

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2012322093 C1**

(54) Title
Antibody polypeptides that antagonize CD40L

(51) International Patent Classification(s)
C07K 16/28 (2006.01) **A61K 39/395** (2006.01)

(21) Application No: **2012322093** (22) Date of Filing: **2012.10.12**

(87) WIPO No: **WO13/056068**

(30) Priority Data

(31) Number	(32) Date	(33) Country
61/546,800	2011.10.13	US
61/655,110	2012.06.04	US

(43) Publication Date: **2013.04.18**

(44) Accepted Journal Date: **2016.06.02**

(44) Amended Journal Date: **2016.12.22**

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(56) Related Art
WO 2006/030220



- (51) **International Patent Classification:**
C07K 16/28 (2006.01) *A61K 39/395* (2006.01)
- (21) **International Application Number:**
PCT/US2012/059977
- (22) **International Filing Date:**
12 October 2012 (12.10.2012)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
61/546,800 13 October 2011 (13.10.2011) US
61/655,110 4 June 2012 (04.06.2012) US
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(81) **Designated States** (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))
- with sequence listing part of description (Rule 5.2(a))

(54) **Title:** ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40L

FIG. 1B

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EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYY
CYKVGKDAKSDYRGGGLTVTVSSASTEPKSSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLDHQLNGKEVCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNVKTPPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSPGK
(MW=77,984 daltons)

dAb
Linker
Modified IgG1 Fc from Abatacept (Cys→Ser; Pro→Ser)

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(57) **Abstract:** Antibody polypeptides that specifically bind human CD40L are provided. The antibody polypeptides do not activate platelets. The antibody polypeptides are useful in the treatment of diseases involving CD40L activation, such as graft-related diseases and autoimmune diseases. The antibody polypeptides may be domain antibodies (dAbs) comprising a single VH or VK domain. The half-life of the antibody polypeptides may be increased by modifying the antibody polypeptides to be dual specific reagents that can also bind human serum albumin (HSA) or another antigen.

ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40L**TECHNICAL FIELD**

Antibodies and fragments thereof that target CD40L, compositions comprising the same, and methods of using the same for treatment of diseases involving CD40L activity are provided.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on October 8, 2012, is named 20089600.txt and is 1,254,371 bytes in size.

BACKGROUND

CD40 ligand (CD40L), also known as CD154, gp39, TNF-related activation protein (TRAP), 5c8 antigen, or T-BAM, is a trimeric transmembrane protein of the tumor necrosis factor (TNF) superfamily of molecules. CD40L is primarily expressed on activated T cells, as well as on activated leukocytes, eosinophils, basophils, natural killer cells, mast cells, and non-immune cells such as platelets and activated endothelial cells. CD40L also exists in soluble form (sCD40L) that is produced by microsomal stimulus-dependent cleavage of the membrane-bound CD40L. Most of sCD40L in circulation (>90%) is platelet-derived.

CD40L binds CD40, a type I transmembrane glycoprotein belonging to the TNF receptor (TNFR) family. Although all monomeric, dimeric, and trimeric forms of sCD40L can bind to CD40, the trimeric form of sCD40L has the most potent biological activity through oligomerization of cell surface CD40, a common feature of TNFR family. The highest expression of CD40 has been observed on antigen presenting cells (APCs), such as B cells, macrophages, and dendritic cells, while lower expression of this receptor is noted on a variety of other cell types, including stromal cells and thymic epithelium. The CD40-CD40L interaction is essential for normal T-B cell interactions, including increased co-stimulation, T-cell priming, cytokine production, antibody-class switching and affinity maturation, and antibody and autoantibody production.

The crucial role of CD40-CD40L interactions in immune and inflammatory responses has made them a promising target for treatment of pathological immuno-inflammatory

processes. Blockade of CD40-CD40L interactions by means of specific CD40L monoclonal antibodies (mAbs) successfully prevents allograft rejection in primates and treats autoimmune diseases and atherosclerosis in animal models. Montgomery et al., *Transplantation* 74: 1365-1369 (2002).

In humans, two different anti-CD40L mAb clones have been used in clinical trials for treatment of different autoimmune diseases. Maribel et al., *Mol. Immunol.* 45: 937-44 (2008). Monoclonal antibodies, however, can display unusually high incidence of thromboembolic (TE) complications, such as atherothrombotic central nervous system events, myocardial infarction, pulmonary embolism, and deep vein thrombosis. For example, the usefulness of the anti-CD40L mAb clone hu5c8 (anti-CD40L mAb, Biogen) is limited by an unusually high incidence of TE complications. TE by these antibodies is thought to result from the formation of higher-order immune complexes (IC) of the mAbs with membrane-bound CD40L on platelets, or sCD40L shed from platelets, that can ligate and thereby aggregate neighboring platelets via their FcγRIIa receptors, resulting in thrombi formation. The risk of thromboembolism has led to a halt in all ongoing clinical trials. Boumpas et al., *Arthritis & Rheumatism* 48: 719-727 (2003).

SUMMARY

In a first aspect, the invention provides an isolated antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the first variable domain comprises:

- (a) a CDR1 region having a sequence Trp-X₁-Leu-Met-Gly (SEQ ID NO: 2), wherein X₁ is Glu or Gln;
- (b) a CDR2 region having a sequence Gly-Ile-Glu-Gly-Pro-Gly-Asp-Val-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (SEQ ID NO: 3); and
- (c) a CDR3 region having a sequence Lys-X₂-Y₂-Z₂-Ser-Asp-Tyr (SEQ ID NO: 4), wherein X₂ is Asp or Glu, Y₂ is Ala or Ser, and Z₂ is Lys, Asn, or Arg.

In further aspects, the invention provides an isolated nucleic acid encoding the antibody polypeptide of the invention, a vector comprising such a nucleic acid, and an isolated host cell comprising such a vector.

In additional aspects, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of the antibody polypeptide of the invention

and a pharmaceutically acceptable carrier, and a method of treating an immune disease in a patient having, or at risk of having an immune disease, comprising administering to the patient a therapeutically effective amount of an isolated polypeptide of the invention. A further aspect is the use of an antibody polypeptide of the invention for the preparation of a medicament for the treatment of a patient, wherein the patient has or is at risk of having an immune disease.

The invention is as defined in the claims. However, the description which follows may refer to additional polypeptides and other subject matter outside the scope of the present claims. This description is retained for technical information.

Anti-CD40L antibody antagonists that are less likely to cause platelet aggregation and thus cause thromboembolism are still needed in a clinical setting. Novel antibody polypeptides that specifically bind human CD40L are provided. The antibody polypeptides advantageously do not cause platelet aggregation. The antibody polypeptides are useful in the treatment of diseases involving CD40L activation, including autoimmune diseases, transplant rejection, and allergic responses. The antibody polypeptides comprise a variable domain. Exemplary antibody polypeptides are in the form of a domain antibody (dAb) that contains a single variable domain. Alternatively, the dAbs can be bi-specific reagents that comprise a second variable domain that can bind another antigen, such as human serum albumin (HSA), for example.

An antibody polypeptide is provided comprising a first variable domain that specifically binds human CD40L, wherein the first variable domain comprises the amino acid sequence of one of the variable domains selected from the BMS2h lineage. Further provided is an isolated antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the first variable domain comprises: (a) a CDR1 region which differs from the CDR1 region of BMS2h-572-633 by up to three amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS2h-572-633 by up to three amino acids, (c) a CDR3 region which differs from the CDR3 region of BMS2h-572-633 by up to three amino acids, (d) a FR1 region which differs from the FR1 region of BMS2h-572-633 by up to three amino acids, (e) a FR2 region which differs from the FR2 region of BMS2h-572-633 by up to three amino acids, (f) a FR3 region which differs from the FR3 region of

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BMS2h-572-633 by up to three amino acids, and (g) a FR4 region which differs from the FR4 region of BMS2h-572-633 by up to three amino acids; and wherein the antibody polypeptide inhibits binding of CD40L to CD40 with an EC₅₀ of 100 pM to 100 nM. Also provided is an antibody polypeptide, wherein the amino acid sequence of the first variable domain comprises: (a) a CDR1 region which differs from the CDR1 region of BMS2h-572-633 by up to three amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS2h-572-633 by up to three amino acids, and (c) a CDR3 region which differs from the CDR3 region of BMS2h-572-633 by up to three amino acids. Alternatively, the amino acid sequence of the first variable domain can differ from the amino acid sequence of BMS2h-572-633 by up to and including 10 amino acids. Furthermore, the amino acid sequence of the first variable domain can differ from the amino acid sequence of BMS2h-572-633 by up to and including 5 amino acids. The amino acid sequence of the first variable domain can also differ from the amino acid sequence of BMS2h-572-633 by up to and including 2 amino acids. Alternatively, the first variable domain differs from the amino acid sequence of BMS2h-572-633 by 1 amino acid.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-572, wherein the amino acid sequence of the first variable domain further comprises: (a) a CDR1 region having a sequence Trp-X₁-Leu-Met-Gly (SEQ ID NO: 2), wherein X₁ is Glu or Gln; (b) a CDR2 region having a sequence Gly-Ile-Glu-Gly-Pro-Gly-Asp-Val-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (SEQ ID NO: 3); and (c) a CDR3 region having a sequence Lys-X₂-Y₂-Z₂-Ser-Asp-Tyr (SEQ ID NO: 4), wherein X₂ is Asp or Glu, Y₂ is Ala or Ser, and Z₂ is Lys, Asn, or Arg. Also provided is the antibody polypeptide, wherein the amino acid sequence of the first variable domain further comprises: (a) a FR1 region having a sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Asn (SEQ ID NO: 5); (b) a FR2 region having a sequence Trp-X₁-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser (SEQ ID NO: 6), wherein X₁ is Ala or Val; (c) a FR3 region having a sequence Arg-Thr-Phe-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Val-Lys-Val-Gly (SEQ ID NO: 7); and (d) a FR4 region having a sequence Arg-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 8). Alternatively, the first variable domain of the antibody polypeptide can comprise the amino acid sequence of BMS2h-572-633.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-719, comprising a first variable domain with the following consensus sequence: Glu-Val-Gln-

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Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-X₁-Y₁-Tyr-Glu-Met-Z₁-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ser-Ile-Ser-Ser-Asp-Gly-Ser-Phe-Thr-Tyr-Tyr-Ala-A₁-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-B₁-Pro-Phe-Thr-Glu-C₁-Asp-Tyr-Trp-Gly-His-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 9), wherein X₁ is Lys or Asn; Y₁ is Arg, Lys, Ser, or Thr; Z₁ is Met or Gln; A₁ is Asp or Glu; B₁ is Asp or Glu; and C₁ is Phe, Met, or Leu.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-503, comprising a first variable domain with the following consensus sequence: Asp-Ile-Gln-Met-Thr-Gln-Ser-Pro-Ser-Ser-Leu-Ser-Ala-Ser-Val-Gly-Asp-Arg-Val-Thr-Ile-Thr-Cys-Arg-Ala-Ser-His- X₁-Ile-Gln-Arg-Tyr-Leu-Ser-Trp-Tyr-Gln-Gln-Lys-Pro-Gly-Lys-Ala-Pro-Lys-Leu-Leu-Ile-Leu-Trp-Gly-Ser-Gln-Leu-Gln-Ser-Gly-Val-Pro-Ser-Arg-Phe-Ser-Gly-Ser-Gly-Ser-Gly-Thr-Asp-Phe-Thr-Leu-Thr-Ile-Ser-Ser-Leu-Gln-Pro-Glu-Asp-Phe-Ala-Thr-Tyr-Tyr-Cys-Gly-Gln-Trp-Trp-Ala-Pro-Pro-Gln-Thr-Phe-Gly-Gln-Gly-Thr-Lys-Val-Glu-Ile-Lys-Arg (SEQ ID NO: 10), wherein X₁ is His or Asp.

Also provided is an antibody polypeptide selected from the lineage group of BMS2h-116, comprising a first variable domain with the following consensus sequence: Asp-Ile-Gln-Met-Thr-Gln-Ser-Pro-Ser-Ser-Leu-Ser-Ala- X₁-Val-Gly-Asp-Arg-Val-Thr-Ile-Thr-Cys-Arg-Ala-Ser-Gln-Pro-Ile-Gly-Pro-Asp-Leu-Leu-Trp-Tyr-Gln-Gln-Lys-Pro-Gly-Lys-Ala-Pro-Lys-Leu-Leu-Ile-Tyr-Gln-Thr-Ser-Ile-Leu-Arg-Ser-Gly-Val-Pro-Ser-Arg-Phe-Ser-Gly-Ser-Gly-Ser-Glu-Thr-Asp-Phe-Thr-Leu-Thr-Ile-Ser-Asn-Leu-Gln-Pro-Glu-Asp-Y₁-Ala-Z₁-Tyr-Tyr-Cys-Gln-Gln-Tyr-Trp-Ala-Phe-Pro-Val-Thr-Phe-Gly-A₁-Gly-Thr-Lys-Val-Val-Ile-Lys-Arg (SEQ ID NO: 11), wherein X₁ is Ser or Tyr; Y₁ is Leu or Phe; Z₁ is Thr or Lys; and A₁ is Lys, Arg, or Gln.

Also provided is an antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein the antibody polypeptide is a domain antibody (dAb). The antibody polypeptide can be a fusion polypeptide comprising the first variable domain and an Fc domain. Alternatively, the fusion polypeptide can comprise an IgG4 Fc domain. The fusion polypeptide also can comprise an IgG1 Fc domain. The fusion polypeptide can also comprise an IgG1 Fc domain. Alternatively, the fusion polypeptide can comprise a CT-Long domain. The fusion polypeptide can also comprise a CT-short domain. Alternatively, the fusion polypeptide can comprise a N297Q Long Fc domain. The fusion polypeptide can alternatively comprise a N297Q Short Fc domain.

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Also provided is an antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, wherein the second antigen is an antigen other than human CD40L. The second antigen can be a cluster of differentiation (CD) molecule or a Major Histocompatibility Complex (MHC) Class II molecule. Alternatively, the second antigen can be serum albumin (SA).

Also provided is a nucleic acid encoding any of the antibody polypeptides provided herein. Further contemplated is a vector comprising the nucleic acid. An isolated host cell can comprise such vector.

A pharmaceutical composition is provided comprising a therapeutically-effective amount of the presently provided antibody polypeptide and a pharmaceutically acceptable carrier. The pharmaceutical composition can further comprise an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

A method of treating an immune disease in a patient in need of such treatment is provided comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition described herein. An exemplary method administers the pharmaceutical composition in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. The immune disease can be an autoimmune disease or a graft-related disease. Alternatively, the immune disease is a graft-related disease.

Furthermore, the graft-related disease can comprise solid organ, tissue and/or cell transplant rejection. Alternatively, the graft-related disease is graft versus host disease (GVHD). The graft-related disease can further be an acute transplant rejection. Alternatively, the graft-related disease can be a chronic transplant rejection.

Also provided is the method of treating a graft-related disease, wherein the pharmaceutical composition is co-administered with a CTLA4 mutant molecule. The CTLA4 mutant molecule can be L104EA29Y-Ig (belatacept).

A method of treating an immune disease in a patient in need of such treatment is also provided comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition provided herein, wherein the immune disease is selected from the group consisting of selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease,

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hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction. Alternatively, the immune disease can be myasthenia gravis, idiopathic thrombocytopenic purpura, or systemic sclerosis.

Also provided is a use of an isolated antibody polypeptide disclosed herein for the preparation of a medicament for the treatment of a patient, wherein the patient has or is at risk of having an immune disease. Further provided is a use of an isolated antibody polypeptide disclosed herein for preparation of a medicament for alleviating at least one symptom of an immune disease in a patient in need thereof.

Further provided herein is an isolated antibody polypeptide comprising a first variable domain, wherein said antibody polypeptide specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of BMS2h-572-633, and wherein the antibody polypeptide inhibits binding of CD40L to CD40 with an EC₅₀ of 100pM to 100nM. In one aspect, the first variable domain comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS2h-572, BMS2h-719, BMS2h-503, and BMS2h-116. In another aspect, the first variable domain comprises an amino acid sequence at least 95% identical to BMS2h-572-6, BMS2h-572-608, BMS2h-572-614, BMS2h-572-619, BMS2h-572-633, BMS2h-572-634, BMS2h-572-635, BMS2h-719-2, BMS2h-719-202, BMS2h-719-203, BMS2h-719-213, BMS2h-719-214, BMS2h-719-215, BMS2h-719-218, BMS2h-719-225, BMS2h-503-1, BMS2h-503-2, BMS2h-116-1312, BMS2h-116-1313, or BMS2h-116-1320. In yet another aspect, the first variable domain comprises the amino acid sequence of BMS2h-572-6, BMS2h-572-608, BMS2h-572-614, BMS2h-572-619, BMS2h-572-633, BMS2h-572-634, BMS2h-572-635, BMS2h-719-2, BMS2h-719-202, BMS2h-719-203, BMS2h-719-213, BMS2h-719-214, BMS2h-719-215, BMS2h-719-218, BMS2h-719-225, BMS2h-503-1, BMS2h-503-2, BMS2h-116-1312, BMS2h-116-1313, or BMS2h-116-1320.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1A depicts the domain antibody that comprises a V_H variable domain BMS2h-572-633 fused to a modified Fc tail from Abatacept IgG1.

FIG. 1B shows the amino acid sequence (SEQ ID NO: 1355) of the variable domain BMS2h-572-633. The Fc fusion protein is a dimer of molecular weight 77,984 Daltons, with each polypeptide chain consisting of 354 amino acids. The variable domain is fused by a linker to the mutated Fc construct of human IgG1, wherein three cysteine residues are substituted with serine, and one proline is substituted with a serine residue.

FIG. 2 depicts a working model for the CD40-40L pathway. The top panel demonstrates initial stages of an encounter between a T cell and an APC. The initial encounter driven by T cell receptor (TCR) engagement of pMHC complex (signal 1) coupled with an early CD28-CD80 interaction (signal 2) is sufficient for the cell surface expression of trimeric CD40L (bottom panel). Engagement of CD40 by CD40L results in numerous biological responses outlined in the grey box.

FIG. 3 provides sequences (SEQ ID NOS 1356-1361, respectively, in order of appearance) of various Fc domains. Linker regions are shown in boxes.

FIG. 4 shows examples of various Fc-formatted domain antibodies (SEQ ID NOS 1362-1365, respectively, in order of appearance). Linker regions are indicated by boxes.

FIG. 5 depicts SPR sensorgram data for the binding of 12.5-0.39nM BMS-986004 (2:1 dilution series) to biot-IZ-hCD40L captured on a streptavidin SPR sensor chip at 25°C. Colored lines show the double-referenced sensorgram data, and black lines show the 1:1 Langmuir fit to the data, with an avidity-influenced apparent K_d value of 0.11 nM.

FIG. 6 shows ITC data for titrations of 19 μ M IZ-hCD40L into 2 μ M BMS-986004 (black) or 18 μ M BMS-986004 into 2 μ M IZ-hCD40L (blue). The molar ratio (apparent stoichiometry) is defined per mole of IZ-hCD40L trimer and per mole of bivalent BMS-986004 Fc-dimer. Molar ratio values obtained as the equivalence points on the abscissa suggest more than one mole of BMS-986004 can bind per mole of IZ-hCD40L trimer; however, an exact structural model for the complex cannot be determined from the ITC data alone. Squares represent the integrated heat of binding data and solid lines represent the best fit to a "2 sets of sites model."

FIG. 7 shows in vivo efficacy of mouse CD40L surrogate dAb-Fc (KLH-induced antibody response).

FIG. 8 demonstrates that mouse dAb BMS-2m-126-24-Fc and antibody MR-1 inhibit TNBS-induced colitis in mice.

FIG. 9 shows that BMS-2m-126-24-Fc and CTLA4-Ig work synergistically to prolong the survival of cardiac allografts.

FIG. 10 provides a hypothetical model for anti-CD40 monoclonal antibody-mediated platelet aggregation.

FIG. 11A shows plasma concentration vs. time profile of BMS-986004 after IV dosing of 11 mg/kg in monkeys.

FIG. 11B demonstrates plasma concentration vs. time profiles of BMS-986003 after IV dosing of 2 mg/kg in monkeys.

FIG. 12 presents plasma concentrations vs. time profiles of BMS-986003 (after SC dosing at 0.2, 2 and 20 mg/kg in monkeys) and of 5c8 IgG1 (after IV dosing at 20 mg/kg in monkeys).

FIG. 13 shows plasma concentrations vs. time profiles of BMS-2m-126-24-CT after 1 mg/kg IV and SC dosing, and 10 mg/kg SC dosing to mice.

FIG. 14 demonstrates PK/PD modeling of BMS-986003 and 5c8-IgG1 plasma exposures and anti-KLH antibody response (IgG Titers).

FIG. 15 shows PK/PD modeling of BMS-986004 plasma exposures and *ex vivo* RO on peripheral blood mononuclear cells (PBMC).

FIG. 16 demonstrates that IV.3 blocks 5c8/sCD40L IC-mediated activation of platelets in human blood.

FIG. 17 shows the effect of Fc variants on platelet activation in human blood.

FIG. 18 demonstrates activation of platelets with 5c8-CT/sCD40L IC in blood from human donors genotyped for FcγRIIa polymorphism.

FIG. 19 diagrams platelet activation by various antibodies in blood from human donors.

FIG. 20 shows levels of platelet activation by various antibodies, including BMS-986003, in hFcγRIIa-expressing transgenic mice.

FIGS. 21, 22, 23, and 24 show is ClustalW2 alignments of representative domain antibody polypeptides from lineages BMS2h-572, BMS2h-719, BMS2h-503, and BMS2h-116, respectively. FIG. 21 discloses SEQ ID NOS 243, 251, 257, 262 and 274-276, respectively, in order of appearance, FIG. 22 discloses SEQ ID NOS 352, 354-355 and 357-361, respectively, in order of appearance, FIG. 23 discloses SEQ ID NOS 1087-1088, respectively, in order of appearance, and FIG. 24 discloses SEQ ID NOS 970-971 and 974, respectively, in order of appearance.

FIG. 25 shows SPR sensorgram data for binding experiments using monovalent dAbs BMS2h-503-1, BMS2h-572-6, BMS2h-719-17, and monovalent Fab fragment of 5c8, where the indicated molecules compete with each other for binding to CD40L (biotinylated IZ-hCD40L).

FIG. 26 shows SPR sensorgram data for experiments testing the binding of BMS2h-572-619-CT-long, BMS2h-572-633-CT-long, BMS2h-572-6-CT-long, BMS2h-719-202-CT-long, BMS2h-572-608-CT-long, BMS2h-572-634-CT-long, BMS2h-572-614-CT-long, BMS2h-572-635-CT-long, and 5c8-CT-long molecules to either CD40L monomer (upper 3 panels) or CD40L trimer (lower 3 panels).

DETAILED DESCRIPTION

Antibody polypeptides that specifically bind to human CD40L are provided. The antibody polypeptides do not activate platelets, and the antibody polypeptides are useful in the treatment of diseases involving CD40L activation, such as graft-related diseases and autoimmune diseases. The antibody polypeptides may be selected using a primary screen that utilizes cell binding assays, followed by one or more rounds of error-prone or degenerate oligonucleotide-directed affinity maturation. As a result, a genus of antibody polypeptides that specifically bind CD40L are provided.

A “lineage” is a set of related antibody polypeptides that were prepared from a common precursor by error-prone or degenerate oligonucleotide-directed affinity maturation, as disclosed in the examples below, and that are expected to bind CD40L. The nomenclature of the antibody polypeptides is used to designate the various lineages. The nomenclature “BMS2h-572,” for example, refers to antibody polypeptides of lineage 572, which were

raised against human CD40L. “Lineage BMS2h-572” antibody polypeptides include BMS2h-572-1 through BMS2h-572-19, BMS2h-572-21 through BMS2h-572-24, BMS2h-572-601 through BMS2h-572-627, and BMS2h-572-630 through BMS2h-572-635.

Accordingly, in one aspect, an antibody polypeptide comprises a variable domain that specifically binds human CD40L, where the antibody polypeptide competes with the binding of any one of the domain antibodies (dAbs) listed in TABLE 1 or TABLE 3. For example, the antibody polypeptide may compete with a dAb selected from the 2h lineage. The dAb also may be selected from a lineage selected from the group consisting of BMS2h-116, BMS2h-503, BMS2h-572, and BMS2h-719, such as the dAb BMS2h-572-633, BMS2h-572-608, or BMS2h-572-614, for instance. In another aspect, an antibody polypeptide specifically binds human CD40L as any one of the dAbs listed in TABLE 1 and TABLE 3. For example, the antibody polypeptide may comprise a variable domain that specifically binds human CD40L as the dAb BMS2h-572-633, BMS2h-572-608, or BMS2h-572-614, for instance.

The antibody polypeptides may be a domain antibody containing a single variable domain. The antibody polypeptides also may comprise additional domains, such as an Fc domain. For instance, the antibody polypeptide may comprise a second variable domain that specifically binds human serum albumin (HSA). Such dual specific antibody polypeptides may have an increased half-life, for example.

As used herein, “specific binding” refers to the binding of an antigen by an antibody polypeptide with a dissociation constant (K_d) of about 1 μ M or lower as measured, for example, by surface plasmon resonance (SPR). Suitable assay systems include the BIAcore™ surface plasmon resonance system and BIAcore™ kinetic evaluation software (e.g., version 2.1). The affinity or K_d for a specific binding interaction may be about 1 μ M or lower, about 500 nM or lower or about 300 nM or lower.

The term “about” will be understood by persons of ordinary skill in the art and will vary to some extent on the context in which it is used. Generally, about encompasses a range of values that are plus/minus 10% of a referenced value.

In accordance with this detailed description, the following abbreviations and definitions apply. It must be noted that as used herein, the singular forms “a”, “an”, and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “an antibody” includes a plurality of such antibodies and reference to

“the dosage” includes reference to one or more dosages and equivalents thereof known to those skilled in the art, and so forth.

1. CD40L and CD40L Activities

Antibody polypeptides are provided that bind human CD40L. CD40L is also known as CD154, gp39, TNF-related activation protein (TRAP), 5c8 antigen, or T-BAM. Relevant structural information for human CD40L can be found, for example, at UniProt Accession Number P29965. “Human CD40L” refers to the CD40L comprising the following amino acid sequence:

	<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>
<u>60</u>	MIETYNQTSP	RSAATGLPIS	MKIFMYLLTV	FLITQMIGSA	LFAVYLHRRL
	DKIEDERNLH				
	<u>70</u>	<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>
<u>120</u>	EDFVFMKTIQ	RCNTGERSLS	LLNCEEIKSQ	FEGFVKDIML	NKEETKKENS
	FEMQKGDQNP				
	<u>130</u>	<u>140</u>	<u>150</u>	<u>160</u>	<u>170</u>
<u>180</u>	QIAAHVISEA	SSKTTSVLQW	AEKGYTMSN	NLVTLENGKQ	LTVKRQGLYY
	IYAQVTFCNS				
	<u>190</u>	<u>200</u>	<u>210</u>	<u>220</u>	<u>230</u>
<u>240</u>	REASSQAPFI	ASLCLKSPGR	FERILLRAAN	THSSAKPCGQ	QSIHLGGVFE
	LQPGASVFN				
	<u>250</u>	<u>260</u>			
	VTDPQVSHG	TGFTSFGLLK	L		
	(SEQ ID NO: 1)				

CD40L has also been sequenced in *Sus scrofa*, *Mus musculus*, *Canis familiaris*, *Bos taurus*, *Macaca mulatta*, *Aotus tigris*, *Callithrix jacchus*, *Cercopithecus aethiops*, *Macaca nemestrina*, *Rattus norvegicus*, *Gallus gallus*, *Felis catus*, and *Sus scrofa*.

Binding of the present antibody polypeptides to CD40L antagonizes CD40L activity. “CD40L activities” include, but are not limited to, costimulation and activation an APC in association with T cell receptor stimulation by MHC molecules on the APC, secretion of all immunoglobulin isotypes in the presence of cytokines, stimulation of B cell proliferation, cytokine production, antibody class switching and affinity maturation. For example, patients with X-linked hyper-IgM syndrome express functional CD40 on their B cells, but their

activated T cells have a defective CD40L protein, resulting in its inability to activate B cells and induce immunoglobulin isotype switching. Aruffo *et al.*, *Cell* 72:291-300 (1993).

CD40L activities can be mediated by interaction with other molecules. “CD40 activities” include the functional interaction between CD40L and the following molecules: CD40 (CD40L receptor), $\alpha 5\beta 1$ integrin, and $\alpha \text{IIb}\beta 3$. For example, CD40L binds its receptor, CD40, which is expressed on a variety of APCs, such as B cells, macrophages, and dendritic cells, as well as on stromal cells, vascular endothelial cells, and platelets.

As used herein, the terms “activate,” “activates,” and “activated” refer to an increase in a given measurable CD40L activity by at least 10% relative to a reference, for example, at least 10%, 25%, 50%, 75%, or even 100%, or more. A CD40L activity is “antagonized” if the activity is reduced by at least 10%, and in an exemplary embodiment, at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, or even 100% (i.e., no detectable activity), relative to the absence of the antagonist. For example, an antibody polypeptide may antagonize some or all CD40L activity. In one embodiment, the antibody polypeptide does not activate B cell proliferation. In another embodiment, the antibody polypeptide does not activate cytokine secretion by T cells or dendritic cells (DCs), where the cytokine is at least one cytokine selected from the group consisting of IL-2, IL-6, IL-10, IL-12, IL-13, IL-17, IL-23, TNF- α , and IFN- γ .

2. Antibody Polypeptides

The antibody polypeptides comprise a variable domain. In one embodiment, the antibody polypeptides are in the form of a dAb that contains a single variable domain. Antibody polypeptides may be full-length anti-CD40L immunoglobulin molecules comprising two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. In this embodiment, the amino terminal portion of each chain includes a variable domain (V_L or V_H) of about 100-120 amino acids. The complementarity determining regions (CDRs) contained therein are primarily responsible for antigen recognition, although framework residues can play a role in epitope binding. The carboxy-terminal “half” of each heavy chain defines a constant region (Fc) primarily responsible for effector function.

Antibody polypeptides also may be “fragments” comprising a portion of the full-length anti-CD40L immunoglobulin molecule that comprises a variable domain that specifically binds CD40L. Thus, the term “antibody polypeptides” includes an antigen-binding heavy chain, light chain, heavy chain-light chain dimer, Fab fragment, $F(ab')_2$

fragment, Fv fragment, single chain Fv (scFv), and dAb, for example. The term “antibody polypeptides” thus includes polypeptides made by recombinant engineering and expression, as well as monoclonal antibodies produced by natural recombination and secretion by hybridoma cell clones.

Light chains are classified as kappa (κ) or lambda (λ), and are characterized by a particular constant region, C_L , as known in the art. Heavy chains are classified as γ , μ , α , δ , or ϵ , and define the isotype of an antibody as IgG, IgM, IgA, IgD, or IgE, respectively. The heavy chain constant region is comprised of three domains (CH1, CH2, and CH3) for IgG, IgD, and IgA; and four domains (CH1, CH2, CH3, and CH4) for IgM and IgE. Anti-CD40L antibodies may have a heavy chain constant region selected from any of the immunoglobulin classes (IgA, IgD, IgG, IgM, and IgE).

Each light chain variable domain (V_L) and heavy chain variable domain (V_H) is composed of three CDRs and four framework regions (FRs), arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4. The three CDRs of the light chain are referred to as “LCDR1, LCDR2, and LCDR3” and the three CDRs of the heavy chain are referred to as “HCDR1, HCDR2, and HCDR3.”

As used herein, the term “Fc domain” refers to the constant region antibody sequences comprising CH2 and CH3 constant domains as delimited according to Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The Fc domain may be derived from an IgG1 or an IgG4 Fc region, for example.

A variable domain may be fused to an Fc domain. Examples of various Fc-formatted domain antibodies and their potency are provided in TABLE 6. FIG. 3 provides sequences of various Fc domains provided herein. Linker regions are shown in boxes. As used in TABLE 6, “Fc” indicates that the dAb is fused to a human IgG1 short Fc. “CT Long Fc,” also called CT-L2, refers to the Fc from CTLA4. The underlined S are cysteine-to-serine point mutations made to eliminate the disulfides in the Fc hinge. “CT Short,” also called CT-S1, is shorter than CT Long by 7 amino acids. “N297Q Long Fc,” also referred to as N297Q-L4, is the Fc domain of human IgG1 with a N297Q mutation made to eliminate the N-linked carbohydrate in the Fc. “N297Q Short Fc,” also called N297Q-S3, is short than N297Q Long Fc by 7 amino acids, and is a human IgG1 with a N297Q point mutation made to eliminate the N-linked carbohydrate in the Fc domain. “CT-Fc SP5” is the CT Long Fc, where SP5 refers to the octeonectin signal peptide used for secretion from the mammalian expression

host. Cleavage site is indicated by “^”. FIG. 4 further provides examples of various Fc domain formats.

When a variable domain is fused to an Fc domain, the carboxyl terminus of the variable domain (either a V_L or V_H domain, including dAbs) may be linked or fused to the amino terminus of the Fc CH2 domain. Alternatively, the carboxyl terminus of the variable domain may be linked or fused to the amino terminus of a CH1 domain, which itself is fused to the Fc CH2 domain. The protein may comprise the hinge region between the CH1 and CH2 domains in whole or in part.

The CDRs contain most of the residues that form specific interactions with the antigen. In one embodiment, the variable domain of an antibody polypeptide comprises CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of one of the dAbs listed in TABLE 1 or TABLE 3 or that each differ from the CDR1, CDR2, and CDR3 regions by one, two, or three amino acids. For example, the antibody polypeptide may comprise CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of BMS2h-572-633, BMS2h-572-608, or BMS2h-572-614, for example.

A “domain antibody” (dAb) comprises a single variable (V_L or V_H) domain that is capable of specifically and monovalently binding an antigen, such as CD40L. For example, a dAb may have a V_{HH} structure, characteristic of a camelid dAb. A “V_H domain” as used herein is meant to include a V_{HH} structure. In another embodiment, the V_H domains (including all features and combination of features presented as embodiments herein) are other than V_{HH} domains. dAbs may form homo- or heterodimers in solution. While not limited by any particular theory, it is believed that the dAbs disclosed herein do not cause platelet aggregation, because the antibodies containing mutated Fc constructs do not bind FcγRIIIa (also known as CD32a) on the platelet surface and do not activate platelets.

As used herein, the term “variable domain” refers to immunoglobulin variable domains defined by Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The numbering and positioning of CDR amino acid residues within the variable domains is in accordance with the well-known Kabat numbering convention.

The term “human,” when applied to antibody polypeptides, means that the antibody polypeptide has a sequence, e.g., framework regions and/or CH domains, derived from a

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human immunoglobulin. A sequence is “derived from” a human immunoglobulin coding sequence when the sequence is either: (a) isolated from a human individual or from a cell or cell line from a human individual; (b) isolated from a library of cloned human antibody gene sequences or of human antibody variable domain sequences; or (c) diversified by mutation and selection from one or more of the polypeptides above. An “isolated” compound as used herein means that the compound is removed from at least one component with which the compound is naturally associated with in nature.

Antibody polypeptides can be administered to human patients while largely avoiding the anti-antibody immune response often provoked by the administration of antibodies from other species, *e.g.*, mouse. For example, murine antibodies can be “humanized” by grafting murine CDRs onto a human variable domain FR, according to procedures well known in the art. Human antibodies as disclosed herein, however, can be produced without the need for genetic manipulation of a murine antibody sequence.

Variable domains may comprise one or more FR with the same amino acid sequence as a corresponding framework region encoded by a human germline antibody gene segment. For example, a domain antibody may comprise the V_H germline gene segments DP47, DP45, or DP38, the V_κ germline gene segment DPK9, the J_H segment JH4b, or the J_κ segment Jκ1.

Changes may be made to antibody polypeptide sequences while retaining the ability to bind CD40L specifically. Specifically, the antibody polypeptides (*e.g.*, a dAb) may comprise a variant variable domain that retains the function of specifically binding CD40L as the dAb BMS2h-572-633. In one embodiment, the variant variable domain may compete with BMS2h-572-633 for specific binding to CD40L. Error-prone affinity maturation, as disclosed in the examples below, provides one exemplary method for making and identifying antibody polypeptides with variant sequences that specifically bind CD40L.

For example, a variant variable domain may differ from one of the variable domains listed in TABLE 1 and TABLE 3 by up to 10 amino acids or any integral value between, where the variant variable domain specifically binds CD40L. Alternatively, the variant variable domain may have at least 90% sequence identity (*e.g.*, at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity) relative to a sequence listed in the present Sequence Listing. Non-identical amino acid residues or amino acids that differ between two sequences may represent amino acid substitutions, additions, or deletions. Residues that

differ between two sequences appear as non-identical positions, when the two sequences are aligned by any appropriate amino acid sequence alignment algorithm, such as BLAST.

In one embodiment, amino acid substitutions may be made to individual FR regions, such that a FR comprises 1, 2, 3, 4, or 5 amino acid differences relative to the amino acid sequence of the corresponding FR encoded by a human germline antibody gene segment. In another embodiment, the variant variable domain may contain one or two amino acid substitutions in a CDR. In other embodiments, amino acid substitutions to FR and CDR regions may be combined. Representative variable domains that specifically bind CD40L are listed in TABLE 1 and TABLE 3.

The information regarding the boundaries of the V_L or V_H domains of heavy and light chain genes may be used to design PCR primers to amplify the variable domain from a cloned heavy or light chain coding sequence encoding an antibody polypeptide known to bind CD40L. The amplified variable domain may be inserted into a suitable expression vector, *e.g.*, pHEN-1 (Hoogenboom et al. (1991) *Nucleic Acids Res.* 19:4133-4137) and expressed, either alone or as a fusion with another polypeptide sequence, using techniques well known in the art. Based on the disclosed amino acid and polynucleotide sequences, the fusion protein can be produced and purified using only ordinary skill in any suitable mammalian host cell line, such as CHO, 293, COS, NSO, and the like, followed by purification using one or a combination of methods, including protein A affinity chromatography, ion exchange, reverse phase techniques, or the like.

In one aspect, the antibody polypeptide is a “dual specific” antibody polypeptide comprising a first variable domain that specifically binds human CD40L. Dual specific antibody polypeptides comprise a second variable domain that specifically binds a second antigen that is other than human CD40L.

In another embodiment, the second antigen may be a cell surface molecule of an immune effector cell or a soluble molecule such as a cytokine, for example. Binding of the dual specificity antibody polypeptide could be used to antagonize CD40L and antagonize a biological activity of the second antigen. Cell surface molecules of immune effector cells include the cluster of differentiation (CD) molecules. Representative CD markers are listed on the Internet at hypertext transfer protocol

http://en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation (last modified on August 8, 2012). Cell surface molecules of immune effector cells also include Major

Histocompatibility Complex (MHC) Class II molecules. Antibodies against these cell surface molecules are known in the art and can be used a source of a variable domain to construct a dual specific antibody polypeptide.

In one embodiment, antibody polypeptides of a dual specific ligand may be linked by an “amino acid linker” or “linker.” For example, a dAb may be fused to the N-terminus of an amino acid linker, and another dAb may be fused to the C-terminus of the linker. Although amino acid linkers can be any length and consist of any combination of amino acids, the linker length may be relatively short (*e.g.*, five or fewer amino acids) to reduce interactions between the linked domains. The amino acid composition of the linker also may be adjusted to reduce the number of amino acids with bulky side chains or amino acids likely to introduce secondary structure. Suitable amino acid linkers include, but are not limited to, those up to 3, 4, 5, 6, 7, 10, 15, 20, or 25 amino acids in length. Representative amino acid linker sequences include (GGGS)_n (SEQ ID NO: 12), where n may be any integer between 1 and 5. Other suitable linker sequences may be selected from the group consisting of AS, AST, TVAAPS (SEQ ID NO: 13), TVA, and ASTSGPS (SEQ ID NO: 14).

The binding of the second antigen can increase the *in vivo* half-life of the antibody polypeptide. For example, the second variable domain of the dual specific antibody polypeptide may specifically bind serum albumin (SA), *e.g.*, human serum albumin (HSA). The antibody polypeptide formatted to bind I can have an increased *in vivo* t-α (“alpha half-life”) or t-β (“beta half-life”) half-life relative to the same unformatted antibody polypeptide. The t-α and t-β half-lives measure how quickly a substance is distributed in and eliminated from the body. The linkage to I may be accomplished by fusion of the antibody polypeptide with a second variable domain capable of specifically binding I, for example. Anti-human serum albumin antibodies are well-known in the art. *See, e.g.*, Abcam®, Human Serum Albumin antibodies ab10241, ab2406, and ab8940, available on the Internet at hypertext transfer protocol www.abcam.com/index.html, or GenWay, ALB antibody, available on the Internet at hypertext transfer protocol www.genwaybio.com. Variable domains that specifically bind I can be obtained from any of these antibodies, and then fused to an antibody polypeptide of the disclosure using recombinant techniques that are well known in the art.

Alternatively, the linking of the antibody polypeptide to I can be accomplished by directly fusing the antibody polypeptide sequence to an I coding sequence using techniques well known to the skilled artisan. The I coding sequences can be obtained by PCR using

primers derived from the cDNA sequence available at GenBank Accession No. NM000477, for example.

In one embodiment, the t_{α} -half-life of the I-linked domain antibody composition is increased by 10% or more. In another embodiment, the t_{α} -half-life of the I-linked domain antibody composition is in the range of 0.25 hours to 6 hours. In another embodiment, the t_{β} -half-life of the I-linked domain antibody composition is increased by 10% or more. In another embodiment, the t_{β} -half-life of the I-linked domain antibody composition is in the range of 12 to 48 hours.

In another embodiment, an antibody polypeptide may be formatted to increase its *in vivo* half-life by PEGylation. In one embodiment, the PEG is covalently linked. In another embodiment, the PEG is linked to the antibody polypeptide at a cysteine or lysine residue. In yet another embodiment, the PEG-linked antibody polypeptide has a hydrodynamic size of at least 24 kD. In yet another embodiment, the total PEG size is from 20 to 60 kD, inclusive. In yet another embodiment, the PEG-linked domain antibody has a hydrodynamic size of at least 200 kD.

PEGylation can be achieved using several PEG attachment moieties including, but not limited to N-hydroxylsuccinimide active ester, succinimidyl propionate, maleimide, vinyl sulfone, or thiol. A PEG polymer can be linked to an antibody polypeptide at either a predetermined position, or can be randomly linked to the domain antibody molecule.

PEGylation can also be mediated through a peptide linker attached to a domain antibody. That is, the PEG moiety can be attached to a peptide linker fused to an antibody polypeptide, where the linker provides the site (e.g., a free cysteine or lysine) for PEG attachment. Methods of PEGylating antibodies are well known in the art, as disclosed in Chapman, et al., "PEGylated antibodies and antibody fragments for improved therapy: a review," *Adv. Drug Deliv. Rev.* 54(4):531-45 (2002), for example.

Antibody polypeptides also may be designed to form a dimer, trimer, tetramer, or other multimer. Antibody polypeptides, e.g., dAbs, can be linked to form a multimer by several methods known in the art, including, but not limited to, expression of monomers as a fusion protein, linkage of two or more monomers via a peptide linker between monomers, or by chemically joining monomers after translation, either to each other directly, or through a linker by disulfide bonds, or by linkage to a di-, tri- or multivalent linking moiety (e.g., a multi-arm PEG). In one embodiment, the multimer can bind a single molecule of CD40.

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3. Pharmaceutical Compositions and Methods of Treatment

A pharmaceutical composition comprises a therapeutically-effective amount of one or more antibody polypeptides and optionally a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include, for example, water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof.

Pharmaceutically acceptable carriers can further comprise minor amounts of auxiliary substances, such as wetting or emulsifying agents, preservatives, or buffers that enhance the shelf-life or effectiveness of the fusion protein. The compositions can be formulated to provide quick, sustained, or delayed release of the active ingredient(s) after administration. Suitable pharmaceutical compositions and processes for preparing them are well known in the art. *See, e.g.,* Remington, THE SCIENCE AND PRACTICE OF PHARMACY, A. Gennaro, et al., eds., 21st ed., Mack Publishing Co. (2005).

The pharmaceutical composition further may comprise an immuno-suppressive/immunomodulatory and/or anti-inflammatory agent. A method of treating an immune disease in a patient in need of such treatment may comprise administering to the patient a therapeutically effective amount of the pharmaceutical composition. Antagonizing CD40L-mediated T cell activation could inhibit undesired T cell responses occurring during autoimmunity, transplant rejection, or allergic responses, for example. Inhibiting CD40L-mediated T cell activation could moderate the progression and/or severity of these diseases.

As used herein, a “patient” means an animal, e.g. mammal, including humans. The patient may be diagnosed with an immune disease. “Treatment” or “treat” or “treating” refers to the process involving alleviating the progression or severity of a symptom, disorder, condition, or disease. An “immune disease” refers to any disease associated with the development of an immune reaction in an individual, including a cellular and/or a humoral immune reaction. Examples of immune diseases include, but are not limited to graft-related disease, inflammation, allergy, and autoimmune disease. The autoimmune disease may be selected from the group consisting of systemic lupus erythematosus, multiple sclerosis, rheumatoid arthritis, diabetes, psoriasis, scleroderma, atherosclerosis, inflammatory bowel disease, and ulcerative colitis.

