala Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1483

<211> 24

<212> DNA

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<400> 1483

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24

<210> 1484

<211> 8

<212> PRT

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<400> 1484

Gly Phe Ala Phe Asn Asp Tyr Thr
1 5

<210> 1485

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1485

attagttgga atagtaatag taaa

24

<210> 1486

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1486

Ile Ser Trp Asn Ser Asn Ser Lys
1 5

<210> 1487

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

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51

<210> 1488

<211> 17

<212> PRT

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

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Val	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Ser	Leu	Tyr	Ala	Leu	Asp
1				5					10					15	

Val

<210> 1489

<211> 372

<212> DNA

<213> Artificial Sequence

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<400> 1489

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ccagggaagg	gcctagagtg	ggtctcagat	attagttgga	atagtggtag	taaaggctat	180
gcggactctg	tgaagggccg	attcaccatc	tccagagaca	acgccaagga	ttccctatat	240
ctgcagatgg	acagtctgag	agctgcagac	acggccttct	attactgtgc	aaaagataaa	300
agtggctacg	gccacttcta	ctactacgct	atggacgtct	ggggccaagg	gaccacggtc	360
accgtctcct	ca					372

<210> 1490

<211> 124

<212> PRT

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<220>

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<400> 1490

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly	Arg
1				5					10					15	

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Asp Asp Tyr
20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asp Ser Leu Tyr
65 70 75 80

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

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1491
<211> 24
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<220>
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<400> 1491
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24

<210> 1492
<211> 8
<212> PRT
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<220>
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<400> 1492

Gly Phe Lys Phe Asp Asp Tyr Thr
1 5

10296W001-Sequence.txt

<210> 1493
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<213> Artificial Sequence

<220>
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<400> 1493
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24

<210> 1494
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<212> PRT
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<220>
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<400> 1494

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1495
<211> 51
<212> DNA
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<400> 1495
gcaaaagata aaagtggtc cggccacttc tactactacg ctatggacgt c

51

<210> 1496
<211> 17
<212> PRT
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<400> 1496

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Ala Met Asp
1 5 10 15

Val

<210> 1497
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1497
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 ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag taaaggctat 180
 gcggactctg taaagggccg attcaccatc tccagagaca atgacaagaa ctccctgtat 240
 ctgcaaatga acagtctgag aggtgaggac acggccttgt attactgtgc aaaagatgga 300
 agtggctacg ggaggttcca cttctacgct atcgacgtct ggggccaagg gaccacggtc 360
 accgtctcct ca 372

<210> 1498
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1498

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Lys Phe Ala Asp Tyr
 20 25 30

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

10296W001-Sequence.txt

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Phe Tyr Ala Ile Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1499
<211> 24
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<220>
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<400> 1499
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24

<210> 1500
<211> 8
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<220>
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<400> 1500

Gly Phe Lys Phe Ala Asp Tyr Thr
1 5

<210> 1501
<211> 24
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<213> Artificial Sequence

<220>

<223> synthetic

<400> 1501

attagttgga atagtggtag taaa

24

<210> 1502

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 1502

Ile Ser Trp Asn Ser Gly Ser Lys

1 5

<210> 1503

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1503

gcaaaagatg gaagtggtc cgggaggttc cacttctacg ctatcgacgt c

51

<210> 1504

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1504

Ala Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Phe Tyr Ala Ile Asp

1 5 10 15

Val

<210> 1505

<211> 372

10296W001-Sequence.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1505

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tcctgtgtag cctctggatt cacctttgat gattattcca tgcactgggt ccggcaagct      120
ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag caaagactat      180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240
ctgcaaatga acagtctgag agctgaagac acggccttgt attactgtgc aaaatatgga      300
agtggctacg ggaagttcta ccactacggt ttggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                              372

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<210> 1506

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1506

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
          50           55           60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80

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10296W001-Sequence.txt

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1507
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<212> DNA
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<220>
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<400> 1507
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24

<210> 1508
<211> 8
<212> PRT
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<220>
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<400> 1508

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1509
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1509
attagttgga atagtggtag caaa

24

<210> 1510
<211> 8

<212> PRT
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<220>
 <223> synthetic

<400> 1510

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1511
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1511
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<210> 1512
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1512

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
 1 5 10 15

Val

<210> 1513
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1513
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10296W001-Sequence.txt

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tcctgtgcag cctctggatt cacctttgct gattatacca tgcactgggt ccggcaggct      120
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gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa atccctgtat      240
ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatgga      300
agtggctacg ggaaatactt cttctacgct atggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                              372

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<210> 1514
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1514

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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Tyr Phe Phe Tyr Ala Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1515
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 <212> DNA
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<400> 1515
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24

<210> 1516
 <211> 8
 <212> PRT
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<220>
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<400> 1516

Gly Phe Thr Phe Ala Asp Tyr Thr
 1 5

<210> 1517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1517
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24

<210> 1518
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 1518

Ile Ser Trp Asn Ser Gly Ser Met
 1 5

<210> 1519
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<210> 1520
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<220>
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<400> 1520

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Tyr Phe Phe Tyr Ala Met Asp
 1 5 10 15

Val

<210> 1521
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1521
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 ccagggaagg gcctggagtg ggtctcagat attagttagga atagtggtag taaaggctat 180
 acggactctg tgaagggccg attcaccatt tccagagaca acgccaagaa gtccctgtat 240
 ctacaaatga acagtctgag agctgaggac acggccttgt actactgtgt aaaagatgga 300

10296W001-Sequence.txt

agtggctacg ggaaatacca cttctacgct atggacgtct ggggcccaagg gaccctggtc 360
accgtctcct ca 372

<210> 1522
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1522

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly Lys Tyr His Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 1523
<211> 24
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<223> synthetic

<400> 1523

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24

<210> 1524

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1524

Gly Phe Thr Phe Ser Asp Tyr Thr
1 5

<210> 1525

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> synthetic

<400> 1525

attagttgga atagtggtag taaa

24

<210> 1526

<211> 8

<212> PRT

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<223> synthetic

<400> 1526

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1527

<211> 51

<212> DNA

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

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<210> 1528

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<213> Artificial Sequence

<220>

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<400> 1528

Val	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Lys	Tyr	His	Phe	Tyr	Ala	Met	Asp
1				5				10					15		

Val

<210> 1529

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

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<400> 1529

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ccagggaagg gcctggaatg ggtctcagat attagttaga atagtggtag cagaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagata atgccgagaa ctccctgtac 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataaa 300

agtggctacg gccactacta ctactacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> 1530

<211> 124

10296W001-Sequence.txt

<212> PRT
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<220>
<223> synthetic

<400> 1530

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Tyr Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1531
<211> 24
<212> DNA
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<220>
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<400> 1531

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24

<210> 1532
 <211> 8
 <212> PRT
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<400> 1532

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 1533
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1533
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24

<210> 1534
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1534

Ile Ser Trp Asn Ser Gly Ser Arg
 1 5

<210> 1535
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1535
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51

10296W001-Sequence.txt

<210> 1536
 <211> 17
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 <213> Artificial Sequence

<220>
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<400> 1536

Ala	Lys	Asp	Lys	Ser	Gly	Tyr	Gly	His	Tyr	Tyr	Tyr	Tyr	Ala	Met	Asp
1				5				10						15	

Val

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 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1537

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ccagggaagg	gcctggaatg	ggtctcagat	attagttgga	atagtggcac	cagaggctat	180
gcggactctg	tgaggggccc	attcaccatc	tccagagaca	acgccaagaa	gtccctgtat	240
ctgcaaatga	acagtctgag	atctgaggac	acggccttgt	attactgtgt	gaaagatgga	300
agtggctacg	ggagatataa	tttctacgct	atggacgtct	ggggccaagg	gaccacggtc	360
accgtctcct	ca					372

<210> 1538
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<220>
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<400> 1538

10296W001-Sequence.txt

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1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

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

Ser Asp Ile Ser Trp Asn Ser Gly Thr Arg Gly Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly Arg Tyr Asn Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1539
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1539
ggattcacct ttgctgatta tacc

24

<210> 1540
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1540

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> 1541

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1541

attagttgga atagtggcac caga

24

<210> 1542

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1542

Ile Ser Trp Asn Ser Gly Thr Arg
1 5

<210> 1543

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1543

gtgaaagatg gaagtggcta cgggagatat aatttctacg ctatggacgt c

51

<210> 1544

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1544

Val Lys Asp Gly Ser Gly Tyr Gly Arg Tyr Asn Phe Tyr Ala Met Asp
 1 5 10 15

Val

<210> 1545

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1545

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 ccaggaagg gcctggagtg ggtctcagat attggttgga atagtaatac tataggctat 180
 gcggactctg tgaagggccg attcgccatc tccagagaca acgccaagaa ctccctgtat 240
 cttcaaatga acagtctgcg acctgaggac acggccttat attactgtgt aaaggataaa 300
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 gtctcctca 369

<210> 1546

<211> 123

<212> PRT

<213> Artificial Sequence

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<223> synthetic

<400> 1546

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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
 20 25 30

10296W001-Sequence.txt

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

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

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1547
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24

<210> 1548
<211> 8
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<400> 1548

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> 1549
<211> 24

<212> DNA
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<220>
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<400> 1549
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24

<210> 1550
 <211> 8
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<220>
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<400> 1550

Ile Gly Trp Asn Ser Asn Thr Ile
 1 5

<210> 1551
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 <212> DNA
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<220>
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<400> 1551
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48

<210> 1552
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 <212> PRT
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<220>
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<400> 1552

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
 1 5 10 15

<210> 1553
 <211> 369

10296W001-Sequence.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1553

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ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaacag tataggctat      180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240
ctccaaatga acagtctgag acctgaggac acggccttgt atttctgtgt aaaggataaa      300
agtggctacg ggaaatTTTT catcggtttg gacgtctggg gccaaaggac aatggtcacc      360
gtctcttca                                     369
  
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<210> 1554

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1554

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30

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

Ser Asp Ile Gly Trp Asn Ser Asn Ser Ile Gly Tyr Ala Asp Ser Val
          50           55           60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80
  
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10296W001-Sequence.txt

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Phe Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 1555
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<400> 1555
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24

<210> 1556
<211> 8
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<220>
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<400> 1556

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 1557
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1557
attggttgga atagtaacag tata

24

<210> 1558
<211> 8

<212> PRT
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<220>
 <223> synthetic

<400> 1558

Ile Gly Trp Asn Ser Asn Ser Ile
 1 5

<210> 1559
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1559
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<210> 1560
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1560

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
 1 5 10 15

<210> 1561
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1561
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 ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaatac taaaggctat 180

10296W001-Sequence.txt

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ttccctgtat 240
 ctccaaatga acagtctgag acctgaggac acggccttgt atttctgtgt gaaggataaa 300
 agtggctacg ggaaatTTTT catcggtttg gacgtctggg gccaaaggac aatggtcacc 360
 gtctcttca 369

<210> 1562
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1562

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Asp Ile Gly Trp Asn Ser Asn Thr Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Phe Cys
 85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
 100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

<210> 1563
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1563
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24

<210> 1564
 <211> 8
 <212> PRT
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<220>
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<400> 1564

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 1565
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1565
 attggttgga atagtaatac taaa

24

<210> 1566
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1566

Ile Gly Trp Asn Ser Asn Thr Lys
 1 5

10296W001-Sequence.txt

<210> 1567

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1567

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48

<210> 1568

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1568

Val	Lys	Asp	Lys	Ser	Gly	Tyr	Gly	Lys	Phe	Phe	Ile	Gly	Leu	Asp	Val
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<210> 1569

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1569

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ccagggacgg gcctggagtg ggtctcagat attggttgga gtggtggtag tttaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ttggaaatga acaatctgcg acctgaagac acggccttgt attatttgtt aaaggataaa 300

agtggctacg ggaaattcca gtacggtttg gacgtctggg gccaaaggac cacggtcacc 360

gtctcctca 369

<210> 1570

<211> 123

10296W001-Sequence.txt

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1570

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Thr Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Ser Gly Gly Ser Leu Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Glu Met Asn Asn Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1571
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1571

ggattcacct ttgctgatta tacc

24

<210> 1572
 <211> 8
 <212> PRT
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<220>
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<400> 1572

Gly Phe Thr Phe Ala Asp Tyr Thr
 1 5

<210> 1573
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1573
 attggttgga gtggtggtag ttta

24

<210> 1574
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1574

Ile Gly Trp Ser Gly Gly Ser Leu
 1 5

<210> 1575
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1575
 gtaaaggata aaagtggtc cgggaaattc cagtacgggtt tggacgctc

48

10296W001-Sequence.txt

<210> 1576
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1576

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1				5					10					15	

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<211> 369
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1577

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ccagggaagg	gcctggagtg	ggtctcagat	attggttgga	atagtaacac	tataggctat	180
gcggactctg	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	ctccctgtat	240
ctccaaatga	acagtctgag	accagaggac	acggccttgt	atttctgtgt	aaaggataaa	300
agtggctacg	ggaaatTTTT	catcggtttg	gacgtctggg	gccaagggac	aatggtcacc	360
gtctcttca						369

<210> 1578
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1578

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Asp Gly Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Phe Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 1579
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1579
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24

<210> 1580
<211> 8
<212> PRT
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<220>
<223> synthetic

<400> 1580

Gly Phe Lys Phe Asp Gly Tyr Thr
1 5

<210> 1581
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1581
 attggttgga atagtaacac tata

24

<210> 1582
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1582

Ile Gly Trp Asn Ser Asn Thr Ile
 1 5

<210> 1583
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1583
 gtaaaggata aaagtggtta cgggaaattt ttcacgggtt tggacgtc

48

<210> 1584
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1584

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
 1 5 10 15

10296W001-Sequence.txt

<210> 1585
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1585
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 ccagggaagg gcctggagtg ggtctcagat attggttggga atagtaatac tataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctccctgtat 240
 ctgcaaatga acagtctgcg acctgaagac acggccttat attactgtgt aaaggataaa 300
 agtggctacg ggaaattcca atacggtttg gacgtctggg gccaaaggac cacggtcacc 360
 gtctcctca 369

<210> 1586
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1586

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

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

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1587
<211> 24
<212> DNA
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<220>
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<400> 1587
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24

<210> 1588
<211> 8
<212> PRT
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<220>
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<400> 1588

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 1589
<211> 24
<212> DNA
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<220>
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<400> 1589
attggttgga atagtaatac tata

24

<210> 1590
 <211> 8
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<220>
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<400> 1590

Ile Gly Trp Asn Ser Asn Thr Ile
 1 5

<210> 1591
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1591
 gtaaaggata aaagtggcta cgggaaattc caatacgggtt tggacgtc 48