Diseases that can be treated by administering the pharmaceutical composition may be selected from the group consisting of Addison’s disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye,

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autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products (*e.g.*, Factor VII in hemophiliacs), systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, and vasculitis. Autoimmune-mediated conditions include, but are not limited to, conditions in which the tissue affected is the primary target, and in some cases, the secondary target. Such conditions include, but are not limited to, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus' phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

Preferred indications for administration of the present pharmaceutical compositions are, for example, immune thrombocytopenic purpura, systemic sclerosis, myasthenia gravis, allograft rejection, and graft-versus-host disease.

The pharmaceutical composition may be administered alone or in combination therapy, (*i.e.*, simultaneously or sequentially) with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. Different immune diseases can require use of specific auxiliary compounds useful for treating immune diseases, which can be determined on a patient-to-patient basis. For example, the pharmaceutical composition may be administered in combination with one or more suitable adjuvants, *e.g.*, cytokines (IL-10 and IL-13, for example) or other immune stimulators, *e.g.*, chemokines, tumor-associated antigens, and peptides. Suitable adjuvants are known in the art.

For example, the disclosed pharmaceutical composition may be co-administered, concomitantly or sequentially, with a cytotoxic T-lymphocyte antigen 4 (CTLA4) mutant molecule, such as L104EA29Y-Ig (belatacept). CTLA4 binds to CD80 (B7-1) and CD86 (B7-2) with higher avidity than CD28, and it is transiently expressed on T cells following their activation, where it interrupts the interaction between CD28 and CD80/86. Oosterwegel et al., *Curr. Opin. Immunol.* 11: 294-300 (1999). This creates a negative feedback signal for T cell activation.

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CTLA4 mutant molecules, including L104EA29Y-Ig, have increased binding avidity to CD80/86 compared to wild-type CTLA4. Intervention of the CD28-CD80/86 pathway by L104EA29Y-Ig has been successfully pursued, for example, to treat graft-related diseases in non-human primate transplant models, alone or in combination with other immunosuppressive agents. Larsen et al., *Amer. J. Transplant.* 5: 443 (2005). U.S. Patent Application number 2010/0166774 describes the structure of L104EA29Y-Ig, methods of producing it, and a formulation comprising a CTLA4 molecule; and the application is herein incorporated by reference. U.S. Patent Nos 7,094,874 and 7,482,327 further disclose administration (including co-administration with one or more other drugs) and dosage schedule of L104EA29Y-Ig, and the disclosures of these patents are herein incorporated by reference.

Any suitable method or route can be used to administer the antibody polypeptide or the pharmaceutical composition. Routes of administration include, for example, oral, intravenous, intraperitoneal, subcutaneous, or intramuscular administration. A therapeutically effective dose of administered antibody polypeptide(s) depends on numerous factors, including, for example, the type and severity of the immune disease being treated, the use of combination therapy, the route of administration of the antibody polypeptide(s) or pharmaceutical composition, and the weight of the patient. A non-limiting range for a therapeutically effective amount of a domain antibody is 0.1-20 mg/kg, and in an aspect, 1-10 mg/kg, relative to the body weight of the patient. The dose of antibody polypeptide(s) can be further guided by the amount of antibody polypeptide(s) required for CD40 antagonism in *in vitro* and/or *in vivo* models of disease states. Representative models are described below and in the examples.

4. *In Vitro* and *In Vivo* Models

The ability of antibody polypeptides of the disclosure to antagonize CD40L can be tested in one of several available *in vitro* or *in vivo* model systems. Appropriate human, animal, and cell model systems are described below. Further cell assay systems are described in the examples.

4.1. Immune Thrombocytopenic Purpura (ITP) *In Vivo* Model:

The potential role of CD40-CD40L in the pathogenesis of ITP is reported by Patel et al., *British J. Haematology* 141: 545-548 (2008). Antiplatelet autoantibodies in patients with

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ITP bind to circulating platelets and accelerate their destruction. The primary mechanism by which anti-CD40L antibodies are thought to increase the platelet count in ITP is by blocking T-cell based activation of autoreactive B cells that produce anti-platelet antibodies. Anti-CD40L antibodies may also block expression of CD40L on platelets, thus preventing autresentation of platelet glycoprotein antigens to macrophages. Furthermore, anti-CD40L mAbs inhibit direct interactions between platelet CD40L and other cells, such as plasmacytoid dendritic cells (DCs), which have recently been implicated in driving the type 1 interferon (IFN) response in human lupus patients. Duffau et al., *Sci. Transl. Med.* 2: 47 (2010).

Patel *et al.* demonstrated efficacy of two humanized anti-CD40L monoclonal antibodies, hu5c8 and IDEC-131, in 46 human patients with chronic ITP refractory to conventional therapies. The patients had an overall 24% response rate, characterized by increased platelet counts. This demonstrated the potential role of CD40-CD40L in the pathogenesis of ITP.

4.2. Lupus *In Vivo* and *In Vitro* Models:

Glomerular and tubular CD40 expression is markedly upregulated in proliferative nephritis. Several studies have reported hyperexpression of CD40L by T cells and elevated soluble sCD40L concentrations in human lupus. Kimura et al., *Therapeutic Apheriss and Dialysis* 9: 64-68 (2005); Vakkalanka et al., *Arthritis & Rheumatism* 42: 871-881 (1999).

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease characterized by the production of multiple autoantibodies and by B cell hyperactivity. Grammer et al., *J. Clin. Invest.* 112: 1506-1520 (2003) reports the results of treatment of patients with SLE with humanized anti-CD40L mAb 5c8 (BG9588). *See also* Huang et al., *Arthritis & Rheumatism* 46: 1554-1562 (2002). Grammer et al. report that CD19+ peripheral B cells were examined before and after treatment with the anti-CD40L mAb. Before treatment, SLE patients manifested activated B cells that expressed CD40L, CD69, CD38, CD5, and CD27. The activated B cells disappeared from the periphery during and post-treatment. Before treatment, active SLE patients had circulating CD38^{bright} Ig-secreting cells that were not found in normal individuals. Disappearance of these plasma cells during treatment was associated with decreases in anti-double stranded DNA (anti-dsDNA) Ab levels, proteinuria, and SLE disease activity index. Consistent with this finding, peripheral B cells cultured *in vitro* spontaneously proliferated and secreted Ig in a manner that was inhibited by anti-CD40L

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mAb. The CD38+/++IgD+, CD38+++, and CD38+IgD- B cell subsets present in the peripheral blood of SLE patients also disappeared following treatment with the anti-CD40L mAb. Together, these results suggest that spontaneous CD40L-CD40 interactions in active SLE patients drive B cell activation, proliferation, and differentiation to autoantibody-secreting plasma cells that mediate proteinuria and disease activity.

Proliferative lupus glomerulonephritis is a protracted autoimmune disease with a waxing and waning course, characterized by increased level of anti-dsDNA antibodies, decreased serum C3 concentrations, and hematuria. Boumpas et al, *Arthritis & Rheumatism* 48: 719-727 (2003) report results of a phase II, multicenter, open-label study evaluating the toxicity and efficacy of BG9688, a humanized anti-CD40L monoclonal antibody, in patients with proliferative lupus glomerulonephritis. Although the study had to be terminated prematurely because of thromboembolic events occurring in patients in several BG9588 protocols, a short course of the anti-CD40L antibody treatment in patients with proliferative lupus nephritis reduced anti-dsDNA antibodies, increased C3 concentrations, and decreased hematuria, suggesting that the drug has immunomodulatory function.

4.3. Inflammatory Bowel Disease (IBD) *In Vivo* Models:

Crohn's disease (CD) and ulcerative colitis (UC) are IBDs that are characterized by leukocytic infiltrates in inflamed intestinal mucosa, which consists primarily of activated CD25+ cells, B cells, and macrophages. Ludwiczek et al., *Int. J. Colorectal Dis.* 18: 142-147 (2003) report that in CD patients, plasma levels of sCD40L were significantly higher than in healthy individuals. Moreover, CD patients with fistulas and/or abscesses had significantly higher levels of sCD40L than patients with uncomplicated CD. It has also been reported that the CD40-CD40L pathway contributes to the proinflammatory function of intestinal epithelial cells in IBD. Borchering et al., *Am. J. Pathol.* 176: 1816-1827 (2010). Patients with CD also have an increased risk of systemic thromboembolism, and the hyperactive state of platelets from such patients likely results from the enhanced release of sCD40L as a consequence of their higher endogenous content of CD40L. Menchen et al., *Gut* 58: 920-928 (2009); *see also* Danese et al., *Gut* 52: 1435-1441 (2003).

Kasran et al., *Aliment. Pharmacol. Ther.* 22: 111-122 (2005) investigated the use of a chimeric anti-human CD40 mAb ch5D12 to treat Crohn's disease. The mAb was administered to 18 patients with moderate to severe CD in a single dose, open-label dose escalation phase I/Ia study. Of the 18 patients, 13 (or 72%) experienced a favorable

response to the antibody infusion, and 4 patients (or 22%) experienced a remission. Treatment with the anti-CD40 mAb reduced microscopic disease activity and intensity of the lamina propria cell infiltrate, and the mAb was well tolerated.

4.4. Rheumatoid Arthritis (RA), Juvenile Idiopathic Arthritis (JIA), and Psoriatic Arthritis (PsA) *In Vivo* Models:

Rheumatoid arthritis is a systemic autoimmune disease with intra-articular inflammation as a dominant feature that affects up to 1% of the population. The disease can be subdivided clinically by the presence or absence of autoantibodies (antibodies to cyclic citrullinated peptide (CCP) or rheumatoid factor (RF), both of which are highly correlated to each other. Raychaudhuri et al., *Nature Genetics* 40: 1216-1223 (2008) reported that they conducted a meta-analysis of two published genome-wide association (GWA) studies totaling 3,393 cases and 12,462 controls, in order to identify RA risk loci in European populations. They genotyped 31 top-ranked short nucleotide polymorphisms (SNPs) not previously associated with RA in an independent replication of 3,929 autoantibody-positive RA cases and 5,807 matched controls from eight separate collections. They identified a common variant at the CD40 gene locus, which implied a central role for the CD40 signaling pathway in RA pathogenesis. The strong association of the CD40 gene with susceptibility to RA was robustly replicated in another study in a large UK cohort of 3,962 patients with RA. Orozso et al., *Ann. Rheum. Dis.* 69: 813-816 (2010).

A major role of CD40L has also been found in the pathogenesis of juvenile idiopathic arthritis (JIA). Prahalad et al., *Pediatric Rheumatology* 6: 1-8 (2008). JIA is a heterogeneous group of arthropathies of unknown etiology. It was found that sCD40L was significantly elevated in the serum of children with JIA, along with some cytokines. Logistic regression analysis suggested that sCD40L, as well as IL-6 and TNF α , were positively associated with JIA. sCD40L was elevated in all JIA subtypes, with highest levels among more severe subtypes. These results implicated sCD40L as a potential biomarker for treatment and monitoring of patients with JIA.

It has also been demonstrated that activated T cells from patients with psoriatic arthritis (PsA), and particularly those with active disease, have a significantly increased expression of CD40L. Daoussis et al., *Rheumatology* 46: 227-231 (2007). These results indicate a role of the CD40-CD40L pathway in the pathogenesis of PsA and that a therapy selectively targeting CD40L could benefit PsA patients.

4.5. Systemic Sclerosis *In Vivo* Models:

Systemic sclerosis (SSc) is an autoimmune connective tissue disorder characterized by fibrous and vascular changes in the skin and internal visceral organs. In a study involving 52 Japanese patients with SSc, serum sCD40L levels were elevated when compared with healthy controls. Komura et al., *J. Rheumatol.* 31: 514-519 (2004). Moreover, levels of sCD40L in patients with SSc were higher than in patients with systemic lupus erythematosus (SLE) who had elevated sCD40L levels compared to controls, and sCD40L levels correlated positively with C reactive peptide levels in SSc patients. It has also been reported that blockade of CD40L with anti-CD40L antibody in cultured T and B cells from SSc patients inhibited anti-topoisomerase I antibody production. Kuwana et al., *J. Immunol.* 155: 2703-2714 (1995). These results suggest that inhibition of CD40-CD40L interactions may be potential therapeutic targets in therapy of SSc as well as SLE.

4.6. Atherosclerosis *In Vivo* Models:

Several studies have suggested a role of CD40-CD40L signaling pathway during atherogenesis. Mach et al. demonstrated that in mice, treatment with monoclonal anti-CD40L antibody limited atherosclerosis in mice lacking receptor for low-density lipoprotein that had been fed a high-cholesterol diet for 12 weeks. *Nature* 394: 200-203 (1998). The antibody reduced the size of aortic atherosclerotic lesions by 59% and their lipid content by 79%. Additionally, atheroma of mice treated with anti-CD40L antibody contained significantly fewer macrophages and T lymphocytes, and exhibited decreased expression of vascular cell adhesion molecule-1.

Anti-CD40L antibody treatment of low-density lipoprotein receptor-deficient mice during the second half of a 26-week regimen of a high-cholesterol diet did not regress, but did significantly reduce further progression of established atherosclerotic lesions within the aortic arch and particularly the thoracic and abdominal aorta, as compared to control treatment. Schonbeck et al., *Proc. Natl. Acad. Sci.* 97: 7458-7463 (2000). Furthermore, anti-CD40L treatment changed the composition of atheroma in manners thought to favor plaque stability, e.g., reduced relative content of macrophages and lipid, as well as increased relative content of smooth muscle cells and collagen. These studies lend support to the importance of the CD40-CD40L signaling pathway in atherosclerosis and its complications, such as coronary artery disease.

4.7. Allograft Rejection *In Vivo* Models:

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Targeting the CD40-CD40L pathway has long been of much interest for prevention of rejection of solid organ transplants (SOT), particularly in light of the promising data from numerous published transplant studies in non-human primates. It has been demonstrated that reduced CD40L expression on *ex vivo* activated CD4⁺ T lymphocytes correlates with excellent renal allograft function. Lederer et al., *Int. Arch. Allergy Immunol.* 133: 276-284 (2004). Furthermore, several studies have demonstrated that anti-CD40L mAbs can both prevent and reverse acute allograft rejection in primates. For example, Kirk et al., *Proc. Natl. Acad. Sci. USA* 94: 8789-8794 (1997) reported that, in rhesus monkeys transplanted with renal allografts, anti-CD40L mAb 5C8 alone or in combination with CTLA4-Ig significantly prolonged rejection-free survival. The CD40L-specific mAb hu5c8 alone also allowed for allogeneic islet engraftment and long-term insulin independence in rhesus monkeys that were transplanted an adequate number of viable pancreatic islets. Kenyon et al., *Proc. Natl. Acad. Sci. USA* 96: 8132-8137 (1999). Preston et al., *Amer. J. Transplantation* 5: 1032-1041 (2005) performed renal transplants in MHC-mismatched rhesus monkeys and treated the recipients with combinations of CD40L-specific mAb IDEC-131, and/or sirolimus, and/or pre-transplant donor-specific transfusion. IDEC-131 was highly effective in preventing renal allograft rejection in primates. In cynomolgus monkeys that underwent renal allotransplantation, treatment with anti-CD40L mAb ABI793 effectively prevented graft rejection. Schuler et al., *Transplantation* 77: 717-726 (2004). In addition to preventing allograft rejection, CD40L-specific mAbs induced donor specific tolerance in primate transplant models. Preston et al., *Amer. J. Transplantation* 5: 1032-1041 (2005); Kenyon et al., *Proc. Natl. Acad. Sci. USA* 96: 8132-8137 (1999).

In pediatric human patients that were undergoing acute graft rejection after liver or small-bowel transplantation, a correlation was observed between the expression of CD40L on CD8⁺ T cells and the risk of transplant rejection. Ashokkumar et al., *Amer. J. Transplantation* 9: 179-191 (2009) and Ashokkumar et al., *Surgery* 146: 166-173 (2009). Similarly, in adult patients that were undergoing allograft rejection following liver or renal transplantation, histological analysis demonstrated an association between CD40L expression and acute or chronic rejection. Bartlett et al., *Amer. J. Transplantation* 3: 1363-1368 (2003) and Biancone et al., *Nephrol. Diall. Transplant.* 13: 716-722 (1998).

Several studies support targeting CD40L over CD40 to achieve better efficacy in transplantation. For example, graft survival is longer and more durable when CD40L is selectively blocked, compared to CD40. Gilson et al., *J. Immunol.* 183: 1625-35 (2009).

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Furthermore, recent data suggest that CD40L blockade may enhance induction of Tregs and/or suppressor cells to promote graft survival. Garcia et al., *J. Clin. Inv.* 120: 2486-96 (2010). Also, blockade of CD40L, but not CD40, has demonstrated induction of long-lived immunological tolerance resulting in indefinite graft survival, particularly when combined with blockade of the B7 pathway. Kenyon et al., *Proc. Natl. Acad. Sci. USA* 96: 8132-8137 (1999); Kawai et al., *Amer. J. Transplantation* 4: 1391-1398 (2004); Preston et al., *Amer. J. Transplantation* 5: 1032-1041 (2005); Adams et al., *J. Immunol.* 174: 542-50 (2005). The synergy of blocking CD40-40L and B7-CD28 pathways in enhancing graft survival is especially important, because it presents the presently disclosed domain antibodies as a natural choice for combination with belatacept (CTLA4-Ig) for SOT.

4.8. Graft-versus-Host Disease *In Vivo* Model:

Chronic and acute graft-versus-host disease (cGVHD and aGVHD) are complications that can occur after a stem cell or bone marrow transplant in which the transplanted donor cells attack the transplant recipient's body. Acute GVHD in humans takes place withing about 60 days post-transplantation and results in damage to the skin, liver, and gut by the action of cytolytic lymphocytes. Chronic GVHD occurs later and is a systemic autoimmune disease that affects primarily the skin, resulting in the polyclonal activation of B cells and the hyperproduction of Ig and autoantibodies.

CD40L-CD40 interactions appear to be critical in the development of both cGVHD and aGVHD. Durie et al., *J. Clin. Invest.* 94: 1333-1338 (1994). In a mouse *in vivo* model, anti-CD40L antibodies blocked the following cGVHD-associated phenomena: splenomegaly, in vitro polyclonal Ig production, elevated levels of serum IgE and serum anti-DNA autoantibodies, and the generation of anti-host cytotoxic T cells. Antibody production remained inhibited for extended periods of time after the end of anti-CD40L antibody administration. In mice with aGVHD, which is associated with the induction of a profound antiallogenic cytotoxic T cell (CTL) response, treatment with anti-CD40L prevented the generation of H-2b-derived CTL. The results of the study suggest that CD40L-CD40 interactions are critical in GVHD and that CD40L may be a valuable ligand for targeting immunotherapeutic agents to control GVHD.

4.9. Myasthenia Gravis *In Vivo* Model:

Myasthenia gravis (MG) and its animal model, experimental autoimmune MG (EAMG), are T-cell dependent autoimmune disorders caused by autoantibodies against the

nicotinic acetylcholine receptors (AChR) at the neuromuscular junction of skeletal muscle. The role of CD40-CD40L in EAMG was shown in CD40L (CD40L^{-/-}) knockout mice. Shi et al, *Eur. J. Immunol.* 28: 3587-3593 (1998). The CD40L knockout mice were completely resistant to EAMG induction and had diminished Th1 and Th2 responses as well as severely impaired T-cell dependent AChR-reactive B cell responses.

It has also been demonstrated that blockade of CD40L-CD40 signaling by anti-CD40L antibodies is capable of suppressing EAMG. Im et al., *J. Immunol.* 166: 6893-6898 (2001). Antibodies given to rats at the chronic stage of EAMG suppress the clinical progression of the autoimmune response and lead to a decrease in the AChR-specific humoral response and delayed-type hypersensitivity. The effect of anti-CD40L treatment during the chronic phase of EAMG is of particular relevance to human MG, which is a chronic disease. It suggests that antagonizing CD40L can be used for immunotherapy of MG and other antibody-mediated autoimmune diseases.

5. Thromboembolism

CD40-CD40L interactions on T and antigen presenting cells are important for adaptive immune responses, such as B-cell proliferation, immunoglobulin (Ig) production, upregulation of co-stimulatory activity (CD80, CD86), cytokine production, and Ig class-switching. The receptor and ligand are also expressed on platelets (off-target cell population), where CD40 is constitutively found on platelets, while CD40L is expressed on activated platelets and cleaved to sCD40L (>90% of circulating sCD40L is derived from platelets). Feroni et al., *Curr. Med. Chem.* 14: 2170-2180 (2007). At least three anti-CD40L monoclonal antibodies (mAb) caused TE in the clinic and/or nonclinical studies conducted in non-human primates (NHP). hu5c8 (BG9588) caused TE in multiple clinical trials (lupus and renal transplantation). Boumpas et al., *Arthritis & Rheumatism* 48: 719-727 (2003). IDEC131 caused TE in one patient in a Crohn's disease trial, leading to termination of ongoing trials at the time. Sidiropoulus & Boumpas, *Lupus* 13: 391-397 (2004). Both hu5c8 and ABI1793 (which binds CD40 at a different epitope from 5c8) caused TE/thrombosis in renal transplantation studies in cynomolgus or rhesus monkeys. Schuler et al., *Transplantation* 77: 717-726 (2004); Kanmaz et al., *Transplantation* 77: 914-920 (2004); Koyama et al., *Transplantation* 77: 460-461 (2004). In a non-published disclosure, Biogen reported a thrombosis incidence of 1/4 and 6/12 in rhesus monkeys given 5 and 20 mg/kg

weekly, respectively, for 6-months, but not in cynomolgus monkeys given 50 mg/kg at the same frequency and duration. The basis for the species difference is not clear.

One of the hypotheses is that the TE associated with administration of these antibodies is mediated by anti-CD40Lmab-CD40L immune complex (IC)-mediated cross linking of platelets, facilitated by IC binding to FcγRIIa, an IgG Fc receptor, causing activation and aggregation (FIG. 10). Blocking the interaction of Fc moiety of IgG with FcγRIIa is, therefore, expected to mitigate platelet cross linking and thrombosis. Approaches and methods developed to evaluate the risk for TE/thrombosis are described in Examples below.

EXAMPLES

TABLE 1 lists representative anti-human CD40L VH domain amino acid sequences useful for the disclosed antibody polypeptides. TABLE 2 discloses representative nucleic acids that encode the VH domain sequences listed in TABLE 1. TABLE 3 lists representative anti-human CD40L VK domain amino acid sequences useful for the antibody polypeptides of the present disclosure. TABLE 4 in turn discloses representative nucleic acids that encode the VK domain sequences listed in TABLE 3. As well known in the art, multiple codons can encode the same amino acid. Nucleic acids encoding a protein sequence thus include nucleic acids having codon degeneracy. The antibody polypeptides disclosed in TABLE 1 and TABLE 3 specifically bind CD40L. They were made using the reiterative initial/primary screening and affinity methodologies described in the examples that follow.

TABLE 1

Anti-human CD40L VH Domain Amino Acid Sequences

BMS2h-10 (SEQ ID NO: 15)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFI AYDMSWVRQA PGKGLEWVSW IDEWGLQTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKT PEE----- FDYWGQGTLV TVSS

BMS2h-11 (SEQ ID NO: 16)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFG DYEMSWVRQA PGKGLEWVSG IDGEGSDTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RS----- FDYWGQGTLV TVSS

BMS2h-111 (SEQ ID NO: 17)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFE RYPMTWVRQA PGKGLEWVST IHGSGSATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP YTSRHNSLGH FDYWGQGTLV TVSS

BMS2h-112 (SEQ ID NO: 18)

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EVQLLES GGG LVQPGGSLRL SCAASGFTFM DYPMGWVRQA PGKGLEWVSS IGPVGMSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYG GTSGRHNTK- FDYWGQGTLV TVSS

BMS2h-113 (SEQ ID NO: 19)

EVQLLES GGG LVQPGGSLRL SCAASGFTFT EYPMSWVRQA PGKGLEWVSV ISPLGFTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWT GSGILNSS- FDYWGQGTLV TVSS

BMS2h-114 (SEQ ID NO: 20)

EVQLLES GGG LVQPGGSLRL SCAASGFRVS NYDLTWVRQA PGKGLEWVST ISATNGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAAVT WWLLRHNDN- LGFWGQGTLV TVSS

BMS2h-115 (SEQ ID NO: 21)

EVQLLES GGG LVQPGGSLRL SCAASGFSIS YKNMAWVRQA PGKGLEWVSA IKAANGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCATGS QKKRTYT--- FDFWGQGTLV TVSS

BMS2h-12 (SEQ ID NO: 22)

EVQLLES GGG LVQPGGSLRL SCAASGFTFR LYEMAWVRQA PGKGLEWVSG IDILGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDL SWQG----- FDYWGQGTLV TVSS

BMS2h-120 (SEQ ID NO: 23)

EVQLLES GGG LVQPGGSLRL SCAASGFTFR SYTMGWVRQA PGKGLEWVSS INPMGYQTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHG VGKGTKPHN FDYWGQGTLV TVSS

BMS2h-121 (SEQ ID NO: 24)

EVQLLES GGG LVQPGGSLRL SCAASGFTFE LYRMSWVRQA PGKGLEWVSE ISGSGFPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSL HDKTQHHQE FDYWGQGTLV TVSS

BMS2h-123 (SEQ ID NO: 25)

EVQLLES GGG LVQPGGSLRL SCAASGFTFI EYPMRWVRQA PGKGLEWVSL ISPSGVFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD ESST FDYWGQGTLV TVSS

BMS2h-124 (SEQ ID NO: 26)

EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYDMDWVRQA PGKGLEWVST IGSSGYPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAERM PGYFPGFARQ FDYWGQGTLV
TVSS

BMS2h-125 (SEQ ID NO: 27)

EVQLLES GGG LVQPGGSLRL SCAASGFTFW RYAMGWVRQA PGKGLEWVST INDEGRETTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKR VSSSVNAPYE FDYWGQGTLV TVSS

BMS2h-126 (SEQ ID NO: 28)

EVQLLES GGG LVQPGGSLRL SCAASGFTFA NYSMSWVRQA PGKGLEWVSS IDRLGHTHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVL ADLIAGHAE FDYWGQGTLV TVSS

BMS2h-127 (SEQ ID NO: 29)

EVQLLES GGG LVQPGGSLRL SCAASGFTFP SYDMAWVRQA PGKGLEWVSG ISRSGSMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGV DAHVYYMEPF FDYWGQGTLV TVSS

BMS2h-128 (SEQ ID NO: 30)

EVQLLES GGG LVQPGGSLRL SCAASGFTFE RYQMAWVRQA PGKGLEWVST ISSDGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG TV FDYWGQGTLV TVSS

BMS2h-129 (SEQ ID NO: 31)

EVQLLES GGG LVQPGGSLRL SCAASGFTFP KYEMAWVRQA PGKGLEWVSS IDGDGKSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD QF FDYWGQGTLV TVSS

BMS2h-13 (SEQ ID NO: 32)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS YYSMYWVRQA PGKGLEWVSS ISPFGWGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYG ETSGPISEN FDYWGQGTLV TVSS

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BMS2h-130 (SEQ ID NO: 33)
 EVQLLES GGG LVQP GGS LRL SCTAS GFTFA GYQMS WVRQA PGKGLEW VSS ITNEGVSTYY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKPG KY FDYWGQGGLTV TVSS

5 BMS2h-131 (SEQ ID NO: 34)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG EYEMW WVRQA PGKGLEW VSS ITSDGLSTYY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKPG IRFDYWGQGGLTV TVSS

0 BMS2h-132 (SEQ ID NO: 35)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA DYDMA WVRQA PGKGLEW VSG IVDDGLMTYY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKPD VAFDYWGQGGLTVTVSN

5 BMS2h-133 (SEQ ID NO: 36)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFI GYAMA WVRQA PGKGLEW VSS IGPLGATTYY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKLP AGTSSHSVDFDYWGQGGLTV TVSS

10 BMS2h-134 (SEQ ID NO: 37)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA DYEMT WVRQA PGKGLEW VSS ITSDGVSTYY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKPS VQ FDYWGQGGLTV TVSS

15 BMS2h-135 (SEQ ID NO: 38)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR RYVMG WVRQA PGKGLEW VSW IEADGRTTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKGL TDQHVIE FDYWGQGGLTV TVSS

20 BMS2h-136 (SEQ ID NO: 39)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD GYRMG WVRQA PGKGLEW VSS IAPDGNITY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKFW GMQFDYWGQGGLTV TVSS

25 BMS2h-137 (SEQ ID NO: 40)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA SYPMG WVRQA PGKGLEW VSS IGPIGFTTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAEMK SPYKPQ---- FDYWGQGGLTV TVSS

30 BMS2h-138 (SEQ ID NO: 41)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFL AYWMW WVRQA PGKGLEW VSS ISPSGHTTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRVED TAVYYCAKYT EPGLGS---- FDYWGQGGLTV TVSS

35 BMS2h-139 (SEQ ID NO: 42)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS NYEMG WVRQA PGKGLEW VSV ISEVGS LTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKPH DSSIG----- FDYWGQGGLTV TVSS

40 BMS2h-14 (SEQ ID NO: 43)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFW SYDMT WVRQA PGKGLEW VSS IMASGDDTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKWD RD----- FDYWGQGGLTV TVSS

45 BMS2h-15 (SEQ ID NO: 44)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE EYVMS WVRQA PGKGLEW VST ISPIGLTTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAEFP LIILPD---- FDYWGQGGLTV TVSS

50 BMS2h-16 (SEQ ID NO: 45)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFM EYAMI WVRQA PGKGLEW VSI ISPLGLSTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKYQ DSSDSQYTN- FDYWGQGGLTV TVSS

55 BMS2h-17 (SEQ ID NO: 46)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE DYGMG WARQA PGKGLEW VSS IGPLGLWTYY
 ADSAKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKSP LEGLITN--- FDYWGQGGLTV TVSS

60 BMS2h-176 (SEQ ID NO: 47)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD AYEMG WVRQA PGKGLEW VSI IDWDGNSTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKPG DNVGI----- FDYWGQGGLTV TVSS

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BMS2h-177 (SEQ ID NO: 48)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS NY YM WVRQA PGK GLEW VSA IDEW GFATYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKHW EFTSDTSR—FDYWGQGTLV TVSS

5 BMS2h-178 (SEQ ID NO: 49)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE DFDMA WVRQA PGK GLEW VSS INDQGS LTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPD QF----- FDYWGQGTLV TVSS

0 BMS2h-179 (SEQ ID NO: 50)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYDMM WVRQA PGK GLEW VSR ISPQGQRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKIR GQSRIPMR—FDYWGQGTLV TVSS

5 BMS2h-18 (SEQ ID NO: 51)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFP EYDMT WVRQA PGK GLEW VSY ISSDGYSTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPH GSPRE----- FDYWGQGTLV TVSS

0 BMS2h-180 (SEQ ID NO: 52)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT DYEMGWVRQA PGK GLEW VST ITS LGESTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPG RI----- FDYWGQGTLV TVSS

5 BMS2h-181 (SEQ ID NO: 53)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA FYPMM WVRQA PGK GLEW VSW IDATGTRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAEGN YGSSYTMGV- FDYWGQGTLV TVSS

5 BMS2h-182 (SEQ ID NO: 54)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD EYPMY WVRQA PGK GLEW VSS IGPSGPNTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKSP YFDVIPSY—FDYWGQGTLV TVSS

0 BMS2h-183 (SEQ ID NO: 55)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA DYGMGWVRQA PGK GLEW VSS IQSSGLRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKRA NSRRG----- FDYWGQGTLV TVSS

5 BMS2h-184 (SEQ ID NO: 56)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYEMMWVRQA PGK GLEW VSS ITSHGGSTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPD KD----- FDYWGQGTLV TVSS

40 BMS2h-185 (SEQ ID NO: 57)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA HYPMS WVRQA PGK GLEW VSS IGR LGNR TYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKRA TPVPIKGL—FDYWGQGTLV TVSS

45 BMS2h-186 (SEQ ID NO: 58)
 EVQLLES GGG LVQP GGS LRL SCAAS GLTFG RYEMAWVRQA PGK GLEW VSS IDSDGWVTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAQPD SL----- FDYWGQGTLV TVSS

50 BMS2h-187 (SEQ ID NO: 59)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS SYSMWVRQA PGK GLEW VSG INRGGTRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGW RRG----- FDYWGQGTLV TVSS

55 BMS2h-188 (SEQ ID NO: 60)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT RYRMS WVRQA PGK GLEW VSG ISR DGYRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGM TAS----- FDYWGQGTLV TVSS

60 BMS2h-189 (SEQ ID NO: 61)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFQ MYPMG WVRQA PGK GLEW VSM IEPAGDLTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKYQ EQPW----- FDYWGQGTLV TVSS

BMS2h-19 (SEQ ID NO: 62)
 EVQLLES GGG LVQP GGS LRL SCAAS GFPPF QYQMA WVRQA PGK GLEW VSM ITS DGLDTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPE PL----- FDYWGQGTLV TVSS

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BMS2h-190 (SEQ ID NO: 63)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS MYDMH WVRQA PGK GLEWVST ILSDG TDTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKYG AM----- FDYWGQGTLV TVSS

5 BMS2h-191 (SEQ ID NO: 64)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK LYPMT WVRQA PGK GLEWVSS IDAGGHETYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKDW WDYL----- FDYWGQGTLV TVSS

0 BMS2h-192 (SEQ ID NO: 65)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS RYPMS WVRQA PGK GLEWVSS INRSGMRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAEGH QAP----- FDYWGQGTLV TVSS

5 BMS2h-193 (SEQ ID NO: 66)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT GYAMS WVRQA PGK GLEWVST INANGIRTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGG VWRWGTG HK- FDYWGQGTLV TVSS

0 BMS2h-194 (SEQ ID NO: 67)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK QYDMR WVRQA PGK GLEWVST ISQNGTKTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKSR TGRY----- FDYWGQGTLV TVSS

5 BMS2h-195 (SEQ ID NO: 68)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG TYDMG WVRQA PGK GLEWVSR INWQGDRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKAG FGHYVDGLG- FDYWGQGTLV TVSS

0 BMS2h-196 (SEQ ID NO: 69)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS GYEMA WVRQA PGK GLEWVSS ITDMGDSTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPG TA----- FDYWGPGTLV TVSS

5 BMS2h-197 (SEQ ID NO: 70)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA KYKM WVRQA PGK GLEWVSS ITPKG HSTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKRP MTP----- FDYWGQGTLV TVSS

0 BMS2h-198 (SEQ ID NO: 71)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE RYNMS WVRQA PGK GLEWVSS IRPRGGKTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKWR REGYT GSK—FDYWGQGTLV TVSS

40 BMS2h-199 (SEQ ID NO: 72)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE RYGMT WVRQA PGK GLEWVSS IWPRGQKTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGN SRYV----- FDYWGQGTLV TVSS

45 BMS2h-2 (SEQ ID NO: 73)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYEMM WVRQA PGK GLEWVST ITSDGISTYY
 ADSVKGRFTI FRD NSKNTLY LQMNS LRAED TAVYYCAKSG RF----- FDYWGQGTLV TVSS

50 BMS2h-20 (SEQ ID NO: 74)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS GYQMA WVRQA PGK GLEWVSG ISSEGLTTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKLG RR----- FDYWGQGTLV TVSS

55 BMS2h-200 (SEQ ID NO: 75)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT NYSMG WVRQA PGK GLEWVST IRPNGTKTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKRS SAHLQR---- FDYWGQGTLV TVSS

60 BMS2h-201 (SEQ ID NO: 76)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG NYSMG WVRQA PGK GLEWVSS IGRHGGRTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKKG STYPR----- FDYWGQGTLV TVSS

BMS2h-202 (SEQ ID NO: 77)
 EVQLLES GGG LVQP GGS LRL SCTAS GFTFS HYEMG WVRQA PGK GLEWVSS IEPFGGGTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKVY PQGS----- FDYWGQGTLV TVSS

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BMS2h-203 (SEQ ID NO: 78)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS NYTMGWVRQA PGKGLEWVSS IRPDGKITYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEVY SSCAMCTPLL FDYWGQGTLV TVSS

BMS2h-204 (SEQ ID NO: 79)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK RYMAWVRQA PGKGLEWVSD IGPRGFSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG RGQRDTSQP- FDYWGQGTLV TVSS

BMS2h-205 (SEQ ID NO: 80)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA SYQMAWVRQA PGKGLEWVSG ITSGGLSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RG----- FDYWGQGTLV TVSS

BMS2h-206 (SEQ ID NO: 81)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA SYEMTWVRQA PGKGLEWVSG ISSDGLSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VL----- FDYWGQGTLV TVSS

BMS2h-207 (SEQ ID NO: 82)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD KYLSWVRQA PGKGLEWVSG IEPLGDVTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKEA SGD----- FDYWGQGTLV TVSS

BMS2h-208 (SEQ ID NO: 83)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT EYEMSWVRQA PGKGLEWVSS IDNVGSSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KL----- FDYWGQGTLV TVSS

BMS2h-209 (SEQ ID NO: 84)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA DYEMWWVRQA PGKGLEWVSA ISRQGFATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDL ERDD----- FDYWGQGTLV TVSS

BMS2h-21 (SEQ ID NO: 85)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA NYEMGWARQA PGKGLEWVSV ISEWGYSTYY
 ADSAKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLV GGTQYE---- FDYWGQGTLV TVSS

BMS2h-22 (SEQ ID NO: 86)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFH NYEMSWVRQA PGKGLEWVSS ISSGGSSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VK----- FDYWGQGTLV TVSS

BMS2h-23 (SEQ ID NO: 87)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG LYEMTWVRQA PGKGLEWVSS ITGDGISTYY
 ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKAG RK----- FDYWGQGTLV TVSS

BMS2h-24 (SEQ ID NO: 88)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS NYQMAWVRQA PGKGLEWVSS ITSEGGSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KN----- FDYWGQGTLV TVSS

BMS2h-24-1 (SEQ ID NO: 89)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYQMAWVRQA PGKGLEWVSS ITSEGGSTYY
 ADSVKGRFTI SRDNSKNTVY LQMNSLRAED TAVYYCAKPG KN----- FDYWGQGTLV TVSS

BMS2h-25 (SEQ ID NO: 90)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD NYEMTWVRQA PGKGLEWVST ITSQGTSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RS----- FDYWGQGTLV TVSS

BMS2h-26 (SEQ ID NO: 91)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR SYEMTWVRQA PGKGLEWVSS ITSDGGTTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KT----- FDYWGQGTLV TVSS

BMS2h-27 (SEQ ID NO: 92)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN LYEMTWVRQA PGKGLEWVSS ITSDGVSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD SP----- FDYWGQGTLV TVSS

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5 BMS2h-28 (SEQ ID NO: 93)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG HYDMAWVRQA PGKGLEWVST ISDNGNGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RD----- FDYWGQGTLV TVSS

10 BMS2h-29 (SEQ ID NO: 94)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG RYQMAWVRQA PGKGLEWVSS ISSDGGGTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RA----- FDYWGQGTLV TVSS

15 BMS2h-30 (SEQ ID NO: 95)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA RYQMAWVRQA PGKGLEWVST ISDDGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLD KL----- FDYWGQGTLV TVSS

20 BMS2h-300 (SEQ ID NO: 96)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NDEMTWVRQA PGKGLEWVSA IDTTGGQTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG KE----- FDYWGQGTLV TVSS

25 BMS2h-301 (SEQ ID NO: 97)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EEMSWVRQA PGKGLEWVSS ILDEGSGTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KD----- FDYWGQGTLV TVSS

30 BMS2h-302 (SEQ ID NO: 98)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG EEEMSWVRQA PGKGLEWVSA ITDDGDDTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN AGA----- FDYWGQGTLV TVSS

35 BMS2h-303 (SEQ ID NO: 99)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE VYDMAWVRQA PGKGLEWVSG IVNDGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD KD----- FDYWGQGTLV TVSS

40 BMS2h-304 (SEQ ID NO: 100)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG NTEMTWVRQA PGKGLEWVSS IADDGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG QA----- FDYWGQGTLV TVSS

45 BMS2h-31 (SEQ ID NO: 101)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE EYQMAWVRQA PGKGLEWVST ISDDGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD LY----- FDYWGQGTLV TVSS

50 BMS2h-32 (SEQ ID NO: 102)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE VYQMGWVRQA PGKGLEWVSF IVPGGDLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETW PE----- FDYWGQGTLV TVSS

55 BMS2h-4 (SEQ ID NO: 103)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NYEMTWVRQA PGKGLEWVSS ITSDGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN PP----- FDYWGQGTLV TVSS

60 BMS2h-40 (SEQ ID NO: 104)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK AYDMGWVRQA PGKGLEWVSQ IGRDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPR RYAIF----- TFDRGQGTLV TVSS

65 BMS2h-400 (SEQ ID NO: 105)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK QYPMWVRQA PGKGLEWVST ISTNGVRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWT DISSSE--- FDYWGQGTLV TVSS

70 BMS2h-401 (SEQ ID NO: 106)
EVQLLESGGG LVQPGGSLRL SCAASGFTFF NYDMSWVRQA PGKGLEWVSA ISGSGGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVF VWSADIDFD- FDYWGQGTLV TVSS

75 BMS2h-402 (SEQ ID NO: 107)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS WYDMSWVRQA PGKGLEWVSH IASWGGKTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVT VKDGGYLM- FDYWGQGTLV TVSS

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5 BMS2h-403 (SEQ ID NO: 108)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFA EYAMA WVRQA PGK GLEWVSS IGRD GAVTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKWK AAKER GSW—FDYWG QGTLV TVSS

10 BMS2h-404 (SEQ ID NO: 109)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFQ AYQM QWVRQA PGK GLEWVST ISPNG LFTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKWL SS----- FDYWG QGTLV TVSS

15 BMS2h-407 (SEQ ID NO: 110)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFA MY SMAWVRQA PGK GLEWVSG ISPRG VETYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKTN WNGVDL---- FDYWG QGTLV TVSS

20 BMS2h-408 (SEQ ID NO: 111)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFP TYMMS WVRQA PGK GLEWVST INTNG RDTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKGD SNMSF----- FDYWG QGTLV TVSS

25 BMS2h-409 (SEQ ID NO: 112)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE GYSMT WVRQA PGK GLEWVSS INASG TLTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKDG NRSEVF---- FDYWG QGTLV TVSS

30 BMS2h-41 (SEQ ID NO: 113)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFF EYEMT WVRQA PGK GLEWVSS IANDG STTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKPD RQ----- FDYWG QGTLV TVSS

35 BMS2h-410 (SEQ ID NO: 114)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFQ DY LMAWVRQA PGK GLEWVSE INQDG TVTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAESS PY----- FDYWG QGTLV TVSS

40 BMS2h-411 (SEQ ID NO: 115)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFD NYAMS WVRQA PGK GLEWVSS ISR DGHVTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKLS SKGGTFASS- FDYWG QGTLV TVSS

45 BMS2h-412 (SEQ ID NO: 116)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AVPMT WVRQA PGK GLEWVSA ITDDG LRTTY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKGH IYGDY----- FDYWG QGTLV TVSS

50 BMS2h-413 (SEQ ID NO: 117)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE LYRMM WVRQA PGK GLEWVSA ISSDG DTTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAEHW LGTTL SLRD- FDYWG QGTLV TVSS

55 BMS2h-414 (SEQ ID NO: 118)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFY RYTMA WVRQA PGK GLEWVSQ ISPRG NITYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKSG VAGAESPEY- FDYWG QGTLV TVSS

60 BMS2h-415 (SEQ ID NO: 119)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFL GYYMS WVRQA PGK GLEWVST IGPIG GGTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKSQ NIYGP----- FDYWG QGTLV TVSS

65 BMS2h-416 (SEQ ID NO: 120)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE QYDMA WVRQA PGK GLEWVSE ISR DGGRTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAEEY PY----- FDYWG QGTLV TVSS

70 BMS2h-417 (SEQ ID NO: 121)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFP QYSMV WVRQA PGK GLEWVST ISPLG SSTYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKMS KLLSRE--- FDYWG QGTLV TVSS

75 BMS2h-418 (SEQ ID NO: 122)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFA MY SMAWVRQA PGK GLEWVSG ISPRG VETYY
ADSVK GRFTI SRD NSKNTLY LQMNS LRAED TAVYY CAKTN WNGVDL---- FDYWG QGTLV TVSS

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BMS2h-419 (SEQ ID NO: 123)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FT RHGMA WVRQA PGKGLEW VST ITPTGN TTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDA HDEGY----- FDYWGQGTLV TVSS

BMS2h-42 (SEQ ID NO: 124)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FG PYEMTWVRQA PGKGLEW VSS IVGDGLD TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RV----- FDYWGQGTLV TVSS

BMS2h-420 (SEQ ID NO: 125)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FG STPMWVRQA PGKGLEW VSE IRDTGLATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCASVS ----- FDYWGQGTLV TVSS

BMS2h-421 (SEQ ID NO: 126)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FH LGDMHWVRQA PGKGLEW VSS ISGTGHT TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPM NDQG----- FDYWGQGTLV TVSS

BMS2h-422 (SEQ ID NO: 127)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FM DEDMLWVRQA PGKGLEW VSR INSLGHT TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSF MM----- FDYWGQGTLV TVSS

BMS2h-423 (SEQ ID NO: 128)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FR NYQMHWVRQA PGKGLEW VSG IDATGRATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARST RS----- FDYWGQGTLV TVSS

BMS2h-424 (SEQ ID NO: 129)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FT NADMWVRQA PGKGLEW VSS ISGSGGSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGY LTSH----- FDYWGQGTLV TVSS