<210> 1592
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1592

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
 1 5 10 15

<210> 1593
 <211> 369
 <212> DNA
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<400> 1593
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10296W001-Sequence.txt

tcctgtgcag cctctggatt caagtttgat gattatacca tgcactgggt ccggcaaggt	120
ccagggaagg gcctggagtg ggtctcagac attagttgga gtggtggtag catagactat	180
acggactctg tgaagggccg attctccatc tccagagaca acgccaagaa ctccctgtat	240
ctgcaaataa acagtctgag agttgaagac acggccttgt attatttgtt aaaagataaa	300
agtggctacg ggaagtactc ttacggtttg gacgtctggg gccaaaggac cacggtcacc	360
gtctcctca	369

<210> 1594
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1594

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Asp Asp Tyr	
20 25 30	

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

Ser Asp Ile Ser Trp Ser Gly Gly Ser Ile Asp Tyr Thr Asp Ser Val	
50 55 60	

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
65 70 75 80	

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

Val Lys Asp Lys Ser Gly Tyr Gly Lys Tyr Ser Tyr Gly Leu Asp Val	
100 105 110	

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1595
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1595
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24

<210> 1596
 <211> 8
 <212> PRT
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<220>
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<400> 1596

Gly Phe Lys Phe Asp Asp Tyr Thr
 1 5

<210> 1597
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1597
 attagttgga gtggtggtag cata

24

<210> 1598
 <211> 8
 <212> PRT
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<220>
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<400> 1598

10296W001-Sequence.txt

Ile Ser Trp Ser Gly Gly Ser Ile
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<210> 1599
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1599
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<210> 1600
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1600

Val Lys Asp Lys Ser Gly Tyr Gly Lys Tyr Ser Tyr Gly Leu Asp Val
1 5 10 15

<210> 1601
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1601
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ccaggaagg ggctggagtg ggttgccgt attaaaagca taagtgatgg tgggacaaca 180
gactacgtg catccgtgaa aggcagattc accatctcaa gagaagattc aaaaaatatg 240
ctgtttctgg aaatgaatag tctgaaaacc gaggacacag ccgtgtttta ctgtaccaca 300
gaggtcgcta gaactccgaa ctactggggc cggggaaccc tggtcaccgt ctctca 357

10296W001-Sequence.txt

<210> 1602
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1602

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

Ser Leu Arg Ile Ser Cys Ala Ala Ser Gly Phe Ser Phe Ile Asn Ala
 20 25 30

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

Gly Arg Ile Lys Ser Ile Ser Asp Gly Gly Thr Thr Asp Tyr Ala Ala
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asp Ser Lys Asn Met
 65 70 75 80

Leu Phe Leu Glu Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Phe
 85 90 95

Tyr Cys Thr Thr Glu Val Ala Arg Thr Pro Asn Tyr Trp Gly Arg Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 1603
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1603

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<210> 1604
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1604

Gly Phe Ser Phe Ile Asn Ala Trp
 1 5

<210> 1605
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1605
 attaaaagca taagtgatgg tgggacaaca

30

<210> 1606
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1606

Ile Lys Ser Ile Ser Asp Gly Gly Thr Thr
 1 5 10

<210> 1607
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1607
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30

10296W001-Sequence.txt

<210> 1608
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1608

Thr Thr Glu Val Ala Arg Thr Pro Asn Tyr
 1 5 10

<210> 1609
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1609

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cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag caagggatac	180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac	240
cttcaaata ga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc	300
agtggttatg gcaagtttta tcattatgga ctggacgtgt ggggacaagg gacaacagtg	360
acagtgagta gc	372

<210> 1610
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1610

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1611
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1611
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24

<210> 1612
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1612

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1613
<211> 24
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<400> 1613
atatcatgga actcaggaag caag

24

<210> 1614
<211> 8
<212> PRT
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<220>
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<400> 1614

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1615
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1615
gcaaaatagc gcagtgggta tggcaagttt tatcattatg gactggacgt g

51

<210> 1616
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1616

10296W001-Sequence.txt

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
1 5 10 15

Val

<210> 1617
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1617
gaagtacaac tggtcgaatc tggaggaggt cttgttcaac ctggtcgatc acttcgcctt 60
tcttgtgccg cttctggttt cactttcgac gattatagca tgcattgggt acgacaggct 120
cccgaaaaag ggctggaatg ggtgtcagga attagttgga actcaggaag tattggatac 180
gctgattcag tcaaaggacg cttcacaatc tcaagggaca acgctaaaaa ctcactttat 240
ttgcaaatga actctctccg cgctgaagat accgctctct attattgcgc caaagatggg 300
tctggttacg gttattttta ctactatgga atggacgttt ggggccaagg aacaactgtc 360
acagtatcat cc 372

<210> 1618
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1618

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

10296W001-Sequence.txt

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1619
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1619
ggtttcactt tcgacgatta tagc

24

<210> 1620
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1620

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1621
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1621

attagttgga actcaggaag tatt

24

<210> 1622

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1622

Ile Ser Trp Asn Ser Gly Ser Ile

1 5

<210> 1623

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1623

gccaaagatg ggtctgggta cggttatattt tactactatg gaatggacgt t

51

<210> 1624

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1624

Ala Lys Asp Gly Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met Asp

1 5 10 15

Val

10296W001-Sequence.txt

<210> 1625
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1625
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 tcttgcgctg catccggatt tacatttgac gactattcaa tgcactgggt acggcaagcc 120
 ccaggtaaag gactcgaatg ggtaagcggc atatcttgga actcaggcag tattggctac 180
 gcagattcag taaaaggaag attcactatt tcaagggata atgctaagaa cagtctctac 240
 ttgcaaata atagcttgcg cgcagaagat acagcacttt attattgtgc aaaagatgga 300
 agcggttatg ggaaatttta ttattatggt atggatgtat ggggtcaagg tacaacagtt 360
 actgtgtcaa gt 372

<210> 1626
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1626

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

10296W001-Sequence.txt

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1627
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1627
 ggatttacat ttgacgacta ttca

24

<210> 1628
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1628

Gly Phe Thr Phe Asp Asp Tyr Ser
 1 5

<210> 1629
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1629
 atatcttgga actcaggcag tatt

24

<210> 1630
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1630

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1631
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1631

gcaaaagatg gaagcgggta tgggaaattt tattattatg gtatggatgt a

51

<210> 1632
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1632

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 1633
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

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<400> 1633
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc      60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgta      180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc      300
caagggacac gactggagat taaa                                             324

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<210> 1634
<211> 108
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 1634

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

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
          20           25           30

```

```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45

```

```

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

```

```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
          85           90           95

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```

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
          100          105

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<210> 1635
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1635
 cagagcatta gcagctat

18

<210> 1636
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1636

Gln Ser Ile Ser Ser Tyr
 1 5

<210> 1637
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1637
 gctgcatcc

9

<210> 1638
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1638

Ala Ala Ser
 1

10296W001-Sequence.txt

<210> 1639
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic
 <400> 1639
 caacagagtt acagtacccc tccgatcacc 30

<210> 1640
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1640

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
 1 5 10

<210> 1641
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1641
 gaagtgcagc tggtaggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttaga atagtggtag tataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300
 agtggctacg gtcactacta ctacggaatg gacgtctggg gccaaaggac cacggtcacc 360
 gtcgcctca 369

<210> 1642
 <211> 123

10296W001-Sequence.txt

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1642

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
115 120

<210> 1643
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1643

ggattcacct ttgatgatta tacc

24

<210> 1644
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1644

Gly Phe Thr Phe Asp Asp Tyr Thr
 1 5

<210> 1645
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1645
 attagttgga atagtggtag tata

24

<210> 1646
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1646

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1647
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1647
 gcaaaagata atagtggtcga cggtcactac tactacggaa tggacgctc

48

10296W001-Sequence.txt

<210> 1648
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1648

Ala	Lys	Asp	Asn	Ser	Gly	Tyr	Gly	His	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
1				5				10						15	

<210> 1649
<211> 320
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1649

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ctctcctgca	gggccagtc	gagtgtagc	agcaacttag	cctggtacca	gcaaaaacct	120
ggccaggctc	ccaggctcct	catctatggt	gcatccacca	gggccactgg	tatcccagcc	180
aggttcagtg	gcagtgggtc	tgggacagag	ttcactctca	ccatcagcag	cctgcagtct	240
gaagattttg	cagtttatta	ctgtcagcac	tatattaact	ggcctctcac	tttcggcgga	300
gggaccaagg	tggagatcaa					320

<210> 1650
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1650

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

Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser
			20					25					30		

10296W001-Sequence.txt

Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
 65 70 75 80

Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro
 85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 1651
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1651
 cagagtgtta gcagcaac

18

<210> 1652
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1652

Gln Ser Val Ser Ser Asn
 1 5

<210> 1653
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1653

ggtgcatcc

9

<210> 1654

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1654

Gly Ala Ser

1

<210> 1655

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1655

cagcactata ttaactggcc tctcact

27

<210> 1656

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1656

Gln His Tyr Ile Asn Trp Pro Leu Thr

1

5

<210> 1657

<211> 369

<212> DNA

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 1657

gaagtgcac	tggtggagtc	tgggggaggc	ttagtacagc	ctggcgggtc	cctgagactc	60
tcctgtgcag	ccactggatt	cacctttgat	gattttacca	tgcactgggt	ccggcaagct	120
ccaggaagg	gcctggagtg	ggtctcaggt	atcagttgga	atagtggtag	cataggctat	180
gtggactctg	tgaagggccg	attcaccatc	tccagagaca	acgccaagaa	ctccctgtat	240
ctgcaaatga	acagtctgag	agctgaggac	acggccttgt	actactgtgc	aaaagataat	300
agtggctacg	gctattatta	ctacggtatg	gacgtctggg	gccaagggac	cacggtcacc	360
gtctcctca						369

<210> 1658

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1658

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

10296W001-Sequence.txt

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1659
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1659
 ggattcacct ttgatgattt tacc

24

<210> 1660
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1660

Gly Phe Thr Phe Asp Asp Phe Thr
 1 5

<210> 1661
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1661
 atcagttgga atagtggtag cata

24

<210> 1662
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1662

Ile Ser Trp Asn Ser Gly Ser Ile

1 5

<210> 1663

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1663

gcaaaagata atagtggcta cggctattat tactacggta tggacgtc 48

<210> 1664

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1664

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val

1 5 10 15

<210> 1665

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1665

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca cagtgttagc aggaactcag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240

10296W001-Sequence.txt

gaagattttg caatttatta ctgtcagcag tataataatt ggcctctcac tttcggcgga 300
gggaccaagg tggagatcaa a 321

<210> 1666
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1666

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser His Ser Val Ser Arg Asn
20 25 30

Ser Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1667
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1667
cacagtgtta gcaggaac

18

<210> 1668
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1668

His Ser Val Ser Arg Asn
1 5

<210> 1669
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1669
ggtgcatcc

9

<210> 1670
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1670

Gly Ala Ser
1

<210> 1671
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1671
cagcagtata ataattggcc tctcact 27

<210> 1672
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1672

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> 1673
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1673
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180
gcggaactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300
agtggctacg gtcactacta ctacggaatg gacgtctggg gccaaaggac cacggtcacc 360
gtcgcctca 369

<210> 1674
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1674

10296W001-Sequence.txt

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
115 120

<210> 1675
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1675
ggattcacct ttgatgatta tacc

24

<210> 1676
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1676

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> 1677

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1677

attagttgga atagtggtag tata

24

<210> 1678

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1678

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 1679

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1679

gcaaaagata atagtggtgta cggtcactac tactacggaa tggacgtc

48

<210> 1680

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1680

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
 1 5 10 15

<210> 1681

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1681

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
 ctctcctgca gggccagtca gagtggttagc agcaacttag cctggtacca gcaaaaacct 120
 ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180
 aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240
 gaagattttg cagtttatta ctgtcagcac tatattaact ggcctctcac tttcggcgga 300
 gggaccaagg tggagatcaa a 321

<210> 1682

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1682

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

10296W001-Sequence.txt

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1683
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<220>
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<400> 1683
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18

<210> 1684
<211> 6
<212> PRT
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<220>
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<400> 1684

Gln Ser Val Ser Ser Asn
1 5

<210> 1685
<211> 9
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<220>
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<400> 1685
ggtgcatcc

9

<210> 1686
 <211> 3
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 <213> Artificial Sequence

<220>
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<400> 1686

Gly Ala Ser
 1

<210> 1687
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1687
 cagcactata ttaactggcc tctcact

27

<210> 1688
 <211> 9
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<220>
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<400> 1688

Gln His Tyr Ile Asn Trp Pro Leu Thr
 1 5

<210> 1689
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1689
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tcctgtgctg cgtctggatt taccttcaga agttatgcc a tgcactgggt ccgccaggct 120

10296W001-Sequence.txt

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ccaggcaagg ggctggagtg ggtggcaatg gtatactatg atggaaataa tcaatactat      180
gcagactccg tgagggggccg attcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct      300
gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca              354
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<210> 1690
 <211> 118
 <212> PRT
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<220>
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<400> 1690

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

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
              20              25              30
```

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

```
Ala Met Val Tyr Tyr Asp Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
              50              55              60
```

```
Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65              70              75              80
```

```
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Phe Cys
              85              90              95
```

```
Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
              100             105             110
```

```
Leu Val Thr Val Ser Ser
              115
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<210> 1691
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1691
 ggatttacct tcagaagtta tgcc

24

<210> 1692
 <211> 8
 <212> PRT
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<220>
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<400> 1692

Gly Phe Thr Phe Arg Ser Tyr Ala
 1 5

<210> 1693
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1693
 gtatactatg atggaaataa tcaa

24

<210> 1694
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1694

Val Tyr Tyr Asp Gly Asn Asn Gln
 1 5

10296W001-Sequence.txt

<210> 1695
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1695
gcgcgagggc ctgggtacaa ctggctcgac ccc

33

<210> 1696
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 1696

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 1697
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
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<400> 1697
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgca gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccggcc 180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240
gaagattttg cagtttatta ctgtcagcag tataataact ggcctctcac tttcggcgga 300
gggaccaagg tggatgatcaa a 321

<210> 1698
<211> 107
<212> PRT
<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 1698

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Val Ile Lys
100 105

<210> 1699

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1699

cagagtgtta gcaggaac

18

<210> 1700

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1700

Gln Ser Val Ser Arg Asn
1 5

<210> 1701

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1701

ggtgcatcc

9

<210> 1702

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1702

Gly Ala Ser
1

<210> 1703

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1703

cagcagtata ataactggcc tctcact

27

<210> 1704

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1704

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> 1705

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1705

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gcctgtgttg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct	120
ccaggcaagg gactgcagtg ggtggcaatg atttactatg atggttaagaa taaatattat	180
gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacactgtat	240
ctgcaaatga acaatctgag agtcgaggac acggctatgt atttctgtgc gcgagggcct	300
gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcactgtttc ctca	354

<210> 1706

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1706

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

Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr	
20 25 30	

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

10296W001-Sequence.txt

Ala Met Ile Tyr Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 1707
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1707
ggattcacct tcagaagtta tggc