BMS2h-425 (SEQ ID NO: 130)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FR DYMAWVRQA PGKGLEW VST ITPSGLT TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS QAVTRS---- FDYWGQGTLV TVSS

BMS2h-426 (SEQ ID NO: 131)
 EVQLLES GGD LVQP GGS LRL SCAAS GFT FS DEGMMWVRQA PGKGLEW VSE INQQGSATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTI GM----- FDYWGQGTLV TVSS

BMS2h-427 (SEQ ID NO: 132)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FT DQPMWVRQA PGKGLEW VSS IGARGGP TTY
 ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCAKWF DIIAWDPFS- FDYWGQGTLV TVSS

BMS2h-428 (SEQ ID NO: 133)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FN QYPMWVRQA PGKGLEW VSS ITPSGFL TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWN PFITT----- FDYWGQGTLV TVSS

BMS2h-429 (SEQ ID NO: 134)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FG HQQMAWVRQA PGKGLEW VST ITPNGYY TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFD YSLR----- FDYWGQGTLV TVSS

BMS2h-43 (SEQ ID NO: 135)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FA SYEMAWVRQA PGKGLEW VSS IGSDGGP TTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED SAVYYCAKPD RA----- FDYWGQGTLV TVSS

BMS2h-430 (SEQ ID NO: 136)
 EVQLLES GGG LVQP GGS LRL SCAAS GFT FS AEQMTWARQA PGKGLEW VST ITPHGDSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWR TLVDWPTSES FDYWGQGTLV
 TVSS

BMS2h-44 (SEQ ID NO: 137)

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EVQLLES GGG LVQPGGSLRL SCAASGFTFT SYEMGWVRQA PGKGLEWVSS IEPTGITTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPH FTELG----- FDYWGQGLTV TVSS

5 BMS2h-449 (SEQ ID NO: 138)
EVQLLES GGG LVQPGGSLRL SCAASGFTFE GEQMAWVRQA PGKGLEWVST ITLPGPYTFY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGN GTF----- FDYWGQGLTV TVSS

0 BMS2h-45 (SEQ ID NO: 139)
EVQLLES GGG LVQPGGSLRL SCAASGFTFG NYAMAWVRQA PGKGLEWVSK IGAQGLHTYY
AGSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQT TMDYER---- FDYWGQGLTV TVSS

5 BMS2h-450 (SEQ ID NO: 140)
EVQLLES GGG LVQPGGSLRL SCAASGFTFD EVDMSWVRQA PGKGLEWVSA IGNNGLKTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSA LSYPVPPV--- FDYWGQGLTV TVSS

10 BMS2h-451 (SEQ ID NO: 141)
EVQLLES GGG LVQPGGSLRL SCAASGFTFQ DDTMSWVRQA PGKGLEWVST ITLKGPSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSR DGLY----- FDYWGQGLTV TVSS

15 BMS2h-452 (SEQ ID NO: 142)
EVQLLES GGG LVQPGGSLRL SCAASGFTFA SSPMAWVRQA PGKGLEWVSS IGRDGSTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS PYRR----- FDYWGQGLTV TVSS

20 BMS2h-453 (SEQ ID NO: 143)
EVQLLES GGG LVQPGGSLRL SCAASGFTFT DYSMWVRQA PGKGLEWVST IVSHGGTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGK GYNAQY---- FDYWGQGLTV TVSS

25 BMS2h-454 (SEQ ID NO: 144)
EVQLLES GGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFD YSLR----- FDYWGQGLTV TVSS

30 BMS2h-455 (SEQ ID NO: 145)
EVQLLES GGG LVQPGGSLRL SCAASGFTFN DYDMIWVRQA PGKGLEWVST ISSHGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD VF----- FDYWGQGLTV TVSS

35 BMS2h-456 (SEQ ID NO: 146)
EVQLLES GGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS DS----- FDYRGQGLTV TVSS

40 BMS2h-457 (SEQ ID NO: 147)
EVQLLES GGG LVQPGGSLRL SCAASGFTFA DYEMAWVRQA PGKGLEWVSG IQSNGNITY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAN SQVEY----- FDYWGQGLTV TVSS

45 BMS2h-458 (SEQ ID NO: 148)
EVQLLES GGG LVQPGGSLRL SCAASGFTFG VEPMSWVRQA PGKGLEWVSN IGRDGSMTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG KHGT----- FDYWGQGLTV TVSS

50 BMS2h-459 (SEQ ID NO: 149)
EVQLLES GGG LVQPGGSLRL SCAASGFTFP EYRMMWVRQA PGKGLEWVSW IDERGS�TY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRR KGTKQ----- FDYWGQGLTV TVSS

55 BMS2h-46 (SEQ ID NO: 150)
EVQLLES GGG LVQPGGSLRL SCAASGFTFE LYAMAWVRQA PGKGLEWVSG IGAVGETTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKEA NNLSNLT---FDYWGQGLTV TVSS

60 BMS2h-460 (SEQ ID NO: 151)
EVQLLES GGG LVQPGGSLRL SCAASGFTFG HQQMAWVRQA PGKGLEWVST ITPNGYYTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWS VEW----- FDYWGQGLTV TVSS

60 BMS2h-461 (SEQ ID NO: 152)

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EVQLLES GGG LVQPGGSLRL SCAASGFTFN SYTMNWVRQA PGKGLEWVSS INPWGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL VL----- FDYWGQGTLLV TVSS

BMS2h-462 (SEQ ID NO: 153)

EVQLLES GGG LVQPGGSLRL SCAASGFTFD GDMMSWVRQA PGKGLEWVSS ITQLGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQN WRTL----- FDYWGQGTLLV TVSS

BMS2h-463 (SEQ ID NO: 154)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN AYGMWVRQA PGKGLEWVSS ILSDGVITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSA RGNF----- FDYWGQGTLLV TVSS

BMS2h-464 (SEQ ID NO: 155)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG HYMMWVRQA PGKGLEWVSS ITPHGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEFN AIFSEA----- FDYWGQGTLLV TVSS

BMS2h-465 (SEQ ID NO: 156)

EVQLLES GGG LVQPGGSLRL SCAASGFTFR DYMAWVRQA PGKGLEWVST ITPSGLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS QAVTRS----- FDYWGQGTLLV TVSS

BMS2h-466 (SEQ ID NO: 157)

EVQLLES GGG LVQPGGSLRL SCAASGFTFD LYAMWVRQA PGKGLEWVSM IGRDGRFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLA GSLRGR----- FDYWGQGTLLV TVSS

BMS2h-467 (SEQ ID NO: 158)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN KASMGWVRQA PGKGLEWVST ITPHGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQR WGVE----- FDYWGQGTLLV TVSS

BMS2h-468 (SEQ ID NO: 159)

EVQLLES GGG LVQPGGSLRL SCAASGFTFQ GYSMGWVRQA PGKGLEWVSS IAGRGGVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL YIYHSL----- FDYWGQGTLLV TVSS

BMS2h-469 (SEQ ID NO: 160)

EVQLLES GGG LVQPGGSLRL SCAASGFTFP GMEMSWVRQA PGKGLEWVSA ITGTGSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGY HP----- FDYWGQGTLLV TVSS

BMS2h-470 (SEQ ID NO: 161)

EVQLLES GGG LVQPGGSLRL SCAASGFTFP MVAMSWVRQA PGKGLEWVSS IARDGNVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED AAVYYCAKVS PTG----- FDYWGQGTLLV TVSS

BMS2h-471 (SEQ ID NO: 162)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG HQDMSWVRQA PGKGLEWVSG ITDDGESTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD YD----- FDYWGQGTLLV
TVSS

BMS2h-472 (SEQ ID NO: 163)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG EYNMMWVRQA PGKGLEWVSQ ITRDGSRTYY
ADSVRGRFTI SRDNSRNTLY LQMNSLRAED SAVYYCAKLS NIG----- FDYWGQGTLLV TVSS

BMS2h-473 (SEQ ID NO: 164)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS DYSMIWARQA PGKGLEWVSS ITPYGSYTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTD YL----- FDYWGQGTLLV TVSS

BMS2h-474 (SEQ ID NO: 165)

EVQLLES GGG LVQPGGSLRL SCAASGFTFD TYSMMWVRQA PGKGLEWVST ITPYGSSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWG LV----- FDYWGQGTLLV TVSS

BMS2h-475 (SEQ ID NO: 166)

EVQLLES GGG LVQPGGSLRL SCAASGFTFT TGPMMWVRQA PGKGLEWVSA IGIGGDTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLT PSNQ----- FDYWGQGTLLV TVSS

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BMS2h-476 (SEQ ID NO: 167)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK QYQMM WVRQA PGKGLEW VSS ITPSGFLTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWN PFIST----- FDYWGQGTLV TVSS

5 BMS2h-477 (SEQ ID NO: 168)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFP NYDMW WVRQA PGKGLEW VSS ISALGNVTYY
 ADSVKGRFTI SRDNSKNTLY LQTNSLRAED TAVYYCAKWR SAITGN----
 FDYWGQGTLV TVSS

0 BMS2h-478 (SEQ ID NO: 169)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK EYQMS WVRQA PGKGLEW VST ISPSGMNTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWR SVVRPWPGV- FDYWGQGTLV
 TVSS

5 BMS2h-479 (SEQ ID NO: 170)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD DESMA WVRQA PGKGLEW VSS ITPHGTFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLH LKLYESH--- FDYWGQGTLV TVSS

0 BMS2h-480 (SEQ ID NO: 171)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE GGEMG WVRQA PGKGLEW VSM IPMDGSATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG ST----- FDYWGQGTLV TVSS

5 BMS2h-481 (SEQ ID NO: 172)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD FMPMA WVRQA PGKGLEW VSS IGRDGAYTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLA SPAQ----- FDYWGQGTLV TVSS

0 BMS2h-482 (SEQ ID NO: 173)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DEPML WVRQA PGKGLEW VSS IGGTGTTTTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGN QGDFINR--- FHYWGQGTLV TVSS

5 BMS2h-483 (SEQ ID NO: 174)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFH AYNMA WVRQA PGKGLEW VST ISPRGSYTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWP PPSSH----- FDYWGQGTLV TVSS

5 BMS2h-5 (SEQ ID NO: 175)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD GYEMA WVRQA PGKGLEW VSS ITS DGTSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG LR----- FDYWGQGTLV TVSS

40 BMS2h-505 (SEQ ID NO: 176)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE GYMMY WVRQA PGKGLEW VSS ISPQGHFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAELR ELPRL----- FDYWGQGTLV TVSS

45 BMS2h-506 (SEQ ID NO: 177)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS SYAMG WVRQA PGKGLEW VSS IDASGGPTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAN GKKFPFTKY- FDYWGQGTLV TVSS

50 BMS2h-507 (SEQ ID NO: 178)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFP SVHMA WVRQA PGKGLEW VSG INLTGVDTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSA TTRQAHPLY- FDYWGQGTLV TVSS

55 BMS2h-515 (SEQ ID NO: 179)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK EGEMY WVRQA PGKGLEW VST ISTNGLTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKST RDLG----- FAYWGQGTLV TVSS

BMS2h-516 (SEQ ID NO: 180)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE EYEMA WARQA PGKGLEW VSF ISPRGHFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPA KT----- FDYWGQGTLV TVSS

BMS2h-517 (SEQ ID NO: 181)

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EVQLLES GGG LVQPGGSLRL SCAASGFTFD TYEMLWVRQA PGKGLEWVSR ISVDGSITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTR MR----- FDYWGQGTLV TVSS

BMS2h-518 (SEQ ID NO: 182)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS SYAMSWVRQA PGKGLEWVSN ISRDGSKTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAQ SGLRSLTT FDYWGQGTLV TVSS

BMS2h-519 (SEQ ID NO: 183)

EVQLLES GGG LVQPGGSLRL SCADSGFTFS SYAMSWVRQA PGKGLEWVSS IGRDGAYTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG PKGIA----- FDYWGQGTLV TVSS

BMS2h-520 (SEQ ID NO: 184)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS PHAMAWVRQA PGKGLEWVSG IDGGGSMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSD PP----- FDYWGQGTLV TVSS

BMS2h-521 (SEQ ID NO: 185)

EVQLLES GGG LVQPGGSLRL SCAASGFTFH AGEMHWVRQA PGKGLEWVSS ITLPGDMTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN TGYT----- FDYWGQGTLV TVSS

BMS2h-522 (SEQ ID NO: 186)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG NYGMSWVRQA PGKGLEWVSS ISWDGSLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQNT RL----- FDYWGQGTLV TVSS

BMS2h-523 (SEQ ID NO: 187)

EVQLLES GGG LVQPGGSLRL SCAASGFTFH DADMLWVRQA PGKGLEWVSG ILSPGEDTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFG LP----- FDYWGQGTLV TVSS

BMS2h-524 (SEQ ID NO: 188)

EVQLLES GGG LVQPGGSLRL SCAASGFTFR TDQMNWVRQA PGKGLEWVSS ISPSGAYTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL GA----- FDYWGQGTLV TVSS

BMS2h-525 (SEQ ID NO: 189)

EVQLLES GGG LVQPGGSLRL SCAASGFIFE QYQMWWVRQA PGKGLEWVSW ISPDGHTHTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFS LRKMEK----- FDYWGQGTLV TVSS

BMS2h-526 (SEQ ID NO: 190)

EVQLLES GGG LVQPGGSLRL SCAASGFTFQ DEQMAWVRQA PGKGLEWVSS IASDGMSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQPG KN----- FDHWGQGTLV TVSS

BMS2h-527 (SEQ ID NO: 191)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS DYAMSWVRQA PGKGLEWVSS ITTGGERTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRW NLYTES----- FDYWGQGTLV TVSS

BMS2h-528 (SEQ ID NO: 192)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG GQPMDWVRQA PGKGLEWVSS IAPDGIHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNL GQG----- FDYWGQGTLV TVSS

BMS2h-529 (SEQ ID NO: 193)

EVQLLES GGG LVQPGGSLRL SCAASGFTFE RYQMTWVRQA PGKGLEWVSS ISPSGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWK AL----- FDYWGQGTLV TVSS

BMS2h-530 (SEQ ID NO: 194)

EVQLLES GGG LVQPGGSLRL SCAASGFTFP HSTMYWVRQA PGKGLEWVSL ILPSGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFS DER----- FDYWGQGTLV TVSS

BMS2h-531 (SEQ ID NO: 195)

EVQLSESGGG LVQPGGSLRL SCAASGFTFG DGNMDWVRQA PGKGLEWVSG ISSDGVTTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR GQG----- FDYWGQGTLV TVSS

BMS2h-532 (SEQ ID NO: 196)

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EVQLLES GGG LVQPGGSLRL SCAASGFTFD DYMMWVVRQA PGKGLEWVSS ISPHGVYTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWL HT----- FDYWGQGTLLV TVSS

BMS2h-533 (SEQ ID NO: 197)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS NYTMAWGRQA PGKGLEWVSF IAGPGNYTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG STATYNNGQ- FDYWGQGTLLV TVSS

BMS2h-534 (SEQ ID NO: 198)

EVQLLES GGG LVQPGGSLRL SCAASGFTFT EYSMWVVRQA PGKGLEWVSS ISGSGRVTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWL KLVRAPNP—FDYWGQGTLLV TVSS

BMS2h-535 (SEQ ID NO: 199)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS NYQMAWVRQA PGKGLEWVSG ISKTGHSTYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKAS HSLGPL---- FDYWGQGTLLV TVSS

BMS2h-54 (SEQ ID NO: 200)

EVQLLES GGG LVQPGGSLRL SCAASGFTFT AYRMAWVRQA PGKGLEWVSW ISPSGSGTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTL TDSPSGHYE- FDYWGQGTLLV TVSS

BMS2h-55 (SEQ ID NO: 201)

EVQLLES GGG LVQPGGSLRL SCAASGFTFA RYEMGWVRQA PGKGLEWVSR ITAQGLGTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYL TDFSSGHQE- FDYWGQGTLLV TVSS

BMS2h-553 (SEQ ID NO: 202)

EVQLLES GGG LVQPGGSLRL SCAASGFTFD DYGMSWVRQV PGKGLEWVSG ISHNGMLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYW PSTSWETD—FDYWGQGTLLV TVSS

BMS2h-554 (SEQ ID NO: 203)

EVQLLES GGG SVQPGGSLRL SCAASGFTFG NEPMWVVRQA PGKGLEWVSS IEMQGKNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDR GQG----- FDYWGQGTLLV TVSS

BMS2h-555 (SEQ ID NO: 204)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG EEEMSWVRQA PGKGLEWVSC IDNLGSPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED AAVYYCAKTI SHQYDR---- FDYWGQGTLLV TVSS

BMS2h-556 (SEQ ID NO: 205)

EVQLLES GGG LVQPGGSLRL SCAASGFTFG EEEMSWVRQA PGKGLEWVSS IDEGGRWTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKWT PHKQLS---- FDYWGQGTLLV TVSS

BMS2h-557 (SEQ ID NO: 206)

EVQLLES GGG LVQPGGSLRL SCAASGFSFA DEYMWVARQA PGKGLEWVSE IDPLGTGTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYG TA----- FDYWGQGTLLV TVSS

BMS2h-558 (SEQ ID NO: 207)

EVQLLES GGG LVQPGGSLRL SCAASGFTFS THDMMWVRQA PGKGLEWVSS ISDDGISTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD MSLIE----- FDYWGQGTLLV TVSS

BMS2h-559 (SEQ ID NO: 208)

EVQLLES GGG LVQPGGSLRL SCAASGFTFD GTPMWVVRQA PGKGLEWVSG ISGDGRNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPY ALTSSKP--- FDYWGQGTLLV TVSS

BMS2h-56 (SEQ ID NO: 209)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN DYTGMWVRQA PGKGLEWVSW IHGTGGQTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAL ADRSGGVVE- FDYWGQGTLLV TVSS

BMS2h-560 (SEQ ID NO: 210)

EVQLLES GGG LVQPGGSLRL SCAASGFTFE AETMAWVRQA PGKGLEWVSC ISNDGNNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKES LISPGL---- FDYWGQGTLLV TVSS

BMS2h-561 (SEQ ID NO: 211)

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EVQLLES GGG LVQP GGS LRL SCAAS GFT FT GEYMN WVRQA PGK GLEWVST INETGYMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS TRGVP----- FDYWGQGTLV TVSS

BMS2h-562 (SEQ ID NO: 212)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FR SYDMGWVRQA PGK GLEWVST ISPMGVFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSN QHAHDP---- FDYWGQGTLV TVSS

BMS2h-563 (SEQ ID NO: 213)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FS DYDMGWVRQA PGK GLEWVSS ISPMGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAA LTPM----- FDYWGQGTLV TVSS

BMS2h-564 (SEQ ID NO: 214)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FR DYDMGWVRQA PGK GLEWVST ISPLGHFTYY
ADSVKGRSTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAE EA----- FDYWGQGTLV TVSS

BMS2h-565 (SEQ ID NO: 215)

EVQLLES GGG LVQP GGS LRL SCAAS GFAP RYGMTWVRQA PGK GLEWVSN IDQFGMKTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEEY AS----- FDYWGQGTLV TVSS

BMS2h-566 (SEQ ID NO: 216)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FD KYDMGWVRQA PGK GLEWVST ISPMGVFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGR GNTSD----- FDYWGQGTLV TVSS

BMS2h-567 (SEQ ID NO: 217)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FS NYDMAWVRQA PGK GLEWVST ISGAGHFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSF PRDE----- FDYWGQGTLV TVSS

BMS2h-568 (SEQ ID NO: 218)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FP KYEMRWVRQA PGK GLEWVSE IGLDGSPTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG DPNG----- FDYWGQGTLV TVSS

BMS2h-569 (SEQ ID NO: 219)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FP TSEMDWVRQA PGK GLEWVSG IGPDLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHA DW----- FDYWGQGTLV TVSS

BMS2h-57 (SEQ ID NO: 220)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FS EYDMYWVRQA PGK GLEWVSW IDTDGGDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG LK----- FDYWGQGTLV TVSS

BMS2h-570 (SEQ ID NO: 221)

EVQLLES GGG LVQP GGS LRL SCTAS GFT FE NASMQWVRQA PGK GLEWVSS IEGQGNATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSS SWS----- FDYWGQGTLV TVSS

BMS2h-571 (SEQ ID NO: 222)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FT RNEMGWVRQA PGK GLEWVST ITPTGTFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTD PGNRY----- FDYWGQGTLV TVSS

BMS2h-572 (SEQ ID NO: 223)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FN WQLMGWVRQA PGK GLEWVSG IEGPGDVTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-1 (SEQ ID NO: 224)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FN WQLMGWFRQA PGK GLEWVSG IEGPGDVTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-10 (SEQ ID NO: 225)

EVQLLES GGG LVQP GGS LRL SCAAS GFT FN WQLMGWVRQA PGK GLEWVSG IEGPGDVTTY
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-11 (SEQ ID NO: 226)

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EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-12 (SEQ ID NO: 227)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-13 (SEQ ID NO: 228)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKDRFTI SRDNSKNTLY LLMNSLRAED TAVYYCAKVG KESN----- FDYWGQGTLV TVSS

BMS2h-572-14 (SEQ ID NO: 229)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-15 (SEQ ID NO: 230)

EVRLLES GGG LVQPGGSLRL SCAASGFNFN WQLMGWIRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-16 (SEQ ID NO: 231)

EVQLLES GGG LVRPGGSLRL SCVASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-17 (SEQ ID NO: 232)

EVQLLES GGG LVQTGGSLRL SCAASGFTYN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRADD TAVYYCVKVG KESN----- FDYRGHGTLV TVSS

BMS2h-572-18 (SEQ ID NO: 233)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRKA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-19 (SEQ ID NO: 234)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-2 (SEQ ID NO: 235)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESK----- FDYLGQGTLV TVSS

BMS2h-572-21 (SEQ ID NO: 236)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
AESVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- LDYRGQGTLV TVSS

BMS2h-572-22 (SEQ ID NO: 237)

EVQLFES GGG SVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-23 (SEQ ID NO: 238)

EVQLLES GGG LVQPGGSLRL TCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-24 (SEQ ID NO: 239)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSTNTLY LQMNSLRAED TAVYYCAKVG KESE----- FDYRGQGTLV TVSS

BMS2h-572-3 (SEQ ID NO: 240)

EVRLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI TRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- LDYRGQGTLV TVSS

BMS2h-572-4 (SEQ ID NO: 241)

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EVQLLVSGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-5 (SEQ ID NO: 242)

EVQLLVSGGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- FDYRGQGTLV TVSS

BMS2h-572-6 (SEQ ID NO: 243)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-601 (SEQ ID NO: 244)

EVQLLES GGG LVQPGGSLRL SCAASGFTFK WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-602 (SEQ ID NO: 245)

EVQLLES GGG LVQPGGSLRL SCAASGFTFK WHLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESS----- SDYRGQGTLV TVSS

BMS2h-572-603 (SEQ ID NO: 246)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WHLMAWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV
TVSS

BMS2h-572-604 (SEQ ID NO: 247)

EVQLLES GGG LVQPGGSLRL SCAASGFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-605 (SEQ ID NO: 248)

EVQLLES GGG LVQPGGSLRL SCAASGFTFK WQLMAWARQA PGKGLEWVSG IEGPGDITYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-606 (SEQ ID NO: 249)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WHLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-607 (SEQ ID NO: 250)

EVQLLES GGG LVQPGGSLRL SCAASGFTFK WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-608 (SEQ ID NO: 251)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-609 (SEQ ID NO: 252)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESN----- SDYRGQGTLV TVSS

BMS2h-572-610 (SEQ ID NO: 253)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK----- SDYRGQGTLV TVSS

BMS2h-572-611 (SEQ ID NO: 254)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRRA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK----- SDYRGQGTLV TVSS

BMS2h-572-612 (SEQ ID NO: 255)

EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSN----- SDYRGQGTLV TVSS

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BMS2h-572-613 (SEQ ID NO: 256)
 EVQLLES GGG LAQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK----- SDYRGQGTLV TVSS

5 BMS2h-572-614 (SEQ ID NO: 257)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDAK----- SDYRGQGTLV TVSS

0 BMS2h-572-615 (SEQ ID NO: 258)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDKN----- SDYRGQGTLV TVSS

5 BMS2h-572-616 (SEQ ID NO: 259)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESK----- SDYRGQGTLV TVSS

10 BMS2h-572-617 (SEQ ID NO: 260)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG RDSK----- SDYRGQGTLV TVSS

15 BMS2h-572-618 (SEQ ID NO: 261)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KYSN----- SDYRGQGTLV TVSS

20 BMS2h-572-619 (SEQ ID NO: 262)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSR----- SDYRGQGTLV TVSS

25 BMS2h-572-620 (SEQ ID NO: 263)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDDS----- SDYRGQGTLV TVSS

30 BMS2h-572-621 (SEQ ID NO: 264)
 EVQLLEFGGG LVQPGGSLRF SCAASGFTFN WQLMGWFRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG RDSN----- SDYRGQGTLV TVSS

35 BMS2h-572-622 (SEQ ID NO: 265)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDST----- SDYRGQGTLV TVSS

40 BMS2h-572-623 (SEQ ID NO: 266)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KESS----- SDYRGQGTLV TVSS

45 BMS2h-572-624 (SEQ ID NO: 267)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSA----- SDYRGQGTLV TVSS

50 BMS2h-572-625 (SEQ ID NO: 268)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG NDSY----- SDYRGQGTLV TVSS

55 BMS2h-572-626 (SEQ ID NO: 269)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSS----- SDYRGQGTLV TVSS

60 BMS2h-572-627 (SEQ ID NO: 270)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSA----- SDYRGQGTLV TVSS

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BMS2h-572-630 (SEQ ID NO: 271)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDAK----- SDYRGQGTLV TVSS

5 BMS2h-572-631 (SEQ ID NO: 272)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSR----- SDYRGQGTLV TVSS

0 BMS2h-572-632 (SEQ ID NO: 273)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK----- SDYRGQGTLV TVSS

5 BMS2h-572-633 (SEQ ID NO: 274)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDAK----- SDYRGQGTLV TVSS

10 BMS2h-572-634 (SEQ ID NO: 275)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSR----- SDYRGQGTLV TVSS

15 BMS2h-572-635 (SEQ ID NO: 276)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN WELMGWARQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCVKVG KDSK----- SDYRGQGTLV TVSS

20 BMS2h-572-7 (SEQ ID NO: 277)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN WQLMGWARQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED SAVYYCAKVG KESN----- FDYLGQGTLV TVSS

25 BMS2h-572-8 (SEQ ID NO: 278)
 EVQLLES GGG LVQP GGS LRL SCVAS GFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

30 BMS2h-572-9 (SEQ ID NO: 279)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN WQLMGWVRQA PGKGLEWVSG IEGPGDVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG KESN----- SDYRGQGTLV TVSS

35 BMS2h-573 (SEQ ID NO: 280)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS GWEMGWVRQA PGKGLEWVSS IDESGLNITYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGA PQYQIT---- FDYWGQGTLV TVSS

40 BMS2h-574 (SEQ ID NO: 281)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFP NYGMWVRQA PGKGLEWVSY ISRRGLLITYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTS HYMNNG---- FDYWGQGTLV TVSS

45 BMS2h-575 (SEQ ID NO: 282)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFV DYTMAWVRQA PGKGLEWVSS ISPIGTFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDP YGMEDGLTW- FDYWGQGTLV TVSS

50 BMS2h-576 (SEQ ID NO: 283)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD AYDMQWVRQA PGKGLEWVST ITSEGLSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS DL----- FDYWGQGTLV TVSS

55 BMS2h-577 (SEQ ID NO: 284)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD GYDMGWVRQA PGKGLEWVST ISRGGWFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGT SQSSTGS--- FDYWGQGTLV TVSS

60 BMS2h-578 (SEQ ID NO: 285)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR RYDMLWARQA PGKGLEWVSE ISPTGALITYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG ST----- FDYWGQGTLV TVSS

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BMS2h-579 (SEQ ID NO: 286)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFF PYMSWVRQA PGKGLEWVSS ISGTGGLTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTT QNATL----- FDYWGQGTLV TVSS

5 BMS2h-58 (SEQ ID NO: 287)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE VYTMWVRQA PGKGLEWVST IDESGRDTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VW----- FDYWGQGTLV TVSS

0 BMS2h-580 (SEQ ID NO: 288)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA FYKMGWVRQA PGKGLEWVST ITPKGHTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVF KGKGWTRPSG FDYWGQGTLV
 TVSS

5 BMS2h-581 (SEQ ID NO: 289)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN EYSMMWVRQA PGKGLEWVSS IGRRGWLTYT
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAV LLDSTK---- FDYWGQGTLV TVSS

10 BMS2h-582 (SEQ ID NO: 290)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD EYPMTWVRQA PGKGLEWVST ISARGPFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGR HWLRNGR--- FDYWGQGTLV TVSS

15 BMS2h-583 (SEQ ID NO: 291)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG MQSMQWVRQA PGKGLEWVSS ITDDGTSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RV----- FDYWGQGTLV TVSS

20 BMS2h-584 (SEQ ID NO: 292)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG AADMWVRQA PGKGLEWVSL ITNDGISTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG DR----- FDYWGQGTLV TVSS

25 BMS2h-586 (SEQ ID NO: 293)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN KYRMQWVRQA PGKGLEWVSS IDSSGELTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEEV PMGNQTF--- FDYWGQGTLV TVSS

30 BMS2h-587 (SEQ ID NO: 294)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT DYTMGWVRQA PGKGLEWVSS ITSQGAFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAT GTDSS----- FDYWGQGTLV TVSS

35 BMS2h-588 (SEQ ID NO: 295)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE DYEMSWVRQA PGKGLEWVSC IGPGGKPTYT
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVD GH----- FDYWGQGTLV TVSS

40 BMS2h-589 (SEQ ID NO: 296)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS QYDMGWVRQA PGKGLEWVST ISSRGWLTYT
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP GGRRR----- FDYWGQGTLV TVSS

45 BMS2h-59 (SEQ ID NO: 297)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFL DYAMGWVRQA PGKGLEWVST ISPMGMGTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSS AISFTSDISN FDYWGQGTLV TVSS

50 BMS2h-590 (SEQ ID NO: 298)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYPMSWVRQA PGKGLEWVSS ISWSGFQTYT
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VARMPGTGIA- FDYWGQGTLV TVSS

55 BMS2h-591 (SEQ ID NO: 299)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYEMQWVRQA PGKGLEWVSS IDSAGTFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF GM----- FDYWGQGTLV TVSS

60 BMS2h-592 (SEQ ID NO: 300)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS EYPMKWVRQA PGKGLEWVST IDRQGDRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKTV RRGLPRPSRY FDYWGQGTLV TVSS

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BMS2h-593 (SEQ ID NO: 301)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYDMGWVRQA PGKGLEWVSS ISPMGTFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL SVYSGLD--- FDYWGQGTLV TVSS

BMS2h-594 (SEQ ID NO: 302)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS HYDMGWVRQA PGKGLEWVSD IDYIGKTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAS DEVG VNTSK- FDYWGQGTLV TVSS

BMS2h-595 (SEQ ID NO: 303)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA RYDMGWVRQA PGKGLEWVST ISPTGVLTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGF ED----- FDYWGQGTLV TVSS

BMS2h-596 (SEQ ID NO: 304)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE AYPMSWVRQA PGKGLEWVSL ISHTGHATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGH WP----- FDYRGQGT LI TVSS

BMS2h-597 (SEQ ID NO: 305)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE DEWMSWVRQA PGKGLEWVSD ISPGGWTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGY RPFDE----- FDYWGQGTLV TVSS

BMS2h-598 (SEQ ID NO: 306)
 EVQLLES GGG LVQP GGS LRL SCAAS GVTFD AIEMSWVRQA PGKGLEWVSS ISRHGEYTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEDA WSRH----- FDYWGQGTLV TVSS

BMS2h-599 (SEQ ID NO: 307)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD STDMSWVRQA PGKGLEWVSG ILDN GSNTYY
 ADSVKGRFTI SRDNSKNM LY LQMNSLRAED TAVYYCAKGA RD----- FDYWGQGTLV TVSS

BMS2h-600 (SEQ ID NO: 308)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG RQSMQWVRQA PGKGLEWVSS IDDDGFSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGD PWG----- FDYWGQGTLV TVSS

BMS2h-601 (SEQ ID NO: 309)
 EVQLLES GGG LVQP GGS LRL SCTAS GFTFS DTQMAWVRQA PGKGLEWVSG ID DGGVSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPD RH----- FDYWGQGTLV TVSS

BMS2h-602 (SEQ ID NO: 310)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG STTMGWVRQA PGKGLEWVSV ISDDGGFTYY
 ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKVD GYGV----- FDYWGQGTLV TVSS

BMS2h-603 (SEQ ID NO: 311)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR SGDMNWVRQA PGKGLEWVST ITNDGTSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSD SD----- FDYWGQGTLV TVSS

BMS2h-61 (SEQ ID NO: 312)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA AYAMTWVRQA PGKGLEWVSY ISPNGTATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEYV GMRWNS---- FDYWGQGTLV TVSS

BMS2h-62 (SEQ ID NO: 313)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS SYEMAWVRQA PGKGLEWVSS ITSLGTSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RK----- FDYWGQGTLV TVSS

BMS2h-65 (SEQ ID NO: 314)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFN EYEMTWVRQA PGKGLEWVST ITSEGS GTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPN GK----- FDYWGQGTLV TVSS

BMS2h-66 (SEQ ID NO: 315)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYEMLWVRQA PGKGLEWVST ITSEGHSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG TS----- FDYWGQGTLV TVSS

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5 BMS2h-67 (SEQ ID NO: 316)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYEMSWVRQA PGKGLEWVST IDSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG VK----- FDYWGQGTLV TVSS

0 BMS2h-68 (SEQ ID NO: 317)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFK DYEMTWVRQA PGKGLEWVSS ISSTGQSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG NK----- FDYWGQGTLV TVSS

5 BMS2h-69 (SEQ ID NO: 318)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFL DYGMAWVRQA PGKGLEWVSA ISPLGLSTYY
ADSVKSRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKEV RVGRGVHPPK FDYWGQGTLV TVSS

5 BMS2h-7 (SEQ ID NO: 319)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFN LYEMTWVRQA PGKGLEWVSS ITSDGVSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG VI----- FDYWGQGTLV TVSS

0 BMS2h-70 (SEQ ID NO: 320)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE NYAMSWVRQA PGKGLEWVST IAPLGVPTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKKK VGAWLQSR- FDYWGQGTLV TVSS

5 BMS2h-701 (SEQ ID NO: 321)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFM DYEMHWVRQA PGKGLEWVST IGASGHYTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYL DMLLFG---- FDYWGQGTLV TVSS

0 BMS2h-702 (SEQ ID NO: 322)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFA EYEMMWARQA PGKGLEWVSR IAGNGSRTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIML SH----- FDYWGQGTLV TVSS

5 BMS2h-703 (SEQ ID NO: 323)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFY NYDMSWVRQA PGKGLEWVSG IDSMGLVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGS NASDWV--- FDYWGQGTLV TVSS

5 BMS2h-704 (SEQ ID NO: 324)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFA SYHMTWVRQA PGKGLEWVSS IADTGDRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLR GMARVWG--- FDYWGQGTLV TVSS

40 BMS2h-705 (SEQ ID NO: 325)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFS YYDMMWVRQA PGKGLEWISS ISDRGLQTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFT EIPLDWLEV- FDYWGQGTLV TVSS

45 BMS2h-706 (SEQ ID NO: 326)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFG SYKMLWVRQA PGKGLEWVSS ITNSGTETYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSM YPDLEIVH—FDYWGQGTLV TVSS

50 BMS2h-707 (SEQ ID NO: 327)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE TYRMSWVRQA PGKGLEWVSA IDQEGSATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNS GTRPGLR--- FDYWGQGTLV TVSS

55 BMS2h-708 (SEQ ID NO: 328)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFS SYDMLWVRQA PGKGLEWVSR IDASGYFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQLL KLSLNPN--- FDYWGQGTLV TVSS

60 BMS2h-709 (SEQ ID NO: 329)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFS SYAMSWVRQA PGKGLEWVSS IHNTGLSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGT QHRFV--- FDYWGQGTLV TVSS

60 BMS2h-71 (SEQ ID NO: 330)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE GYPMSWVRQA PGKGLEWVST ISPLGPDYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLL MGEYLSRT- FDYWGQGTLV TVSS

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5 BMS2h-710 (SEQ ID NO: 331)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN TYSMSWVRQA PGKGLEWVSW IDADGWVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQTG HT----- FDYWGQGTLV TVSS

0 BMS2h-711 (SEQ ID NO: 332)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DGEMGWARQA PGKGLEWVSR IVDPGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG DQ----- FDYWGQGTLV TVSS

5 BMS2h-712 (SEQ ID NO: 333)
EVQLLESGGG LVQPGGSLRL SCAASGFTFP EYEMKWVRQA PGKGLEWVST ITPSGGHTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED AAVYYCAIPL SS----- FDYWGRTGLV TVSS

5 BMS2h-713 (SEQ ID NO: 334)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NYVMIWVRQA PGKGLEWVSL INGAGDMTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGG ARSFGVPPN- FDYWGQGTLV TVSS

0 BMS2h-714 (SEQ ID NO: 335)
EVQLLESGGG LVQPGGSLRL SCAASGFTFT DGEMGWARQA PGKGLEWVSR IVDPGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG DQ----- FDYWGQGTLV TVSS

5 BMS2h-715 (SEQ ID NO: 336)
EVQLLESGGG LVQPGGSLRL SCVASGFTFT LYNMSWVRQA PGKGLEWVSV ISSKGDSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQTS SV----- FDYWGQGTLV TVSS

0 BMS2h-716 (SEQ ID NO: 337)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE AYYMSWVRQA PGKGLEWVSG IVNNGLLTYY
ADSVKGRFTI SRDNSKNMLY LQMNSLRAED TAVYYCAKSA VHPSYRAEL- FDYWGQGTLV TVSS

5 BMS2h-717 (SEQ ID NO: 338)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYEMAWVRQA PGKGLEWVSR IEPDGSNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGP DNFTM----- FDYWGQGTLV TVSS

5 BMS2h-718 (SEQ ID NO: 339)
EVQLLESGGG LVQPGGSLRL SCAASGFTFN KYMMGWVRQA PGKGLEWVSS IDSLGHYTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAE FP----- FDYWGQGTLV TVSS

40 BMS2h-719 (SEQ ID NO: 340)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGQGTLV TVSS

45 BMS2h-719-1 (SEQ ID NO: 341)
EVQLLESGGG MVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGQGTQV TVSS

50 BMS2h-719-10 (SEQ ID NO: 342)
EVQLLESGGG MVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGQGTLV TVSS

50 BMS2h-719-11 (SEQ ID NO: 343)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRKA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSENTLY LQMNSLRAED TAVYYCADPF TE----- FDYWGQGTLV TVSS

55 BMS2h-719-12 (SEQ ID NO: 344)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- FDYWGQGTLV TVSS

60 BMS2h-719-13 (SEQ ID NO: 345)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCADPF TE----- LDYWGHGTLV TVSS

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BMS2h-719-14 (SEQ ID NO: 346)
 EVQLLES GGG LVRPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYFCADPF TE----- FDYWGQGTLLV TVSS

BMS2h-719-15 (SEQ ID NO: 347)
 EVQLLES GGG LVQPGGSLRL SCAASGFAFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LHMNSLRAED TAVYYCADPF TE----- IDYWGQGTLLV TVSS

BMS2h-719-16 (SEQ ID NO: 348)
 EVQLLES GGG LVQPGGSLRL SCAASGFPFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYRAQGTLLV TVSS

BMS2h-719-17 (SEQ ID NO: 349)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMSWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- IDYWGQGTQV TVSS

BMS2h-719-18 (SEQ ID NO: 350)
 EVQLLES GGG LVHPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRDED TAVYYCAEPF TE----- FDYGGQGTLLV TVSS

BMS2h-719-19 (SEQ ID NO: 351)
 EVQLLES GGG WVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- FDYWGQGTLLV TVSS

BMS2h-719-2 (SEQ ID NO: 352)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGHGTLV TVSS

BMS2h-719-20 (SEQ ID NO: 353)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- IDYRGQGTLLV TVSS

BMS2h-719-202 (SEQ ID NO: 354)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK KYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGHGTLV TVSS

BMS2h-719-203 (SEQ ID NO: 355)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFN SYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGHGTLV TVSS

BMS2h-719-21 (SEQ ID NO: 356)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- FDYWGQGTLLV TVSS

BMS2h-719-213 (SEQ ID NO: 357)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- MDYWGHGTLV TVSS

BMS2h-719-214 (SEQ ID NO: 358)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- FDYWGHGTLV TVSS

BMS2h-719-215 (SEQ ID NO: 359)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- LDYWGHGTLV TVSS

BMS2h-719-218 (SEQ ID NO: 360)
 EVQLLES GGG LVQPGGSLRL SCAASGFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
 AESVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWGHGTLV TVSS

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5 BMS2h-719-225 (SEQ ID NO: 361)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFN TYEMQWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWG HGTLV TVSS

0 BMS2h-719-226 (SEQ ID NO: 362)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFN KYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWG HGTLV TVSS

5 BMS2h-719-3 (SEQ ID NO: 363)
EVQLSESGGG LVQP GGS LRL SCAAS GFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- FDYWG QGTLV TVSS

5 BMS2h-719-4 (SEQ ID NO: 364)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFK RYEMMWVRQT PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWG QGTLV TVSS

0 BMS2h-719-5 (SEQ ID NO: 365)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LEMNSMRAED TAVYYCAEPF TE----- FDNWG QGTLV TVSS

5 BMS2h-719-6 (SEQ ID NO: 366)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWG QGTQV TVSS

0 BMS2h-719-7 (SEQ ID NO: 367)
EVQLLES GGG LVQP GGS LRL SCAAS GFNFK RYEMTWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPF TE----- FDYWG QGTLV TVSS

5 BMS2h-719-8 (SEQ ID NO: 368)
EVQLLES GGD LVQP GGS LRL SCAAS GFTFK RYEMMWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYRG QGTLV TVSS

5 BMS2h-719-9 (SEQ ID NO: 369)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFK RYEMSWVRQA PGKGLEWVSS ISSDGSFTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPF TE----- FDYWG RGTLV TVSS

40 BMS2h-72 (SEQ ID NO: 370)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFE AYPMSWVRQA PGKGLEWVSS ISPLGLWTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS AGAETHVYRL FDYWG QGTLV TVSS

45 BMS2h-720 (SEQ ID NO: 371)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFG NYEMMWVRQA PGKGLEWVSS IGVLGHTTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLM SLRTFENL—FDYWG QGTLV TVSS

50 BMS2h-722 (SEQ ID NO: 372)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFT KYPMWVRQA PGKGLEWVSG IDANGNRTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGT WRRHFAL--- FDYWG QGTLV TVSS

50 BMS2h-723 (SEQ ID NO: 373)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFD LYDMWVRQA PGKGLEWVSS ISDLGTLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKNG FRVTSNDRR- FDYWG QGTLV TVSS

55 BMS2h-724 (SEQ ID NO: 374)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFT GGDMMWVRQA PGKGLEWVSM IEGGGVTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAELD LRTGQ----- FDYWG QGTLV TVSS

60 BMS2h-725 (SEQ ID NO: 375)
EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- FDYWG QGTLV TVSS

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5 BMS2h-725-1 (SEQ ID NO: 376)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYFCADPS DPTK----- FDYWGQGTLV TVSS

10 BMS2h-725-10 (SEQ ID NO: 377)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK----- FDYWGQGTLV TVSS

15 BMS2h-725-11 (SEQ ID NO: 378)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMSSLRAED TAVYYCADPS DPTK----- FDYWGQGTLV TVSS

20 BMS2h-725-12 (SEQ ID NO: 379)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFP AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDDSKNTLY LQMNSLRVED TAVYYCAEPS DPTM----- FVYWGQGTLV TVSS

25 BMS2h-725-13 (SEQ ID NO: 380)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTM----- FVYWGQGTLV TVSS

30 BMS2h-725-14 (SEQ ID NO: 381)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTM----- FDYWGQGTLV TVSS

35 BMS2h-725-15 (SEQ ID NO: 382)
 EVQLLES GGG MVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSMRAED TAVYYCADPS DPTK----- FDYWGQGTLV TVSS

40 BMS2h-725-16 (SEQ ID NO: 383)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVTL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTM----- FDYWGQGTLV TVSS

45 BMS2h-725-17 (SEQ ID NO: 384)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- LDYWGQGTLV TVSS

50 BMS2h-725-18 (SEQ ID NO: 385)
 EVQLSES GGG LVQP GGS LRL TCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK----- FVYWGQGTLV TVSS

55 BMS2h-725-19 (SEQ ID NO: 386)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK----- FVYWGQGTLV TVSS

60 BMS2h-725-2 (SEQ ID NO: 387)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- FVYWGQGTPV TVSS

65 BMS2h-725-3 (SEQ ID NO: 388)
 VQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSRNMLY LQMKSLRAED TAVYYCADPS DPTK----- FVYWGQGTPV TVSS

70 BMS2h-725-4 (SEQ ID NO: 389)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI FRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK----- FVYWGQGTLV TVSS

75 BMS2h-725-5 (SEQ ID NO: 390)
 EVQLLES GGG LLQP GGS LRL SCAAS GFTFS DYTGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- FDYWGRGTLV TVSS

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BMS2h-725-6 (SEQ ID NO: 391)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- FVYWGQGTLV TVSS