24

<210> 1708
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1708

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> 1709
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1709

atttactatg atggtaagaa taaa

24

<210> 1710

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1710

Ile Tyr Tyr Asp Gly Lys Asn Lys

1 5

<210> 1711

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1711

gcgcgagggc ctgggtacaa ttggctcgac ccc

33

<210> 1712

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1712

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro

1 5 10

<210> 1713

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

10296W001-Sequence.txt

<223> synthetic

<400> 1713

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ctctcctgca gggccagtc  gagaattagc agcaacttgg cctggtacca gcaaaaacct      120
ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc      180
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct      240
gaggatgttg cagtttatta ctgtcagcaa catcataact ggctctcac tttcggcgga      300
gggaccaagg tggagatcaa a                                           321

```

<210> 1714

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1714

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Asn
          20           25           30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
          35           40           45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ser Pro Ala Arg Phe Ser Gly
          50           55           60

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His His Asn Trp Pro Leu
          85           90           95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
          100          105

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<210> 1715
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1715
 cagagaatta gcagcaac

18

<210> 1716
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1716

Gln Arg Ile Ser Ser Asn
 1 5

<210> 1717
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1717
 ggtgcatcc

9

<210> 1718
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 1718

Gly Ala Ser
 1

<210> 1719
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1719
 cagcaacatc ataactggcc tctcact

27

<210> 1720
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1720

Gln Gln His His Asn Trp Pro Leu Thr
 1 5

<210> 1721
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1721

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
 50 55 60

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 1722
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1722

Gly Tyr Thr Phe Thr Arg Tyr Thr
1 5

<210> 1723
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1723

Ile Asn Pro Ser Arg Gly Tyr Thr
1 5

<210> 1724
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1724

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
1 5 10

<210> 1725

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1725

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1726

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1726

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
1 5 10

<210> 1727

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1727

Asp Thr Ser

1

<210> 1728

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1728

Gln Gln Trp Ser Ser Asn Pro Leu Thr
1 5

<210> 1729

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1729

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60

agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct 120

cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag caagggatac 180

gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240

10296W001-Sequence.txt

cttcaaata gactctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
 agtgggttatg gcaagtttta tcattatgga ctggacgtgt ggggacaagg gacaacagtg 360
 acagtgagta gc 372

<210> 1730
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1730

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1731
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1731
gggtttacat tcgacgatta cagc

24

<210> 1732
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1732

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1733
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1733
atatcatgga actcaggaag caag

24

<210> 1734
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1734

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1735
<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1735

gcaaaatacg gcagtgggta tggcaagttt tatcattatg gactggacgt g 51

<210> 1736

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1736

Ala	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	His	Tyr	Gly	Leu	Asp
1				5					10					15	

Val

<210> 1737

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1737

gaagtacagt tggtagaatc tggaggagga ctcgtgcaac caggacgatc attgcggttg 60

agttgtgctg ctagtggatt cacattcgac gactatgcta tgcattgggt aagacaggct 120

ccaggaaaag gactcgaatg ggtgtcagga ataagttgga actccggaag cattgggtac 180

gcagattcag tcaaagggcg attcaccata tcccagagata acgctaagaa ctcactttac 240

cttcaaata actctcttcg agcagaggac actgcacttt attattgcgc taaggacggc 300

tccggttatg gatattttta ttattatgga atggacgtat ggggacaagg cactactgtt 360

accgttagtt cc 372

10296W001-Sequence.txt

<210> 1738

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1738

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1739

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1739

ggattcacat tcgacgacta tgct

<210> 1740
 <211> 8
 <212> PRT
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<220>
 <223> synthetic

<400> 1740

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 1741
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1741
 ataagttgga actccggaag catt

24

<210> 1742
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1742

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1743
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1743
 gctaaggacg gctccggtta tggatatattt tattattatg gaatggacgt a

51

<210> 1744
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1744

Ala	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Tyr	Phe	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 1745
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1745

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tcttgtgccg cttctggttt cactttcgac gattatagca tgcattgggt acgacaggct	120
cccggaaaag ggctggaatg ggtgtcagga attagttgga actcaggaag tattggatac	180
gctgattcag tcaaaggacg cttcacaatc tcaagggaca acgctaataaa ctcactttat	240
ttgcaaatga actctctccg cgctgaagat accgctctct attattgcgc caaagatggg	300
tctggttacg gttatTTTTA ctactatgga atggacgttt ggggccaagg aacaactgtc	360
acagtatcat cc	372

<210> 1746
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

<400> 1746

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1747

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1747

ggtttcactt tcgacgatta tagc

24

<210> 1748

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1748

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1749

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1749

attagttgga actcaggaag tatt

24

<210> 1750

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1750

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 1751

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1751

gccaaagatg ggtctggtta cggttatattt tactactatg gaatggacgt t

51

<210> 1752

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1752

Ala	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Tyr	Phe	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 1753

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1753

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tcatgcgtag cttccggatt tacatttgac gattacgcaa tgcactgggt tagacaggca	120
ccaggaaaag gactggagtg ggtgagcggg atttcatgga acagcggcag tatcggttat	180
gcagactcag ttaaaggaag attcaccatc agtagagaca acgcaaaaaa ttccctttat	240
ctccaaatga actctcttag ggccgaagat acagcattgt actactgcgc aaaagacgga	300
tcaggttacg gaaaatttta ctactatggt atggatgtat ggggtcaggg aaccacagta	360
actgtatcaa gc	372

<210> 1754

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1754

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		

10296W001-Sequence.txt

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1755
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1755
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24

<210> 1756
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1756

Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 1757
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1757
 atttcatgga acagcggcag tatc

24

<210> 1758
 <211> 8
 <212> PRT
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<220>
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<400> 1758

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1759
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1759
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51

<210> 1760
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1760

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 1761
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1761
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 tcttgcgctg catccggatt tacatttgac gactattcaa tgcactgggt acggcaagcc 120
 ccaggtaaag gactcgaatg ggtaagcggc atatcttgga actcaggcag tattggctac 180
 gcagattcag taaaaggaag attcactatt tcaagggata atgctaagaa cagtctctac 240
 ttgcaaatga atagcttgcg cgcagaagat acagcacttt attattgtgc aaaagatgga 300
 agcggttatg ggaaatttta ttattatggt atggatgtat ggggtcaagg tacaacagtt 360
 actgtgtcaa gt 372

<210> 1762
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1762

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1763
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1763
ggatttacat ttgacgacta ttca

24

<210> 1764
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1764

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1765
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1765
 atatcttgga actcaggcag tatt

24

<210> 1766
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1766

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1767
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1767
 gcaaaagatg gaagcgggta tgggaaattt tattattatg gtaggatgt a

51

<210> 1768
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1768

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 1769
 <211> 372
 <212> DNA
 <213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 1769

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agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct      120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggatac      180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac      240
cttcaaataa actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc      300
agtggttatg gcaagtttta tcattatgga ctggacgtgt ggggacaagg gacaacagtg      360
acagtgagta gc                                                              372

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<210> 1770

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1770

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
          50           55           60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95

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10296W001-Sequence.txt

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1771
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1771
 gggtttacat tcgacgatta cagc

24

<210> 1772
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1772

Gly Phe Thr Phe Asp Asp Tyr Ser
 1 5

<210> 1773
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1773
 atatcatgga actcaggaag catc

24

<210> 1774
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1774

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 1775

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1775

gcaaaatacg gcagtgggta tggcaagttt tatcattatg gactggacgt g 51

<210> 1776

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1776

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
1 5 10 15

Val

<210> 1777

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1777

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60

agttgcgcag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120

10296W001-Sequence.txt

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cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag caagggatac 180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
cttcaaata ga actctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc 300
agtggttatg gcaagtttta tcattatgga ctggacgtgt ggggacaagg gacaacagtg 360
acagtgagta gc 372
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<210> 1778
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1778

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1779
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1779
 gggtttacat tcgacgatta cagc

24

<210> 1780
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1780

Gly Phe Thr Phe Asp Asp Tyr Ser
 1 5

<210> 1781
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1781
 atatcatgga actcaggaag caag

24

<210> 1782
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1782

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1783
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1783
 gcaaaagacg gcagtgggta tggcaagttt tatcattatg gactggacgt g 51

<210> 1784
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1784

Ala	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	His	Tyr	Gly	Leu	Asp
1				5				10						15	

Val

<210> 1785
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1785
 gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60
 agttgcgag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120
 cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag caagggatac 180
 gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
 cttcaaatga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
 agtggttatg gcaagtttta ttattatgga ctggacgtgt ggggacaagg gacaacagtg 360

acagtgagta gc

<210> 1786
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1786

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1787
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 1787

gggtttacat tcgacgatta cagc

24

<210> 1788

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1788

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1789

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1789

atatcatgga actcaggaag caag

24

<210> 1790

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1790

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1791

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1791

gcaaaatacg gcagtgggta tggcaagttt tattattatg gactggacgt g

51

<210> 1792

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1792

Ala	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	Tyr	Tyr	Gly	Leu	Asp
1				5				10						15	

Val

<210> 1793

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1793

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60

agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct 120

cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag caagggatac 180

gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240

cttcaaata actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300

agtggttatg gcaagtttta tcattatgga atggacgtgt ggggacaagg gacaacagtg 360

acagtga gta gc 372

<210> 1794

<211> 124

<212> PRT

<213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 1794

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1795

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1795

gggtttacat tcgacgatta cagc

24

<210> 1796

<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1796

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1797
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1797
atatcatgga actcaggaag caag

24

<210> 1798
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1798

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1799
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1799
gcaaaatacg gcagtgggta tggcaagttt tatcattatg gaatggacgt g

51

<210> 1800
<211> 17

10296W001-Sequence.txt

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1800

Ala	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	His	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 1801
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1801

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg	60
agttgcgcag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct	120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggatac	180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac	240
cttcaaata gaactctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc	300
agtggttatg gcaagtttta tcattatgga ctggacgtgt ggggacaagg gacaacagtg	360
acagtga gta gc	372

<210> 1802
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1802

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

10296W001-Sequence.txt

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1803
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1803
gggtttacat tcgacgatta cagc

24

<210> 1804
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1804

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1805
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1805
atatcatgga actcaggaag catc

24

<210> 1806
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1806

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 1807
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1807
gcaaaagacg gcagtgggta tggcaagttt tatcattatg gactggacgt g

51

<210> 1808
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1808

10296W001-Sequence.txt

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
1 5 10 15

Val

<210> 1809
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1809
gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60
agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct 120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggatac 180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
cttcaaata gaactctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
agtggttatg gcaagtttta ttattatgga ctggacgtgt ggggacaagg gacaacagtg 360
acagtgagta gc 372

<210> 1810
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1810

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

10296W001-Sequence.txt

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1811
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1811
gggtttacat tcgacgatta cagc

24

<210> 1812
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1812

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1813
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1813

atatcatgga actcaggaag catc

24

<210> 1814

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1814

Ile Ser Trp Asn Ser Gly Ser Ile

1 5

<210> 1815

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1815

gcaaaatacg gcagtgggta tggcaagttt tattattatg gactggacgt g

51

<210> 1816

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1816

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Leu Asp

1 5 10 15

Val

10296W001-Sequence.txt

<210> 1817
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1817
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 agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct 120
 cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggatac 180
 gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
 cttcaaatga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
 agtggttatg gcaagtttta tcattatgga atggacgtgt ggggacaagg gacaacagtg 360
 acagtgagta gc 372

<210> 1818
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1818

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

10296W001-Sequence.txt

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1819
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1819
 gggtttacat tcgacgatta cagc

24

<210> 1820
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1820

Gly Phe Thr Phe Asp Asp Tyr Ser
 1 5

<210> 1821
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1821
 atatcatgga actcaggaag catc

24

<210> 1822
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1822

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1823
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 1823

gcaaaatacg gcagtgggta tggcaagttt tatcattatg gaatggacgt g

51

<210> 1824
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1824

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Met Asp
 1 5 10 15

Val

<210> 1825
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

<400> 1825
gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60
agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct 120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag caagggatac 180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
cttcaaatac actctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc 300
agtggttatg gcaagtttta ttattatgga ctggacgtgt ggggacaagg gacaacagtg 360
acagtgagta gc 372

<210> 1826
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1826

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1827
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1827
gggtttacat tcgacgatta cagc

24

<210> 1828
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1828

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1829
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1829
atatcatgga actcaggaag caag

24

<210> 1830
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1830

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1831

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1831

gcaaaagacg gcagtgggta tggcaagttt tattattatg gactggacgt g 51

<210> 1832

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1832

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Leu Asp
 1 5 10 15

Val

<210> 1833

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1833

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60

agttgcgcag ctagtggggt tacattcgac gattacagca tgcattgggt gaggcaagct 120

cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag caagggatac 180

gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240

10296W001-Sequence.txt

cttcaaata gactctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc 300
 agtgggttatg gcaagtttta tcattatgga atggacgtgt ggggacaagg gacaacagtg 360
 acagtga gta gc 372

<210> 1834
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1834

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1835
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1835
gggtttacat tcgacgatta cagc

24

<210> 1836
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1836

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1837
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1837
atatcatgga actcaggaag caag

24

<210> 1838
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1838

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1839
<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1839

gcaaaagacg gcagtgggta tggcaagttt tatcattatg gaatggacgt g 51

<210> 1840

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1840

Ala	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	His	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 1841

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1841

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60

agttgcgcag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120

cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag caagggatac 180

gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240

cttcaaata actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300

agtggttatg gcaagtttta ttattatgga atggacgtgt ggggacaagg gacaacagtg 360

acagtgagta gc 372

10296W001-Sequence.txt

<210> 1842

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1842

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1843

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1843

gggtttacat tcgacgatta cagc

10296W001-Sequence.txt

<210> 1844
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1844

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1845
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1845
atatcatgga actcaggaag caag

24

<210> 1846
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1846

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> 1847
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1847
gcaaaatacg gcagtgggta tggcaagttt tattattatg gaatggacgt g

51

<210> 1848
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1848

Ala	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	Tyr	Tyr	Gly	Met	Asp
1				5					10					15	

Val

<210> 1849
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1849

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg	60
agttgcgag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct	120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag catcggatac	180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac	240
cttcaaata actctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc	300
agtggttatg gcaagtttta ttattatgga ctggacgtgt ggggacaagg gacaacagtg	360
acagtgagta gc	372

<210> 1850
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

10296W001-Sequence.txt

<400> 1850

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1851

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1851

gggtttacat tcgacgatta cagc

24

<210> 1852

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1852

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1853

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1853

atatcatgga actcaggaag catc

24

<210> 1854

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1854

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 1855

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1855

gcaaaagacg gcagtgggta tggcaagttt tattattatg gactggacgt g

51

<210> 1856

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1856

Ala	Lys	Asp	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	Tyr	Tyr	Gly	Leu	Asp
1				5					10					15	

Val

<210> 1857

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1857

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg	60
agttgcgcag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct	120
cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag catcggatac	180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac	240
cttcaaata gaactctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc	300
agtggttatg gcaagtttta tcattatgga atggacgtgt ggggacaagg gacaacagtg	360
acagtgagta gc	372

<210> 1858

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1858

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
			20					25					30		

10296W001-Sequence.txt

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Met Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1859
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1859
 gggtttacat tcgacgatta cagc

24

<210> 1860
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1860

Gly Phe Thr Phe Asp Asp Tyr Ser
 1 5

<210> 1861
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1861
 atatcatgga actcaggaag catc

24

<210> 1862
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1862

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1863
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1863
 gcaaaagacg gcagtgggta tggcaagttt tatcattatg gaatggacgt g

51

<210> 1864
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1864

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Met Asp
 1 5 10 15

Val

<210> 1865
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1865
 gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60
 agttgcgag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120
 cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag catcggatac 180
 gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240
 cttcaaatga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300
 agtggttatg gcaagtttta ttattatgga atggacgtgt ggggacaagg gacaacagtg 360
 acagtgagta gc 372

<210> 1866
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1866

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

10296W001-Sequence.txt

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1867
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1867
gggtttacat tcgacgatta cagc

24

<210> 1868
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1868

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1869
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1869
 atatcatgga actcaggaag catc

24

<210> 1870
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1870

Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 1871
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1871
 gcaaaatacg gcagtgggta tggcaagttt tattattatg gaatggacgt g

51

<210> 1872
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1872

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
 1 5 10 15

Val

<210> 1873
 <211> 372
 <212> DNA
 <213> Artificial Sequence

10296W001-Sequence.txt

<220>

<223> synthetic

<400> 1873

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gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg      60
agttgcgtag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct      120
cctggtaaag gattggaatg ggtagcggg atatcatgga actcaggaag caagggatac      180
gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac      240
cttcaaataa actctcttag ggcagaagac acagcattgt attattgcgc aaaagacggc      300
agtggttatg gcaagtttta ttattatgga atggacgtgt ggggacaagg gacaacagtg      360
acagtgagta gc                                                              372