BMS2h-725-7 (SEQ ID NO: 392)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGTWTYY
 ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCADPS DPTK----- FDYWGQGTLV TVSS

BMS2h-725-8 (SEQ ID NO: 393)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGKGLEWVSL IGDRGSWTYY
 ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- FDYWGQGTLV TVSS

BMS2h-725-9 (SEQ ID NO: 394)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMGWVRQA PGMGLEWVSL IGDRGSWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPS DPTK----- FDYWGQGTLV TVSS

BMS2h-726 (SEQ ID NO: 395)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD NYKMYWVRQA PGKGLEWVSS ISEIGNLTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIAL TR----- FDYWGQGTLV TVSS

BMS2h-727 (SEQ ID NO: 396)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA SYRMWVRQA PGKGLEWVSY IDPPGSRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSL NLSFPYIN—FDYWGQGTLV TVSS

BMS2h-728 (SEQ ID NO: 397)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE RYEMLWVRQA PGKGLEWVSR ISHSGRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAQLD GP----- FDYWGQGTLV TVSS

BMS2h-729 (SEQ ID NO: 398)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK RYYMDWVRQA PGKGLEWVSR INHNGSVTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKMP QGTSDWYY—FDYWGQGTLV TVSS

BMS2h-73 (SEQ ID NO: 399)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS KYDMSWVRQA PGKGLEWVST ILEDGLTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPG RL----- FDYWGQGTLV TVSS

BMS2h-74 (SEQ ID NO: 400)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS DYPMTWVRQA PGKGLEWVST ILSPGTETYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAE KD----- FDYWGQGTLV TVSS

BMS2h-741 (SEQ ID NO: 401)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE GGEMGWVRQA PGKGLEWVSM IPMDGSATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG EV----- FDYWGQGTLV TVSS

BMS2h-742 (SEQ ID NO: 402)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR EYHMKWARQA PGKGLEWVSG ISRDGMNTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIQL AL----- FDYWGQGTLV TVSS

BMS2h-743 (SEQ ID NO: 403)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR DYEMLWARQA PGKGLEWVSG ILPSGGATYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAG SGNGPIL--- FDYWGQGTLV TVSS

BMS2h-744 (SEQ ID NO: 404)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK EHDMFWVRQA PGKGLEWVSG IGAEGWWTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPT MSNGSQSR—FDYWGQGTLV TVSS

BMS2h-745 (SEQ ID NO: 405)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD NTEMAWVRQA PGKGLEWVSG IIEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

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5 BMS2h-745-1 (SEQ ID NO: 406)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

10 BMS2h-745-10 (SEQ ID NO: 407)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

15 BMS2h-745-11 (SEQ ID NO: 408)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNFKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

20 BMS2h-745-12 (SEQ ID NO: 409)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSMNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

25 BMS2h-745-13 (SEQ ID NO: 410)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG IIEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

30 BMS2h-745-14 (SEQ ID NO: 411)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

35 BMS2h-745-15 (SEQ ID NO: 412)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSKNALY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGGLTLV TVSS

40 BMS2h-745-16 (SEQ ID NO: 413)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

45 BMS2h-745-17 (SEQ ID NO: 414)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG IIEDGNRTYY
 ADSVKGRFTI SRDNSKNRLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

50 BMS2h-745-18 (SEQ ID NO: 415)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYHCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

55 BMS2h-745-19 (SEQ ID NO: 416)
 EVQLLESGGG LVQPEGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG IIEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

60 BMS2h-745-2 (SEQ ID NO: 417)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ISEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED SAVYYCAKIR NLHWDVGRQ- FVYWGQGTLV TVSS

65 BMS2h-745-3 (SEQ ID NO: 418)
 EVQLLESGGG LVEPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMSSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

70 BMS2h-745-4 (SEQ ID NO: 419)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ISEDGNRTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYHCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

75 BMS2h-745-5 (SEQ ID NO: 420)
 EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
 ADSVKGRFII SRDNSKNTLN LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

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5 BMS2h-745-6 (SEQ ID NO: 421)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGRGLEWVSG VTEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLLV TVSS

10 BMS2h-745-7 (SEQ ID NO: 422)
EVQLLESGGG LVQPGGSLRL SCEASGFTFD NTEMAWIRQA PGKGLEWVSG IIEDGNRTYY
ADSVKGRFTI SRDNTKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLLV TVSS

15 BMS2h-745-8 (SEQ ID NO: 423)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD NTEMAWIRQA PGKGLEWVSG ITEDGDRTYY
ADSVKGRFTI SRDNSKSSLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLLV TVSS

20 BMS2h-745-9 (SEQ ID NO: 424)
EVQLLESGGG SVQPGGSLRL SCAASGFTFD NTEMAWVRQA PGKGLEWVSG ITEDGNRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FVYWGQGTLLV TVSS

25 BMS2h-746 (SEQ ID NO: 425)
EVQLLESGGG LVQPGGSLRL SCAASGFTFG SAEMGWVRQA PGKGLEWVSG ISRPGQVTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLLV TVSS

30 BMS2h-747 (SEQ ID NO: 426)
EVQLLESGGG LVQPGGSLRL SCAASGFTFD DGTMGWARQA PGKGLEWVSL ILPSGSRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHS LTNRP----- FDYWGQGTLLV TVSS

35 BMS2h-748 (SEQ ID NO: 427)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS KYDMRWARQA PGKGLEWVSD IDAVGTRTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIPG GT----- FDYWGQGTLLV TVSS

40 BMS2h-749 (SEQ ID NO: 428)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE MYGMMWARQA PGKGLEWVSS IEGAGHATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAIVL GM----- FDYWGQGTLLV TVSS

45 BMS2h-75 (SEQ ID NO: 429)
EVQLLESGGG LVQPGGSLRL SCAASGFTFL QYPMGWVRQA PGKGLEWVST ISPVGLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLF EGSRIQRDVG FDYWGQGTLLV TVSS

50 BMS2h-750 (SEQ ID NO: 430)
EVQLLESGGG LVQPGGSLRL SCAASGFTFE KYQMGWARQA PGKGLEWVSS IRGSGLVTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVH TTLHTEVIG- FDYWGQGTLLV TVSS

55 BMS2h-751 (SEQ ID NO: 431)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS QYTMWARQA PGKGLEWVSE ISHSGSNTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAISG LH----- FDYWGQGTLLV TVSS

60 BMS2h-752 (SEQ ID NO: 432)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYAMAWVRQA PGKGLEWVSR IGVEGGDTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLL RLYRLG---- FDYWGQGTLLV TVSS

65 BMS2h-753 (SEQ ID NO: 433)
EVQLLESGGG LVQPGGSLRL SCAASGFTFA KYDMTWVRQA PGKGLEWVSK INSDGGLTTY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGL HGRGFVI--- FDYWGQGTLLV TVSS

70 BMS2h-754 (SEQ ID NO: 434)
EVQLLESGGG LVQPGGSLRL SCAASGFTFS RYDMVWVRQA PGKGLEWVSR INSMGLATYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDY SVAPHGYPLG FDYWGQGTLLV TVSS

75 BMS2h-755 (SEQ ID NO: 435)
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYSMMWVRQA PGKGLEWVST ITDNGTSTYY
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHM SLATYLQF—FDYWGQGTLLV TVSS

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5 BMS2h-756 (SEQ ID NO: 436)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFM EYDMLWVRQA PGKGLEWVSR ISSDGLWTTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGV SALAPFDIG- FDYWGQGTLV TVSS

10 BMS2h-757 (SEQ ID NO: 437)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK EYNMAWVRQA PGKGLEWVSS INFAGRTTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLS LPLDIFS--- FDYWGQGTLV TVSS

15 BMS2h-758 (SEQ ID NO: 438)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY----- FDYWGQGTLV TVSS

20 BMS2h-758-1 (SEQ ID NO: 439)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNMLY LRMNSLRAED TAVYYCAETS GY----- YEYWGQGTLV TVSS

25 BMS2h-758-2 (SEQ ID NO: 440)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY----- FEYWGQGTLV TVSS

30 BMS2h-758-3 (SEQ ID NO: 441)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS SY----- FEYWGQGTLV TVSS

35 BMS2h-758-4 (SEQ ID NO: 442)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCAETS GY----- YEYWGHGTLV TVSS

40 BMS2h-758-5 (SEQ ID NO: 443)
 EVQLLES GGG LVQP GGS LRL SCAAS GFAFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY----- FEYWGQGTLV TVSS

45 BMS2h-758-6 (SEQ ID NO: 444)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGMNWVRQA PGKGLEWVSH ISSNGRFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAETS GY----- FEYWGQGTLV TVSS

50 BMS2h-759 (SEQ ID NO: 445)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR EYVMGWVRQA PGKGLEWVST INGLGNVTYY
 ADSVKGRFTI SRDNTKNTLY LQMNSLRAEE TAVYYCAIQL PN----- FDYWGQGTLV TVSS

55 BMS2h-760 (SEQ ID NO: 446)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG NDGMWWVRQA PGKGLEWVSF INVDGRETTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEWS PGRVQ----- FDYWGQGTLV TVSS

60 BMS2h-761 (SEQ ID NO: 447)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG GWDMAWVRQA PGKGLEWVSS IAHEGGETYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYV PGSPL----- FDYWGQRTLTV TVSS

65 BMS2h-762 (SEQ ID NO: 448)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD QGWMYWVRQA PGKGLEWVSG IGSNGPRTSY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSG EY----- FDYWGQGTLV TVSS

70 BMS2h-763 (SEQ ID NO: 449)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR QSDMWWVRQA PGKGLEWVSV IGNNGEFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDN WLL----- FDYWGQGTLV TVSS

75 BMS2h-764 (SEQ ID NO: 450)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD LSTMYWVRQA PGKGLEWVST IGGDGSHTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEGT QY----- FDYWGQGTLV TVSS

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BMS2h-765 (SEQ ID NO: 451)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS AYTMEWVRQA PGKGLEWVSS IGV TGYDTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGG QG----- FDYWGQGTLV TVSS

BMS2h-766 (SEQ ID NO: 452)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG DYGM SWVRQA PGKGLEWVSY IDPLGRLTTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAEDL SSLQYGVSPN FDYWGQGTLV TVSS

BMS2h-767 (SEQ ID NO: 453)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFF HYSMSWVRQA PGKGLEWVSS IGPVGRETTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKMI QSPLFKD--- FDYWGQGTLV TVSS

BMS2h-768 (SEQ ID NO: 454)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE WYDMYWVRQA PGKGLEWVSR IDSGGNQTTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAEAS LWKWRL---- FDYWGQGTLV TVSS

BMS2h-77 (SEQ ID NO: 455)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE EYGMWVRQA PGKGLEWVST ISPLGISTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKHA TSQESLRS—FDYWGQGTLV TVSS

BMS2h-770 (SEQ ID NO: 456)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFS KYEMMWVRQA PGKGLEWVSA ISGSGGSTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGP LPDAFWTRG- FDYWGQGTLV TVSS

BMS2h-771 (SEQ ID NO: 457)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG TYSMWVRQA PGKGLEWVST IDRHGLATYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKTP GSSWQTV--- FGYWGQGTLV TVSS

BMS2h-772 (SEQ ID NO: 458)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE SYPMGWVRQA PGKGLEWVSS IDHHGHSTYY
 ADSAKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKLL RVSMIFG--- FDYWGQGTLV TVSS

BMS2h-773 (SEQ ID NO: 459)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFV QYGM SWVRQA PGKGLEWVSW ISSSGTYTTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAETS RM----- FDYWGQGTLV TVSS

BMS2h-774 (SEQ ID NO: 460)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR EYDMGWVRQA PGKGLEWVSL ISPPGRTTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKVV ILGYTNR--- FDYWGQGTLV TVSS

BMS2h-775 (SEQ ID NO: 461)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFP NYGMLWVRQA PGKGLEWVSS INSSGMETYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKFF RLNDHNSVFG FDYWGQGTLV TVSS

BMS2h-776 (SEQ ID NO: 462)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFK DYKMMWIRQA PGKGLEWVSS IVGSGSMTYY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKGP GY----- FDYWGQGTLV TVSS

BMS2h-777 (SEQ ID NO: 463)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFH NYAMGWVRRQA PGKGLEWVSS IDEHGTITY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKDS LDRVWI---- FDYWGQGTLV TVSS

BMS2h-778 (SEQ ID NO: 464)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA DYPMTWVRQA PGKGLEWVSS IYSAGSPTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKLY HREPILFG—FDYWGQGTLV TVSS

BMS2h-78 (SEQ ID NO: 465)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE RYQMAWVRQA PGKGLEWVST ISSDGGGTY
 ADSVKGRFTI SRD NSKNTLY LQMNS LRAED TAVYYCAKPG HR----- FDYWGQGTLV TVSS

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5 BMS2h-780 (SEQ ID NO: 466)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG SYTMMWVRQA PGKGLEWVSE IDRTGERTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEPG FASLP----- FDYWGQGTLV TVSS

10 BMS2h-781 (SEQ ID NO: 467)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFT DYTMYWVRQA PGKGLEWVSK ISPSGRSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDP FG----- FDYWGQGTLV TVSS

15 BMS2h-782 (SEQ ID NO: 468)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD DAEMFWVRQA PGKGLEWVSS IDARGLTTY
 ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAEAT SAMYP----- FDYWGQGTLV TVSS

20 BMS2h-783 (SEQ ID NO: 469)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR DYDMGWVRQA PGKGLEWVST ISPLGHFTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKSG FHEYTEG---- FDYWGQGTLV TVSS

25 BMS2h-784 (SEQ ID NO: 470)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD RAGMGWVRQA PGKGLEWVSL IGRGGDITY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIR NLHWDVGRQ- FDYWGQGTLV TVSS

30 BMS2h-80 (SEQ ID NO: 471)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFG RYQMAWVRQA PGKGLEWVSS ISSDGGGTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPS RR----- FDYWGQGTLV TVSS

35 BMS2h-81 (SEQ ID NO: 472)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE LYPMAWVRQA PGKGLEWVSS ISPVGFLTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKGH EGSYTPRSA- FDYWGQGTLV TVSS

40 BMS2h-82 (SEQ ID NO: 473)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFV AYPMAWVRQA PGKGLEWVST IAPLGGNTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKRP EGLQIDSQN- FDYWGQGTLV TVSS

45 BMS2h-83 (SEQ ID NO: 474)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFA LYQMAWVRQA PGKGLEWVSS IDSSGSDTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPE RD----- FDYWGQGTLV TVSS

50 BMS2h-84 (SEQ ID NO: 475)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR QYQMAWARQA PGKGLEWVST IASDGVSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKVG RD----- FDYWGQGTLV TVSS

55 BMS2h-85 (SEQ ID NO: 476)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE QYDMRWVRQA PGKGLEWVSW IDEAGHETYY
 ADSVKGRFTI SRDNSRNTLY LQMNSLRAED TAVYYCAKGM DG----- FDYWGQGTLV TVSS

60 BMS2h-92 (SEQ ID NO: 477)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFV DYPMGWVRQA PGKGLEWVST ISTGGFSTYY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKAR YYYLSQIKN- FDYWGQGTLV TVSS

65 BMS2h-93 (SEQ ID NO: 478)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD IYGMTWVRQA PGKGLEWVSS ISPLGLVTTY
 ADPVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLG EHGDVP---- FDYWGQGTLV TVSS

70 BMS2h-94 (SEQ ID NO: 479)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE LYPMSWVRQA PGKGLEWVST ISPTGLLTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKFK RSGKTDDTN- FDYWGQGTLV TVSS

75 BMS2h-95 (SEQ ID NO: 480)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFR EYDMLWVRQA PGKGLEWVST IVGDGNGTY
 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKQD RQ----- FDYWGQGTLV TVSS

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BMS2h-97 (SEQ ID NO: 481)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE EYGMS WVRQA PGKGLEWVST ISPIGV TTTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKNA YDRKSN---- FDYWGQGTLV TVSS

5 BMS2h-98 (SEQ ID NO: 482)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFD RYVMW WVRQA PGKDLEWVSG ITPSGRR TTY
 ADSVKGRFTI SRDNS KDTLY LQMNS LRAED TAVYYCAKVL GRHFDPLLP FDYWGQGTLV TVSS

0 BMS2h-99 (SEQ ID NO: 483)
 EVQLLES GGG LVQP GGS LRL SCAAS GFTFE DYAMS WVRQA PGKGLEWVST ITPGGFW TTY
 ADSVKGRFTI SRDNS KNTLY LQMNS LRAED TAVYYCAKTS SGELQLVED-FDYWGQGTLV TVSS

TABLE 2

Human Anti-CD40L VH Domain Encoding Nucleotide Sequences

5 BMS2h-10 (SEQ ID NO: 484)
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTAGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATTGCTTATGATATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTGATGAGTGGGGTCTGCAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 10 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGACG
 CCTGAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

15 BMS2h-11 (SEQ ID NO: 485)
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGAGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGATGGTGAGGGTTCTGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGGG
 20 AGGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

0 BMS2h-111 (SEQ ID NO: 486)
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGTTATCCTATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCATGGTTCTGGTAGTGCTACATACTAC
 5 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCCG
 TATACTAGTCGGCATAATAGTCTTGGGCATTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

40 BMS2h-112 (SEQ ID NO: 487)
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATGGATTATCCTATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGCCTGTTGGTATGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 45 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATGGG
 GGGACTAGTGGTAGGCATAATACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

50 BMS2h-113 (SEQ ID NO: 488)
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACTGAGTATCCTATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTTCTCCTCTTGGTTTTACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGACT
 55 GGTGGGAGTGGTATTTTGAATTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

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BMS2h-114 (SEQ ID NO: 489)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTAGGGTTAGCAATTACGATTTGACCTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTATCAACCATTAGTGCCACAAACGGTAGCACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTATTGCGCGCAGTGACG
 TGGTGGTTGTTGCGTCATAACGACAACCTTGGGGTTTTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-115 (SEQ ID NO: 490)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTAGCATTAGCTATAAGAATATGGCCTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTATCAGCCATTAAGGCGGCAAACGGTAGCACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTATTGCGCGACAGGGAGT
 CAGAAGAAGCGGACCTACACGTTTCGACTTTTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-12 (SEQ ID NO: 491)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGGTTGTATGAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGATATTTTGGGTTGAGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCTG
 TCGTGGCAGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-120 (SEQ ID NO: 492)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGGTCTTATACGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTAATCCTATGGGTTATCAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACATGGG
 GTGGGGAAGGGTACTAAGCCGCATAATTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-121 (SEQ ID NO: 493)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGCTGTATAGGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAGTGGTAGTGGTTTTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTCTG
 CATGATAAGACTCAGCATCATCAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-123 (SEQ ID NO: 494)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATTGAGTATCCTATGCGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTCTCCGTCTGGTGTGTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAT
 GAGTCTAGTACTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-124 (SEQ ID NO: 495)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGCGGTATGATATGGATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGGAGTTGCGGTTATCCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAAGGATG
 CCTGGTTATTTTCTGGGTTTGCTCGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

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BMS2h-125 (SEQ ID NO: 496)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTGGCGGTATGCTATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAATGATGAGGGTCGGGAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGCGG
 GTGTCTAGTTCTGTGAATGCTCCGTATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-126 (SEQ ID NO: 497)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCGAATTATAGTATGAGTTGGGTCCGCCAGGCC
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATCGTCTTGGTACGCATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAATACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTGCTG
 GCTGATCTTATTGCTGGGCATGCGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-127 (SEQ ID NO: 498)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCCGTCGTATGATATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTTGAGGTCTGTTCTATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 TTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGTT
 GATGCGCATGTTTATTATATGGAGCCTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-128 (SEQ ID NO: 499)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGAGGTATCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTTCTGATGGTGGGGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 ACTGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-129 (SEQ ID NO: 500)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACATTTCCGAAGTATGAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGGTGATGGTAAGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGAT
 CAGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-13 (SEQ ID NO: 501)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCTTATTATTCGATGTATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTGCGCTTTTGTTGGGGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGGACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGG
 GAGACGAGTGGTCCGATTTCTGAGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-130 (SEQ ID NO: 502)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTACAGCCTCCGGATTACCTTTGCGGGTTATCAGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTAATGAGGGTGTCTTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 AAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-131 (SEQ ID NO: 503)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGTATGAGATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTACGTCGGATGGTCTGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 ATTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-132 (SEQ ID NO: 504)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGATATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGTTGATGATGGTCTTATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
 GTTGCTTTTGACTACTGGGGTCAGGGGACCCTGGTCACCGTCTCGAAC

BMS2h-133 (SEQ ID NO: 505)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATTGGTTATGCTATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTCCTTTGGGTGCGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGCCT
 GCTGGTACGAGTAGTCATAGTGTGGATTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-134 (SEQ ID NO: 506)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCGGATTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTGATGGTGTCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTCG
 GTTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-135 (SEQ ID NO: 507)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTAGGTATGTTATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGAGGCTGATGGTCGTACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCTT
 ACGGATCAGCATGTTATTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-136 (SEQ ID NO: 508)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATGGTTATCGTATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCTCCGGATGGTAATTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGG
 GGGATGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-137 (SEQ ID NO: 509)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTTCGTATCCGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTCCTATTGGTTTTACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAATGAAG
 TCGCCTTATAAGCCGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-138 (SEQ ID NO: 510)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTTGGCTTATTGGATGGTTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTCCGTCCGGTACGCATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGTGAGGACACCGCGGTATATTACTGTGCGAAATATACT
 GAGCCGGGGTTGGGTTCTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-139 (SEQ ID NO: 511)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGAATTATGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGTGATTTCTGAGGTGGGTTCTCTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCAT
 GATAGTTCGATTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-14 (SEQ ID NO: 512)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTGGTCTTATGATATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTATGGCTTCGGGTGATGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGGAT
 CGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-15 (SEQ ID NO: 513)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGTTATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTTCTCCTATTGGTCTGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATTTCT
 TTGATTATTCTTCTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-16 (SEQ ID NO: 514)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATGGAGTATGCGATGATTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAATTATTTCTCCGCTTGTTTGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAG
 GATTCGTCTGATAGTCAGTATACGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-17 (SEQ ID NO: 515)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
 TGTGCAGCCTCCGGATTCACCTTTGAGGATTATGGGATGGGGTGGGCCCGCCAGGCTCCAGGG
 AAGGGTCTAGAGTGGGTCTCAAGTATTGGTCCTCTGGGTCTTTGGACATACTACGCAGACTCCG
 CGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAG
 CCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCGCTTGAGGGTTTGATTACG
 AATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-176 (SEQ ID NO: 516)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATGCGTATGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAATTATTGATTGGGATGGTAATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGG
 GATAATGTTGGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-177 (SEQ ID NO: 517)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTAATTATTATATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGATGAGTGGGGTTTTGCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATTGG
 GAGTTTACGTCTGATACGTGCGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-178 (SEQ ID NO: 518)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGGATTTTGATATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGATCAGGGTTCTCTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
 CAGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-179 (SEQ ID NO: 519)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTGCTTATGATATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTAGTCCTCAGGGTCAGCGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
 GGGCAGTCGCGGATTCTATGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-18 (SEQ ID NO: 520)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCTGAGTATGATATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATATATTAGTTCTGATGGTTATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGCAT
 GGGAGTCCGCGGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-180 (SEQ ID NO: 521)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTACGGATTATGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTAGTTTGGGTGAGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
 CGTATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-181 (SEQ ID NO: 522)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCTTTTTATCCTATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGATGCTACGGGTACGAGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGTAAT
 TATGGGAGTTCGTATACTATGGGGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-182 (SEQ ID NO: 523)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATGAGTATCCGATGTATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTCCTTCTGGTCCGAATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCG
 TATTTTGATGTTATTCCTAGTTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

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BMS2h-183 (SEQ ID NO: 524)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCGGATTACGGTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTCGTCGGGTTTGGCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACGGGCT
 AATTCTCGTAGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-184 (SEQ ID NO: 525)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCTGATTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTCATGGTGGGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGAT
 AAGGATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-185 (SEQ ID NO: 526)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCGCATTATCCGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTAGGCTGGGTAATCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTGCT
 ACGCCTGTGCCGATTAAGGGTTTGTGTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-186 (SEQ ID NO: 527)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGACTCACCTTTGGGAGGTATGAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATTTCGGATGGTTGGGTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACCGGAT
 TCGTTGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-187 (SEQ ID NO: 528)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCTAGTTATTCTATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATCGGGGTGGTACTCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTGG
 AGGAGGGGGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-188 (SEQ ID NO: 529)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTACGCGTTATAGGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGGGATTTTCGAGGGATGGTTATCGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTATG
 ACTGCGTCGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-189 (SEQ ID NO: 530)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCAGATGTATCCGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTGAGCCGGCTGGTGATCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAG
 GAGCAGCCTTGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-19 (SEQ ID NO: 531)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCCCCTTTCCGCAGTATCAGATGGCGTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTACTTCTGATGGTCTTGATACATATTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGAG
CCTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-190 (SEQ ID NO: 532)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAGTATGTATGATATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTTGTCTGATGGTACGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGG
GCTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-191 (SEQ ID NO: 533)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAAGTTGTATCCGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGCGGGGGTTCATGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATTGG
TGGGATTATCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-192 (SEQ ID NO: 534)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGCGGTATCCGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATCGTTCGGGTATGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGCAT
CAGGCGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-193 (SEQ ID NO: 535)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTACGGGGTATGCTATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGCGAATGGTATTCGGACATACTAC
GCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGGG
GTTTGGAGGTGGGGGACTGGGCATAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-194 (SEQ ID NO: 536)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAAGCAGTATGATATGCGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTTCGAGAATGGTACTAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGAGG
ACTGGTAGGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-195 (SEQ ID NO: 537)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGGGACTTATGATATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATTGGCAGGGTGATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGG
TTTGGTCATTATGTTGATGGTCTTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-196 (SEQ ID NO: 538)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAGTGGGTATGAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTGATATGGGTGATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

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CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGG
ACTGCGTTTGACTACTGGGGTCCGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-197 (SEQ ID NO: 539)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGCGAAGTATAAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCGAAGGGTCATTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGGCCG
ATGACTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-198 (SEQ ID NO: 540)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGAGCGGTATAATATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGGCCGCGGGGTGGGAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCGG
CGGGAGGGGTATACTGGTTCTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-199 (SEQ ID NO: 541)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGAGAGGTATGGTATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTGGCCGAGGGGTGAGAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAAT
AGTCGGTATGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-2 (SEQ ID NO: 542)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCTGATTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTTCGGATGGTATTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGTGGG
AGGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-20 (SEQ ID NO: 543)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTTCGGGTTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTTCGGAGGGTCTTACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGGGG
CGTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-200 (SEQ ID NO: 544)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTACTAATTATAGTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCGTCCTAATGGTACTAAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACGGTCG
TCTGCGCATCTTCAGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-201 (SEQ ID NO: 545)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGGTAATTATTCGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTCGTCATGGTGGGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGGG
AGTACTTATCCTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-202 (SEQ ID NO: 546)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTACAGCCTCCGGATTACCTTTTCGCATTATGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGAGCCTTTTGGTGGTGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTGTAT
 CCTCAGGGTTCTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-203 (SEQ ID NO: 547)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTAATTATACTATGGGGTGGGTCCGTCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCCGGCCTGATGGTAAGATTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGTTTAT
 TCTTCGTGTGCGATGTGTACTCCGCTTTTGTGTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-204 (SEQ ID NO: 548)

GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAAGCGGTATTTCGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTGGGCCGAGGGGTTTTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGGT
 CGTGGTCAGCGTGATACTAGTCAGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-205 (SEQ ID NO: 549)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCTTCTTATCAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACTTCGGGTGGTCTTAGTACGTACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 AGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-206 (SEQ ID NO: 550)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGTGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCTTCTTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTCTTCTGATGGTCTGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 GTGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-207 (SEQ ID NO: 551)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCTGGATTACCTTTGATAAGTATTTGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTGAGCCTCTGGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGCT
 TCGGGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-208 (SEQ ID NO: 552)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGGTTACCTTTACTGAGTATGAGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAATGTGGGTAGTAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGG
 AAGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-209 (SEQ ID NO: 553)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

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TCCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTAGGCAGGGTTTTGCTACATACTAC
 GCAGACTCCGTGAAAGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCTG
 GAGCGGGATGATTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-21 (SEQ ID NO: 554)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCGAATTATGAGATGGGGTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTTCTGAGTGGGGTATTCTACATACTAC
 GCAGACTCCGCGAAGGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAACTTTGTG
 GGTGGGACTCAGTATGAGTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-22 (SEQ ID NO: 555)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTATAATTATGAGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTTCGGGTGGTTCTTCTACATACTAC
 GCAGACTCCGTGAAAGGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 GTTAAGTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-23 (SEQ ID NO: 556)

GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGCTGTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACGGGTGATGGTATTTGACATACTAC
 GCAGACTCCGTGAAAGGGCCGGTTACCATTCTCCGCGACAATTCCAGGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGG
 AGGAAGTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-24 (SEQ ID NO: 557)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTAGTGAGGGTGGTTGACATACTAC
 GCAGACTCCGTGAAAGGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACACTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 AAGAATTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-24-1 (SEQ ID NO: 558)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGACTAGAGTGGGTCTCAAGTATTACTAGTGAGGGTGGTTGACATACTAC
 GCAGACTCCGTGAAAGGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACAGTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 AAGAATTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-25 (SEQ ID NO: 559)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGTGCGAGGGTACTAGTACATACTAC
 GCAGACTCCGTGAAAGGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
 CGTTCTTTTGA TACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-26 (SEQ ID NO: 560)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCTAGTTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTACGTGCGATGGTGGTACTACATACTAC
 GCAGACTCCGTGAAAGGGCCGGTTACCATTCTCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT

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AAGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-27 (SEQ ID NO: 561)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAATTTGTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTGATGGTGTCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
 TCTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-28 (SEQ ID NO: 562)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGCATTATGATATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTGATAATGGTAATGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 CGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-29 (SEQ ID NO: 563)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGTCGTTATCAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTGATGGTGGGGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGG
 CGGGCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-30 (SEQ ID NO: 564)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCGAGGTATCAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTTCTGATGATGGTGATTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTGGAT
 AAGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-300 (SEQ ID NO: 565)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATAATGATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATACGACGGGTGGGCAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
 AAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-301 (SEQ ID NO: 566)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGGAGAGTGAGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTCTTGATGAGGGTTCTGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
 AAGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-302 (SEQ ID NO: 567)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGGAGGAGGAGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACTGATGATGGTGATGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTAAT
 GCGGGTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-303 (SEQ ID NO: 568)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

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TCCTGTGCAGCCTCCGGATTCACCTTTGAGGTGTATGATATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGTTAATGATGGTTCTTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
 AAGGATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-304 (SEQ ID NO: 569)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGTAATACGGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGGATGATGGTTCTAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
 CAGGCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-31 (SEQ ID NO: 570)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCCGATGATGGTTCTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
 CTTTATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-32 (SEQ ID NO: 571)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGTGTATCAGATGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTGTGCCTGGGGGTGATTTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGG
 CCGGAGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-4 (SEQ ID NO: 572)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGAGTGATGGTACTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTAAT
 CCGCCGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-40 (SEQ ID NO: 573)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGGCGTATGATATGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGGGAGGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCGT
 CCGTATGCTATTTTTACTTTTGATCGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-400 (SEQ ID NO: 574)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGCAGTATCCGATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTACTAATGGTGTGAGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGACG
 GATATTATTTCTGCTTCGGAGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

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BMS2h-401 (SEQ ID NO: 575)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTTTAATTATGATATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTTTT
 GTGTGGTCCGGCTGATATTGATTTTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-402 (SEQ ID NO: 576)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGTGGTATGATATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACATATTGCGAGTTGGGTGGTAAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGACG
 GTGAAGGATGGGGGTATCTGATGGATTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-403 (SEQ ID NO: 577)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTGAGTATGCTATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTGGGCGGGATGGTGCGGTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAAG
 GCGGCGAAGGAGCGGGGTTCTTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-404 (SEQ ID NO: 578)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCAAGGCTTATCAGATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTTGAGTGGGTCTCAACTATTAGTCCTAATGGTCTTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTTG
 AGTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-407 (SEQ ID NO: 579)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTATGTATTTCGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTTCGCCTCGTGGTGTGAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATAAT
 TGGAATGGTGTGGATCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-408 (SEQ ID NO: 580)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCTACGTATATGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATACGAATGGTTCGTGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAT
 AGTAATATGTCGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-409 (SEQ ID NO: 581)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTTATTTCGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGCGTCGGGTACTCTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATGGT
 AATAGGTCTGAGGTTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-41 (SEQ ID NO: 582)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTTTGTAGTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCGAATGATGGTTCGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
 CGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-410 (SEQ ID NO: 583)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTTCAGGATTATTTGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAATCAGGATGGTACTGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAAGTTCT
 CCGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-411 (SEQ ID NO: 584)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTGATAATTATGCGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTCGGGATGGTCATGTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTTCT
 TCTAAGGGGGGGACGTTTGCTAGTTCTTTTACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-412 (SEQ ID NO: 585)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTAGTGCTGTTCCGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACGGATGATGGTCTTCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCAT
 ATTTATGGGGATTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-413 (SEQ ID NO: 586)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTGTAGCTTTATAGGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGTGATGGTGATACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACATTGG
 TTGGGTACTACGTTGTCTTTGAGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-414 (SEQ ID NO: 587)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTATCGTTATACGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGCGCTAGGGGTAATATTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGGT
 GTGGCGGGGGCGGAGTCGCCTGAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-415 (SEQ ID NO: 588)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGTTTGGTGCAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTTTGGGTTATTATATGAGTTGGATCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGGCCGATTGGTGGTGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCAG
 AATATTTATGGTCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-416 (SEQ ID NO: 589)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

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TCCTGTGCAGCCTCCGGATTCACCTTTGAGCAGTATGATATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAGTCGTGATGGTGGGCGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGAGTAT
 CCTTATTTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-417 (SEQ ID NO: 590)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCCGCAGTATAGTATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTTGAAGTGGGTCTCAACTATTTCCGCTCTGGGTTCTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATGAGT
 AAGTTGTTGCTGTGAGGGAGTTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-418 (SEQ ID NO: 591)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTATGTATTGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCCGCTCTGGTGTGAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATAAT
 TGGAATGGTGTGGATCTGTTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-419 (SEQ ID NO: 592)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACGCGTCATGGTATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGCCTACTGGTAATACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATGCT
 CATGATGAGGGGTATTTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-42 (SEQ ID NO: 593)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTCCGTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGTTGGTGTGGTCTGGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
 CGGGTTTTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-420 (SEQ ID NO: 594)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTAGTACGCCTATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAGGGATACGGGTCTGGCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAGTGTTTCG
 TTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-421 (SEQ ID NO: 595)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTATGATGAGGATATGCATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTAGTGGGACGGGTCTACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTATG
 AATGATCAGGGGTTTGACTIONTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-422 (SEQ ID NO: 596)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATGGATGAGGATATGTTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATTCGCTGGGTACTCATACATACTAC
 GCAGACTCCGTGAAGGGCCGATTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT

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CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATCGTTT
ATGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-423 (SEQ ID NO: 597)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGTAATTATCAGATGCATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGCGACTGGTCGGGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAGATCTACT
AGGTCAATTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-424 (SEQ ID NO: 598)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTACGAATGCGGATATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGGTAGTGGTGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTAT
TTGACTTCGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-425 (SEQ ID NO: 599)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAGGGATTATTCTATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGTGCGGTCTTACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGTCT
CAGGCGGTTACTCGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-426 (SEQ ID NO: 600)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCTGATGAGGGTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTAATCAGCAGGGTTCGGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGATT
GGGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-427 (SEQ ID NO: 601)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTACTGATCAGCCGATGGTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGGGCGCGTGGTGGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTTT
GATATTATTGCTTGGGATCCTTTTAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-428 (SEQ ID NO: 602)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAATCAGTATCCTATGATGTGGGTTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCTTCTGTTTTTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGAAT
CCTTTTATTACTACGTTTGACTACTGGGGTCAGGGAACCCTGGTGACCGTCTCGAGC

BMS2h-429 (SEQ ID NO: 603)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGAT
TATTCGCTTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-43 (SEQ ID NO: 604)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCTTCTTATGAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGTAGTGATGGTGGGCCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACTCCGCGGTATATTACTGTGCGAAACCTGAT
 AGGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-430 (SEQ ID NO: 605)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCTGCGGAGCAGATGACTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGCATGGTGATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCGG
 ACTTTGGTTGATTGGCCTACGAGTGAGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-44 (SEQ ID NO: 606)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTACGTCTTATGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGAGCCTACTGGTATTACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCAT
 TTTACTGAGCTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-449 (SEQ ID NO: 607)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGGGGGAGCAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGCTGCCTGGTCCGTATACATTCTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAAT
 GGGACGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-45 (SEQ ID NO: 608)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGTAATTATGCGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTGGGGCGCAGGGTCTTCATACATACTAC
 GCAGGCTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGACG
 ACGATGGATTATGAGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-450 (SEQ ID NO: 609)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATGAGGTTGATATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGCTATTGGTAATAATGGTCTTAAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGCT
 CTGTCGTATAGGCCTCCTGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-451 (SEQ ID NO: 610)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGGATGATACTATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGCTTAAGGGTCCGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGAGG
 GATGGGTTGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-452 (SEQ ID NO: 611)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

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TCCTGTGCAGCCTCCGGATTACCTTTGCTTCGTCTCCGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTCGGGATGGTAGTACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTTCG
 CTTATCGGCGGTTTGA TACTG GGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-453 (SEQ ID NO: 612)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTACTGATTATTCGATGGTTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGTGAGTCATGGTGGTACTACATACTAC
 GCAGACTCCGTGAAGGGCCGATTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAG
 GGTATAATGCGCAGTATTTTGA TACTG GGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-454 (SEQ ID NO: 613)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGAT
 TATTCGCTTCGTTTTGA TACTG GGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-455 (SEQ ID NO: 614)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAATGATTATGATATGATTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTTCGCATGGTGATAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAT
 GTTTTTTTTGA TACTG GGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-456 (SEQ ID NO: 615)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAATGGTCG
 GATTCTTTTGA TACTA CAGGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-457 (SEQ ID NO: 616)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCTGATTATGAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTCACTAATGGTAATATTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTAAT
 TCTCAGGTTGAGTATTTTGA TACTG GGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-458 (SEQ ID NO: 617)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGGTGGAGCCTATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAAATATTGGTCGTGATGGTTGATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGGGG
 AAGCATGGTACTTTTGA TACTG GGGGT CAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-459 (SEQ ID NO: 618)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCCGGAGTATCGGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTGATGAGCGGGGTTTCGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGCGG

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AAGGGTACTAAGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-46 (SEQ ID NO: 619)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGTTGTATGCTATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGTGCTGTGGGTGAGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGCT
 AATAATCTTTCTGATAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-460 (SEQ ID NO: 620)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGCATCAGCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGAATGGTTATTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTCG
 GTTGAGTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-461 (SEQ ID NO: 621)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAATAGTTATACGATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAATCCTTGGGGTAGTCGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTCTG
 GTGCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-462 0 (SEQ ID NO: 622)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATGGTGATATGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTCAGCTTGGTAGTAGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGAAT
 TGCGGACTCTTACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-463 (SEQ ID NO: 623)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGCGCAGCCTCCGGATTACCTTTAATGCTTATGGGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCTTTCTGATGGTGTTATTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGCT
 CGGGGTGCGAATTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-464 (SEQ ID NO: 624)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGCATTATATGATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTACGCCTCATGGTACGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATTTAAT
 GCTATTTTATGAGGCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-465 (SEQ ID NO: 625)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGGGATTATTCTATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGTCCGGTCTTACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGTCT
 CAGGCGGTTACTCGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-466 (SEQ ID NO: 626)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATCTTTATGCGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTGGGAGGGATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACGCGGTATATTACTGTGCGAAATTGGCT
 GGTTGCTGAGAGGGTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-467 (SEQ ID NO: 627)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATAAGGCTAGTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGCCTCATGGTTCGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGCGG
 TGGGGTGTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-468 (SEQ ID NO: 628)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCAAGGGTATAGTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTGGGCGTGGTGGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTTG
 TATATTTATCATAGTCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-469 (SEQ ID NO: 629)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCTGGTATGGAGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACTGGGACTGGTAGTACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTAT
 CATCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-470 (SEQ ID NO: 630)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCCGATGGTGGCTATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTCGGGATGGTAATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGTTTCG
 CCGACTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-471 (SEQ ID NO: 631)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGCATCAGGATATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACGGATGATGGTGAGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAT
 TATGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-472 (SEQ ID NO: 632)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGTATAATATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTACGAGGGATGGTTCTAGGACATACTAC
 GCAGACTCCGTGAGGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACTCCGCGGTATATTACTGTGCGAAACTGTCG
 AATATTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-473 (SEQ ID NO: 633)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATTCTATGATTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACGCCGTATGGTTCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

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CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACCTGAT
TATTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-474 (SEQ ID NO: 634)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATACGTATAGTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTTGAGTGGGTCTCAACTATTACTCCTTATGGTAGTTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGGGT
CTGGTGTGTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-475 (SEQ ID NO: 635)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGACTC
TCCTGTGCAGCCTCCGGATTCACCTTTACTACGGGTCTTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGTATTGGGGGTGATACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTCTATTACTGTGCGAAATTGACT
CCGTCTAATCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-476 (SEQ ID NO: 636)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGCAGTATCAGATGATGTGGGTTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCTTCTGGTTTTTTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGAAT
CCTTTTATTAGTACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-477 (SEQ ID NO: 637)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTAATTATGATATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTGCTTTGGGTAATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAACGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTACTGTGCGAAATGGCGT
AGTGCTATTACTGGTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-478 (SEQ ID NO: 638)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGTATCAGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTGCGCGTCGGGTATGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGCGG
TCGGTTGTTCTCCTTGCCGGGTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-479 (SEQ ID NO: 639)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGATGAGAGTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTCCTCATGGTACTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCAT
CTTAAGTTGTATGAGTCTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-480 (SEQ ID NO: 640)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGGGTGGTGAGATGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTCCGATGGATGGTAGTGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGG
AGTACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-481 (SEQ ID NO: 641)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATTTTATGCCGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGAGGGATGGTGCTTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTGCT
 TCGCCGGCGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-482 (SEQ ID NO: 642)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGTGATGAGCCTATGCTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGGGTACGGGTACGACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAT
 CAGGGTGATTTTATTAATCGGTTTCACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-483 (SEQ ID NO: 643)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCATGCGTATAATATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCCGCGGGGTCTTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCCG
 CCGCCTTCGTCTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-5 (SEQ ID NO: 644)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATGGGTATGAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGAGTGATGGTACGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 CTGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-505 (SEQ ID NO: 645)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGGGTTATATGATGTATTGGGTCCACCAGGCT
 CCGGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTCCTCAGGGTCATTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACTTCGT
 GAGCTTCCTCGTCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-506 (SEQ ID NO: 646)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTAGTTATGCTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGCGAGTGGTGGTCCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGAAT
 GGGAAGAAGTTTCTTTTACTAAGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-507 (SEQ ID NO: 647)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCTAGTGTCATATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTAATCTGACGGGTGTTGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGCT
 ACTACTAGGCAGGCGCATCCGTTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

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BMS2h-515 (SEQ ID NO: 648)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGGGTGAGATGTATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTGACTAATGGTCTTACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTACT
 CGTGATCTGGGTTTTGCCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-516 (SEQ ID NO: 649)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGAGATGGCTTGGGCCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTTCTCCTCGTGGTCATTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGCT
 AAGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-517 (SEQ ID NO: 650)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATACGTATGAGATGCTTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTTCTGTTGATGGTAGTATTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACGCGG
 ATGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-518 (SEQ ID NO: 651)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTTCTGATGCTATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAATATTTCTCGTGATGGTTCGAAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGCAG
 TCTGGGGGGCTTCGGTCGGGTTTACTACGTTTACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-519 (SEQ ID NO: 652)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGACTCCGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGAGGGATGGTGCTTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGG
 CCGAAGGGTATTGCGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-520 (SEQ ID NO: 653)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTCCGCATGCTATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTGATGGGGGGGGTTCGATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGAT
 CCTCCGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-521 (SEQ ID NO: 654)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGCGCAGCCTCCGGATTCACCTTTTCATGCGGGGGAGATGCATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACGCTGCCTGGTGATATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGAAT
 ACTGGGTATACTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-522 (SEQ ID NO: 655)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGAATTATGGTATGTCGTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTGTTGGGATGGTTCTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAATACG
CGGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-523 (SEQ ID NO: 656)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCATGATGCGGATATGCTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTGTCTCCGGGTGAGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGGT
CTGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-524 (SEQ ID NO: 657)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGTAATGATCAGATGAATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTCCTAGTGGTGCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTCTT
GGTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-525 (SEQ ID NO: 658)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCATCTTTGAGCAGTATCAGATGGTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTTGCGCTGATGGTACGCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTAGT
TTGCGTAAGATGGAGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-526 (SEQ ID NO: 659)

GAGGTGCAGCTGTTGGAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCAGGATGAGCAGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCGTCTGATGGTATGTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAATAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACCTGGG
AAGAATTTTGACCACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-527 (SEQ ID NO: 660)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGCGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTACTGGGGGTGAGCGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTTGG
AATCTGTATACGGAGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-528 (SEQ ID NO: 661)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTGGTACGCCGATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTCCTGATGGTATTCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTTG
GGTCAGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-529 (SEQ ID NO: 662)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGGTATCAGATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTCCTAGTGGTACGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATGGAAG
GCGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-530 (SEQ ID NO: 663)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCTCATTGACTATGTATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTGCCGTGCGGTAGTCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTTCT
 GATGAGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-531 (SEQ ID NO: 664)

GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATGGGAATATGGATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCTAGTGATGGTGTGACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGG
 GGTGAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-532 (SEQ ID NO: 665)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCTTCCGGATTCACCTTTGATGATTATATGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTCCGCATGGTGTTTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGTTG
 CATACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-533 (SEQ ID NO: 666)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTGAATTATACGATGGCGTGGGGCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATTATTGCTGGTCCGGGTAATTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
 AGTACTGCGACGTATAATAATGGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-534 (SEQ ID NO: 667)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACGGAGTATAGTATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTAGTGGGAGTGGTCTGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGCTT
 AAGCTGGTTAGGGCTCCTAATCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-535 (SEQ ID NO: 668)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCTAAGACTGGTCATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTTCG
 CATTCGTTGGGGCCTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-54 (SEQ ID NO: 669)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACGGCGTATAGGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTTGCTTCTGGTTCGGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACCTTTG
 ACGGATTCGCCGTCGGGGCATTATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

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BMS2h-55 (SEQ ID NO: 670)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCGCGGTATGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTACTGCTCAGGGTCTTGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATCTT
 ACTGATTTTAGTAGTGGGCATCAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-553 (SEQ ID NO: 671)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATGATTATGGTATGTCGTGGGTCCGCCAGGTT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTAGTCATAATGGTATGTTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATTGG
 CCGTCTACTAGTTGGGAGACTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-554 (SEQ ID NO: 672)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGAATGAGCCTATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGAGATGCAGGGTAAGAATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGG
 GTTCAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-555 1 (SEQ ID NO: 673)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGGAGGAGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATGTATTGATAATCTGGGTAGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCGCGGTATATTACTGTGCGAAAACGATT
 TCTCATCAGTATGATAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-556 (SEQ ID NO: 674)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGGAGGAGGAGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGAGGGGGGTGGGTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGACG
 CCGCATAAGCAGTTGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-557 (SEQ ID NO: 675)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCAGCTTTGCTGATGAGTATATGGTTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTGATCCGTTGGGTACTGGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGG
 ACGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-558 (SEQ ID NO: 676)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCTACGCATGATATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTGATGATGGTATTAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATTTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGAT
 ATGTCTCTTATTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-559 (SEQ ID NO: 677)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

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TCCTGTGCAGCCTCCGGATTCACCTTTGATGGTACTCCGATGGTTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTAGTGGTGATGGTAGGAATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCTTAT
 GCGCTTACTTCGTCTAAGCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-56 (SEQ ID NO: 678)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATGATTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTATGGGACTGGTGGTCAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTTTG
 GCTGATAGGAGTGGGGGGGTTGTTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-560 (SEQ ID NO: 679)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCGGAGACGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATGTATTAGTAATGATGGTAATACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTCT
 CTGATTAGTCCTGGTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-561 (SEQ ID NO: 680)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACTGGTGAGTATATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGAGACTGGTTATATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAATAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTTCT
 ACGAGGGGGGTGCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-562 (SEQ ID NO: 681)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGGTCGTATGATATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTGCGCTATGGGTGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTAAT
 CAGCATGCTCATGATCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-563 (SEQ ID NO: 682)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGATATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTGCGCTATGGGTACGTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGCT
 TTGACTGAGCCTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-564 (SEQ ID NO: 683)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGTGATTATGATATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTCTTGGTCATTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTCCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTGAG
 GAGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-565 (SEQ ID NO: 684)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
 TCCTGTGCAGCCTCCGGATTCGCTTTTCTAGGTATGGTATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAAATATTGATCAGTTTGGTATGAAGACATACTAC

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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGAGTAT
GCTTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

5 BMS2h-566 (SEQ ID NO: 685)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAAGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTGCCTATGGGTGTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGG
GGTAATACTTCGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

5 BMS2h-567 (SEQ ID NO: 686)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAATTATGATATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTGGGGCGGGTCATTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTTT
CCGCGTGATGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

10 BMS2h-568 (SEQ ID NO: 687)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGAAGTATGAGATGAGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTGGTCTGGATGGTTCGCCTACATACTAC
15 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGGGG
GATCCGAATGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

20 BMS2h-569 (SEQ ID NO: 688)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCGACTAGTGAGATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTGGGCCTGATGGTTTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
25 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATGCG
GATTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

30 BMS2h-57 (SEQ ID NO: 689)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCTGAGTATGATATGTATTGGGTCCGCCAGGCT
40 CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGATACTGATGGTGGGGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
CTGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

45 BMS2h-570 (SEQ ID NO: 690)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTACAGCCTCCGGATTCACCTTTGAGAATGCTTCTATGCAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGAGGGGCAGGGTAATGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
50 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTTCG
TCTTGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

55 BMS2h-571 (SEQ ID NO: 691)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGCGTAATGAGATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGCCGACTGGTACGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGAT
60 CCTGGTAATAGGTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-572 (SEQ ID NO: 692)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTTTGACTACCGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-1 (SEQ ID NO: 693)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTTTGACTACCGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-10 (SEQ ID NO: 694)

GAGGTGCAGCTGTTGGAGTCTGGTGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-11 (SEQ ID NO: 695)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCAGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGATTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGAGGGAACCAGGTACCGTCTCGAGC

BMS2h-572-12 (SEQ ID NO: 696)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-13 (SEQ ID NO: 697)

GAGGTGCAGTTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGACCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCTAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTAGGG
 AAGGAGAGTAATTTTGACTACTGGGGTCAAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-14 (SEQ ID NO: 698)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGCATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCAGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-15 (SEQ ID NO: 699)

GAGGTGCGGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACTTTAATTGGCAGCTGATGGGTTGGATCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC

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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCAGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTCTGACTACCGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

5 BMS2h-572-16 (SEQ ID NO: 700)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCACTGCGTCTC
TCCTGTGTAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTACTACCGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

5 BMS2h-572-17 (SEQ ID NO: 701)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGACTGGGGGGTCCCTGCGTCTC
5 TCCTGTGCAGCCTCCGGATTCACCTATAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
10 CTGCAAATGAACAGCCTGCGTGCCGATGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTTTACTACCGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

5 BMS2h-572-18 (SEQ ID NO: 702)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCAAGGCT
CCTGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
15 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTACTACCGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

10 BMS2h-572-19 (SEQ ID NO: 703)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
20 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTTACTACCGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

40 BMS2h-572-2 (SEQ ID NO: 704)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTTGAAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
45 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAAGTTTACTACCTGGGTACAGGGAACCCTGGTCACCGTCTCGAGC

45 BMS2h-572-21 (SEQ ID NO: 705)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGAATCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
50 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATCTTACTACCGGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

55 BMS2h-572-22 (SEQ ID NO: 706)

GAGGTGCAGCTGTTTGAAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
60 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTCTGACTACCGGGGGTCAGGGGACCCTGGTCACCGTCTCGAGC

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BMS2h-572-23 (SEQ ID NO: 707)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 ACCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCGGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCATCATCTCCCGCGACAATTCCAAGAACACGCTATAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-24 (SEQ ID NO: 708)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCGGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCACGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTGAATTTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-3 (SEQ ID NO: 709)

GAGGTGCGGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCACCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
 AAGGAGAGTAATCTTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-4 (SEQ ID NO: 710)

GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTTTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-5 (SEQ ID NO: 711)

GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCTGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
 CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
 AAGGAGAGTAATTTTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-572-6 (SEQ ID NO: 712)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-601 (SEQ ID NO: 713)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTCATGGGGTGGGCCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
 AAGGAGAGTAATTCTGACTACCGGGGTGTCAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-602 (SEQ ID NO: 714)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCACCTGATGGGGTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC

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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAGTTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

5 BMS2h-572-603 (SEQ ID NO: 715)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGCACCTGATGGCCTGGGCCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

5 BMS2h-572-604 (SEQ ID NO: 716)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGCACCTGATGGGCTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTCAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
10 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

15 BMS2h-572-605 (SEQ ID NO: 717)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGCACCTGATGGCCTGGGCCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATATTACATACTAC
20 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

25 BMS2h-572-606 (SEQ ID NO: 718)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGCACTTGATGGGCTGGGCCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
30 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

40 BMS2h-572-607 (SEQ ID NO: 719)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGCACCTCATGGGGTGGGCCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
45 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

50 BMS2h-572-608 (SEQ ID NO: 720)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGGAGCTGATGGGCTGGGCCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
55 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

60 BMS2h-572-609 (SEQ ID NO: 721)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAACTGGCACCTCATGGGCTGGGCCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTTGGG
AAGGAGAGTAATTCTGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

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BMS2h-572-610 (SEQ ID NO: 722)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
 AAGGACAGCAAGTCCGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-611 (SEQ ID NO: 723)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTCGGG
 AAGGACAGCAAGTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-612 (SEQ ID NO: 724)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTCGGG
 AAGGACAGCAACTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-613 (SEQ ID NO: 725)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGCACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
 AAGGACAGCAAGTCCGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-614 (SEQ ID NO: 726)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
 AAGGACGCCAAGTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-615 (SEQ ID NO: 727)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
 AAGGACAAGAACTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-616 (SEQ ID NO: 728)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
 AAGGAGAGCAAGTCCGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-617 (SEQ ID NO: 729)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AGGGACAGCAAGTCGGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

5 BMS2h-572-618 (SEQ ID NO: 730)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCGGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTCGGG
AAGTACAGCAACTCGGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

5 BMS2h-572-619 (SEQ ID NO: 731)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
10 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAGGTTCGGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

15 BMS2h-572-620 (SEQ ID NO: 732)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
20 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACGACAGCTTCGGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

25 BMS2h-572-621 (SEQ ID NO: 733)

GAGGTGCAGCTGTTGGAGTTTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTTTT
TCCTGTGCAGCTTCCGGATTACCTTTAATTGGCAGCTGATGGGTTGGTTCGGCAGGCT
CCAGGGAAGGGTTTAGAGTGGGTTTCAGGTATTGAGGGTCCAGGTGATGTTACATATTAC
30 GCAGATTCCGTGAAGGGCCGGTTCACCATTTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCTTGCCTGCGGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACAGCAATTCCGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

35 BMS2h-572-622 (SEQ ID NO: 734)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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40 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGACAGCACCTTCGGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

45 BMS2h-572-623 (SEQ ID NO: 735)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
50 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
AAGGAGAGCAGCTTCGGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

55 BMS2h-572-624 (SEQ ID NO: 736)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
60 GCAGACTCCGTGAAGGGCCGGTTCACCATCTTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCGCGTCCGACTACCGGGGTTCAGGGAACCCTGGTCACCGTATCGAGC

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BMS2h-572-625 (SEQ ID NO: 737)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTCGGC
 AACGACAGCTACTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-626 (SEQ ID NO: 738)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCTGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACGGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGG
 AAGGACAGCAGCTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-627 (SEQ ID NO: 739)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTGGCAGCTGATGGGTTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGATATATTACTGTGTGAAAGTGGGC
 AAGGACAGCGCGTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-630 (SEQ ID NO: 740)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
 AAGGACGCCAAGTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-631 (SEQ ID NO: 741)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
 AAGGACAGCAGGTTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-632 (SEQ ID NO: 742)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGCAGCTGATGGGCTGGGTCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
 AAGGACAGCAAGTCCGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-633 (SEQ ID NO: 743)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGTGAAAGTGGGG
 AAGGACGCCAAGTCGGACTACCGGGGTGAGGGAACCCTGGTCACCGTATCGAGC

BMS2h-572-634 (SEQ ID NO: 744)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC

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GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAGGTCGGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

5 BMS2h-572-635 (SEQ ID NO: 745)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGGAGCTGATGGGCTGGGCCCGGCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCAGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAAGTGGGC
AAGGACAGCAAGTCCGACTACCGGGGTCAGGGAACCCTGGTCACCGTATCGAGC

5 BMS2h-572-7 (SEQ ID NO: 746)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGCAGCTGATGGGATGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCCTGGTGATGTTACATACTAC
GCAGACTCCGTGAAGGGTCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
10 CTACAAATGAACAGCCTGCGTGCCGAGGACTCCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTGACTACCTGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

15 BMS2h-572-8 (SEQ ID NO: 747)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGTAGCCTCCGGATTCACCTTTAACTGGCAGCTGATGGGTTGGGTCCGCCAGGCG
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCCTGGTGATGTTACATACTAC
20 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGG
AAGGAGAGTAATTTGACTACCTGGGTCAGGGAACCCTGGTCACCGTTTCGAGC

25 BMS2h-572-9 (SEQ ID NO: 748)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACTGGCAGCTGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGAGGGTCCCTGGTGATGTTACATACTAC
30 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGG
AAGGAGAGTAATTTGACTACCTGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

40 BMS2h-573 (SEQ ID NO: 749)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTGGGTGGGAGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGAGTCTGGTCTTAATACATACTAC
45 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGTGCG
CCGCAGTATCAGATTACATTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

50 BMS2h-574 (SEQ ID NO: 750)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTAATTATGGGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATATATTTGCGGAGGGGTTTGTGACATACTAC
55 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGTCG
CATTATATGAATAATGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

60 BMS2h-575 (SEQ ID NO: 751)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTGGATTATACGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTAGTCCGATTGGTACTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
65 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCCT
TATGGGATGGAGGATGGTCTGACGTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

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BMS2h-576 (SEQ ID NO: 752)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATGCGTATGATATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAACGATTACGTCGGAGGGTCTTTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTAGT
 GATTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-577 (SEQ ID NO: 753)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGATGGGTATGATATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCGTGGGGGTGGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGACG
 AGTCAGTCGTCTACGGGGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-578 (SEQ ID NO: 754)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGTCGGTATGATATGCTTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTTGCGCTACGGGTGCTCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTGGT
 TCGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-579 (SEQ ID NO: 755)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTTTCCGTATTATATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGTACGGGTGGGCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGACG
 CAGAATGCGACGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-58 (SEQ ID NO: 756)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGGTTTATACTATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAACGATTGATGAGTCTGGTCGTGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
 GTTTGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-580 (SEQ ID NO: 757)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCGTTTTATAAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTCCTAAGGGTCATCATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTTTT
 AAGGGTAAGGGTTGGACTCGTCCGAGTGGGTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-581 (SEQ ID NO: 758)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAATGAGTATAGTATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGAGGCGTGGTTGGCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGTG
 CTGCTGGATTCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-582 (SEQ ID NO: 759)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATGAGTATCCGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTGCGCGTGGTCCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGG
 CATTGGCTTCGTAATGGTTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-583 (SEQ ID NO: 760)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTATGCAGTCGATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTGATGATGGTACTAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAT
 CGGGTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-584 (SEQ ID NO: 761)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGGCGGCTGATATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACTGATTACTAATGATGGTATTTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
 GATCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-586 (SEQ ID NO: 762)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATAAGTATAGGATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAGTTCTGGTGAGCTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGAGGTT
 CCGATGGGGAATCAGACTTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-587 (SEQ ID NO: 763)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACTGATTATACTATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACGTCTCAGGGTGCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTACG
 GGTACGGATTCGTCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-588 (SEQ ID NO: 764)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATTATGAGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATGTATTGGGCCGGGGGGTAAGCCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGAT
 GGGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-589 (SEQ ID NO: 765)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTCAGTATGATATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTTCGAGGGGTTGGCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCCG
 GGGGGTCGTCGGCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-59 (SEQ ID NO: 766)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCTGGATTATGCGATGGGTTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTTCTCCGATGGGTATGGGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGAGT
 GCTATTTCTGTTACTTCTGATATTTCTAATTTTGACTACTGGGGTCAGGGAACCTGGTC
 ACCGTCTCGAGC

BMS2h-590 (SEQ ID NO: 767)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATCCGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTTGGTCTGGTTTTTCAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCTGGT
 GTTGCAGGATGCCTACTGGGATTGCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC
 GTCTCGAGC

BMS2h-591 (SEQ ID NO: 768)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTGCTTATGAGATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAGTGCTGGTACTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTCTATTACTGTGCGGAACCTTTT
 GGGATGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC

BMS2h-592 (SEQ ID NO: 769)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGGAGTATCCGATGAAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCGGCAGGGTGATCGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGTG
 CGGAGGGGTCTTCCTCGTCCGAGTCGTTATTTTGACTACTGGGGTCAGGGAACCTGGTC
 ACCGTCTCGAGC

BMS2h-593 (SEQ ID NO: 770)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTGATTATGATATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTTCGCTATGGGTACGTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCTG
 AGTGTGATTCGGGTCTTGATTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCG
 AGC

BMS2h-594 (SEQ ID NO: 771)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGCGCAGCCTCCGGATTCACCTTTTCTCATTATGATATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGATATTGATTATATTGGTAAGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCTCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTTCG
 GATGAGGTGGGTGTTAATACTTCCAAGTTTGACTACTGGGGTCAGGGAACCTGGTCACC
 GTCTCGAGC

BMS2h-595 (SEQ ID NO: 772)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCGCGGTATGATATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTACTGGTGTGTTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTTT
 GAGGATTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC

BMS2h-596 (SEQ ID NO: 773)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC

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TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCTTATCCGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACTGATTTCTCATACGGGTCATGCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAT
 TGGCCTTTTGA TACTACCGGGGTCAGGGAACCCTGATCACCGTCTCGAGC

BMS2h-597 0 (SEQ ID NO: 774)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGGGGTCCCTGCGCCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATGAGTGGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTAGCCCGGGTGGTTGGACTACATACTAC
 GCCGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTAT
 CGTCCGTTTGATGAGTTTGA TACTGAGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-598 (SEQ ID NO: 775)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGAGTCACCTTTGATGCTATTGAGATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCGATTTGCGGTCATGGTGAGTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGATGCT
 TGGTCTCGGCATTTTGA TACTGAGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-599 (SEQ ID NO: 776)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAGTACGGATATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTTGGATAATGGTAGTAATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACATGCTGTAT
 CTGCAAATGAATAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGGCG
 AGGGATTTTGA TACTGAGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-600 (SEQ ID NO: 777)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCTTCCGGATTCACCTTTGGTAGGCAGAGTATGCAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGATGATGGTTTTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAT
 CCGTGGGGTTTTGACTACTGAGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-601 (SEQ ID NO: 778)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTACAGCCTCCGGATTCACCTTTAGTGATACGCAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGATGGGGGTGTGAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGAT
 CGTCATTTTGA TACTGAGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-602 (SEQ ID NO: 779)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGAGTACGACGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGTGATTTTCGGATGATGGTGGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAGGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGAT
 GGTTATGGTGGTTTTGACTACTGAGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-603 (SEQ ID NO: 780)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGGAGTGGGGATATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACGAATGATGGTACGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAATACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTGAT

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TCTGATTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-61 (SEQ ID NO: 781)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCTGCTTATGCTATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATATATTAGTCCGAATGGTACGGCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAATATGTG
 GGGATGCGTTGGAATTCTTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-62 (SEQ ID NO: 782)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTTCGAGTTATGAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGAGTCTTGGTACTTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 AGGAAGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-65 (SEQ ID NO: 783)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAATGAGTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTAGTGAGGGTAGTGGGACATACTAC
 GCAGACTCCGTAAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTAAT
 GGTAAGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-66 (SEQ ID NO: 784)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCTGATTATGAGATGTTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTACTAGTGAGGGTCATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGG
 ACTTCGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-67 (SEQ ID NO: 785)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTGATTATGAGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATTCTGATGGTAGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 GTGAAGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-68 (SEQ ID NO: 786)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAAGGATTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTACTGGTCAGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGT
 AATAAGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-69 (SEQ ID NO: 787)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCTTGATTATGGTATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTGCTTGGTCTTAGTACATACTAC
 GCAGACTCCGTGAAGAGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGGTG
 AGGGTGGGTAGGGGTGTTTCATCCTCCGAAGTTTGACTIONACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-7 (SEQ ID NO: 788)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATTTGTATGAGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACTAGTGATGGTGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGG
 GTGATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-70 (SEQ ID NO: 789)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGAATTATGCTATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGCTCCGCTGGGTGTTCCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAAGAAG
 GTTGGGGCGTGGCTGCAGTCGCGGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-701 (SEQ ID NO: 790)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATGGATTATGAGATGCATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGTGCTTCTGGTCATTATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCTT
 GATATGCTGCTGTTTGGGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-702 (SEQ ID NO: 791)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCTGAGTATGAGATGATGTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCTGGTAATGGTTCTCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATAATGCTT
 TCTCATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-703 (SEQ ID NO: 792)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTATAATTATGATATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATTGATGGGTCTTGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGTCT
 AATGCGAGTGATTGGGTTGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-704 (SEQ ID NO: 793)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGCGTCGTATCATATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGGATACGGGTGATCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACTGCGGTATATTACTGTGCGAAATTGCGT
 GGGATGGCTCGGGTTTGGGGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-705 (SEQ ID NO: 794)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTTATTATGATATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGATCTCATCTATTTCCGATCGTGGTCTTCAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTACG
 GAGATTCCGTTGGATTGGTTGGAGGTGTTTACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-706 (SEQ ID NO: 795)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGGGAGTTATAAGATGTTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACTAATTCTGGTACTGAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGATG
 TATCCGGATTTGGAGATTGTGCATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTC
 TCGAGC

BMS2h-707 (SEQ ID NO: 796)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGACTTATCGTATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATCAGGAGGGTTCTGCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATAGT
 GGGACGAGGCCGGGGCTTCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-708 (SEQ ID NO: 797)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTAGTTATGATATGCTTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATGCGAGTGGTTATTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAATTGTTG
 AAGCTGTCGTTGAATCCTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-709 1 (SEQ ID NO: 798)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTACATAACTGGTTTGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGACT
 CAGCATCGTTTTGTTGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-71 (SEQ ID NO: 799)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGGGTTATCCTATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTCCTTTGGGTCTGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTGTTG
 ATGGGGGAGTATTTGAATTCTAGGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-710 (SEQ ID NO: 800)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAATACGTATAGTATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATGGATTGATGCTGATGGTTGGGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAAGTGGG
 CATACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-711 (SEQ ID NO: 801)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTACGGATGGGGAGATGGGTTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGTGGATCCTGGTGATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
 GATCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-712 (SEQ ID NO: 802)

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCTGAGTATGAGATGAAGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGTCGGGTGGTCATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGATACCTCTT
 TCTAGTTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-713 (SEQ ID NO: 803)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCTAATTATGTGATGATTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTAATGGTGCTGGTGATATGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGGAAGGGGGT
 GCGCGTTCGTTTGGGGTTCGCGCTAATTTTACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-714 (SEQ ID NO: 804)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACGGATGGGGAGATGGGTGGGCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGTGGATCCTGGTGATTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGCGGGT
 GATCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-715 (SEQ ID NO: 805)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGTAGCCTCCGGATTCACCTTTACGCTGTATAATATGTCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAGTTATTTCTAGTAAGGGTGATAGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGCAAACGAGT
 AGTGTTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-716 (SEQ ID NO: 806)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCGTATTATATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGTTAATAATGGTTTGTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAATCGGCT
 GTTCATCCTTCGTATAGGGCGGAGTTGTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-717 (SEQ ID NO: 807)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGTTCGTATGAGATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGAGCCTGATGGTAGTAATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGGTCCG
 GATAATTTTACTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-718 (SEQ ID NO: 808)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAATAAGTATATGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAGTCTTGGTCATTATACATACTAC
 GCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGGAAGCGGAG
 TTTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719 (SEQ ID NO: 809)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-1 (SEQ ID NO: 810)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCATGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCAGGTACCGTCTCGAGC

BMS2h-719-10 (SEQ ID NO: 811)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCATGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-11 (SEQ ID NO: 812)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCAAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCGAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGTTTGACTATTGGGGTCAGGGTACCCTGGTCACCGTCTCGAGC

BMS2h-719-12 (SEQ ID NO: 813)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGACCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-13 (SEQ ID NO: 814)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCGTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATACCAAGAACACGCTGTAT
CTACAGATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGACCCGTTT
ACTGAGCTTGACTACTGGGGTCATGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-14 (SEQ ID NO: 815)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTTCTGTGCAGATCCGTTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-15 (SEQ ID NO: 816)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCGCTTTAAGAGGTATGAGATGACATGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCCTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCATATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
ACTGAGATTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC

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BMS2h-719-16 (SEQ ID NO: 817)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCCCTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACCGGGCTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-17 (SEQ ID NO: 818)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAAGAGGTATGAGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCTTCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
 ACTGAGATTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGC

BMS2h-719-18 (SEQ ID NO: 819)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACATCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCTTCCGGATTACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGACGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACGGGGTTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-19 (SEQ ID NO: 820)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCAGGATTACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
 ACTGAGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-2 (SEQ ID NO: 821)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACTGGGGTCATGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-20 (SEQ ID NO: 822)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACTCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGATTGACTACCGGGTTCAGGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-202 (SEQ ID NO: 823)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAAGAAGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACTGGGGTCATGGAACCCCTGGTCACCGTCTCGAGC

BMS2h-719-203 (SEQ ID NO: 824)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAACAGCTATGAGATGATGTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-21 (SEQ ID NO: 825)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCATTT
ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-213 (SEQ ID NO: 826)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGACCCGTTT
ACGGAGATGGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-214 (SEQ ID NO: 827)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGACCCGTTT
ACGGAGTTTCTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-215 (SEQ ID NO: 828)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTA
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAGCCGTTT
ACGGAGTTGGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-218 (SEQ ID NO: 829)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTGGAGTGGGTCTCATCGATTTTCGTCGGACGGTTCTTTCACGTA
GCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-225 (SEQ ID NO: 830)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACACGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-226 (SEQ ID NO: 831)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAACAGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGTCGGATGGTTCTTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
ACTGAGTTTGACTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-719-3 (SEQ ID NO: 832)

GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAATACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGATCCGTTT
 ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-4 (SEQ ID NO: 833)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGACT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCAGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCAAGC

BMS2h-719-5 (SEQ ID NO: 834)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGGAAATGAACAGCATGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACAACCTGGGGTCAGGGAACCCTCGTCACCGTCTCGAGC

BMS2h-719-6 (SEQ ID NO: 835)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCAGAACCGTTT
 ACTGAGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAGC

BMS2h-719-7 (SEQ ID NO: 836)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACTTTAAGAGGTATGAGATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCAGACCCGTTT
 ACTGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-8 (SEQ ID NO: 837)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCACGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACAGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-719-9 (SEQ ID NO: 838)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATGAGATGTCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGTCGGATGGTTCTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAACCGTTT
 ACTGAGTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-72 (SEQ ID NO: 839)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGCGTATCCTATGTCGTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCCCCTCTTGTTTTGTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTAGT
 GCTGGGGCGGAGACTCATGTTTATCGGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-720 (SEQ ID NO: 840)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATTATGAGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGGGTGTGGGTGCATACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAACTTATG
 TCGTTGAGGACGTTTGAATCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-722 (SEQ ID NO: 841)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACGAAGTATCCTATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGCTAATGGTAATAGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGACT
 TGGCGTAGGCATTTTGCATTTTGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-723 (SEQ ID NO: 842)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATCTGTATGATATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTGATCTGGGTACGCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATGGT
 TTTAGGGTTACGAGTAATGATCGTAGGTTTGTACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-724 (SEQ ID NO: 843)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTACTGGTGGGGATATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTGAGGGTGGTGGTGTGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCTTGAT
 CTTCCGACGGGTCAGTTTGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725 (SEQ ID NO: 844)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
 GATCCTACTAAGTTTGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-1 (SEQ ID NO: 845)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCATCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTTCTGTGCGGATCCGTCG
 GATCCTACTAAGTTTGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-10 (SEQ ID NO: 846)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGTGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTGCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-11 (SEQ ID NO: 847)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAGCAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTGCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-12 (SEQ ID NO: 848)

GAGGTGCAGCTGTTGGAGTCTGGGGGTGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCCCGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACGATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGTCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCTCG
GATCCTACTATGTTTGTCTACTGGGGTCAGGGAACCCTTGTACCGTCTCGAGC

BMS2h-725-13 (SEQ ID NO: 849)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGCTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCTCTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCTCG
GATCCTACTATGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-14 (SEQ ID NO: 850)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCATCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGTGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCA
GATCCTACTATGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-15 (SEQ ID NO: 851)

GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCATGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCATGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTGCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-16 (SEQ ID NO: 852)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTACACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCTCG
GATCCTACTATGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-17 (SEQ ID NO: 853)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACACTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGCGCGGAACCGTCTCG
GATCCTACTAAGTTAGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-725-18 (SEQ ID NO: 854)

GAGGTGCAGCTGTCGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 ACCTGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
 GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-19 (SEQ ID NO: 855)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAGATCCGTCG
 GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-2 (SEQ ID NO: 856)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCC
 TGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCTCCAGGGA
 AGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGTTCTTGGACATACTACGCAGACTCCGT
 GAAGGGCCCGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
 CTGCGTGCCGAGGACACCGCGGTATATTACTGCGCGGAACCGTCGGATCCTACTAAGTTTGTCT
 ACTGGGGTCAGGGAACCCCGGTACCGTCTCGAGC

BMS2h-725-3 (SEQ ID NO: 857)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCGCTTATTGGGGATCGTGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACATGCTGTAT
 CTGCAAATGAAAAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGCGCGGATCCGTCG
 GATCCTACTAAGTTTGTCTACTGGGGTCAAGGAACCCAGGTACACCGTCTCGAGC

BMS2h-725-4 (SEQ ID NO: 858)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGATCCGTCG
 GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-5 (SEQ ID NO: 859)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGATTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
 GATCCTACTAAGTTTCGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-6 (SEQ ID NO: 860)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGTTCTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCACGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCC
 GATCCTACTAAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-7 (SEQ ID NO: 861)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTACTTGGACATATTAC
GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACACTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTATTGTGCGGATCCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-8 (SEQ ID NO: 862)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-725-9 (SEQ ID NO: 863)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTCGGCTTATACTATGGGTTGGGTCCGCCAGGCT
CCAGGGATGGGTCTGGAGTGGGTCTCACTTATTGGGGATCGTGGTCTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGTCG
GATCCTACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-726 (SEQ ID NO: 864)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCCGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATTATAAGATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTTCGGAGATAGGTAATCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATAGCTCTG
ACGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-727 (SEQ ID NO: 865)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGAGTTATCGTATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATATATTGATCCGCCGGGTAGTCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTTG
AATTTGTCGTTTCCTTATATTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-728 (SEQ ID NO: 866)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCGGTATGAGATGCTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTTCTCATTCCGGTCCGACGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAATTGGAT
GGTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-729 (SEQ ID NO: 867)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGAGGTATTATATGGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATCATAATGGTTCTGTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATGCCG
CAGGGTACTTCTGATTGGTATTATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-73 (SEQ ID NO: 868)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTAAGTATGATATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTCTGGAGGATGGTCTGACTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

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CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGG
CGTTTGTGTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-74 (SEQ ID NO: 869)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGGATTATCCTATGACGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTCTGTCTCCGGGTACGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGAG
AAGGATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-741 (SEQ ID NO: 870)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGAGGGTGGTGAGATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAATGATTCCGATGGATGGTAGTGCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGT
GAGGTGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-742 (SEQ ID NO: 871)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAGGGAGTATCATATGAAGTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTAGTAGGGATGGTATGAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATACAGCTT
GCTTTGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-743 (SEQ ID NO: 872)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGTGATTATGAGATGCTTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTCTTCGTCCGGTGGGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGT
TCGGGGAATGGGCCTATTCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-744 (SEQ ID NO: 873)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAAGGAGCATGATATGTTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGGGCTGAGGGTGTGTTGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCGACG
ATGTCTAATGGTTCTCAGTCGCGTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-745 (SEQ ID NO: 874)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-1 (SEQ ID NO: 875)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTTTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT

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AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-10 (SEQ ID NO: 876)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAACCTGCGTGCCGAAGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-11 (SEQ ID NO: 877)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTTCAAGAACACGCTGTAT
CTGCAGATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-12 (SEQ ID NO: 878)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGATTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCATGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-13 (SEQ ID NO: 879)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAAACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-14 (SEQ ID NO: 880)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGTTACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-15 (SEQ ID NO: 881)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCTGGATTACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCTGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-16 (SEQ ID NO: 882)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-17 (SEQ ID NO: 883)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACAGGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGCACCCCTGGTCACC
GTTTCGAGC

BMS2h-745-18 (SEQ ID NO: 884)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATCACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTCGTCACC
GTCTCGAGC

BMS2h-745-19 (SEQ ID NO: 885)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGAGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-2 (SEQ ID NO: 886)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGAGAGGACTCCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-3 (SEQ ID NO: 887)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAGAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCGCCAGGCT
CCTGGGAAGGGTCTCGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAGCAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-745-4 (SEQ ID NO: 888)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTGAGGATGGTAATCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATTCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATCACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGTCTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

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BMS2h-745-5 (SEQ ID NO: 889)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
 GCTGACTCCGTGAAGGGCCGGTTCATCATCTCCCGCGACAATTCCAAGAACACGCTGAAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
 AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-745-6 (SEQ ID NO: 890)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTGTTACTGAGGATGGTAATCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
 AATCTGCATTGGGATGTGGGGAGGCAATTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-745-7 (SEQ ID NO: 891)

GAGGTGCAGCTGTTGGAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGAAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTATTGAGGATGGTAATCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTATTGTGCGAAAATTCGT
 AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGT

BMS2h-745-8 (SEQ ID NO: 892)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGATCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTGATCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAGCTCGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
 AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCCAGC

BMS2h-745-9 (SEQ ID NO: 893)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATAATACTGAGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGAGGATGGTAATCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACTCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
 AATCTGCATTGGGATGTGGGGAGGCAGTTTGCTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-746 (SEQ ID NO: 894)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGGTCCGCTGAGATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTGAGGCCTGGTCAGGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATTCGT
 AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-747 (SEQ ID NO: 895)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATGATGGTACTATGGGGTGGGCCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTGCCGTCCGGTAGTCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATTCTG

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CTGACTAATCGTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-748 (SEQ ID NO: 896)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTAAGTATGATATGCGGTGGGCCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTGATGCTGTTGGTACTCGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATACCGGGG
 GGGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-749 (SEQ ID NO: 897)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGATGTATGGTATGATGTGGGCCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGAGGGTGCGGGTGATGCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACTGCGGTATATTACTGTGCGATAGTGCTT
 GGTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-75 (SEQ ID NO: 898)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTTGCAGTATCCGATGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTGTTGGTTTGACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTGTTT
 GAGGGGTCGAGGATTCAGCGTGATGTGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-750 (SEQ ID NO: 899)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGAGAAAGTATCAGATGGGTGGGCCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGGGGTCTGGTCTTGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGCAT
 ACTACGCTGCATACGGAGGTGATTGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-751 (SEQ ID NO: 900)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCGGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTAGTCAGTATACGATGTATTGGGCCCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTTCTCATAGTGGTTCTAATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGATATCGGGG
 CTGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-752 (SEQ ID NO: 901)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGATTATGCGATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACGTATTGGTGTGGAGGGTGGGGATACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGTTG
 CGGCTTTATCGTCTGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-753 (SEQ ID NO: 902)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTGCTAAGTATGATATGACGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTAATTCTGATGGTGGTCTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTG
 CATGGTAGGGGGTTTGTTATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

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BMS2h-754 (SEQ ID NO: 903)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTTCGCGGTATGATATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTAATTCTATGGGTCTGGCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATTAT
 TCGGTTGCGCCGCATGGGTATCCTTTGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-755 (SEQ ID NO: 904)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGGATTATTTCGATGATGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACTGATAATGGTACGTCTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATATG
 TCGCTTGCTACTTATCTGCAGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC

BMS2h-756 (SEQ ID NO: 905)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTATGGAGTATGATATGCTTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTTCTGTCGGATGGTCTTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTG
 AGTGCGCTTGCTCCTTTTGATATTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-757 (SEQ ID NO: 906)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAAGGAGTATAATATGGCTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTAATTTTGCTGGTTCGGACGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTGTCT
 CTTCTTTGGATATTTTTCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC

BMS2h-758 (SEQ ID NO: 907)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACTAGT
 GGTTATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-1 (SEQ ID NO: 908)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTAT
 CTGCGAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACTAGT
 GGTTATTATGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-2 (SEQ ID NO: 909)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACTAGT
 GGTTATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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BMS2h-758-3 (SEQ ID NO: 910)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCC
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
 AGTTATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-4 (SEQ ID NO: 911)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGGTTACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTTT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
 GGTATTATGAGTACTGGGGTCATGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-5 (SEQ ID NO: 912)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCTGCCTCCGGATTCGCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
 GGTATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-758-6 (SEQ ID NO: 913)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGATTATGGTATGAATTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCACATATTTCTTCTAATGGTCGTTTTATATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACTAGT
 GGTACTTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-759 (SEQ ID NO: 914)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTAGGGAGTATGTTATGGGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGGTTGGTAATGTTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATACCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGAGACCGCGGTATATTACTGTGCGGATACAGCTG
 CCTAATTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-760 (SEQ ID NO: 915)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTAATGATGGGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTAATGTTGATGGTAGGGAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAATGGTCT
 CCTGGGCGGGTTCAGTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-761 (SEQ ID NO: 916)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGGTGTTGGGATATGGCGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCTCATGAGGGTGGTGAGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGTT
 CCTGGGTCTCCTCTGTTTGAATACTGGGGTCAGAGAACCCTGGTCACCGTCTCGAGC

BMS2h-762 (SEQ ID NO: 917)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATCAGGGTTGGATGTATTGGGTCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGTTCGAATGGTCCTCGGACATCCTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGGG
GAGTATTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-763 (SEQ ID NO: 918)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTAGGCAGAGTGATATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTGGTAATAATGGTGAGTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAAT
TGGCTGTTGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-764 (SEQ ID NO: 919)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGATCTTAGTACTATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGGTGGGGATGGTAGTCATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGGAAGGTACG
CAGTATTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-765 (SEQ ID NO: 920)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGGCGTATACGATGGAGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGGGTTACGGGTATGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGT
CAGGGTTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-766 (SEQ ID NO: 921)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGGGGATTATGGGATGTCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATATATTGATCCTCTGGGTGCTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGATTG
TCGTGCTGTCAGTATGGGGTGTCGCCTAATTTTGACTIONACTGGGGTCAGGGAACCCTGGT
ACCGTCTCGAGC

BMS2h-767 (SEQ ID NO: 922)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTTTTCATTATTCTATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGGTCCGGTTGGTCCGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGATT
CAGTCGCCGTTGTTTAAGGATTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-768 (SEQ ID NO: 923)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGATATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATAGTGGGGGTAATCAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAATAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGTCG
CTTTGGAAGTGGAGGTTGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-77 (SEQ ID NO: 924)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTGAGGAGTATGGTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCGCTGGGTATTTTCGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT

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CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATGCT
ACGTCTCAGGAGTCTTTGCGGTCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

5 BMS2h-770 (SEQ ID NO: 925)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGTAAGTATGAGATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
0 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCCT
CTGCCTGATGCGTTTTGGACTAGGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

5 BMS2h-771 (SEQ ID NO: 926)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTACTTATTCTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGATCGGCATGGTTTGGCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
10 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACCTCCT
GGTTCTTCTTGGCAGACTGTTTTTGGCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

5 BMS2h-772 (SEQ ID NO: 927)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
15 TCCTGTGCAGCCTCCGGATTCACCTTTGAGTCGTATCCTATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATCATCATGGTCATTTCGACATACTAC
GCAGACTCCGCGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
20 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGCTT
AGGGTTTTGATGATTTTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

5 BMS2h-773 (SEQ ID NO: 928)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
15 TCCTGTGCAGCCTCCGGATTCACCTTTGTGCAGTATGGGATGAGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTAGTAGTAGTGGTACGTATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
20 CTGCAAATGAACAGCCTACGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACGTCT
AGGATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

40 BMS2h-774 (SEQ ID NO: 929)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCGGCCTCCGGATTCACCTTTGCGGAGTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTTATTTGCGCTCCTGGTCGTAACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
45 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTTGTG
ATTCTGGGTTATACGAATAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

50 BMS2h-775 (SEQ ID NO: 930)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTAATTACGGGATGTTGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTAATTCTTCGGGTATGGAGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
55 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTTTT
CGTCTGAATGATCATAATTCTGTGTTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTC
ACCGTCTCGAGC

60 BMS2h-776 (SEQ ID NO: 931)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAAGGATTATAAGATGATGTGGATCCGCCAGGCT

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CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGTTGGGTCTGGTTCGATGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCCT
GGTATTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-777 (SEQ ID NO: 932)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTATAATTATGCTATGGGGTGGGTCCGCCGGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGAGCATGGTACTATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGT
CTGGATCGGGTTTGGATTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-778 (SEQ ID NO: 933)

GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTGTGATTATCCGATGACTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTATTCTGCGGGTTCTCCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTTAT
CATCGGGAGCCGATTCTTTTGGGTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTC
TCGAGC

BMS2h-78 (SEQ ID NO: 934)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTTGA GAGGTATCAGATGGCGTGGGTCCGCCAGGCT
CCGGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTTCTGATGGTGGGGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGGT
CATCGGTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-780 (SEQ ID NO: 935)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTTTCTTATACTATGATGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGAGATTGATCGGACGGGTGAGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACCTGGG
TTTGCTTCTCTTCTTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-781 (SEQ ID NO: 936)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTACGGATTATACTATGTATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAAAGATTTCTCCGAGTGGTCGTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCG
TTTGGGTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-782 (SEQ ID NO: 937)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATGATGCGGAGATGTTTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATGCTCGTGGTTTGACGACATACTAC
GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCGACG
TCGGCTATGTATCCTTTTGA TACTG GGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-783 (SEQ ID NO: 938)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTCTGTGATTATGATATGGGTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTCTTGGTCATTTTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATCTGGG

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TTTCATGAGTATACTGAGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC

BMS2h-784 (SEQ ID NO: 939)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGATCGTGCGGGTATGGGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCACTGATTGGGCGTGGTGGTGATATTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGT
AATCTGCATTGGGATGTGGGGAGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-80 (SEQ ID NO: 940)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGGTCTGTTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTGATGGTGGGGGGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTCT
CGTCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-81 (SEQ ID NO: 941)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTTCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGTTGTATCCGATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCATCGATTTCTCCGGTTGGTTTTCTGACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGCAT
GAGGGGTCTGATACTCCGCGGTCTGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-82 (SEQ ID NO: 942)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGTGGCGTATCCTATGGCGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTGGAGTGGGTCTCAACTATTGCGCCTCTGGGTGGTAATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGCCG
GAGGGGCTGCAGATTGATTCTCAGAAATTTGACTACTGGGGTCAGGGAACCCTGGTCACC
GTCTCGAGC

BMS2h-83 (SEQ ID NO: 943)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGCGTTGTATCAGATGGCTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTCTTCTGGTAGTGATACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTGAG
CGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-84 (SEQ ID NO: 944)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTAGGCAGTACCAGATGGCTTGGGCCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGCGTCGGATGGTGTTTCTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGT
CGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-85 (SEQ ID NO: 945)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTCACCTTTGAGCAGTATGATATGAGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGATGAGGCGGGTCATGAGACATACTAT
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAGGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATG

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GATGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGTTGATTATCCGATGGGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTACGGGGGGTTTTTCGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGCGG
 TATTATTATCTTAGTCAGATTAAGAATTTTACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-93 (SEQ ID NO: 947)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATATTTATGGGATGACTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTGGAGTGGGTCTCAAGTATTTTCGCTCTTGGTCTTGTACATACTAC
 GCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTGAAG
 GAGCATGGGGATGTTCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-94 (SEQ ID NO: 948)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGCTTTATCCGATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTCCTACGGGTTTGTGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTAAG
 AGGAGTGGGAAGACTGATGATACTAATTTTACTACTGGGGTCAGGGAACCCTGGTCACC
 GTCTCGAGC

BMS2h-95 (SEQ ID NO: 949)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCCGGAGTATGATATGCTGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGTGGGGGATGGTAATGGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGAT
 CGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-97 (SEQ ID NO: 950)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGTATGGTATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTTCGCTATTGGTGTACTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATGCT
 TATGATCGGAAGTCTAATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

BMS2h-98 (SEQ ID NO: 951)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGATCGGTATGTGATGGTGTGGGTCCGCCAGGCT
 CCAGGGAAGGATCTAGAGTGGGTCTCAGGTATTACTCCGAGTGGTAGGAGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGGACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTTG
 GGGCGTCATTTTGATCCTCTTCTGCCTTCGTTTACTACTGGGGTCAGGGAACCCTGGTC
 ACCGTCTCGAGC

BMS2h-99 (SEQ ID NO: 952)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTGAGGATTATGCTATGAGTTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCGGGTGGTTTTTGGACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACGTCT
 AGTGGGGAGTTGCAGTTGTTGAGGATTTTACTACTGGGGTCAGGGAACCCTGGTCACC

GTCTCGAGC

TABLE 3

Anti-human CD40L VK Domain Amino Acid Sequences

5	BMS2h-100 (SEQ ID NO: 953) DIQMTQSPSS LSASVGDRVT ITCRASQNIK HSLRWYQQKP GKAPRLLIYH RSQLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VRHRPYTFGQ GTKVEIKR
0	BMS2h-101 (SEQ ID NO: 954) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VALFPYTFGQ GTKVEIKR
5	BMS2h-102 (SEQ ID NO: 955) DIQMTQSPSS LSASVGDRVT ITCRASQHIG HHLRWYQQKP GKAPKLLIYH RSHLQSGVPS RFSGSGSGTD FTLTISSLQP EDSATYYCQQ WDRPPYTFGQ GTKVEIKR
10	BMS2h-103 (SEQ ID NO: 956) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VRAVPYTFGQ GTKVEIKR
15	BMS2h-104 (SEQ ID NO: 957) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VRFSPYTFGQ GTKVEIKR
20	BMS2h-105 (SEQ ID NO: 958) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYARPVTFGQ GTKVEIKR
25	BMS2h-106 (SEQ ID NO: 959) DIQMTQSPSS LSASVGDRVT ITCRASQIN HRLYWYQQKP GKAPKLLIYH RSRLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YKVRPNTFGQ GTKVEIKR
30	BMS2h-107 (SEQ ID NO: 960) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TYSSPHTFGQ GTKVEIKR
35	BMS2h-108 (SEQ ID NO: 961) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ RAVRPFTFGQ GTKVEIKR
40	BMS2h-109 (SEQ ID NO: 962) DIQMTQSPSS LSASVGDRVT ITCRASAIG HRLRWYQQKP GKAPKLLIYH RSKLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TYRPLTFGQ GTKVEIKR
45	BMS2h-110 (SEQ ID NO: 963) DIQMTQSPAS LSASVGDRVT ITCRASQDID PMLRWYQQKP GKAPKLLIYA GSILQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TSIRPYTFGQ GTKVEIKR
50	BMS2h-116 (SEQ ID NO: 964) DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR
55	BMS2h-116-1 (SEQ ID NO: 965) DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDILWYQQKP GKAPKLLIYQ TSILQSGVPS RFSGSESGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR
	BMS2h-116-10 (SEQ ID NO: 966)

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- DIQITQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YWAFPVTFGQ GTKVEIKR
- 5 BMS2h-116-11 (SEQ ID NO: 967)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGRGSGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR
- 0 BMS2h-116-12 (SEQ ID NO: 968)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWTFPVTFGQ GTKVEIKR
- 5 BMS2h-116-13 (SEQ ID NO: 969)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWAFPVTFGQ GTKVVIKR
- 0 BMS2h-116-1312 (SEQ ID NO: 970)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDLATYYCQQ YWAFPVTFGK GTKVVIKR
- 0 BMS2h-116-1313 (SEQ ID NO: 971)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWAFPVTFGR GTKVVIKR
- 5 BMS2h-116-1314 (SEQ ID NO: 972)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYRQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWAFPVTFGQ GTKVVIKR
- 0 BMS2h-116-1319 (SEQ ID NO: 973)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSIMRSGVPS
RFSGSGSETD FTLTISNLQP EDFATYYCQQ YWTFPVTFGQ GTKVEIKR
- 5 BMS2h-116-1320 (SEQ ID NO: 974)
DIQMTQSPSS LSAYVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP EDFAKYYCQQ YWAFPVTFGQ GTKVVIKR
- 40 BMS2h-116-138 (SEQ ID NO: 975)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSETD FTLTISNLQP VDFATYYCQQ YWAFPVTFGQ GTKVVIKR
- 40 BMS2h-116-14 (SEQ ID NO: 976)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWFQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSESGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR
- 45 BMS2h-116-15 (SEQ ID NO: 977)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYRQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWTFPVTFGQ GTKVEIKR
- 50 BMS2h-116-16 (SEQ ID NO: 978)
DIQMTQSPSS LSASVGDRVT ITCRASPID PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTV FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR
- 55 BMS2h-116-17 (SEQ ID NO: 979)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWAFPVTFGQ GTKVEIKR
- 60 BMS2h-116-2 (SEQ ID NO: 980)
DIQMTQSPSS LSASVGDRVT ITCRASPIE PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWASPVTFGQ GTKVEIKR
- 60 BMS2h-116-3 (SEQ ID NO: 981)

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DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ
TSILQSGVPS RFGSGESGTD FTLTISSLQP EDIATYYCQ YWAFPVTFGQ GTRVEIKR

BMS2h-116-4 (SEQ ID NO: 982)
5 DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFGSGESGTD FTLTISSLQP EDFATYYCQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-5 (SEQ ID NO: 983)
0 DIQMTQSPSS LSASVGDRVA ITCRASQPIG PDILWYQQKP GKAPKLLIYQ TSILRSGVPS
RFGSGSGTD FTLTISSLQP EDSATYYCQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-6 (SEQ ID NO: 984)
5 DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFGSGGSVTD FTLTISSLQP EDFATYYCQ YWAFPVTFGQ GTKVGIKR

BMS2h-116-7 (SEQ ID NO: 985)
10 DIQMTQSPSS LSASVGDRVT ITCRASQPID PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFGSGGSRTD FTLTISSLQP EDFATYYCQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-8 (SEQ ID NO: 986)
15 DIQMTQSPSS LSASVGDRVT ITCRASQPIG PDLLWYQQKP GKAPKLLIYQ TSILQSGVPS
RFGSGSGTD FTLTISGLQP EDFATYYCQ YWAFPVTFGQ GTKVEIKR

BMS2h-116-9 (SEQ ID NO: 987)
20 DIQMTQSPSS LSASVGDRVT ITCRASMPIG PDLLWYQQKP GKAPKLLIYQ TSILRSGVPS
RFGSGESGTD FTLTISSLQP EDFATYYCQ YWAFPVTFGQ GTKVEIKR

BMS2h-141 (SEQ ID NO: 988)
25 DIQMTQSPSS LSASVGDRVT ITCRASQWIG DTLTWYQQKL GKAPKLLIYG GSELQSGVPP
RFGSGSGTD FTLTISSLQP EDFATYYCQ CISSPCTFGQ GTKVEIKR

BMS2h-142 (SEQ ID NO: 989)
30 DIQMTQSPSS LSASVGDRVT ITCRASQFIG DSLSWYQQKP GKAPKLLIYF SSILQSGVPS
RFGSGSGTD FTLTISSLQP EDFATYYCQ YHTSPTTFGR GTKVKIKR

BMS2h-143 (SEQ ID NO: 990)
35 DIQMTQSPSS LSASVGDRVT ITCRASQTIE TNLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFGSGSGTD FTLTISSLQP EDLATYYCQ YHGYPTTFGQ GTKVEIKR

BMS2h-144 (SEQ ID NO: 991)
40 DIQMTQSPSS LSASVGDRVT ITCRASQMID QDLEWYQQKP GKAPKLLIYN ASWLQSGVPS
RFGSGSGTD FTLTISSLQP EDFATYYCQ YHGYPTTFGQ GTKVEIKR

BMS2h-145 (SEQ ID NO: 992)
45 DIQMTQSPSS LSASVGDRVT ITCRASQTIY TSLSWYQQKP GKAPKLLIHY GSVLQSGVPS
RFGSGSGTD FTLTISSLQP EDSATYYCQ VHQAPTTFGQ GTKVEIKR

BMS2h-146 (SEQ ID NO: 993)
50 DIRMTQSPSS LSASVGDRVT ITCRASQWIG DSLAWYQQKP GKAPKLLIYG ISELQSGVPS
RFGSGSGTD FTLTISSLQP EDSATYYCQL SSSMPHTFGQ GTKVEIKR

BMS2h-147 (SEQ ID NO: 994)
55 DIQMTQSPSS LSASVGDRVT ITCRASQEIE TNLEWYQQKP GKAPKLLIYD SSSLQSGVPS
RFGSGSGTD FTLTISSLQP EDFATYYCQ YHQNPTTFGQ GTKVEIKR

BMS2h-149 (SEQ ID NO: 995)
60 DIQMTQSPSS LSASVGDRVT ITCRASQWIG RQLVWYQQKP GKAPKLLIYG ATELQSGVPS
RFGSGSGTD FTLTISSLQP EDFATYYCQ QSKGPLTFGH GTKVEIKR

BMS2h-150 (SEQ ID NO: 996)

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DIQMTQSPSS LSASVGDRVT ITCRASQGIG TDLNWYQQKP GKAPKLLIYM GSYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IYSFPITFGQ GTKVEIKR

5 BMS2h-154 (SEQ ID NO: 997)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE EMLHWYQQKP GKAPKLLIYF GSLLQSGVPS
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HHTRPYTFGQ GTKVEIKR

0 BMS2h-155 (SEQ ID NO: 998)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG MDLEWYQQIP GKVPKLLIYD ASYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHKLPTFTFGQ GTKVEIKR

5 BMS2h-156 (SEQ ID NO: 999)
DIQMTQSPSS LSASVGDRVT ITCRASQDIM DNLEWYQQKP GKAPKLLIYA ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHKLPTFTFGQ GTKVEIKR

10 BMS2h-157 (SEQ ID NO: 1000)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE EDLEWYQQKP GNAPKLLIYS ASHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSSYPVTFGQ GTKVEIKR

15 BMS2h-158 (SEQ ID NO: 1001)
DIQMTQSPSS LSASVGDRVT ITCRASQPID EDLEWYQQKP GNAPKLLIYS ASYLQSGVPS
RFSGSGSGTD FTLTISRLQP EDFATYYCQQ YHLLPATFTFGQ GTKVEIKR

20 BMS2h-159 (SEQ ID NO: 1002)
DIQMIQSPSS LSASVGDRVT ITCRASQDIN EDLEWYQQKP GKAPKLLIYN ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP KDFATYYCQQ YHTNPFTFTFGQ GTKVEIKR

25 BMS2h-160 (SEQ ID NO: 1003)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE ADLEWYQQKP GKAPKLLIYH SSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHMSPVTFGQ GTKVEIKR

30 BMS2h-161 (SEQ ID NO: 1004)
DIQMTQSPSS LSASVGDRVT ITCRASQDID SDLEWYQQKP GKAPMLLIYS SSDLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSLPVTFGQ GTKVEIKR

35 BMS2h-162 (SEQ ID NO: 1005)
DIQMTQSPSS LSASVGDRVT ITCRASQDIS DDLEWYQQKP GKAPKLLIYN SSFLQSGVPS
RFSGSGSGAD FTLTISSLQP EDFATYYCQQ YHSLPVTFGQ GTKVEIKR

40 BMS2h-163 (SEQ ID NO: 1006)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE GNLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHHLPTFTFGQ GTKVEIKR

45 BMS2h-164 (SEQ ID NO: 1007)
DIQMTQSPSS LSASVGDRVT ITCRASQSID TDLEWYQQKP GKAPKLLIYD GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YRWIPVTFGQ GTKVEIKR

50 BMS2h-165 (SEQ ID NO: 1008)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE TDLEWYQQKL GKAPKLLIYD ASLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSSLPVTFGQ GTKVEIKR

55 BMS2h-166 (SEQ ID NO: 1009)
DIQMTQSPSS LSASVGDRVT ITCRASQPIT TSLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YWVTPVTFGQ GTKVEIKR

60 BMS2h-167 (SEQ ID NO: 1010)
DIQMTQSPSS LSASVGDRVT ITCRASQNIH TNLEWYQQKP GKAPKLLIYD GSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSANPVTFGQ GTKVGIKR

60 BMS2h-168 (SEQ ID NO: 1011)

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- DIQMTQSPSS LSASVGDRVT ITCRASQWIH TDLEWYQQKP GKAPKLLIYD GSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSVSPVTFGQ GTKVEIKR
- 5 BMS2h-169 (SEQ ID NO: 1012)
DIQMTQSPSS LSASVGDRVT ITCRASQSID NNLEWYQQKP GEAPKLLIYD GSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHLHPVTFGQ GTKVEIKR
- 0 BMS2h-170 (SEQ ID NO: 1013)
DIQMTQSPSS LSASVGDRVT ITCRASQDID TNLEWYQQKP GEAPKLLIYD RSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDSYPVTFGQ GTKVEIKR
- 5 BMS2h-171 (SEQ ID NO: 1014)
DIQMTQSPSS LSASVGDRVT ITCRASQSIE SNLEWYQQKP GKAPKLLIYN ASELQSGVPS
RFSGSGSGTD FTLTISSLRP EDFATYYCQQ YDQWPTTFGQ GTKVEIKR
- 10 BMS2h-172 (SEQ ID NO: 1015)
DIQMTQSPSS LSASVGDRVT ITCRASQAIG NTLRWYQQKP GKAPKLLIYL SSRLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LKKPPYTFGQ GTKVEIKR
- 15 BMS2h-173 (SEQ ID NO: 1016)
DIQMTQSPSS LSASVGDRVT ITCRASQKIK NRLAWYQQKP GKAPKLLIYE VSHLQSGVPS
RFSGSGSGTD FTLTIGSLQP EDFATYYCQQ RRQSPYTFGQ GTKVEIKR
- 20 BMS2h-174 (SEQ ID NO: 1017)
DIQMTQSPSS LSASVGDRVT ITCRASEDIG EELFWYQQKP GKAPKLLIYS ASTLQSEVPS
RFSGSGSGTD FTLTISSLQH EDFATYYCQQ VYEWPYTFGQ GTKVEIKR
- 25 BMS2h-175 (SEQ ID NO: 1018)
DIQMTQSPSS LSASVGDRVT ITCRASQPIS GGLRWYQQKP GKAPKLLIYS TSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LYSAPYTFGQ GTKVEIKR
- 30 BMS2h-305 (SEQ ID NO: 1019)
DIQMTQSPSS LSASVGDRVT ITCRASQDID QDLEWYQQKP GKAPKLLIYN VSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSMNPVTFGQ GTKVEIKR
- 35 BMS2h-306 (SEQ ID NO: 1020)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG NQLKWYQQKP GKAPKLLIYQ ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDLRPQTFGQ GTKVEIKR
- 40 BMS2h-307 (SEQ ID NO: 1021)
DIQMTQSPSF LSASVGDRVT ITCRASQKIS TSLEWYQQKP GKAPRLLIYD SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YEYNPITFGQ GTKVEIKR
- 45 BMS2h-33 (SEQ ID NO: 1022)
DIQMTQSPSS LSASVGDRVT ITCRASQTIG ESLHWYQQKP GKAPRLLIYF ASLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HHMLPSTFGQ GTKVEIKR
- 50 BMS2h-35 (SEQ ID NO: 1023)
DIQMTQSPSS LSASVGDRVT ITCRASQFIG DSLSWYQQKP GKAPKLLIYF SSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YMDIPITFGQ GTKVEIKR
- 55 BMS2h-36 (SEQ ID NO: 1024)
DIQMTQSPSS LSASVGDRVT ITCRASQDID HNLEWYQQKP GKAPKLLIYD SSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSIPVTFGQ GTKVEIKR
- 60 BMS2h-37 (SEQ ID NO: 1025)
DIQMTQSPSS LSASVGDRVT ITCRASQQIE TNLEWYQQKP GKAPKLLIYD GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSLPATFGQ GTKVEIKR
- 60 BMS2h-38 (SEQ ID NO: 1026)

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DIQMTQSPSS LSASVGDRVT ITCRASQDIG NNLEWYQQKP GKAPRLLIYH GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDFNPPTFGQ GTKVEIKR

5 BMS2h-39 (SEQ ID NO: 1027)
DIQMTQSPSS LSASVGDCVT ITCRASQDID GLLWWYQQKP GKAPKLLIYA GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ KAFEPPTFGQ GTKVEIKR

0 BMS2h-405 (SEQ ID NO: 1028)
DIQMTQTPSS LSASVGDRVT ITCRASQSIG HDLEWYQQKP GKAPKLLIYN VSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSHNPPTFGQ GTKVEIKR

5 BMS2h-406 (SEQ ID NO: 1029)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE NDLEWYQQKP GKAPKLLIYS ASHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHLQPTTFGP GTKVEIKR

10 BMS2h-431 (SEQ ID NO: 1030)
DIQMTQSPSS LSASVGDRVT ITCRASQVIE GSNLWYQQKP GKAPKLLIYH RSILQSGVPS
RFSGRGSGTD FTLTISSLQP EDFATYYCQQ TYQLPLTFGQ GTKVEIKR

15 BMS2h-432 (SEQ ID NO: 1031)
DIQMTQSPSS LSASVGDRVT ITCRASRPIN GKLFWYQQKP GKAPKLLIAF ASALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ QAVYPITFGQ GTKVEIKR

20 BMS2h-433 (SEQ ID NO: 1032)
DIQMTQSPSS LSASVGDRVT ITCRASQAIE TNLEWYQQKP GKAPKLLIYD GSLLQSGVPS
RFSGRGSGTD FTLTISSLQP EDFATYYCQQ YHYQPATFGQ GTKVEIKR

25 BMS2h-434 (SEQ ID NO: 1033)
DIQMTQSPSS LSASVGDRVT ITCRASQDIE HDLEWYQQKP GKAPKLLIYS ASQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YQQQPTTFGQ GTKVEIKR

30 BMS2h-435 (SEQ ID NO: 1034)
DIQMTQSPSS LSASVGDRVT ITCRASQIE ESLWWYQQKP GKAPKLLIAD VSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ GVVEPRTFGQ GTKVEIKR

35 BMS2h-436 (SEQ ID NO: 1035)
DIQMTQSPSS LSASVGDRVT ITCRASQYIG LDLEWYQQKP GKAPKLLIYA ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFRQPITFGQ GTKVEIKR

40 BMS2h-437 (SEQ ID NO: 1036)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVEIKR

45 BMS2h-437-1 (SEQ ID NO: 1037)
DIQLTQSPTS LSATVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRHPATFGQ GTKVEIKR

50 BMS2h-437-2 (SEQ ID NO: 1038)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVGIKR

55 BMS2h-437-3 (SEQ ID NO: 1039)
DIQMTQSPSS LSASVGDRVT ITCRVSTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPP
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVEIKR

60 BMS2h-437-4 (SEQ ID NO: 1040)
DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMLDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGCGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGQ GTKVEIKR

60 BMS2h-437-5 (SEQ ID NO: 1041)

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DIQMTQSPSS LSASVGDRVT ITCRASTPIG TMIDWYQQKP GKAPKLLIGH SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HVRPPATFGK GTKVEIKR

BMS2h-438 (SEQ ID NO: 1042)

DIQMTQSPSS LSASVGDRVT ITCRASQYID TNLEWYQQKP GKAPRLLIYD GSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YQVVPVTFGQ GTKVEIKR

BMS2h-439 (SEQ ID NO: 1043)

DIQMTQSPSS LSASVGDRVT ITCRASQSI SYLNWYQQKP GKAPRLLIVD SSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ DRWSPATFGQ GTKVEIKR

BMS2h-440 (SEQ ID NO: 1044)

DIQMTQSPSS LSASVGDRVT ITCRASSRIQ HMLSWYQQKP GKAPKLLIGG HSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ SCAWPLTFGQ GTKVEIKR

BMS2h-441 (SEQ ID NO: 1045)

DIQMTQSPSS LSASVGDRVT ITCRASRGID GDLWWYQQKP GKAPKLLIAD SSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ GAVRPMTFGQ GTKVEIKR

BMS2h-442 (SEQ ID NO: 1046)

DIQMTQSPSS LSASVGDRVT ITCRASRGID TDLWWYQQKP GKAPKLLIAD SSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ GAVRPMTFGQ GTKVEIKR

BMS2h-443 (SEQ ID NO: 1047)

DIQMTQSPSS LSASVGDRVT ITCRASYTIP VALDWYQQKP GKAPKLLIAD ASLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ GWPGPQTFGQ GTKVEIKR

BMS2h-444 (SEQ ID NO: 1048)

DIQMTQSPSS LSASVGDRVT ITCRASQSI TDLEWYQQKP GKAPKLLIYD TSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSYNPSTFGQ GTKVEIKR

BMS2h-445 (SEQ ID NO: 1049)

DIQMTQSPSS LSASVGDRVT ITCRASVPIT EGLSWYQQKP GKAPKLLIQA NSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WEHVPATFGQ GTKVEIKR

BMS2h-446 (SEQ ID NO: 1050)

DIQMTQSPSS LSASVGDRVT ITCRASSMIL YGLDWYQQKP GKAPKLLIGG TSALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WETVPATFGQ GTKVEIKR

BMS2h-447 (SEQ ID NO: 1051)

DIQMTQSPSS LSASVGDRVT ITCRASQPIN GLLIWYQQKP GKAPKLLIYA MSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LARIPFTFGQ GTKVGIKR

BMS2h-448 (SEQ ID NO: 1052)

DIQMTQSPSS LSASVGDRVT ITCRASQLIR TYLAWYQQKP GKAPKLLIYQ SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YNSYPDTFGQ GTKVEIKR

BMS2h-47 (SEQ ID NO: 1053)

DIQMTQSPSS LSASVGDRVT ITCRASQWIG DSLSWYQQKP GKAPKLLIYF GSYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YLHTPSTFGQ GTKVEIKR

BMS2h-484 (SEQ ID NO: 1054)

DIQMTQSPSS LSASVGDRVT ITCRASQDIE ADLEWYQQKP GKAPKLLIYH SSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YGFNPPTFGQ GTKVEIKR

BMS2h-485 (SEQ ID NO: 1055)

DIQMTQSPSS LSASVGDRVT ITCRASSPIE YGLDWYQQKP GKAPKLLIGG GSALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WEVQPATFGQ GTKVEIKR

BMS2h-486 (SEQ ID NO: 1056)

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DIQMTQSPSS LSASVGDRVT ITCRASQRID TDLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YHSAPATFGQ GTKVEIKR

BMS2h-487 (SEQ ID NO: 1057)

DIQMTQSPSS LSASVGDRVT ITCRASGWIG MSLEWHQQKP GKAPKLLIRG ASSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCSQ SRWPPVTFGQ GTKVEIKR

BMS2h-488 (SEQ ID NO: 1058)

DIQMTQSPSS LSASVGDRVT ITCRASRNIS NALSWYQQKP GKAPKLLILG ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCTQ VWDRPPTFGQ GTKVEIKR

BMS2h-489 (SEQ ID NO: 1059)

DIQMTQSPSS LSASVGDRVT ITCRASQDIM SALSWYQQKP GKAPKLLIYS TSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VYLLPVTFGQ GTKVEIKR

BMS2h-490 (SEQ ID NO: 1060)

DIQMTQSPSS LSASVGDRVT ITCRASQEIG IDLEWYQQKP GKAPKLLIYA ASYLQSGVPS
RFSSSGSGTD FTLTISSLQP EDFATYYCQQ YASNPTFGQ GTKVEIKR

BMS2h-491 (SEQ ID NO: 1061)

DIQMTQSPSS LSASVGDRVT ITCRASQMIG DWLNWYQQKP GKAPKLLIYR SSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LYFWPRTFGQ GTKVEIKR

BMS2h-492 (SEQ ID NO: 1062)

DIQMTQSPSS LSASVGDRVT ITCRASQAIE LNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDVYPPTFGQ GTKVEIKR

BMS2h-492-1 (SEQ ID NO: 1063)

DIQMTQSPSS LSASVGDRVT ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YDAYPPTYGQ GTKVEIKR

BMS2h-492-2 (SEQ ID NO: 1064)

DIQMTQSPSS LSASVGDRVT ITCRASRAIE TNLEWYQQKP GKAPKLLFYD ASMLQSGVPS
RFGGSGSGTD FTLTISSLQP EDFATYYCLQ YDVYPPTFGQ GTKVEIKR

BMS2h-492-3 (SEQ ID NO: 1065)

DIQMTQSPSS LSATVGDRVT ITCRASQAIE TNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-492-4 (SEQ ID NO: 1066)

DIQMTQSPSS LSASVGDRVT ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGRGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-492-5 (SEQ ID NO: 1067)

DIQMNQSPSS LSASVGDRVS ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-492-6 (SEQ ID NO: 1068)

DIQMTQSPSS LSASVGDRVT ITCRASQAIE SNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDVYPPTFGQ GTKVEIKR

BMS2h-492-7 (SEQ ID NO: 1069)

DIQMTQSPSS LSASVGDRVT ITCRASQAIE HNLEWYQQKP GKAPKLLIYD ASMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDAYPPTFGQ GTKVEIKR

BMS2h-493 (SEQ ID NO: 1070)

DIQMTQSPSS LSASVGDRVT ITCRASQGID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-494 (SEQ ID NO: 1071)

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DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-494-1 (SEQ ID NO: 1072)

DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSQYPPTFGQ GTKVEIKR

BMS2h-494-2 (SEQ ID NO: 1073)

DIQMTQSPSS LSASVGDRVT ITCRASQSIE EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YFQYPPTFGH GTKVEIKR

BMS2h-494-3 (SEQ ID NO: 1074)

DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYFCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-494-4 (SEQ ID NO: 1075)

EIQMTQSPSS LSASVGDRVT MTCRASQSID KDLEWYQQKP GKAPRLLIYS SSWLQRGVPS
RFSGSGSGTD FTLTISSLRP EDFATYYCQQ YFQYPPTLGQ GTKVEIKR

BMS2h-494-5 (SEQ ID NO: 1076)

DIQMTQSPSS LSASVGDRVT ITCRASQSID EDLEWYQQKP GKAPRLLIYS SSWLQSGVPS
RFSGSGSGTD FTLTISGLQP EDIATYYCKQ YSQYPPTFGQ GTKVEIKR

BMS2h-494-6 (SEQ ID NO: 1077)

DIQMTQSPSS LSASVGDRVT ITCRASQSID KDLEWYQQKP GKAPRLLIYS SSWLQRGVPS
RFSGSGSGTD FTLTISSLQP EDFATYHCQQ YFQYPPTFGQ GTKVEIKR

BMS2h-495 (SEQ ID NO: 1078)

DIQMTQSPSS LSASVGDRVT ITCRASEYIN AELAWYQQKP GKAPKLLIYG SSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCLQ NAMWPITFGQ GTKVEIKR

BMS2h-496 (SEQ ID NO: 1079)

DIQMTQSPSS LSASVGDRVT ITCRASLDIN NGLIWWYQQKP GKAPRLLILG ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCSQ VRSRPFTFGQ GTKVEIKR

BMS2h-497 (SEQ ID NO: 1080)

DIQMTQSPSS LSASVGDRVT ITCRASQDIL SALAWYQQKP GKAPKLLIYG SSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ NYSLPITFGQ GTKVEIKR

BMS2h-498 (SEQ ID NO: 1081)

DIQMTQSPSS LSASVGDRVT ITCRASSPIE SYLRWYQQKP GKAPKLLIRY VSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WFRAPVTFGQ GTKVEIKR

BMS2h-499 (SEQ ID NO: 1082)

DIQMTQSPSS LSASVGDRVT ITCRVSESIN AELHWYQQKP GKAPKLLISG FSGQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ FAMWPFTFGQ GTKVEIKR

BMS2h-500 (SEQ ID NO: 1083)

DIQMTQSPSS LSASVGDRVT ITCRASMMIR FGLDWYQQKP GKAPKLLIGG GSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ HERWPATFGQ GTKVEIKR

BMS2h-501 (SEQ ID NO: 1084)

DIQMTQSPSS LSASVGDRVT ITCRASQSIG TLLRWYQQKP GKAPKLLIYL TSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ MVYRPYTFGQ GTKVEIKR

BMS2h-502 (SEQ ID NO: 1085)

DIQMTQSPSS LSASVGDRVT ITCRASQTIE TNLEWYQQKP GKAPKLLIYD SSQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YDKVPATFGQ GTKVEIKR

BMS2h-503 (SEQ ID NO: 1086)

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DIQMTQSPSS LSASVGDRVT ITCRASHHIQ RYLSWYQQKP GKAPKLLILW GSQSQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWAPPPTFGQ GTKVEIKR

5 BMS2h-503-1 (SEQ ID NO: 1087)
DIQMTQSPSS LSASVGDRVT ITCRASHHIQ RYLSWYQQKP GKAPKLLILW GSQSQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWAPPQTFGQ GTKVEIKR

0 BMS2h-503-2 (SEQ ID NO: 1088)
DIQMTQSPSS LSASVGDRVT ITCRASHDIQ RYLSWYQQKP GKAPKLLILW GSQSQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WWAPPQTFGQ GTKVEIKR

5 BMS2h-504 (SEQ ID NO: 1089)
DIQMTQSPSS LSASVGDRVT ITCRASQYID TNLEWYQQKP GKAPKLLIYD GSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ GAVVPVTFGQ GTKVEIKR

10 BMS2h-508 (SEQ ID NO: 1090)
DIQMTQSPSS LSASVGDRVT ITCRASQDIA FDLEWYQQKP GKAPKLLIYS ASMLQSGVPS
RFSGSGSGSD FTLTISSLQP EDFATYYCQ YNLQPPTFGQ GTKVEIKR

15 BMS2h-509 (SEQ ID NO: 1091)
DIQMTQSPSS LSASVGDRVT ITCRASQDIA TLLRWYQQKP GKAPKLLIYA GSMLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQ MWQRPYTFGQ GTKVEIKR

20 BMS2h-51 (SEQ ID NO: 1092)
DIQMTQSPSS LSASVGDRVT ITCRASQPIV DELDWYQQKP GKAPKLLIYA ASILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCHQ WSTYPTTFGQ GTKVEIKR

25 BMS2h-510 (SEQ ID NO: 1093)
DIQMTQSPSS LSASVGDRVT ITCRASQDIA SYLNWYQQKP GKAPKLLIDG VSGSQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ DWDWPRTFGQ GTKVEIKR

30 BMS2h-511 (SEQ ID NO: 1094)
DIQMTQSPSS LSASVGDRVT ITCRASRNIR DWLRWYQQKP GKAPKLLIDW GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ TWDDPLTFGQ GTKVEIKR

35 BMS2h-511-1 (SEQ ID NO: 1095)
DIQMTQSPSS LSAFVGDRVT ITCRASRNIR DWLRWYQQKP GKAPKLLIDW GSELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ TWYDPLTFGH GTKVEIKR

40 BMS2h-512 (SEQ ID NO: 1096)
DIQMTQSPSS LSASVGDRVT ITCRASIDH GGLTWYQQKP GKAPKLLIVG VSGSQSGVPS
RFSGSGSGTD FTLTISNLQP EDFATYYCAQ VWRPPTFGQ GTKVEIKR

45 BMS2h-513 (SEQ ID NO: 1097)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG SSLWYQQKP GKAPKLLIYA SSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQ TYALPVTFGQ GTKVEIKR

50 BMS2h-514 (SEQ ID NO: 1098)
DIQMTQSPSS LSASVGDRVT ITCRASQIE TNLEWYQQKP GKAPKLLIYD GSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQ YKYLPTTFGQ GTKVEIKR

55 BMS2h-52 (SEQ ID NO: 1099)
DIQMTQSPSS LSASVGDRVT ITCRASQDIG SALRWYQQKP GKAPKLLIYL GSDLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQ TQYFPTTFGQ GTKVEIKR

60 BMS2h-53 (SEQ ID NO: 1100)
DIQMTQSPSS LSASVGDRVT ITCRASQAIY GGLRWYQQKP GKAPKLLIYG ESMLQSGVPS
RFSGSGSGTD FTLTISSLHP EDFATYYCQ VYHKPPTFGQ GTKVEIKR

60 BMS2h-536 (SEQ ID NO: 1101)

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DIQMTQSPSS LSASVGDRVT ITCRASQRIG VWLDWYQQKP GKAPKLLIYD GSFLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TFSSPSTFGQ GTKVEIKR

5 BMS2h-537 (SEQ ID NO: 1102)
DIQMTQSPSS LSASVGDRVP ITCRASQWIG DELYWYQQKP GKAPKLLIYS SSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SFQFPYTFGQ GTKVEIKR

0 BMS2h-538 (SEQ ID NO: 1103)
DIQMTQSPSS LSASVGDRVT ITCRASSNIT GPLEWYQQKP GKAPKLLIPG WSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ VWGEPVTFGQ GTKVEIKR

5 BMS2h-539 (SEQ ID NO: 1104)
DIQMTQSPSS LSASIGDRVT ITCRASQRIA YGLHWYQQKP GKAPRLLIGG RSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ PGMPPDTFGQ GTKVEIKR

10 BMS2h-540 (SEQ ID NO: 1105)
DIQMTQSPSS LSASVGDRVT ITCRASKQIV GGLSWYQQKP GKAPKLLIGR HSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ GVWAPGTFGQ GTKVEIKR

15 BMS2h-541 (SEQ ID NO: 1106)
DIQMTQSPSS LSASVGDRVT ITCRASPAIA AKLDWYQQKP GKAPKLLIGA DSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWAGPPTFGQ GTKVEIKR

20 BMS2h-542 (SEQ ID NO: 1107)
DIQMTQSPSS LSASVGDRVT ITCRASRTIA DGLDWYQQKP GKAPKLLIGA YSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWEGPPTFGQ GTKVEIKR

25 BMS2h-543 (SEQ ID NO: 1108)
DIQMTQSPSS LSASVGDRVT ITCRASQRIY GFLDWYQQKP GKAPKLLIYG VSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TLAWPPTFGQ GTKVEIKR

30 BMS2h-544 (SEQ ID NO: 1109)
DIQMTQSPSS LSASVGDRVT ITCRASQDIR DWLMWYQQKP GKAPKLLIYW GSFLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LYDTPYTFGQ GTKVEIKR

35 BMS2h-545 (SEQ ID NO: 1110)
DIQMTQSPSS LSASVGDRVT ITCRASQNIN TGLDWYQQKP GKAPKLLIYD SSALQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TSYYPYTFGQ GTKVEIKR

40 BMS2h-546 (SEQ ID NO: 1111)
DIQMTQSPSS LSASVGDRVT ITCRASQKIF GWLDWYQQKP GKAPKLLIYG TSKLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ VYSLPYTFGQ GTKVEIKR

45 BMS2h-547 (SEQ ID NO: 1112)
DIQMTQSPSS LSASVGDRVT ITCRASSNIG ADLDWYQQKP GKAPKLLIGG ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWNGPPTFGQ GTKVEIKR

50 BMS2h-548 (SEQ ID NO: 1113)
DIQMTQSPSS LSASVGDRVT ITCRASSPIY DGLDWYQQKP GKAPKLLISG ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWLGPPTFGQ GTKVEIKQ

55 BMS2h-549 (SEQ ID NO: 1114)
DIQMTQSPSS LSASVGDRVT ITCRASSRIY NGLHWYQQKP GKAPKLLIGG RSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ VGEAPSTFGQ GTKVEIKR

60 BMS2h-550 (SEQ ID NO: 1115)
DIQMTQSPSS LSASVGDRVT ITCRASRFIN EELDWYQQKP GKAPKLLISW SSWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCVQ PGGGPPTFGQ GTKVEIKR

60 BMS2h-551 (SEQ ID NO: 1116)

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DIQMTQSPSS LSASVGDRVT ITCRASRDIL DELDWYQQKP GKAPRLLIGG GSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWHGPPTFGQ GTKVEIKR

5 BMS2h-552 (SEQ ID NO: 1117)
DIQMTQSPSS LSASVGDRVT ITCRASSPIY TGLHWYQQKP GKAPKLLIGG RSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCMQ VGTAPATFGQ GTKVEIKR

0 BMS2h-585 (SEQ ID NO: 1118)
DIRMTQSPSS LSASVGDRVT ITCRASQNIS RRLWYQQKP GKAPKLLIYS SSRLQSGVPS
RFGSGSGTD FTLTISSLQP EDFATYYCQQ TYSYPHTFGQ GTKVEIKR

5 BMS2h-604 (SEQ ID NO: 1119)
DIQMTQSPSS LSASVGDRVT ITCRASSPIP QDLYWYQQKP GKAPKLLIVG ISQLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWSAPATFGQ GTKVEIKR

10 BMS2h-605 (SEQ ID NO: 1120)
DIQMTQSPSS LSASVGDRVT ITCRASKSID GMLDWYQQKP GKAPKLLIPG FSG LQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ SVEAPWTFGQ GTKVEIKR

15 BMS2h-606 (SEQ ID NO: 1121)
DIQMTQSPSS LSASVGDRVT ITCRASRYIA HPLDWYQQKP GKAPKLLIPG SSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ SVVVPWTFGQ GTKVEIKR

20 BMS2h-607 (SEQ ID NO: 1122)
DIQMTQSPSS LSASVGDRVT ITCRASRTIE GGLDWYQQKP GKAPKLLIMG GSG LQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWVGPPTFGQ GTKVEIKR

25 BMS2h-608 (SEQ ID NO: 1123)
DIQMTQSPSS LSASVGDRVT ITCRASKFIR DELYWYQQKP GKAPRLLIGG SSLLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWRAPATFGQ GTKVEIKR

30 BMS2h-609 (SEQ ID NO: 1124)
DIQMTQSPSS LSASVGDRVT ITCRASKPIY GGLEWYQQKP GKAPRLLIGG GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ VWGGPVTFGQ GTKVEIKR

35 BMS2h-610 (SEQ ID NO: 1125)
DIRMTQSPSS LSASVGDRVT ITCRASRPIS GCLDWYQQKP GKAPKLLIDG ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ WVEYPPTFGQ GTKVEIKR

40 BMS2h-611 (SEQ ID NO: 1126)
DIQMTQSPSS LSASVGDRVT ITCRASKPIV RDLEWYQQKP GKAPKLLIHG VSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LEAAPATFGQ GTKVEIKR

45 BMS2h-612 (SEQ ID NO: 1127)
DIQMTQSPSS LSASVGDRVT ITCRASRDIG DWLYWYQQKP GKAPRLLIVW ASVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ WGTPTTTFGQ GTKVEIKR

50 BMS2h-613 (SEQ ID NO: 1128)
DIQMTQSPSS LSASVGDRVT ITCRASNRIE YGLDWYQQKP GKAPKLLISG SSRLQSGVPS
RFSSSGSGTD FTLTISSLQP EDFATYYCGQ LEAAPATFGQ GTKVEIKR

55 BMS2h-614 (SEQ ID NO: 1129)
DIQMTQSPSS LSASVGDRVT ITCRASRNIG HFLDWYQQKP GKAPKLLILG GSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LVEPPATFGQ GTKVEIKR

60 BMS2h-615 (SEQ ID NO: 1130)
DIQMTQSPSS LSASVGDRVT ITCRASSSIY SDLYWYQQKP GKAPKLLIDG WSG LQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LHRAPATFGQ GTKVEIKR

65 BMS2h-616 (SEQ ID NO: 1131)

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DIQMTQSPSS LSASVGDRVT ITCRASRFIT DRLDWYQQKP GKAPKLLIGG VSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ SSELPTWTFGQ GTKVEIKR

5 BMS2h-617 (SEQ ID NO: 1132)
DIQMTQSPSS LSASVGDRVT ITCRASRKIG SELYWYQQKP GKAPKLLIGG RSRLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWEPPATFGQ GTKVEIKR

0 BMS2h-618 (SEQ ID NO: 1133)
DIQMTQSPSS LSASVGDRVT ITCRASRNIG NGLDWYQQKP GKAPKLLIGE GSRLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCGQ LWHTPPTFGQ GTKVEIKR

5 BMS2h-619 (SEQ ID NO: 1134)
DIQMTQSPSS LSASVGDRVT ITCRASRNIY GWLSWYQQKP GKAPRLLIGG WSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCAQ DYTLPPTFGQ GTKVEIKR

10 BMS2h-730 (SEQ ID NO: 1135)
DIQMTQSPSS LSASVGDRVT ITCRASQDIK DWLHWYQQKP GKAPKLLIYF ASGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDSATYYCQQ HYSTPYTSGQ GTKVEIKR

15 BMS2h-731 (SEQ ID NO: 1136)
DIQMTQSPSS LSASVGDRVT ITCRASQLIS SHLDWYQQKP GKAPKLLVYD ASELQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ HRSPLPFTFGQ GTKVEIKR

20 BMS2h-732 (SEQ ID NO: 1137)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG GALAWYQQKP GKAPRLLIYQ ISVLQSGIPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YIRSPFTFGQ GTKVEIKR

25 BMS2h-733 (SEQ ID NO: 1138)
DIQMTQSPSS LSASVGDRVT ITCRASQSIG AALNWYQQKP GKAPKLLIYG LSSLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ LFRPLPFTFGQ GTKVEIKR

30 BMS2h-734 (SEQ ID NO: 1139)
DIQMTQSPSS LSASVGDRVT ITCRASQPIG GRLVWYQQKP GKAPKLLIYG SSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YAEAPITFGQ GTKVEIKR

35 BMS2h-735 (SEQ ID NO: 1140)
DIQMTQSPSS LSASVGDRVT ITCRASQNIG SSLIWYQQKP GKAPTLLIYY SSKLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SLSSPYTVGQ GTKVEIKR

40 BMS2h-736 (SEQ ID NO: 1141)
DIQMTQSPSS LSASVGDRVT ITCRASQWIG SELAWYQQKP GKAPKLLIYW TSNLQSGVPS
RFSGSGSGTD FTLTISNLQP EDFATYYCQQ ILETPLTFTGQ GTKVEIKR

45 BMS2h-737 (SEQ ID NO: 1142)
DIQMTQSPSS LSASVGDRVT ITCRASQKIW DALYWYQQKP GKAPKLLIYR GSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ FYRWPHTFGQ GTKVEIKR

50 BMS2h-738 (SEQ ID NO: 1143)
DIQMTQSPSS LSASVGDRVT ITCRASQHIE DSLRWYQQKP GKAPKLLIYY GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ MYKFPITFGQ GTKVEIKR

55 BMS2h-739 (SEQ ID NO: 1144)
DIQTTQSPSS LSASVGDRVT ITCRASQRIN SSLLWYQQKP GKAPKLLIYD TSTLQSGVPS
RFSGSRSGTD FTLTISSLQP EDFATYYCQQ IWGSPPTFGQ GTKVEIKR

60 BMS2h-740 (SEQ ID NO: 1145)
DIQMTQSPSS LSASVGDRVT ITCRASQSIP VGLNWYQQKP GKAPRLLIYS GSTLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ DWYYPNTFGQ GTKVEIKR

60 BMS2h-785 (SEQ ID NO: 1146)

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DIQMTQSPSS LSASVGDRVT ITCRASQPIY GWLNWYQQKP GKAPKLLIYL TSGLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ IHSSPFTFGQ GTKVEIKR

BMS2h-8 (SEQ ID NO: 1147)

DIQMTQSPSS LSASVGDRVT ITCRASQFID TSLEWYQQKP GKAPKLLIYD GSHLQSGVPS
RFSGSGSGTD FTLTISSLQP EDLATYYCQQ YWVLPLTFGQ GTKVEIKR

BMS2h-86 (SEQ ID NO: 1148)

DIQMTQSPSS LSASVGDRVT ITCRASQDIG DALFWYQQKP GKAPKLLIYY SSMLQSGVPS
RFSGGGSGTD FTLTISSLQP EDFATYYCQQ RHSTPATFGQ GTKVEIKR

BMS2h-87 (SEQ ID NO: 1149)

DIQMTQSPSS LSASVGDRVT ITCRASQDID ESLMWYQQKP GKAPRLLIYG VSYLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ RWKAPFTFGQ GTKVEIKR

BMS2h-88 (SEQ ID NO: 1150)

DIQMTQSPSS LSASVGDRVT ITCRASQEIV EDLYWYQQKP GKAAKLLIYG ASWLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TRRRPYTFGQ GTKVEIKR

BMS2h-89 (SEQ ID NO: 1151)

DIQMTQSPAS LSASVGDRVT ITCRASQDID PMLRWYQQKP GKAPKLLIYA GSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ TLVTPYTFGQ GTKVEIKR

BMS2h-90 (SEQ ID NO: 1152)

DIQMTQSPSS LSASVGDRVT ITCRASQSIG DALFWYQQKP GKAPRLLIYY GSVLQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ RFQEPVTFGQ GTKVEIKR

BMS2h-91 (SEQ ID NO: 1153)

DIQMTQSPSS LSASVGDRVT ITCRASQQIS DELNWYQQKP GKAPKLLIYA VSILQSGVPS
RFSGSGSGTD FTLTISSLQP EDFATYYCQQ WLSFPSTFGQ GTKVEIKR

TABLE 4

Human Anti-CD40L VK Domain Encoding Nucleotide Sequences

BMS2h-100 (SEQ ID NO: 1154)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGAGCAAGTCAGAATATTAAGCATTCGTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATCATCGTTCCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTAGGCATCGTCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-101 (SEQ ID NO: 1155)

GACATCCAGATGACCCAGTCTCCATCCTCTCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTGCTTTGTTTCCCTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-102 (SEQ ID NO: 1156)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCATATTGGTCATCATTTAAGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCCAAGCTCCTGATCTATCATAGGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGTGGGATAGGCCGCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-103 (SEQ ID NO: 1157)

GACATCCAGATGACCCAGTCCCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGGTGCGGGCTGTGCCTTATACGTTTGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-104 (SEQ ID NO: 1158)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGGTTGTTTTCTCCTTATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-105 (SEQ ID NO: 1159)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTCTTATGCTAGGCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-106 (SEQ ID NO: 1160)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAAAGTATTAATCATAGGTTATATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAGGATTTTGCTACGTACTACTGTCAACAGTATAAGGTTAGGCCTAATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-107 (SEQ ID NO: 1161)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATTTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGACTTATTCGTCTCCTCATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-108 (SEQ ID NO: 1162)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGAGGGCGGTGAGGCCTTTTACGTTTCGGCCAA
 GGGACCAAAGTGGAAATCAAACGG

BMS2h-109 (SEQ ID NO: 1163)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGGGCATCGGTTACGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATCGGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGACTTATTATCGTCCTCTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-110 (SEQ ID NO: 1164)

GACATCCAGATGACCCAGTCTCCAGCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTGATCCTATGTTAAGGTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTATGCGGGTTCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTAGTATTAGGCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116 (SEQ ID NO: 1165)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-1 (SEQ ID NO: 1166)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATATACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATCTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-10 (SEQ ID NO: 1167)

GACATCCAGATAACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATATTGCGAAGTGGAGTCCCATCA
CGTTTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATCTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-11 (SEQ ID NO: 1168)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTTCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGAGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-12 (SEQ ID NO: 1169)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAACCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCTTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGCGGATCTGGGACTGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGACTTTTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-13 (SEQ ID NO: 1170)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1312 (SEQ ID NO: 1171)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATCTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCAA
GGGACCAAGGTGGTAATCAAACGG

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BMS2h-116-1313 (SEQ ID NO: 1172)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCGA
 GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1314 (SEQ ID NO: 1173)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGAGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCGGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGTAATCAAACGG

BMS2h-116-1319 (SEQ ID NO: 1174)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTATGCGAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGACTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-1320 (SEQ ID NO: 1175)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATATGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCAACCCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTAAGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGTGATCAAACGG

BMS2h-116-138 (SEQ ID NO: 1176)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GTAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTAGTAATCAAACGG

BMS2h-116-14 (SEQ ID NO: 1177)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTTCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-15 (SEQ ID NO: 1178)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATCGGTCCTGATTTACTGTGGTACCGGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGCGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGACTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-16 (SEQ ID NO: 1179)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGATCCTGACTTACTGTGGTACCAGCAGAAACCA

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GGTAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGTTTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCATTTCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-17 (SEQ ID NO: 1180)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCAGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAAGCCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-2 (SEQ ID NO: 1181)

GACATCCAGATGACCCAGTCTCCATCATCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGAACCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTCTCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-3 (SEQ ID NO: 1182)

GACATCCAGATGACCCAGTCACCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCTAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGCGGCAGTGAATCCGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATATTGCAACGTACTACTGTCAACAGTATTGGGCTTTTCTGTGACGTTTCGGCCAA
GGGACCAGGGTGGAAATCAAACGG

BMS2h-116-4 (SEQ ID NO: 1183)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCTTCA
CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-5 (SEQ ID NO: 1184)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCGCC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATATACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCTGTGACGTTTCGGTCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-6 (SEQ ID NO: 1185)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCGTCA
CGTTTCAGTGGCAGTGGATCTGTGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGGAATCAAGCGG

BMS2h-116-7 (SEQ ID NO: 1186)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
ATCACTTGCCGGGCAAGTCAGCCTATTGATCCTGATTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTAGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-116-8 (SEQ ID NO: 1187)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-116-9 (SEQ ID NO: 1188)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTATGCCTATTGGTCCTGATTTACTGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGACGTCCATTTTGCGAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTTTTCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-141 (SEQ ID NO: 1189)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATACGTTAACGTGGTACCAGCAGAAACTA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGTGGTTCCGAGTTGCAAAGTGGGGTCCCACCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTGTATTAGTAGTCCTTGTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-142 (SEQ ID NO: 1190)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTTTATTGGTGATTCTTTATCTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATTTTCTTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATACTTCGCTACTACGTTTCGGCCGA
 GGGACCAAGGTGAAAATCAAACGG

BMS2h-143 (SEQ ID NO: 1191)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGACTATTGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATTCTTCCCAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTAGCTACGTACTACTGTCAACAGTATCATGGGTATCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-144 (SEQ ID NO: 1192)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGATGATTGATCAGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATAATGCGTCCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATGGTTATCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-145 (SEQ ID NO: 1193)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGACGATTTATACTTCGTTAAGTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCCATTATGGTTCCTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTCTGCTACGTACTACTGTCAACAGGTTTCATCAGGCTCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-146 (SEQ ID NO: 1194)

GACATCCGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATTCTTTAGCGTGGTACCAGCAGAAAGCCA

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GGGAAAGCCCCTAAGCTCCTGATCTATGGTATTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACTGTCTAGTAGTATGCCTCATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-147 (SEQ ID NO: 1195)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGAGATTGAGACGAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATTCGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCAGAATCCTCCGACGTTTCGGCCAA
GGAACCAAGGTGGAAATCAAACGG

BMS2h-149 (SEQ ID NO: 1196)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGAGGCAGTTAGTTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGGCGACCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTTAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCAGTCGAAGGGTCCTCTTACGTTTCGGCCAT
GGGACCAAGGTGGAAATCAAACGG

BMS2h-150 (SEQ ID NO: 1197)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGGGATTGGTACTGATTTAAATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATATGGGTTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATTTATTCTTTTCCTATTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-154 (SEQ ID NO: 1198)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGGAGATGTTACATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTTGGTTCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTAGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCATCATACTCGTCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-155 (SEQ ID NO: 1199)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGATGGATTTAGAGTGGTACCAGCAGATACCA
GGGAAAGTCCCTAAGCTCCTGATCTATGATGCGTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAAGCTTCCTGCGACGTTTGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-156 (SEQ ID NO: 1200)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTATGGATAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGGCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAAGTTGCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-157 (SEQ ID NO: 1201)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGAGCAAGTCAGAATATTGGGGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAATGCCCTAAGCTCCTGATCTATAGTGCGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCTAGTTATCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-158 (SEQ ID NO: 1202)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCCGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGCCGATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAATGCCCTAAGCTCCTGATCTATAGTGCGTCTATTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGACTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCTTCTGCCTGCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-159 (SEQ ID NO: 1203)

GACATCCAGATGATCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGGATATTAATGAGGATTTAGAGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATAATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 AAAGATTTTGCTACGTACTACTGTCAACAGTATCATACTAATCCTACTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-160 (SEQ ID NO: 1204)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGGATATTGAGGCGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCATTCTTCCGAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGAAAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATATGTCGCCTGTGACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-161 (SEQ ID NO: 1205)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGGATATTGATAGTGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTATGCTCCTGATCTATTCTTCGTCCGATTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTCTGCCTGTTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-162 (SEQ ID NO: 1206)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGGATATTTCCGATGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATAATTCGTCTTTTTCGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTTTGCCTGTTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-163 (SEQ ID NO: 1207)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGGATATTGAGGGTAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATTCGTCCAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCATCTTCCTACGACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-164 (SEQ ID NO: 1208)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGAGTATTGATACGGATTTAGAGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGGGTCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCGGTGGATTCCTGTTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-165 (SEQ ID NO: 1209)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGAGTATTAGTACTGATTTAGAGTGGTACCAGCAGAACTA

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GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCCTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGAGTCTGCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-166 (SEQ ID NO: 1210)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTACGACGTCTTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGCGTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGTTACGCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-167 (SEQ ID NO: 1211)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACCTGCCGGGCAAGTCAGAATATTCATACGAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTGGGCTAATCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGGAATCAAACGG

BMS2h-168 (SEQ ID NO: 1212)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGTGGATTATACGGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAGTGTGTCGCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-169 (SEQ ID NO: 1213)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATAATAATTTAGAGTGGTACCAGCAGAAACCA
GGGGAAGCCCCTAAGCTCCTGATCTATGATGGGTCCCTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCTTCATCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-170 (SEQ ID NO: 1214)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGATACGAATTTAGAGTGGTATCAGCAGAAACCA
GGGGAAGCCCCTAAGCTCCTGATCTATGATCGTTCCACGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATTCTTATCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-171 (SEQ ID NO: 1215)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGTCTATTGAGTCTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGCGTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCGACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATCAGTGGCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-172 (SEQ ID NO: 1216)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACT
ATCACTTGCCGGGCAAGTCAGGCTATTGGTAATACTTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCTTAGTTCCAGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCTGAAGAAGCCTCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-173 (SEQ ID NO: 1217)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAAGATTAAGAATCGGTTAGCGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGAGGTTTCCCATTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCGGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGAGGAGGCAGTCGCCTTATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-174 (SEQ ID NO: 1218)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTGAGGATATTGGGGAGGAGTTATTTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATTTCGGCGTCCACGTTGCAAAGTGAGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACAT
 GAAGATTTTGCTACGTACTACTGTCAACAGGTTTATGAGTGGCCTTATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-175 (SEQ ID NO: 1219)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTTCTGGGGGTTTAAAGGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATTCTACTTCCATGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGCTTTATTCTGCTCCTTATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-305(SEQ ID NO: 1220)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTGATCAGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATAATGTTTCCCTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTCTATGAATCCTGTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-306 (SEQ ID NO: 1221)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTGGGAATCAGTTAAAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGGCTTCCGGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGATTTGAGGCCTCAGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-307 (SEQ ID NO: 1222)

GACATCCAGATGACCCAGTCTCCATCCTTCCCTGTCTGCATCTGTAGGTGACCGTGTCAACC
 ATCACTTGCCGGGCGAGTCAGAAGATTTCTACGTCTTTAGAGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCTATGATTCTTCCCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGAGTATAATCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-33 (SEQ ID NO: 1223)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGACGATTGGGGAGAGTTTACATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCTATTTTGGTTCCCTGTTGCAAAGTGGGGTCCCATCG
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGCATCATATGCTTCCCTTCTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-35 (SEQ ID NO: 1224)

GACATCCAAATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTTTATTGGTGATTCTTTATCTTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTATTTTTCTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATATGGATATTCTATTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-36 (SEQ ID NO: 1225)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGATCATAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATAGTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATTCTATTCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-37 (SEQ ID NO: 1226)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCAGATTGAGACGAATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTTTGCCTGCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-38 (SEQ ID NO: 1227)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGGTAATAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATCATGGGTCCCTGGTTGCAAAGTGGGGTCCCATCG
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATTTTAATCCTACTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-39 (SEQ ID NO: 1228)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACTGTGTCACC
ATCACTTGCCGGGCAAGTCAGAAATATTGATGGTCTGTTATGGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCGGGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGAAAGGCTTTTGAGCCTTTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-405 (SEQ ID NO: 1229)

GACATCCAGATGACCCAGACTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAGTATTGGTCATGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAATGTGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTTACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAGTCATAATCCTCCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-406 (SEQ ID NO: 1230)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACT
ATCACTTGCCGGGCAAGTCAGCATATTGAGAATGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTGCTTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATCTTCAGCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-431 (SEQ ID NO: 1231)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACT
ATCACTTGCCGGGCAAGTCAGGTTATTGAGGGTAGTTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATAGGTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCCGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTATCAGCTTCCTTTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-432 (SEQ ID NO: 1232)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGTCTATTAATGGTAAGTTATTTTGGTACCAGCAGAAACCA
 GGCAAAGCCCCTAAGCTCCTGATCGCGTTTGCTTCCGCTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGTGCAGCAGGCTGTGTATCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-433 (SEQ ID NO: 1233)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCTATTGAGACGAATTTAGAGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGGGTCCCTTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGAGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCATTATCAGCCTGCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-434 (SEQ ID NO: 1234)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTGAGCATGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATTCGGCGTCCCAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATCAGCAGCAGCCTACTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-435 (SEQ ID NO: 1235)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTTCGCAGATTGAGGAGTCTTTATGGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGCGGATGTTTCCCTGTTGCAAAGTGAGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCTCAGGGTGTGGTGGAGCCTCGTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-436 (SEQ ID NO: 1236)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTATATTGGTCTGGATTTAGAGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCTTCCCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCGGCAGCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-437 (SEQ ID NO: 1237)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGGGCATTTCGTCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCCTCCTGCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-437-1 (SEQ ID NO: 1238)

GACATCCAGTTGACCCAGTCTCCAACCTCCCTGTCTGCAACTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCT
 GGGAAAGCCCCTAAGCTCCTGATCGGGCATTTCGTCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACTGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGCATGTGCGTCATCCTGCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAGCGG

BMS2h-437-2 (SEQ ID NO: 1239)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCGGGCATTTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGACAGCATGTGCGTCCTCCTGCGACGTTGCGCCAA
GGGACCAAGGTGGGAATCAAACGG

BMS2h-437-3 (SEQ ID NO: 1240)

GACATCCAGATGACCCAGTCTCCGTCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGTAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTTCGTCCTGGTTGCAAAGTGGGGTCCCACCA
CGTTTCAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGACAGCATGTGCGTCCTCCTGCGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-437-4 (SEQ ID NO: 1241)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCTGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGACAGCATGTGCGTCCTCCTGCGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-437-5 (SEQ ID NO: 1242)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTACGCCGATTGGTACTATGATAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCATTTCGTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGACAGCATGTGCGTCCTCCTGCGACGTTGCGCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-438 (SEQ ID NO: 1243)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACATGCCGGGCAAGTACAGTATATTGATACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATGATGGTTCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCATCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCAGGTTGTGCCTGTTACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-439 (SEQ ID NO: 1244)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTACAGAGCATTAGCAGCTATTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGTGGATTCTTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGGATCGTTGGTCTCCTGCTACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-440 (SEQ ID NO: 1245)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTTCGCGGATTCAGCATATGTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGGCATTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAATCGTGTGCGTGGCCTCTGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-441 (SEQ ID NO: 1246)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGGGGATTGATGGTGATTTATGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGCGGATTCTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGACAGGGGGCTGTTGCGCCTATGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-442 (SEQ ID NO: 1247)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAGGGGTATTGATACTGATTTATGGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGCGGATTCTTCCCTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGGGGGCTGTTCCGGCCTATGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-443 (SEQ ID NO: 1248)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTTATACTATTCCGGTTGCTTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGCTGATGCGTCCTTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCGCAGGGTTGGCCGGGGCCTCAGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-444 (SEQ ID NO: 1249)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAGTATTGCGACGGACTTAGAGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATACTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATAGTTATAATCCTTCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-445 (SEQ ID NO: 1250)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTGTGCCTATTACTGAGGGTTTATCGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCCAGGCTAATTCCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGTGGGAGCATGTTCCCTGCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-446 (SEQ ID NO: 1251)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAGTATGATTCTTTATGGTTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGGTGGTACTTCCGCGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGTGGGAGACGGTTCCTGCTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-447 (SEQ ID NO: 1252)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTAATGGGCTTTTAATTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCGATGTCCAGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTTGGCTCGGATTCCTTTTACGTTTCGGCCAA
 GGGACCAAGGTGGGAATCAAACGG

BMS2h-448 (SEQ ID NO: 1253)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGAGCAAGTCAGCTGATTCGGACTTATTTAGCGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCAGTCTTCTCAGTTGCAAAGTGGTGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATAATTCTTATCCTGATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-47 (SEQ ID NO: 1254)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATTGTTAAGTTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTATTTTGGTTCCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTGCATACTCCTTCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-484 (SEQ ID NO: 1255)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGAGGCGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCATTCTTCCGAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGGTTTAATCCTCCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-485 (SEQ ID NO: 1256)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTTCTCCTATTGAGTATGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGGGGGGGTCCGCGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGAGTGGGAGGTTTCAGCCTGCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-486 (SEQ ID NO: 1257)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCGGATTGATACTGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATAGTTCACAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATCATAGTGCGCCTGCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-487 (SEQ ID NO: 1258)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTGGGTGGATTGGTATGTCTTTAGAGTGGCACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCGTGGGGCTTCCTCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTAGTCAGTCTCGGTGGCCGCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-488 (SEQ ID NO: 1259)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCGTAATATTTTGAATGCTTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGGGGCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTACTCAGGTGTGGGATAGGCCTTTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-489 (SEQ ID NO: 1260)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTATGTCGGCTTTATCTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTACTTCCATTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTTTATTTGCTGCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-490 (SEQ ID NO: 1261)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGAGATTGGGATTGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCTTCTTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGCTTCTAATCCTCCTACGTTTCGGCCGA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-491 (SEQ ID NO: 1262)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGATGATTGGGGATTGGTTAAATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAACTCCTGATCTATCGTAGTTCGAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTTGATTTTTGGCCTCGTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492 (SEQ ID NO: 1263)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCGATTGAGCTTAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGTTATCCTCCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-1 (SEQ ID NO: 1264)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCGATTGAGCATAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTCCAACCT
 GAAGATTTAGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTACGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-2 (SEQ ID NO: 1265)

GACATCCAGATGACACAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGGGCGATAGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGTTCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCGGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCTACAGTATGATGTTTATCCTCCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-3 (SEQ ID NO: 1266)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAACTGTAGGAGACCGTGTCAACC
 ATCACTTGTCGTGCAAGTCAGGCGATTGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGACTTCACTCTCACCATTAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-4 (SEQ ID NO: 1267)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCGATTGAGCATAACTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGTTTCAGTGGCAGAGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-5 (SEQ ID NO: 1268)

GACATCCAGATGAACCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCTCC
 ATCACTTGCCAGGGCAAGTCAGGCTATTGAGCATAATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
 CGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-6 (SEQ ID NO: 1269)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGCGATTGAGTCTAATTTAGAGTGGTACCAGCAAAAACCA

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GGGAAGGCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGTTTATCCTCCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-492-7 (SEQ ID NO: 1270)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGTGCAAGTCAGGCGATTGAGCATAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCTATGATGCTTCCATGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATGCTTATCCTCCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-493 (SEQ ID NO: 1271)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATTTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494 (SEQ ID NO: 1272)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-1 (SEQ ID NO: 1273)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCAGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTCTCAGTATCCTCCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-2 (SEQ ID NO: 1274)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAGTATTGAAGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGCGGGGTCCCATCA
CGTTTCAGTGGGAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTTCGGCCAT
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-3 (SEQ ID NO: 1275)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTTCTGTCAACAGTATTTTCAGTATCCTCCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-4 (SEQ ID NO: 1276)

GAGATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATGACTTGCCGGGCAAGTCAGAGTATTGATAAGGATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGAGGGGTCCCATCA
CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCGACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATTTTCAGTATCCTCCGACGTTGGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-494-5 (SEQ ID NO: 1277)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACC
 ATCACTTGCCGGGCAAGTCAGAGTATTGATGAGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCT
 GAAGATATCGCTACGTACTACTGTAAACAGTATTCTCAGTATCCTCCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-494-6 (SEQ ID NO: 1278)

GACATCCAGATGACCCAGTCCCCACCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAGTATTGATAAGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCTATTCTAGTTCCCTGGTTGCAAAGAGGGGTCCCATCA
 CGTTTCAGTGGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACCACTGTCAACAGTATTTTCAGTATCCTCCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-495 (SEQ ID NO: 1279)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTGAGTATATTAATGCTGAGTTAGCTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGGAGTTCCGGGTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCTGCAGAATGCGATGTGGCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-496 (SEQ ID NO: 1280)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCTGGATATTAATAATGGTTTAATTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCTTGGGTGCGTCCGGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTTCGCAGGTGCGTTCTCGGCCTTTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-497 (SEQ ID NO: 1281)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTCTGAGTGC GTTAGCTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGGAGTTCCGTTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGAATTATAGTCTTCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-498 (SEQ ID NO: 1282)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTTCTCCTATTGAGTCGTATTTAAGGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCAGGTATGTGTCCGTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTTTCGGGCGCCTGTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-499 (SEQ ID NO: 1283)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGTAAGTGAGTCTATTAATGCTGAGTTACATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTCTGGGTTTTCCGGGTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGTGCAGTTTGCGATGTGGCCTTTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-500 (SEQ ID NO: 1284)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTATGATGATTAGGTTTGGGTAGATTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCGGTGGTGGGTCCTCTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCATGAGCGGTGGCCTGCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-501 (SEQ ID NO: 1285)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAGTATTGGTACTCTTTTACGTTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATCTTACTTCCGTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATGGTTTATCGTCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-502 (SEQ ID NO: 1286)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGACTATTGAGACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATTCTTCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATGATAAGGTTCTGCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-503 (SEQ ID NO: 1287)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCATCATATTAGAGGTATTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGGGTTCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGCTCCTCCTCCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-503-1 (SEQ ID NO: 1288)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCATCATATTAGAGGTATTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGGGTTCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGCTCCTCCTCAGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-503-2 (SEQ ID NO: 1289)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCATGATATTAGAGGTATTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGGGTTCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGCTCCTCCTCAGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-504 (SEQ ID NO: 1290)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACATGCCGGGCAAGTCAGTATATTGATACTAATTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCCTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGGGGGCTGTTGTGCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-508 (SEQ ID NO: 1291)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGCTTTTGATTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTGGCGTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGTCAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAATCTTCAGCCTCCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-509 (SEQ ID NO: 1292)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGAATATTGCTACGCTGTTACGTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGGTTCCATGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGATGTGGCAGCGTCCTTATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-51 (SEQ ID NO: 1293)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGTTGATGAGTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCGTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTGGTCTACTTATCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATTAACGG

BMS2h-510 (SEQ ID NO: 1294)

GACATCCAGATGACCCAATCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTAATCGATGGTGTTCGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGGATTGGGATTGGCCTCGTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-511 (SEQ ID NO: 1295)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTAGGAATATTCGTGATTGGTTACGGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGATTGGGGTCCGTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCTCAGACGTGGGATGATCCTCTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-511-1 (SEQ ID NO: 1296)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATTTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTAGGAATATTCGTGATTGGTTACGGTGGTACCAACAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGATTGGGGTCCGAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCTCAGACGTGGTATGATCCTCTGACGTTTCGGCCAC
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-512 (SEQ ID NO: 1297)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTATTGATATTCATGGTGGTTAACTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGTGGGGGTTTCCGGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCGCAGGTGTGGCGTAGGCCTTTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-513 (SEQ ID NO: 1298)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGGATATTGGGAGTTGTTATCTTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCTTCTTCCCTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGACTTATGCTCTTCCCTGTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-514 (SEQ ID NO: 1299)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCAGCAGATTGAGACGAATTTAGAGTGGTATCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTATAAGTATCTGCCTGTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-52 (SEQ ID NO: 1300)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGTGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGTCTGCGTTAAGGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTGGGTTCGGATTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGCAGTATTTTCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-53 (SEQ ID NO: 1301)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGCGATTTATGGGGGGTTACGGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGGGAGTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCATCCT
GAAGATTTTGCTACGTACTACTGTCAACAGGTTTATCATAAGCCTTTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-536 (SEQ ID NO: 1302)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACGTGCCGGGCAAGTCAGCGTATTGGGGTGTGGTTAGATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGTTCCTTTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACTTTTTCGAGTCCTTCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-537 (SEQ ID NO: 1303)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCCCC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGGATGAGTTATATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATAGTTCTTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGTCGTTTCAGTTTCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-538 (SEQ ID NO: 1304)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGTAATATTACGGGGCCGTTAGAGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCCTGGTTGGTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGGTGTGGGGGGAGCCTGTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-539 (SEQ ID NO: 1305)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCGTCTATAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCGTATTGCTTATGGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGGGGGCGGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGCCTGGGATGCCGCCTGATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-540 (SEQ ID NO: 1306)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAAGCAGATTGTTGGTGGTTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGCGTCATTCTGGGTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGGGGGTTTGGGCTCCTGGGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-541 (SEQ ID NO: 1307)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCCTGCTATTGCTGCTAAGTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGGTGCGGATTCCGGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTGGTCAGCTGTGGGCGGGGCCTCCGACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-542 (SEQ ID NO: 1308)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGTAATGCTGATGGGTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGGGGCGTATTCCGGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTGGTCAGCTTTGGGAGGGTCTCCGACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-543 (SEQ ID NO: 1309)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAGGATTTATGGGTTTTAGATTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGGGTGTCTCGTTGCAAAGTGGGGTCCCATCA
 CGTTTTAGTGGCAGCGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTCAACAGACTTTGGCGTGGCCTTTTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-544 (SEQ ID NO: 1310)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTCGGGATTGGTTAATGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATTGGGGTTCCTTTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTCAACAGCTGTATGATACTCCTTATACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-545 (SEQ ID NO: 1311)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAATATTAATACGGGTTTAGATTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGATAGTTCCGCTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTCAACAGACGTCGTATTATCCTTATACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-546 (SEQ ID NO: 1312)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAAGATTTTTGGTTGGTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGGACTTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTCAACAGGTTTATTCGCTTCCTTATACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-547 (SEQ ID NO: 1313)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTTCGAATATTGGGGCGGATTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGGGGGGCGTCCGGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGTACGTACTACTGTGGGACAGCTGTGGAATGGGCCTCCTACGTTGCGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-548 (SEQ ID NO: 1314)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAGTCCGATTTATGATGGTTTAGATTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTCTGGTGCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGTTGTGGTTGGGTCCTCCGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACAG

BMS2h-549 (SEQ ID NO: 1315)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTTCGCGTATTTATAATGGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTCGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGGTGGGGGAGGCTCCTTCTACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-550 (SEQ ID NO: 1316)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGGTTTATTAATGAGGAGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTCGTGGTCTTCCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGTGCAGCCGGGGGGTGGTCCTGGGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-551 (SEQ ID NO: 1317)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGGGATATTCTGGATGAGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGTGGGGGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGTCAGCTGTGGCATGGGCCTCCGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-552 (SEQ ID NO: 1318)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGTCCTATTTATACGGGTTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGGCGGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTATGCAGGTTGGGACGGCTCCTGCTACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-585 (SEQ ID NO: 1319)

GACATCCGGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGAATATTTCTAGGCGGTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTCTTCTTCCCGGTTGCAAAGTGGGGTCCCATCA
CGTTTCGGTGGCAGTGGATCTGGGACGGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGTATAGCTATCCTCATACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-604 (SEQ ID NO: 1320)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGTCCGATTCCGCAGGATTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGTTGGGATTTCCAGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGTGGAGTGCGCCTGCTACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-605 (SEQ ID NO: 1321)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAAGTCTATTGATGGGATGTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCCTGGTTTTTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTCGGTTGAGGCGCCTTGACGTTGCGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-606 (SEQ ID NO: 1322)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGGTATATTGCTCATCCTTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCCCGGGTTTCGTCCTTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGTCAGTCGGTTGTGGTGCCTTGGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-607 (SEQ ID NO: 1323)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGGACGATTGAGGGTGGTTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCATGGGGGGTTCGGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGTTGTGGGTGGTCTCTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-608 (SEQ ID NO: 1324)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAAGTTTATTAGGGATGAGTTATATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCGGTGGTTTCGTCCTTGTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGCTGTGGCGGGCGCCTGCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-609 (SEQ ID NO: 1325)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAAGCCGATTTATGGTGGTTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCGGGGGGGTTCGGTGTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGGTGTGGGGGGGTCTCTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-610 (SEQ ID NO: 1326)

GACATCCGGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGGCCGATTAGTGGTTGTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCGATGGGGCTTCGGGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGTGGTGGGAGTATCCTCCTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-611 (SEQ ID NO: 1327)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAAGCCTATTGTGAGGGATTTAGAGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCCATGGTGTGTCCACGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGGGCAGCTTGAGGCGGCGCCTGCGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-612 (SEQ ID NO: 1328)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCGGGATATTGGTGATTGGTTATATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCGTTTGGGCGTCCGTGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCGCAGTGGGGGACTCCTCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-613 (SEQ ID NO: 1329)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTAATCGTATTGAGTATGGTTTAGATTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTCGGGGTCTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTAGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTTGAGGCGGCGCCTGCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-614 (SEQ ID NO: 1330)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCGGAATATTGGGCATTTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTTGGGGGGTCTCGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGGTGGAGCCTCCTGCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-615 (SEQ ID NO: 1331)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTTCGAGTATTTATAGTGATTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGATGGGTGGTCCGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTGCATCGTGCTCCTGCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-616 (SEQ ID NO: 1332)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGGTTTATTACTGATCGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTGGTTCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGAGTTCGGAGTTGCCTTGGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-617 (SEQ ID NO: 1333)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCGTAAGATTGGTAGTGAGTTATATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGTGGTAGGTCCCGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGTTGTGGGAGCCTCCTGCGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-618 (SEQ ID NO: 1334)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTAGGAATATTGGTAATGGTTTAGATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCGGGGAGGGTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGGGCAGCTTTGGCATACTCCTCCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-619 (SEQ ID NO: 1335)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCGGAATATTTATGGTTGGTTATCGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCGGTGGTGGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGATTATACGTTGCCTGGTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-730 (SEQ ID NO: 1336)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTAAGGATTGGTTACATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTGCGTCCGGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTCTGCTACGTACTACTGTCAACAGCATTATAGTACGCCTTATACGTCCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-731 (SEQ ID NO: 1337)

GACATCCAGATGACCCAGTCTCCACCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTTGATTTCTTCTCATTTAGATTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGGTCTATGATGCTTCCGAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGCATCGCAGTCTGCCTTTTACGTTTCGGCCAA
 GGGACCAAGGTAGAAATCAAACGG

BMS2h-732 (SEQ ID NO: 1338)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTGGATTGGTGGGGCGTTAGCGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTTATCTATCAGATTTCCGTTTTGCAAAGTGGGATCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATATTCCGTCTCCTTTTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-733 (SEQ ID NO: 1339)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAGTATTGGGGCGGCGTTAAATTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGTCTGTCTCTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGCTGTTTAGGCTTCCTTTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-734 (SEQ ID NO: 1340)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCCTATTGGGGGTCTTTAGTGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGGTCTTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTATGCTGAGGCTCCTATTACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-735 (SEQ ID NO: 1341)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAATATTGGGTCTAGTTTAATTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTACGCTCCTGATCTATTATTCGTCCAAGTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTCTTTGTGAGTCCCTTATACGGTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-736 (SEQ ID NO: 1342)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTGGATTGGGAGTGAGTTAGCGTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATTGGACGTCCAATTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGATTCTGGAGACTCCTTTGACGTTTGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-737 (SEQ ID NO: 1343)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGAAGATTTGGGATGCTTTATATTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATCGTGGGTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTTTTATCGGTGGCCTCATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-738 (SEQ ID NO: 1344)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCATATTGAGGATTCTTTACGGTGGTACCAGCAGAAACCA

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GGGAAAGCCCCTAAGCTCCTGATCTATTATGGTTCCTGTGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATGTATAAGTTTCCTATTACGTTTCGGCCAA
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BMS2h-739 (SEQ ID NO: 1345)

GACATCCAGACGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCGGATTAATTCTTCTTTACTGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATACTTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTAGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTCGCTACGTACTACTGTCAACAGATTTGGGGTTCGCCTCCTACGTTTCGGCCAG
GGGACCAAGGTGGAAATCAAACGG

BMS2h-740 (SEQ ID NO: 1346)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGTCGATTCTGTTGGTTTAAATTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATTCTGGGTCCACTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGGATTGGTATTATCCTAATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-785 (SEQ ID NO: 1347)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGCCTATTTATGGTTGGTTAAATTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTTGACGTCCGGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGATTATAGTTCTCCTTTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-8 (SEQ ID NO: 1348)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGTTTATTGATACGTCGTTAGAGTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGATGGGTCCCATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTAGCTACGTACTACTGTCAACAGTATTGGGTTCTTCTCTGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-86 (SEQ ID NO: 1349)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGGGGATGCTTTATTTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATTATTCTTCCATGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGCGGCATAGTACTCCTGCTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-87 (SEQ ID NO: 1350)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGGATATTGATGAGTCTTTAATGTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAGGCTCCTGATCTATGGGGTGTCTATTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTCGCTACGTACTACTGTCAACAGCGGTGGAAGGCTCCTTTTACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

BMS2h-88 (SEQ ID NO: 1351)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTTACC
ATCACTTGCCGGGCAAGTCAGGAGATTGTGGAGGATTTATATTGGTATCAGCAGAAACCA
GGGAAAGCCGCTAAGCTCCTGATCTATGGTGCGTCTGGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTCAACAGACGCGTAGGCGTCCTTATACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGG

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BMS2h-89 (SEQ ID NO: 1352)

GACATCCAGATGACCCAGTCTCCAGCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGGATATTGATCCTATGTTAAGGTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCGGGTTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGACGCTGGTGACTCCTTATACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-90 (SEQ ID NO: 1353)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGTCGATTTTCGGATGCGTTATTTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAGGCTCCTGATCTATTATGGTTCCGTTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGCGTTTTTCAGGAGCCTGTGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

BMS2h-91 (SEQ ID NO: 1354)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCCGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGCCGGGCAAGTCAGCAGATTAGTGATGAGTTAAATTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGTGTCCATTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTCAACAGTGGTTGAGTTTTCTTCGACGTTTGGCCAA
 GGGACCAAGGTGGAAATCAAACGG

Example 1

Generation of Human Anti-CD40L Variable Domains

BMS2h-2 through BMS2h-785

The following example describes the generation of the 2h lineage of anti-human CD40L variable domains, designated BMS2h-2 through BMS2h-785. Following recombinant expression of a repertoire of single immunoglobulin variable domains on the surface of phage, selection is performed by contacting the phage repertoire with immobilized target antigen, washing to remove unbound phage, and propagating the bound phage. This process is frequently referred to as “panning.” It is applicable to the screening of single immunoglobulin variable domains, as well as other antibody fragments that can be expressed on a display library, e.g., scFv, Fab, and Fab’. Alternatively, phage may be pre-selected for the expression of properly folded member variants by panning against an immobilized generic ligand (e.g., protein A or protein L) that is only bound by folded members. This has the advantage of reducing the proportion of non-functional members, thereby increasing the proportion of members likely to bind a target antigen. Pre-selection with generic ligands is taught in WO 99/20749, for example. The screening of phage antibody libraries is generally described, for example, by Harrison et al., *Meth. Enzymol.* 267: 83-109 (1996).

Screening is commonly performed using purified antigen immobilized on a solid support, for example, plastic tubes or wells, or on a chromatography matrix, for example SepharoseTM (Pharmacia). Screening or selection can also be performed on complex antigens, such as the surface of cells (Marks et al., *BioTechnology* 11: 1145 (1993); de Kruif et al., *Proc. Natl. Acad. Sci. USA* 92: 3938 (1995)). Another alternative involves selection by binding biotinylated antigen in solution, followed by capture on streptavidin-coated beads.

dAb Selection for Clone BMS2h-719 and BMS2h-7xx Series:

Three rounds of selection using decreasing concentrations of antigen (500 nM at round 1; 50 nM at round 2; 50 nM or 5 nM at round 3 depending on the library output used) were performed in parallel against biotinylated (1.2 moles biotin/mole CD40L) human CD40L monomer triple mutant (T211E, S222Y, H224K, [108-261] Construct #7) provided by Bristol-Myers Squibb. Phage from the naïve 4G and 6G Domantis dAb libraries were combined into the pools a) to g) indicated below before initiating selections:

- a) 4G VH CDR3 lengths between 7 – 10 amino acids.
- b) 4G VH CDR3 lengths between 11 – 15 amino acids.
- c) 4G VH CDR3 lengths between 7 – 15 amino acids.
- d) 4G VK
- e) 6G VH CDR3 lengths between 7-9
- f) 6G VH CDR3 lengths between 10-15
- g) 6G VK

Each round of selection involved adding the desired concentration of biotinylated CD40L to a mixture of 200 µl of phage (from one of the naïve library pools indicated above, or subsequent selection output phage) and 1000 µl of 2% MPBS (Phosphate Buffered Saline) containing 2% (w/v) Marvel [Premier Foods, UK]) and incubating at room temperature for 1 hour by mixing end-over-end. The biotinylated antigen phage complex was then captured by adding 100 µl of resuspended Dynabeads M-280 Streptavidin [Invitrogen, UK] and incubated for 5 minutes with mixing end-over-end at room temperature. The Dynabeads were then recovered using a KingFisher magnetic separator [Thermo Fisher Scientific, UK] and washed 7 x 1 ml PBST (PBS containing 0.1% (v/v) polyoxyethylenesorbitan 20 monolaurate [Sigma-Aldrich, UK]) followed by 1 x 1 ml PBS. Bound phage retained on the

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washed Dynabeads were eluted by incubation with 500 µl of trypsin-PBS (50 µl of 10 mg/ml trypsin [Sigma-Aldrich, UK] dissolved in 50 mM Tris-HCl pH 7.4, 1 mM CaCl₂ added to 450 µl PBS). The phage-containing solution was recovered and 250 µl used to infect 1.75 ml of logarithmic growth phase *E. coli* TG1 (at an OD₆₀₀ of 0.4) for 30 minutes at 37°C. The *E. coli* TG1 phage infected culture was centrifuged at 11,600 g in a micro centrifuge for 1 minute and the resulting cell pellet resuspended in 1 ml 2xTY (16 g Tryptone, 10 g Yeast Extract and 5 g NaCl in 1 litre, autoclaved for 15 minutes at 121°C) and plated onto a 9 cm Petri dish containing TYE media supplemented with 15 µg/ml tetracycline. The plates were incubated overnight at 37°C then 2 ml of 2xTY supplemented with 15% glycerol was added to each plate and cells loosened with a glass spreader and mixed thoroughly. Fifty microlitres of the scraped bacteria was used to inoculate 50 ml of 2xTY supplemented with 15 µg/ml tetracycline and grown overnight at 37°C with shaking at 250 rpm. The overnight culture was centrifuged at 3,300 g for 15 min to pellet the bacteria. To precipitate phage, 10 ml PEG/NaCl (20% Polyethylene glycol 8000, 2.5 M NaCl) was added to 40 ml supernatant. The phage/PEG solution was mixed and left on ice for 1 h, then spun at 3,300 g for 30 min at 4°C and the supernatant discarded. The pellet was resuspended in 2 ml PBS and spun at 11,600 g for 10 min in a micro centrifuge to remove the remaining bacterial debris. The resultant supernatant containing phage was then used for the next round of selection against the appropriate concentration of biotinylated CD40L monomer triple mutant antigen.

Phage ELISA:

Monoclonal phage ELISAs were carried out following selection rounds 2 and 3. All washes were performed using 3 washes of 250 µl PBST followed by 3 washes of 250 µl PBS. The plates were coated overnight at 4°C with 50 µl/well of 1 µg/ml NeutrAvidin [Thermo Scientific, UK] in 0.2M carbonate-bicarbonate buffer, pH 9.4. The plates were washed and then blocked with 2% MPBS for 1 hour at room temperature. The plates were then washed and incubated with 50 µl/well of ~1.0 µg/ml biotinylated human CD40L monomer triple mutant in 2% MPBS. The plates were washed and 25 µl/well phage supernatants added to an equal volume of 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and bound phage detected with 50 µl/well anti-M13-HRP conjugate [GE Healthcare, UK] diluted 1:5000 in 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed using 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA]. The colorimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Specific

phage were identified by comparison to wells coated with NeutrAvidin but without biotinylated CD40L monomer triple mutant.

Recovery of dAb genes from MidiPrep pDOM4 Plasmid:

The dAb V-genes from the following round 3 outputs were recovered by DNA restriction enzyme digestion of the phage vector pDOM4:

- a) 4G VH CDR3 lengths between 7 – 10 amino acids (50 nM antigen concentration).
- b) 4G VH CDR3 lengths between 11 – 15 amino acids (50 nM antigen concentration).
- c) 4G VH CDR3 lengths between 11 – 15 amino acids (5 nM antigen concentration).
- d) 4G VH CDR3 lengths between 7 – 15 amino acids (50 nM antigen concentration)..
- e) 4G VK (50 nM antigen concentration).
- f) 4G VK (5 nM antigen concentration).
- g) 6G VH CDR3 lengths between 7-9 (50 nM antigen concentration).
- h) 6G VH CDR3 lengths between 10-15 (5 nM antigen concentration).

Approximately 20 µg of MidiPrep [Qiagen, UK] DNA was digested with *SalI* and *NotI* as follows: 20 µl DNA (~1 µg/µl) was mixed with 1.5 µl *SalI* (20 U/µl) [NEB, UK] and 3 µl *NotI* (10 U/µl) [NEB, UK], 4 µl Buffer 3 [NEB, UK], 0.4 µl BSA (10 mg/ml) [NEB, UK] and tissue culture grade water [Sigma, UK] added to 40 µl. Samples were incubated for 5 hours at 37°C in an air incubator following which the digested dAb genes were isolated by running the digestion mix on a 2% agarose gel [E-gel, Invitrogen, UK], the appropriate DNA bands excised and cleaned using a PCR purification kit [Qiagen, UK]. The purified V-genes were ligated into a *SalI* and *NotI* double digested pDOM5 expression vector.

Soluble dAb ELISA:

Binding dAbs were identified as follows. Ninety-six individual colonies containing dAb V-genes cloned into the soluble dAb expression vector pDOM5 were picked from each output into 200 µl Terrific Broth containing OnEx Autoinduction media [Novagen, UK] and incubated overnight at 37° C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters [Corning Incorporated, USA] sealed with a gas permeable adhesive plastic strip. The cultures were centrifuged to pellet the cells and the supernatants assayed by antigen binding ELISA for dAbs that bound to CD40L monomer triple mutant and IZ-CD40L mutant

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(CD40L containing an isoleucine zipper trimerization domain, supplied by Bristol-Myers Squibb). MaxiSorp 96 well immunoplates [Nunc, USA] were coated overnight at 4°C with 50 µl/well of 1 µg/ml NeutrAvidin in 0.2 M carbonate-bicarbonate buffer, pH 9.4. All washes were as described for the phage ELISA. The plates were blocked for 1 hour at room temperature with 200 µl of PBS containing 1% Tween 20. The plate was then washed and incubated for 1 hour at room temperature with 50 µl/well of 1 µg/ml biotinylated human CD40L monomer triple mutant in PBST or 1 µg/ml biotinylated human IZ-CD40L mutant in PBST (both antigens supplied by Bristol-Myers Squibb). The ELISA plate was washed and dAb-containing culture supernatant clarified by centrifugation at 1,800 g for 10 min at 4°C, then added to the ELISA plate (30 µl/well) to which was added an equal volume of PBST. The plates were incubated for 1 hour at room temperature and then washed. Bound dAb was detected by adding 50 µl/well 9E10 [anti-myc IgG, Sigma-Aldrich, UK] diluted 1:2000 in PBST and incubating for 1 hour at room temperature; the ELISA plate was then washed and 50 µl/well anti-mouse Fc-HRP [Sigma-Aldrich, UK] diluted 1:2000 in PBST added and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed by adding 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA] and the colour allowed to develop. The colourimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Antigen binding dAbs were identified by comparison of the signal intensity from human CD40L monomer triple mutant and human IZ-CD40L mutant wells with control wells not containing antigen.

Expression & Purification of dAb at 50 ml Scale:

Unique dAbs were identified by DNA sequencing ELISA positive clones. The unique dAbs identified were expressed as follows in 250 ml baffled flasks, to which was added:

- a) 50 ml of Terrific Broth [Sigma-Aldrich, UK].
- b) 100 µg/ml carbenicillin [Sigma-Aldrich, UK].
- c) 1 drop of antifoam A204 [Sigma-Aldrich, UK].
- d) Novagen Overnight Express Autoinduction Kit [Novagen, UK].

A bacterial scrape from a fresh confluent 9 cm diameter agar plate or from a glycerol stock of the desired dAb clone was used to inoculate the Terrific Broth, then the flask sealed with Milliwrap PTFE membrane [Millipore, UK], and incubated for 48 hrs, 250 rpm shaking at 30°C. The bacterial overnight culture was clarified by centrifugation and the VH or VK

dAb purified using Streamline Protein A [GE Healthcare, UK] or Protein L agarose [generated in-house] respectively. The resulting purified proteins were assayed by RBA to determine which clones could inhibit the binding of CD40L for CD40.

CD40L Bead Receptor Binding Assay:

Inhibitory dAbs were initially identified by screening purified dAb in a CD40L bead receptor binding assay (RBA). Sphero streptavidin polystyrene beads (0.5% w/v, 6.7µm diameter) [Saxon, Europe] were prepared and washed according to the manufacturer's instructions. The beads were then pelleted at 11,600 g for 1 minute, the supernatant discarded and the beads resuspended in 1 ml PBS by vortexing. The washing step was repeated twice more, the supernatant discarded and the beads resuspended in 1 ml (0.5 mg/ml) of biotinylated human IZ-CD40L in PBS and incubated overnight at room temperature with end-over-end rotation. Following incubation, the beads were pelleted and washed three times with 1 ml PBS as before and then resuspended in 0.5 ml PBS containing 0.1% bovine serum albumin (BSA). The antigen coated beads were then diluted 1:10 in PBS containing 0.1% BSA prior to use. The reagents for the RBA assay were added as follows to duplicate wells in a 384-well black sided clear bottomed FMAT plate [Applied Biosystems, UK]:

- a) 12.5 µl dAb protein or buffer control. The dAb titration starting concentration was typically 10 µM (final concentration) which was diluted 1:3.3 (i.e., 30 µl sample added to 70 µl PBS containing 0.1% BSA) to produce an 8-point titration effect curve.
- b) 12.5 µl CD40-Fc [supplied by Bristol-Myers Squibb, USA; lot CY24Feb06-1] at 0.2 µg/ml (for a final concentration of 0.05 µg/ml) diluted in PBS containing 0.1% BSA.
- c) 12.5 µl Mixture of mouse anti-human Fc [Sigma-Aldrich, UK] at 2 µg/ml (for a final concentration of 0.5 µg/ml) and goat anti-mouse Alexa Fluor 647 [Invitrogen, UK] at 1 µg/ml (for a final concentration of 0.25 µg/ml) diluted in PBS containing 0.1% BSA.
- d) 12.5 µl IZ-CD40L coated beads described above were added to the centre of the well so they did not disperse to the edge of the well.