```

<210> 1874

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1874

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

```

```

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
          20           25           30

```

```

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

```

```

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
          50           55           60

```

```

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80

```

```

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95

```

10296W001-Sequence.txt

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 1875
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1875
gggtttacat tcgacgatta cagc 24

<210> 1876
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1876

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> 1877
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1877
atatcatgga actcaggaag caag 24

<210> 1878
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> synthetic

<400> 1878

Ile Ser Trp Asn Ser Gly Ser Lys

1 5

<210> 1879

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1879

gcaaaagacg gcagtgggta tggcaagttt tattattatg gaatggacgt g 51

<210> 1880

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1880

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp

1 5 10 15

Val

<210> 1881

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1881

gaagtgcagc tgggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgtag cctctggatt cacctttgat gattattcca tgcactgggt ccggcaagct 120

10296W001-Sequence.txt

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ccaggggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag caaagactat      180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240
ctgcaaataga acagtctgag agctgaagac acggccttgt attactgtgc aaaatatgga      300
agtggctacg ggaagttcta ccactacggt ttggacgtct ggggccaagg gaccacggtc      360
accgtctcct ca                                                              372
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<210> 1882
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1882

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 1883
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1883
 ggattcacct ttgatgatta ttcc

24

<210> 1884
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1884

Gly Phe Thr Phe Asp Asp Tyr Ser
 1 5

<210> 1885
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1885
 attagttgga atagtggtag caaa

24

<210> 1886
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1886

Ile Ser Trp Asn Ser Gly Ser Lys
 1 5

<210> 1887
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1887
 gcaaaatatg gaagtggcta cgggaagttc taccactacg gtttggacgt c 51

<210> 1888
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1888

Ala	Lys	Tyr	Gly	Ser	Gly	Tyr	Gly	Lys	Phe	Tyr	His	Tyr	Gly	Leu	Asp
1				5					10					15	

Val

<210> 1889
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1889
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttggaga cagcgtcacc 60
 atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatact gcatccagtt tgctaagtgg ggtcccttca 180
 aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcgg tctgcaccct 240
 gaagattttg caacttactt ctgtcaacag agtttcagta cccctccgat caccttcggc 300
 caaggacac gactggacat taaa 324

<210> 1890
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1890

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu His Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Ser Phe Ser Thr Pro Pro
 85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile Lys
 100 105

<210> 1891
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1891
 cagagcatta acaactat

<210> 1892
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1892

Gln Ser Ile Asn Asn Tyr
 1 5

<210> 1893
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1893
 actgcatcc

9

<210> 1894
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1894

Thr Ala Ser
 1

<210> 1895
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1895
 caacagagtt tcagtacccc tccgatcacc

30

10296W001-Sequence.txt

<210> 1896
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1896

Gln Gln Ser Phe Ser Thr Pro Pro Ile Thr
 1 5 10

<210> 1897
 <211> 207
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1897

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
 1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
 20 25 30

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
 50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
 65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
 85 90 95

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
 100 105 110

10296W001-Sequence.txt

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115 120 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
130 135 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145 150 155 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
165 170 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
180 185 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
195 200 205

<210> 1898

<211> 171

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1898

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1 5 10 15

Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
20 25 30

Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
35 40 45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
50 55 60

Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys
65 70 75 80

10296W001-Sequence.txt

Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys
85 90 95

Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val
100 105 110

Ile Ala Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
115 120 125

Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
130 135 140

Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr
145 150 155 160

Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
165 170

<210> 1899

<211> 490

<212> PRT

<213> Homo sapiens

<400> 1899

Met Glu Ser Ile Ser Met Met Gly Ser Pro Lys Ser Leu Ser Glu Thr
1 5 10 15

Phe Leu Pro Asn Gly Ile Asn Gly Ile Lys Asp Ala Arg Lys Val Thr
20 25 30

Val Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg
35 40 45

Leu Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys
50 55 60

Phe Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu
65 70 75 80

10296W001-Sequence.txt

Asp Ala Leu Thr Lys Thr Asn Ile Ile Phe Val Ala Ile His Arg Glu
85 90 95

His Tyr Thr Ser Leu Trp Asp Leu Arg His Leu Leu Val Gly Lys Ile
100 105 110

Leu Ile Asp Val Ser Asn Asn Met Arg Ile Asn Gln Tyr Pro Glu Ser
115 120 125

Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Asp Ser Leu Ile Val Lys
130 135 140

Gly Phe Asn Val Val Ser Ala Trp Ala Leu Gln Leu Gly Pro Lys Asp
145 150 155 160

Ala Ser Arg Gln Val Tyr Ile Cys Ser Asn Asn Ile Gln Ala Arg Gln
165 170 175

Gln Val Ile Glu Leu Ala Arg Gln Leu Asn Phe Ile Pro Ile Asp Leu
180 185 190

Gly Ser Leu Ser Ser Ala Arg Glu Ile Glu Asn Leu Pro Leu Arg Leu
195 200 205

Phe Thr Leu Trp Arg Gly Pro Val Val Val Ala Ile Ser Leu Ala Thr
210 215 220

Phe Phe Phe Leu Tyr Ser Phe Val Arg Asp Val Ile His Pro Tyr Ala
225 230 235 240

Arg Asn Gln Gln Ser Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn
245 250 255

Lys Thr Leu Pro Ile Val Ala Ile Thr Leu Leu Ser Leu Val Tyr Leu
260 265 270

Ala Gly Leu Leu Ala Ala Ala Tyr Gln Leu Tyr Tyr Gly Thr Lys Tyr
275 280 285

10296W001-Sequence.txt

Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu Gln Cys Arg Lys Gln
290 295 300

Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val Ala Tyr Ser
305 310 315 320

Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn Met
325 330 335

Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu
340 345 350

Glu Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu
355 360 365

Gly Leu Leu Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn
370 375 380

Ala Leu Asn Trp Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr
385 390 395 400

Val Ala Leu Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys
405 410 415

Arg Ala Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe
420 425 430

Val Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Gly Lys Ile Ile
435 440 445

Leu Phe Leu Pro Cys Ile Ser Arg Lys Leu Lys Arg Ile Lys Lys Gly
450 455 460

Trp Glu Lys Ser Gln Phe Leu Glu Glu Gly Met Gly Gly Thr Ile Pro
465 470 475 480

His Val Ser Pro Glu Arg Val Thr Val Met
485 490

10296W001-Sequence.txt

<210> 1900

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1900

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
20 25 30

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

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85 90 95

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
100 105 110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
115 120 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
130 135 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
145 150 155 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn

10296W001-Sequence.txt

165

170

175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
180 185 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
195 200 205

<210> 1901

<211> 171

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1901

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1 5 10 15

Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
20 25 30

Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
35 40 45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
50 55 60

Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys
65 70 75 80

Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys
85 90 95

Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val
100 105 110

Ile Ala Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
115 120 125

10296W001-Sequence.txt

Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
 130 135 140

Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr
 145 150 155 160

Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
 165 170

<210> 1902

<400> 1902
 000

<210> 1903
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1903

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
 20 25

<210> 1904
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1904

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1 5 10 15

Gly

10296W001-Sequence.txt

<210> 1905
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1905

Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 1 5 10 15

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 20 25 30

Thr Ala Leu Tyr Tyr Cys
 35

<210> 1906
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1906

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 1 5 10

<210> 1907
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> VARIANT
 <222> (8)..(8)
 <223> Xaa = Any Amino Acid

<400> 1907

Gly Phe Thr Phe Asp Asp Tyr Xaa
1 5

<210> 1908

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<220>

<221> VARIANT

<222> (8)..(8)

<223> Xaa = Any Amino Acid

<400> 1908

Ile Ser Trp Asn Ser Gly Ser Xaa
1 5

<210> 1909

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<220>

<221> VARIANT

<222> (3)..(3)

<223> Xaa = Any Amino Acid

<220>

<221> VARIANT

<222> (12)..(12)

<223> Xaa = Any Amino Acid

<220>

<221> VARIANT

<222> (15)..(15)

<223> Xaa = Any Amino Acid

<400> 1909

10296W001-Sequence.txt

Ala Lys Xaa Gly Ser Gly Tyr Gly Lys Phe Tyr Xaa Tyr Gly Xaa Asp
1 5 10 15

Val

<210> 1910

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1910

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Tyr Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 1911

<211> 330

10296W001-Sequence.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1911

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

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

10296W001-Sequence.txt

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

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

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

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

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

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

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

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 1912

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1912

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

10296W001-Sequence.txt

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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

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

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

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

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

10296W001-Sequence.txt

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

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

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

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

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

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 1913

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1913

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

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

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

10296W001-Sequence.txt

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

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

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

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

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

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

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

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

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

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

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

10296W001-Sequence.txt

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

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

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

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

Ser Leu Ser Pro Gly Lys
325

<210> 1914
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1914

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

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

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

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

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

10296W001-Sequence.txt

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

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

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

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

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

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

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

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

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

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

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

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

10296W001-Sequence.txt

Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 1915
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1915

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

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

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

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

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

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

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

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

10296W001-Sequence.txt

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

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

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

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

10296W001-Sequence.txt

<210> 1916

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1916

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

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

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

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

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

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

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

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

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

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

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

10296W001-Sequence.txt

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

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

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

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

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

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

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

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

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

Leu Ser Leu Ser Leu Gly Lys
325

<210> 1917

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1917

10296W001-Sequence.txt

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

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

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

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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

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

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

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

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

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

10296W001-Sequence.txt

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
225 230 235 240

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

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

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

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

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
325

<210> 1918
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1918

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

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

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

10296W001-Sequence.txt

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

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

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

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

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

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

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

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

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

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

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
225 230 235 240

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

10296W001-Sequence.txt

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

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

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

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
305 310 315 320

Lys Ser Leu Ser Leu Ser Pro Gly Lys
325

<210> 1919

<211> 326

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1919

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

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

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

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

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

10296W001-Sequence.txt

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

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

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

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

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

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

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

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

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

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

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

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

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

10296W001-Sequence.txt

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

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

Ser Leu Ser Leu Gly Lys
325

<210> 1920
<211> 326
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1920

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

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

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

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

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

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

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

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

10296W001-Sequence.txt

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

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

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

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

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

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

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

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

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

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

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

Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Leu Gly Lys
325

10296W001-Sequence.txt

<210> 1921
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1921

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

10296W001-Sequence.txt

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1922
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1922

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

10296W001-Sequence.txt

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1923

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1923

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

10296W001-Sequence.txt

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

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

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

10296W001-Sequence.txt

Ser Pro Gly Lys
225

<210> 1924
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1924

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

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

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

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

10296W001-Sequence.txt

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Lys
225

<210> 1925
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1925

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

10296W001-Sequence.txt

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

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

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 1926
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1926

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

10296W001-Sequence.txt

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

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

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 1927
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1927

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
20 25 30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
35 40 45

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
50 55 60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
65 70 75 80

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
100 105 110

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
130 135 140

10296W001-Sequence.txt

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
195 200 205

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
210 215 220

Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1928
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1928

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
20 25 30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
35 40 45

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
50 55 60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
65 70 75 80

10296W001-Sequence.txt

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

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
100 105 110

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
130 135 140

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

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
165 170 175

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
180 185 190

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
195 200 205

Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser
210 215 220

Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1929
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1929

10296W001-Sequence.txt

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
130 135 140

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
195 200 205

10296W001-Sequence.txt

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Leu Gly Lys
225

<210> 1930
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1930

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

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

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
130 135 140

10296W001-Sequence.txt

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Leu Gly Lys
225

<210> 1931
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 1931

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
50 55 60

10296W001-Sequence.txt

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65 70 75 80

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
115 120 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
195 200 205

His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
210 215 220

Pro Gly Lys
225

<210> 1932
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

10296W001-Sequence.txt

<400> 1932

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 1 5 10 15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 20 25 30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 35 40 45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 65 70 75 80

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

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 100 105 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 115 120 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 130 135 140

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 165 170 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 180 185 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 195 200 205

10296W001-Sequence.txt

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 210 215 220

Pro Gly Lys
 225

<210> 1933
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 1933

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
 1 5 10 15

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
 20 25 30

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
 35 40 45

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
 50 55 60

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
 65 70 75 80

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
 85 90 95

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
 100 105 110

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
 115 120 125

10296W001-Sequence.txt

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
130 135 140

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145 150 155 160

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
165 170 175

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
180 185 190

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
195 200 205

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn Arg Phe Thr Thr
210 215 220

Lys Ser Phe Ser Arg Thr Pro Gly Lys
225 230

<210> 1934

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1934

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
1 5 10 15

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
20 25 30

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
35 40 45

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
50 55 60

10296W001-Sequence.txt

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
65 70 75 80

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
85 90 95

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
100 105 110

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
115 120 125

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
130 135 140

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145 150 155 160

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
165 170 175

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
180 185 190

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
195 200 205

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
210 215 220

Lys Ser Phe Ser Arg Thr Pro Gly Lys
225 230