Following addition of the reagents to the 384 well plate, it was incubated at room temperature for 6 hours in the dark and then read in an AB8200 FMAT system [Applied Biosystems, UK].

Example 2

dAb Selection for Clone BMS2h-572

Three rounds of selection using decreasing concentrations of antigen (300 nM at round 1; 30 nM at round 2; 3 nM at round 3) were performed in parallel against biotinylated (1.42 moles biotin/mole trimer) human isoleucine zipper-CD40L (IZ-hCD40L) provided by Bristol-Myers Squibb. Phage from the naïve 4G and 6G Domantis dAb libraries were combined into the pools a) to h) indicated below before initiating selections:

- a) 4G VH CDR3 lengths between 7 – 9 amino acids.
- b) 4G VH CDR3 lengths between 10 – 12 amino acids.
- c) 4G VH CDR3 lengths between 13 – 15 amino acids.
- d) 4G VK
- e) 6G VH CDR3 lengths between 7-9
- f) 6G VH CDR3 lengths between 10-12
- g) 6G VH CDR3 lengths between 13-15
- h) 6G VK

Each round of selection involved adding the desired concentration of biotinylated CD40L to a mixture of phage (from one of the naïve library pools indicated above, or subsequent selection output phage) in 1000 µl of 2% MPBS (Phosphate Buffered Saline containing 2% (w/v) Marvel [Premier Foods, UK]) and incubating at room temperature for 1 hour by mixing end-over-end. The biotinylated antigen phage complex was then captured by adding 100 µl of resuspended Dynabeads M-280 Streptavidin [Invitrogen, UK] (rounds 1 and 3) or 50 µl of M-280 tosylactivated Dynabeads (Invitrogen) that had been coupled with NeutrAvidin [Thermo Fisher Scientific, UK] (round 2) and incubated for 5 minutes with mixing end-over-end at room temperature. The Dynabeads were then recovered using a KingFisher magnetic separator [Thermo Fisher Scientific, UK] and washed 7 x 1 ml PBST (PBS containing 0.1% (v/v) polyoxyethylenesorbitan 20 monolaurate [Sigma-Aldrich, UK])

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followed by 1 x 1 ml PBS. Bound phage retained on the washed Dynabeads were eluted by incubation with 500 µl of trypsin-PBS (50 µl of 10 mg/ml trypsin [Sigma-Aldrich, UK] dissolved in 50 mM Tris-HCl pH 7.4, 1 mM CaCl₂ added to 450 µl PBS). The phage-containing solution was recovered and 250 µl used to infect 1.75 ml of logarithmic growth phase *E. coli* TG1 (at an OD₆₀₀ of 0.4) for 30 minutes at 37°C. The *E. coli* TG1 phage infected culture was centrifuged at 11,600 g in a micro centrifuge for 1 minute and the resulting cell pellet resuspended in 1 ml 2xTY (16 g Tryptone, 10 g Yeast Extract and 5 g NaCl in 1 litre, autoclaved for 15 minutes at 121°C) and plated onto a 9 cm Petri dish containing TYE media supplemented with 15 µg/ml tetracycline. The plates were incubated overnight at 37°C then 2 ml of 2xTY supplemented with 15% glycerol was added to each plate and cells loosened with a glass spreader and mixed thoroughly. Fifty microlitres of the scraped bacteria was used to inoculate 50 ml of 2xTY supplemented with 15 µg/ml tetracycline and grown overnight at 37°C with shaking at 250 rpm. The overnight culture was centrifuged at 3,300 g for 15 min to pellet the bacteria. To precipitate phage, 10 ml PEG/NaCl (20% Polyethylene glycol 8000, 2.5 M NaCl) was added to 40 ml supernatant. The phage/PEG solution was mixed and left on ice for 1 h, then spun at 3,300 g for 30 min at 4°C and the supernatant discarded. The pellet was resuspended in 2 ml PBS and spun at 11,600 g for 10 min in a micro centrifuge to remove the remaining bacterial debris. The resultant supernatant containing phage was then used for the next round of selection against the appropriate concentration of biotinylated IZ-hCD40L.

Phage ELISA:

Monoclonal phage ELISAs were carried out following selection rounds 2 and 3. All washes were performed using 3 washes of 250 µl PBST followed by 3 washes of 250 µl PBS. The plates were coated overnight at 4°C with 50 µl/well of 1 µg/ml IZ-hCD40L in PBS. The plates were washed and then blocked with 2% MPBS for 1 hour at room temperature. The plates were washed and 25 µl/well phage supernatants added to an equal volume of 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and bound phage detected with 50 µl/well anti-M13-HRP conjugate [GE Healthcare, UK] diluted 1:5000 in 2% MPBS and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed using 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA]. The colorimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Specific phage were identified by comparison to wells that were not coated with antigen but otherwise identically treated.

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Recovery of dAb genes from pDOM4 plasmid:

The dAb V-genes from round 2 and 3 outputs were recovered by *SalI* and *NotI* restriction enzyme digestion of the phage vector pDOM4 and ligated into a *SalI* and *NotI* double digested pDOM5 expression vector.

Soluble dAb ELISA:

Binding dAbs were identified as follows. Ninety-six individual colonies containing dAb V-genes cloned into the soluble dAb expression vector pDOM5 were picked from each output into 200 µl Terrific Broth containing OnEx Autoinduction media [Novagen, UK] and incubated overnight at 37° C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters [Corning Incorporated, USA] sealed with a gas permeable adhesive plastic strip. The cultures were centrifuged to pellet the cells and the supernatants assayed by antigen binding ELISA for dAbs that bound to IZ-hCD40L. MaxiSorp 96 well immunoplates [Nunc, USA] were coated overnight at 4°C with 50 µl/well of 1 µg/ml IZ-hCD40L in PBS. All washes were as described for the phage ELISA. The plates were blocked for 1 hour at room temperature with 200 µl of PBS containing 1% Tween 20. The ELISA plate was washed and dAb-containing culture supernatant clarified by centrifugation at 1,800 g for 10 min at 4°C, then added to the ELISA plate (30 µl/well) to which was added an equal volume of PBST. The plates were incubated for 1 hour at room temperature and then washed. Bound dAb was detected by adding 50 µl/well 9E10 [anti-myc IgG, Sigma-Aldrich, UK] diluted 1:2000 in PBST and incubating for 1 hour at room temperature; the ELISA plate was then washed and 50 µl/well anti-mouse Fc-HRP [Sigma-Aldrich, UK] diluted 1:2000 in PBST added and incubated for 1 hour at room temperature. The plates were washed and the ELISA developed by adding 50 µl/well SureBlue 1-Component TMB MicroWell Peroxidase solution [KPL Inc, USA] and the colour allowed to develop. The colorimetric reaction was stopped by the addition of an equal volume of 1 M HCl and the ELISA plate read at 450 nm. Antigen binding dAbs were identified by comparison of the signal intensity from IZ-hCD40L wells with control wells not containing antigen.

Example 3**Identification of Clones BMS2h-503-1, BMS2h-719-2, and BMS2h-572-6**

BMS2h-503, BMS2h-719 and BMS2h-572 dAbs were subjected to error-prone affinity maturation to generate BMS2h-503, BMS2h-719 and BMS2h-572 lineages,

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respectively. This was performed using random mutagenesis where on average 3.6 amino acid changes were introduced per dAb. Phage libraries (average size 6×10^8) were selected using biotinylated monomeric and trimeric human CD40L with alternating streptavidin/neutravidin bead capture of the antigen (as described). Three rounds of selections using decreasing concentrations of antigen (100 nM at round 1; 10 nM at round 2; 1 nM at round 3) were performed. Sequencing was used to monitor diversity following each selection round. Selection outputs (round 2 selected on CD40L trimer for BMS2h-572; round 3 selected on CD40L trimer for BMS2h-503 and round 3 selected on CD40L monomer for BMS2h-719) were sub-cloned into soluble expression vector pDOM13 (no C terminal tag) (as described) and screened as monoclonal bacterial micro-culture supernatants by BIAcore for improved off-rates compared to parental clones on both monomeric and trimeric CD40L. Identified improved variants were DNA sequenced and unique dAbs expressed, purified and then assayed using the BMS2h bead RBA as well as cellular CD40L driven assays (as described). As a result, BMS2h-503-1 (sequence listed in TABLE 3), BMS2h-719-2 and BMS2h-572-6 dAbs (sequences listed in TABLE 1) were identified. Activities of these dAbs are listed in TABLE 5 below.

Formatting BMS2h-503-1, BMS2h-719-2 and BMS2h-572-6 as Fc fusions

BMS2h-572-6, BMS2h-503-1 and BMS2h-719-2 dAbs were cloned into pDOM38 vector containing Fc tail derived from human IgG1 to create DMS0502, DMS0500 and DMS0501, respectively. BMS2h-572-6, BMS2h-503-1 and BMS2h-719-2 dAbs were also cloned into pDOM38 vector containing Fc tail derived from human IgG4 to create DMS0505, DMS0506 and DMS0504, respectively. The constructs were transiently expressed in HEK293 cells and the proteins were purified using Protein A. Purified Fc fusions were analysed by Biacore for binding to monomeric and trimeric CD40L as well as in various cell assays (as described).

Identification of clones BMS2h-572-608, BMS2h-572-614 and BMS2h-572-619

BMS2h-572-6 dAb was subjected to affinity maturation using doped oligo approach. Four doped libraries were constructed for this dAb:

Library 1 – 5 residues in CDR1 diversified

Library 2 – 6 residues in CDR2 diversified

Library 3 – 13 residues in CDR2 diversified

Library 4 – 7 residues in CDR3 diversified

In each library, diversification was performed using nnS codons where n retained a large fraction of the parent base (85%) and split the rest between the equimolar amounts of the remaining three bases (5% each) and S stood for G or C. Phage libraries (average size 8×10^8) were selected using biotinylated monomeric and trimeric human CD40L with alternating streptavidin/neutravidin bead capture of the antigen (as described). Libraries 2 and 3 were pulled together during the selection process. Three rounds of selections using decreasing concentrations of antigen (50 nM at round 1; 5 nM at round 2; 1 nM at round 3 with 200 fold excess of competitor – non biotinylated CD40L trimer) were performed. Sequencing was used to monitor diversity following each selection round. Selection outputs (rounds 2 and 3) were sub-cloned into soluble expression vector pDOM13 (no C terminal tag) (as described) and screened as monoclonal bacterial micro-culture supernatants by BIAcore for improved off-rates compared to parental clones on both monomeric and trimeric CD40L. Identified improved variants were DNA sequenced and unique dAbs expressed, purified and then assayed using the BMS2h bead RBA as well as cellular CD40L driven assays (as described). As a result, BMS2h-572-608, BMS2h-572-614 and BMS2h-572-619 dAbs were identified.

Construction of clone BMS2h-572-633

Sequence analysis revealed that all of the amino acid differences between BMS2h-572-608 and the parental dAb BMS2h-572-6 were located in CDR1 and the differences between BMS2h-572-614 and parental dAb BMS2h-572-6 were located in CDR3. Both matured dAbs shared CDR2 with the parental dAb BMS2h-572-6. This created an opportunity to construct a combination mutant which had CDR1 of BMS2h-572-608 and CDR3 of BMS2h-572-614. Firstly, CDR1 region of BMS2h-572-608 was PCR amplified. Secondly, CDR2+CDR3 fragment of BMS2h-572-614 was PCR amplified. This was followed by SOE PCR assembly of the two fragments to create a combination mutant BMS2h-572-633. The assembled dAb PCR product was cloned into soluble expression vector pDOM13 (no C terminal tag), sequence verified, expressed, purified and then assayed using the BMS2h bead RBA as well as cellular CD40L driven assays (as described).

Formatting BMS2h-572-633 as Fc fusion

BMS2h-572-633 dAb was cloned into pDOM38 vector containing Fc tail derived from human IgG1 to create DMS0507. The construct was transiently expressed in HEK293

cells and the protein was purified using Protein A. Purified Fc fusion was analysed by Biacore for binding to monomeric and trimeric CD40L as well as in various cell assays (as described).

Example 4

CD40L Activity Cell Assays

Anti-human CD40L dAbs were assayed functionally for their ability to antagonize CD40L activities. The CD40L activities tested were B cell proliferation and cytokine production by hCD40L-driven activation of primary monocytes-derived dendritic cells (DCs). Unless otherwise noted, all assays were performed in RPMI media supplemented with 10% fetal calf serum (FCS). The results of various assays, described in detail below, are shown in TABLE 5 and TABLE 6.

Soluble IZ-hCD40L-driven primary human B cell proliferation:

1×10^5 tonsillar human B cells were incubated with 0.6 $\mu\text{g/ml}$ of IZ-hCD40L along with varying titration of dAb or mAb in a final volume of 200 $\mu\text{l/well}$ in a 96-well round bottom plate. The plates were incubated at 37°C for 72 hours following which thymidine (^3H ; 0.5 $\mu\text{Ci/well}$) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

CHO-hCD40L-driven primary human B cell proliferation:

CHO cells were transfected with human CD40L to generate a stable cell line expressing high levels of CD40L on the cell surface. CHO-CD40L cells were irradiated at 10,000 Rads before incubation with human B cells. 1×10^5 tonsillar human B cells were incubated with 1×10^3 CHO-CD40L cells (1:100 ratio of CHO-CD40L: human B cells) along with varying titration of dAb or mAb in a final volume of 200 $\mu\text{l/well}$ in a 96-well round bottom plate. The plates were incubated at 37°C for 72 hours following which thymidine (^3H ; 0.5 $\mu\text{Ci/well}$) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

Primary T cell-driven human B cell proliferation:

T cells were isolated from human peripheral blood mononuclear cells (PBMCs) and enriched using via sheep red blood cell (SRBC) affinity. Enriched human T cells were cultured with PM-LCLs (EBV-transformed B cell line; irradiated at 10,000 Rads) at a 5:1 ratio (T:LCL) for 6 days at 37°C to generate a population of allogeneic T cells. At day 6, the expanded T cells were isolated and irradiated at 3000 Rads, and then cultured (5×10^4 T cells/well) with primary human tonsillar B cells (1×10^5 B cells/well) at a 1:2 ratio in 96-well flat bottom plated coated with anti-CD3 mAb (OKT3). Varying titrations of dAbs/mAbs were added to each well; the final volume in each well was 200 μ l. Test plates were incubated at 37°C for 3 days. Human B cell proliferation was determined via the addition of thymidine (^3H ; 0.5 μ ci/well) to the cultures for the last 18 hours. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS). In some instances, the supernatant was harvested and measured for the presence of IL-6.

CHO-hCD40L-driven activation of primary human monocytes-derived dendritic cells (DCs):

Human PBMCs were enriched for monocytes by depleting T cells via SRBC resetting. The monocyte-enriched PBMCs were cultured with 10 ng/ml GM-CSF and 5 ng/ml IL-4 in 6-well plates for six days at 37°C. The cultured plates were replenished with fresh media (with GM-CSF and IL-4) on days 2 and 5. The immature DCs were used in cell assays on day 6. 8×10^4 immature DCs were cultured with 4×10^3 CHO-hCD40L cells (irradiated at 10,000 Rads) along with varying titrations of dAbs/mAbs in a 96-well flat bottom plate. After 24 hours, supernatants were harvested and tested for the presence of various cytokines (IL-12, TNF, IL-23). DC activation was determined by the levels of cytokine production. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

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TABLE 5

Potency of Monomeric dAb Molecules in Various Primary Cell Assays

Clone	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
2h116-13	130.0 ± 40.0	1300.0, 700.0		888.0, >2000.0, 1000.0
2h116-1312	23.0 ± 3.0	530.0 ± 300.0	234 ± 46	112.0 ± 47.0
2h116-1313	29.0 ± 4.0	211.0, 334.0	258 ± 79	136.0 ± 51.0
2h116-1314	41.0 ± 10.0	1300.0, 4400.0	1687 ± 1150	664.0 ± 353.0
2h116-1319	180.0 ± 57.0	>7000.0		
2h116-1320	20.0 ± 7.0	138.0 ± 60.0	191 ± 72	32.0 ± 10.0
2h437	5700.0 ± 1800			
2h437-4	203.0 ± 90.0	>7000.0		1329.0 ± 412.0
2h492	>7000.0			
2h492-3	1100.0 ± 400.0	>7000.0		
2h492-4	1700.0 ± 900.0	>7000.0		
2h492-5	2300.0 ± 700.0			
2h492-6	6300.0 ± 1400.0			
2h492-7	1900.0 ± 600.0			
2h494	6100.0 ± 1200.0			
2h494-2	4800.0 ± 2300.0			
2h494-3	>7000.0			
2h494-4	590.0 ± 250.0	>7000.0		
2h494-6	2000.0 ± 2100.0	>7000.0		
2h503	4200.0 ± 316.0	>7000.0		
2h503-1	24.0 ± 2.0	2300.0 ± 700.0		756.0 ± 333.0

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L- driven DC Activation IL-12 EC50 (nM)
2h503-104	16.0, 19.0			
2h503-2	44.0 ± 6.0	3000.0 ± 1000.0		1562.0 ± 96.0
2h572	>7000.0			
2h572-6	208.0 ± 73.0	>7000.0	>7000.0	>2000.0, 608.0 ± 260.0
2h572-604	254.0, 354.0	>700.0		387.0
2h572-608	96.0 ± 19.0		>7000.0	152.0 ± 61.0
2h572-610	109.0 ± 34.0		>7000.0	207.0± 87.0
2h572-614	93.0 ± 53.0		>7000.0	135.0± 54.0
2h572-616	204.0, 340.0		>7000.0	608.0 ± 136.0
2h572-617	157.0, 189.0		>7000.0	338.0 ± 101.0
2h572-619	90.0 ± 62.0	421.0, 1496.0	>7000.0	188.0± 41.0
2h572-622	301.0, 293.0		>7000.0	281.0± 127.0
2h572-623	181.0, 261.0		>7000.0	280.0 ± 73.0
2h572-630	103.0 ± 71.0			246.0± 240.0
2h572-631	108.0 ± 77.0			230.0 ± 200.0
2h572-632	117.0 ± 91.0			241.0 ± 190.0
2h572-633	20.0 ± 15.0			53.0 ± 60.0
2h572-634	31.0 ± 18.0			77.0 ± 67.0
2h572-635	29.0 ± 19.0			52.0 ± 26.0
2h572-9	324.0, 243.0			>2000.0
2h572-11	140.0 ± 33.0	>7000.0		671.0 ± 165.0
2h572-12	79.0, 76.0			225.0, >2000.0
2h572-14	134.0 ± 12.0	>7000.0		882.0 ± 310.0

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L- driven DC Activation IL-12 EC50 (nM)
2h572-15	168.0 ± 67.0	>7000.0		876.0 ± 391.0
2h572-22	357.0, 305.05			
2h702	>7000.0			
2h703	>7000.0			
2h706	>7000.0			
2h707	>7000.0			
2h710	>7000.0			
2h712	>7000.0			
2h717	>7000.0			
2h719	600.0 ± 640.0			134.0, 646.0
2h719-2	82.0 ± 39.0	>7000.0		196.0 ± 150.0
2h719-202	29.0 ± 12.0			79.0 ± 29.0
2h719-203	81.0, 96.0			
2h719-213	62.0, 98.0			
2h719-214	66.0, 89.0			
2h719-215	92.0, 91.0			
2h719-218	57.0, 60.0			
2h719-225	253.0, 198.0			176.0 ± 84.0
2h719-226	164.0, 247.0			812.0 ± 53.0
2h719-12	358.0 ± 159.0			266.0 ± 66.0
2h719-13	50.0 ± 8.0	659.0, 683.0, 4450.0, 1750.0		219.0 ± 88.0
2h719-17	132.0 ± 50.0	236.0, 268.0		113.0 ± 49.0
2h719-19	138.0 ± 31.0	202.0, >7000.0, >7000.0, 3800.0,		184.0 ± 99.0

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L- driven DC Activation IL-12 EC50 (nM)
		5400.0		
2h722	>7000.0			
2h723	>7000.0			
2h725	6400.0 ± 1200.0			
2h725-2	>7000.0			
2h725-9	>7000.0			
2h725-19	>7000.0			
2h726	>7000.0			
2h730	>7000.0			
2h731	5800.0 ± 2500.0			
2h744	>7000.0			
2h745	6400.0, 3500.0, >7000.0			
2h745-1	>7000.0			
2h745-2	>7000.0			
2h745-9	>7000.0			
2h745-13	>7000.0			
2h745-14	>7000.0			
2h746	>7000.0			
2h747	>7000.0			
2h752	>7000.0			
2h754	6600.0 ± 900.0			
2h757	6400.0 ± 800.0			
2h758	5900.0 ± 1500.0			

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L- driven DC Activation IL-12 EC50 (nM)
2h758-1	>7000.0			
2h758-2	>7000.0			
2h758-3	>7000.0			
2h758-4	>7000.0			
2h758-5	>7000.0			
2h765	>7000.0			
2h766	>7000.0			
2h774	>7000.0			
2h775	>7000.0			
2h780	>7000.0			
2h781	>7000.0			
2h782	>7000.0			
2h783	>2000.0			
2h784	>4700.0			
2h785	3700.0, >7000.0			

TABLE 6

Potency of Fc*-formatted Molecules in Various Primary Cell Assays

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-23 EC50 (nM)	CHO- hCD40L- driven DC Activation TNF EC50 (nM)
2h116-1320- Fc	13.0 ± 2.0	>130.0	244.0 ± 112.0		14.0 ± 11.0			
2h503-1 Fc	4.0 ± 0.5	60.0 ± 20.0	45 ± 6		2.8 ± 2.0			
2h503-1 IgG1	4.5 ± 1.0	67.0 ± 40.0	39.5 ± 12.04		1.4 ± 0.7			
2h503-1 IgG4	2.5 ± 1.0	69.0 ± 50.0	48.3 ± 8.8		18.1 ± 6.4			
2h572-6 Fc	0.6 ± 0.4	3.0 ± 1.0	1.9 ± 0.7		0.22 ± 0.18			
2h572-6 IgG1	1.0 ± 0.4	10.0 ± 5.0	3.1 ± 1.4	2.9 ± 1.7	0.58 ± 0.36			
2h572-6 IgG4	0.9 ± 0.2	11.0 ± 5.0	3.2 ± 1.5	1.3 ± 0.5	1.1 ± 0.5			
2h572-6-CT Long Fc	1.0 ± 0.5	6.0 ± 6.0	13.6 ± 9.2	8.1 ± 3.1	3.0 ± 1.9			

* FIG. 3 provides sequences of various Fc domains. FIG. 4 shows examples of various Fc-formatted dAbs.

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-23 EC50 (nM)	CHO- hCD40L- driven DC Activation TNF EC50 (nM)
2h572-633 Fc	3.5 ± 0.6	3.0 ± 3.0	0.15 ± 0.02	0.11 ± 0.02	0.34 ± 0.17			
2h572-634 Fc	3.0 ± 0.0	3.5 ± 3.0	0.23 ± 0.08	0.19 ± 0.03	0.42 ± 0.05			
2h572-635 Fc	2.0 ± 0.8	2.5 ± 1.0	0.16 ± 0.09	0.11 ± 0.02	0.445 ± 0.14			
2h572-619- Ctshort Fc	1.5 ± 0.6	2.0	0.40 ± 0.1	0.3 ± 0.07	1.8 ± 1.3			
2h572-619- Ctlong Fc	1.6 ± 0.5	2.0 ± 1.0	0.72 ± 0.45	0.43 ± 0.12	1.4 ± 0.6	1.5 ± 0.36	1.5 ± 0.46	2.0 ± 0.7
2h572-619- N297Qshort Fc	0.9 ± 0	1.0 ± 0.6	0.226, 0.216	0.1, 0.1	1.2 ± 0.6			
2h572-619- N297Qlong Fc	0.98 ± 0.05	2.0 ± 0.0	0.480, 0.474	0.22, 0.11	1.1 ± 0.23			
2h572-608- N297Qshort Fc	1.0 ± 0.05	2.0 ± 0.0			0.93 ± 0.4			

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-23 EC50 (nM)	CHO- hCD40L- driven DC Activation TNF EC50 (nM)
2h572-608- CT Long Fc	2.0 ± 1.0	2.0 ± 1.0	0.468 ± 0.156	0.38 ± 0.06	1.6 ± 0.74			
2h572-614- CT Long Fc	2.0 ± 1.0	2.0 ± 0.5	0.283 ± 0.038	0.25 ± 0.02	1.4 ± 0.68			
2h572-633- CT Long Fc	3.0 ± 0.7	1.0 ± 1.0	0.174 ± 0.077	0.13 ± 0.07	1.9 ± 1.3	1.3 ± 0.3	1.2 ± 0.3	1.7 ± 0.43
2h572-633- CT-Fc SP5	5.0 ± 0.5	1.0 ± 0.5	0.161 ± 0.053	0.13 ± 0.04	2.3 ± 1.5	1.5 ± 0.7		2.9 ± 1.3
2h572-634- CT Long Fc	2.0 ± 1.0	1.0 ± 0.6	0.162 ± 0.029	0.13 ± 0.02	1.5 ± 0.91			
2h572-635- CT Long Fc	3.0 ± 1.0	2.0 ± 0.6	0.149 ± 0.014	0.13 ± 0.01	1.6 ± 0.93			
2h719-2 Fc	1.0 ± 0	0.7 ± 0.4	6 ± 1.4		0.13 ± 0.08			
2h719-2 IgG1	1.0 ± 0.5	6.0 ± 0.3	13.8 ± 10.6	2.2 ± 1.3	0.35 ± 0.23			
2h719-2 IgG4	1.5 ± 0.6	16.0 ± 13.0	15.9 ± 10.9	2.1 ± 0.7	1.1 ± 0.48			
2h719-202- N297Qshort	1.8 ± 0.5	1.7 ± 0.7			0.66 ± 0.26			

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Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	T-B cell MLR IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-6 EC50 (nM)	CHO- hCD40L- driven DC Activation IL-23 EC50 (nM)	CHO- hCD40L- driven DC Activation TNF EC50 (nM)
Fc								
2h719-202- CT Long Fc	3.0 ± 1.0	2.5 ± 0.6	1.7 ± 0.7	1.3 ± 0.3	3.1 ± 2.0			

Example 5

Binding Kinetics and CD40L Affinity of Various Antibodies

BMS-986004 is a dimeric fusion protein, composed of a modified Fc fragment of IgG1 linked to the C-terminus of the dAb BMS2h-572-633. Surface plasmon resonance (SPR) was used to characterize the kinetics and affinity of BMS-986004 or the monovalent component domain antibody BMS2h-572-633 binding to CD40L. The BMS-986004 values were compared to those for the benchmark antibodies 5c8-IgG1 and 5c8-CT and the monovalent component 5c8 FAB fragment. The SPR experiments utilized a hCD40L construct containing an N-terminal isoleucine zipper motif (IZ-hCD40L) which facilitates the specific assembly of the CD40L molecule into the native trimeric form. A biotinylated version of IZ-hCD40L (biot-IZ-hCD40L) with equivalent binding activity was also utilized for some SPR experiments.

The monovalent BMS2h-572-633 domain antibody binds biot-IZ-hCD40L with a K_d of 7.8 nM, compared to an affinity of 5.4 nM for the monovalent 5c8 FAB fragment, TABLE 7. Because BMS-986004 is bivalent, and the IZ-hCD40L target is trivalent, the SPR binding data are influenced by avidity regardless of whether CD40L target is on the chip surface or in solution. To estimate the avidity-influenced binding affinity, the SPR data for BMS-986004 binding to a biot-IZ-hCD40L surface was fitted to a 1:1 Langmuir model, suggesting a dissociation constant of less than 1 nM, TABLE 7. Similar results were obtained for 5c8-IgG1 and 5c8-CT.

TABLE 7

IZ-hCD40L kinetic and affinity values as determined using SPR (Biacore)

Anti-CD40L Ab	Temperature (°C)	Model	k_a (M ⁻¹ s ⁻¹)	k_d (s ⁻¹)	K_d (nM)
BMS-986004	25	1:1 Langmuir	2.3 E+06*	2.6 E-04*	0.11*
2h572-633	25	1:1 Langmuir	1.0 E+06	8.1 E-03	7.8
5c8-IgG1	25	1:1 Langmuir	5.4 E+05*	2.3 E-04*	0.42*
5c8-CT	25	1:1 Langmuir	5.8 E+05*	1.3 E-04*	0.22*
5c8 FAB fragment	25	1:1 Langmuir	1.4 E+05	7.6 E-04	5.4

* Value is influenced by avidity due to analyte bivalency.

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FIG. 5 shows SPR sensorgram data for the binding of 12.5-0.39nM BMS-986004 (2:1 dilution series) to biot-IZ-hCD40L captured on a streptavidin SPR sensor chip at 25 °C. Colored lines show the double-referenced sensorgram data, and black lines show the 1:1 Langmuir fit to the data, with an avidity-influenced apparent K_d value of 0.11 nM.

The affinity and thermodynamics of BMS-986004 binding to CD40L were also characterized in solution using isothermal titration calorimetry (ITC) at temperatures ranging from 15–37°C. These data suggested the presence of multiple thermodynamically distinct binding modes (FIG. 6) with K_d values for the different modes beyond the high-affinity limit of detection (K_d <2 nM) (TABLE 8), consistent with the SPR data. The affinity of the monovalent 5c8 FAB fragment for IZ-hCD40L as determined by ITC (3.5 nM) was also consistent with the value determined by SPR.

TABLE 8

IZ-hCD40L affinity as determined using ITC

Molecule in the ITC syringe	Molecule in the ITC cell	K _d (nM)
BMS-986004	IZ-hCD40L	< 2
5c8-CT	IZ-hCD40L	< 2
IZ-hCD40L	BMS-986004	< 2
IZ-hCD40L	5c8-CT	< 2
IZ-hCD40L	5c8 FAB fragment	3.5

Example 6

Fc receptor Affinity of Various Antibodies

The Fc-domain of BMS-986004 (termed “CT”) was engineered from a wild type IgG1 Fc domain to retain the ability to bind FcRn, but to disrupt the binding to Fcγ receptors. To confirm that the engineered molecule has the desired Fc receptor binding profile, the binding affinities of BMS-986004 for human FcRn, and the human Fcγ receptors CD64 (FcγRI), CD32a (FcγRIIa),

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CD32b/c (FcγRIIb/c), CD16a (FcγRIIIa), CD16b (FcγRIIIb) were measured using SPR, in comparison to 5c8-IgG1 and 5c8-CT. For these experiments, BMS-986004 was captured via the domain antibody domains on a biot-IZ-hCD40L sensor surface, and the soluble Fc receptor proteins were tested for binding to the exposed Fc domain. Likewise, 5c8-IgG1 and 5c8-CT were captured on a biot-IZ-hCD40L surface via the FAB domains, with soluble FcR binding.

BMS-986004 bound FcRn with K_d of 670 nM at pH 6.0 which is the relevant pH for binding within the endosome, TABLE 9. However, binding was significantly reduced (K_d >5000 nM) at neutral pH suggesting efficient release of from FcRn under these conditions. BMS-986004 bound CD64 with a K_d of 0.6 nM, and had a statistically weak affinity for CD32a, CD32b/c, CD16a and CD16b (K_d >3000 nM). Both 5c8-IgG1 and 5c8-CT had a similar FcRn affinity as BMS-986004. 5c8-CT, which has the identical "CT" Fc region as BMS-986004, also had a similar FcγR binding properties as BMS-986004, whereas 5c8-IgG1, which has a wild type IgG1 Fc domain, bound more strongly to FcγRs, TABLE 9.

TABLE 9

Fc receptor affinity as determined using SPR (Biacore).

Sample	pH	BMS-986004 K _d (nM)	5c8-IgG1 K _d (nM)	5c8-CT K _d (nM)
hFcRn	6	670	590	720
hFcRn	7.1	>5000	>5000	>5000
CD64	7.1	0.6	<0.05	0.9 ± 0.4
CD32a	7.1	>3000	~10 ⁻⁷ M*	>3000
CD32b/c	7.1	>3000	>3000	>3000
CD16a	7.1	>3000	240±40	>3000
CD16b	7.1	>3000	>3000	>3000

* CD32a binding to 5c8-IgG1 was biphasic. K_d was estimated as ~10⁻⁷ M based on steady state fit to dominant binding even. This K_d is in range of literature reported K_D for CD32a binding to IgG1.

Example 7

In-vitro Cell-based Assays

The potency of BMS-986004 was evaluated in various primary immune cell assays to ensure robust potency across different cell types. The primary human B cell proliferation assays were conducted two ways, as described in detail above in Example 4: (1) recombinant CD40L trimer was used to drive B cell proliferation; and (2) CHO cells expressing CD40L on the membrane (CHO-CD40L) were utilized to induce B cell proliferation. The utility of CHO-CD40L cells was particularly important to ensure that signals from membrane-bound CD40L were inhibited equally well when compared to the soluble CD40L trimer. The CHO-CD40L cells were also used to drive the activation of primary human DCs differentiated from culturing PBMC-derived monocytes in presence of GM-CSF and IL-4. Similarly, the T-B MLR assay measured B cell activation driven by CD40L present on activated T cells. In all of the above described primary assays, BMS-986004 was equipotent to the benchmark 5c8 mAb: potencies ranged from was single-digit nM to sub-nM, depending on the assay (TABLE 10).

TABLE 10

Potency of BMS-986004 in Various Primary Cell Assays

mAb/dAb-Fc	Trimer B cell Assay EC50 (nM)	CHO-CD40L B cell Assay EC50 (nM)	T-B MLR EC50 (nM)	T-B MLR IL-6 EC50 (nM)	CHO-CD40L DC Assay IL-12 EC50 (nM)	CHO-CD40L DC Assay IL-6 EC50 (nM)	CHO-CD40L DC Assay TNF- α EC50 (nM)
5c8	8.0 $\pm$ 3.0	2.0 $\pm$ 2.0	0.54 $\pm$ 0.37	0.23 $\pm$ 0.09	2.0 $\pm$ 1.5		
5c8-IgG1	5.0 $\pm$ 1.0	2.0 $\pm$ 2.0	0.34 $\pm$ 0.13	0.21 $\pm$ 0.06	0.92 $\pm$ 0.94	0.73 $\pm$ 0.5	2.3 $\pm$ 1.3
BMS-986004	5.0 $\pm$ 0.5	1.0 $\pm$ 0.5	0.16 $\pm$ 0.05	0.13 $\pm$ 0.04	3.1 $\pm$ 1.6	1.9 $\pm$ 0.6	3.6 $\pm$ 1.1

Example 8

Assessment of Whole Blood Receptor Occupancy (RO)

A receptor occupancy method was developed to measure CD40L target engagement by BMS-986003 in cynomolgus whole blood samples and, subsequently, in BMS-986004 in human

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whole blood samples. BMS-986003 is a dAb which shares the same amino acid sequence as BMS-986004, except for a non-native glycine residue at its amino-terminus.

Occupancy is measured on CD4+ T cells by flow cytometry using an anti-CD40L mAb that competes for binding to CD40L with BMS-986003 / BMS-986004, and is cross-reactive with human and cynomolgus CD40L. In the presence of bound dAb, the anti-CD40L detection mAb is blocked from binding to CD40L in a concentration-dependent manner, providing a measure of target occupancy. Given that basal CD40L is expressed at low levels on resting T cells in peripheral blood, RO was assessed in both unstimulated blood samples and in samples where phytohemagglutinin (PHA) was used to induce up-regulation of CD40L on the T cell surface. Binding potency curves were generated following *ex vivo* whole blood treatment with BMS-986003 and BMS-986004. The average EC₅₀ and EC₉₀ values obtained are shown in TABLE 11.

TABLE 11

**Binding Potency of BMS-986003 and BMS-986004 on CD4+ T-cells
in *ex vivo* Whole Blood Receptor Occupancy Assay**

BMS-986003	<i>n</i>	Average EC₅₀, nM	Average EC₉₀, nM
Human (basal)	1	0.9	3
Human (PHA-induced)	6	0.8	9
Cyno (basal)	3	0.6	3
Cyno (PHA-induced)	3	0.4	2
BMS-986004			
Human (basal)	3	0.4	3
Human (PHA-induced)	3	0.7	5

The target binding potency in whole blood for BMS-986003 and BMS-986004 closely correlates between human and cynomolgus monkey. The EC₅₀ values for BMS-986003 and BMS-986004 are also similar when bound to basal and PHA-induced CD40L. Additionally, these values are comparable to those obtained in human *in vitro* cell based assays (see TABLE 10). Based on the measured EC₉₀ values, full target saturation in peripheral blood should be achieved at concentrations ≤ 10nM.

To support the preclinical PK/PD profile of BMS-986003 and BMS-986004, RO was assessed in both the cynomolgus KLH study (immunization with keyhole limpet hemocyanin) with BMS-986003 and the IV bridging study with BMS-986004. Further details of these findings can be found in Examples below.

Example 9

In vivo Pharmacology

To show efficacy of a CD40L dAb in mouse disease models, a mouse CD40L dAb 2m126-24 was formatted with mouse IgG1 Fc with D265A point mutation to further lower the Fc effector function. This mouse surrogate dAb 2m126-24-Fc shows potency comparable to BMS-986004 and MR-1, a hamster anti-mouse CD40L antibody (TABLE 12).

TABLE 12

In vitro Potency Comparison

	mAb/dAb-Fc	Trimer B cell Assay EC50 (nM)	CHO-CD40L B cell Assay EC50 (nM)	CHO-CD40L DC Assay IL-6 EC50 (nM)
Human {	5c8	8.0 ± 3.0	2.0 ± 2.0	
	BMS-986004	5.0 ± 0.5	1.0 ± 0.5	1.9 ± 0.6
Mouse {	2m126-24-Fc	4.7 ± 0.9	0.4 ± 0.06	0.5 ± 0.2
	MR-1 (mAb)	1.7 ± 0.4	0.6 ± 0.2	0.6 ± 0.3

Inhibition of KLH Induced Antibody Response by the Mouse CD40L dAb

Female BALB/c mice were injected intraperitoneally (i.p.) with 250 µg KLH on day 0. Mice were dosed subcutaneously (s.c.) with MR-1 or BMS-2m-126-24-Fc at indicated doses on day -1 and day 6. Blood was collected and the serum was analyzed for anti-KLH IgM on day 7 and IgG on day 14 by ELISA. Serum from BALB/c mice collected on day 14 after immunization with KLH was pooled and used as a positive comparator, and the data is expressed as a ratio of the titre of the test serum to the titre of the pooled BALB/c serum. As shown in FIG. 7, BMS-2m-126-24-Fc demonstrated a dose dependent suppression of IgG titers with maximal

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effect shown at 3 mg/kg, with ED50 calculated to be 0.26 mg/kg. Both the CD40L dAb and the antibody were tested at 1 mg/kg, showing 70% vs. 30% reduction in IgG response, respectively. Similar exposure of the dAb and the antibody were observed at 1 mg/kg, suggesting that the dAb is slightly more potent than the antibody at suppressing KLH-induced IgG response. In conclusion, the CD40L dAb has demonstrated at least the same level of efficacy as the anti-CD40L antibody at inhibiting a T cell dependent antibody response.

Inhibition of TNBS-induced Colitis by the Mouse CD40L dAb

Male SJL/J mice were intrarectally administered with 2.5 mg Trinitrobenzene sulfonic acid (TNBS) in 50% EtOH via a catheter inserted 4 cm distal to the anus. Mice were dosed once s.c. with MR-1 or BMS-2m-126-24-Fc at indicated doses 4 hours prior to TNBS injection. FIG. 8 presents the changes in the mean body weight and the percent survival of groups of mice treated with PBS/IgG or varying dose levels of MR-1 or the dAb. Abatacept was used as a positive control (20 mg/kg, i.p. every other day). A typical profile of TNBS-induced colitis was shown in the IgG control group: loss of body weight, peaking at day 3-4; colitis-related death occurring at day 3 and beyond; and the survived mice showing signs of recovery after day 4. Treatment with the CD40L dAb or the antibody (both tested at 2, 8 and 20 mg/kg) caused a dose-dependent inhibition of the body-weight loss and the increase in survival rate; both compounds at 8 mg/kg yielded a degree of efficacy that is comparable to that of Abatacept at 20 mg/kg. In conclusion, the mouse CD40L dAb BMS-2m-126-24-Fc has demonstrated comparable efficacy to the anti-CD40L antibody MR-1 in an acute TNBS-induced colitis model.

Synergistic Effect between CTLA4 Ig and the Mouse CD40L dAb in a

Mouse "Heart-to-Ear" Transplant Model

Heart grafts from neonatal (48-72 hrs) C57BL/6 mice were implanted into a subcutaneous pocket created in the ear pinnae of BALB/c mice. Mice were treated with CTLA4-Ig (i.p. 2x/wk), BMS-2m126-24-Fc (s.c. 1x /wk), or combination of both at indicated doses, with first dosing initiated the day prior to transplantation. Time to rejection was defined by the absence of cardiac contractility for three consecutive days as assessed daily by the electrocardiogram (ECG) device of allograft. As expected, without any treatment, C57BL/6 mice that received the neonatal BALB/c heart rejected the graft shortly thereafter, with median survival time (MST) of

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12 days. The monotherapy with 3, 20 mg/kg of the dAb or 25 mg/kg of CTLA4-Ig had no or little impact on prolonging the survival of the allograft (MST: 12, 15 and 13 days respectively). However, in the groups treated with combination of 20 mg/kg of the dAb and 25 mg/kg of CTLA4-Ig, the graft survival was significantly prolonged showing MST of 35 days (FIG. 9).

5 This data has provided rationale for combining CD40L dAb with belatacept in human renal transplant patients. Future transplant studies in non-human primates will further define the dose level and assess the potential effect on tolerance induction with CD40L dAb BMS-986004.

Example 10

***In vivo* Nonclinical Pharmacokinetics (PK) and Pharmacodynamics (PD)**

0 Various *in vivo* studies were conducted to characterize the PK and PD of BMS-986004, BMS-986003, and a mouse CD40L dAb-Fc surrogate BMS-2m-126-24-CT, in the nonclinical setting. The key findings are summarized below.

ELISA to measure BMS-986004 dAb

5 Enzyme-linked immunosorbency assay (ELISA)-based bioanalytical methods were developed to support the PK studies, acute and chronic efficacy studies in mice, and exploratory PK/PD studies employing cynomolgus monkeys. In all cases, whole blood was obtained and plasma prepared in the presence of EDTA, the samples were then subjected to ELISA analysis.

20 Plasma concentrations of BMS-986004 were measured with an ELISA assay that utilized human CD40L antigen to capture the analyte from test samples. Test samples were thawed at 4°C, mixed well and diluted 1:100 in assay diluent composed of 1× PBS, 0.05% Tween-20, and 1% BSA (PTB). Subsequent dilutions of the sample were made using 1% normal monkey plasma/PTB as diluent. This allowed the test analyte to be assayed at several dilutions (10^2 – 10^5) while keeping the sample matrix at 1%.

25 Recombinant trimeric human CD40L was obtained from Protein Structure and Science (PSS), LVL and was bound to 96 well plates at a final concentration of 2 µg/mL. Test samples, quality control (QC) samples and the standards were detected with affinity-purified rabbit anti-heavy chain (Vh) domain framework polyclonal antibody (Covance Research Products, Denver, PA) diluted to a concentration of 0.25 µg/ml in PTB, followed by horseradish peroxidase-labeled

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donkey anti-rabbit polyclonal secondary antibody (Jackson ImmunoResearch, West Grove, PA) with substrate (TMB - tetramethylbenzidine) added, and the enzymatic reaction stopped with 1 M phosphoric acid. Absorbance was measured at a wavelength of 450 nm. The analysis of BMS-986004 in test samples was conducted using a standard curve. Standard curve calibrators prepared on the day of each run in 1% monkey plasma were used to define the dynamic range of the bioanalytical method. The range of resulting standard curve in 100% plasma was 10 - 1200 ng/mL. The reference standard for BMS-986004 was obtained from Biologics Process and Product Development (BPPD), HPW. The reference standard material was representative of the manufacturing batch and was used in the study protocol. Standard curves and QCs were evaluated using criteria for accuracy and precision of $\leq 20\%$ which was considered to be acceptable for assay performance. Test samples were quantified using a 4-parameter logistic fit regression model weighted by reciprocal concentration ($1/x$) derived from the calibrators.

Performance of the QC samples, measured by the deviation of the calculated concentration from its nominal value indicated the reference material was stable in neat monkey plasma at concentrations of 30 - 1000 ng/ml when stored at -70°C for over 2 months.

ELISA to measure a mouse surrogate dAb

Mouse CD40L-specific dAb BMS-2m-126-24-CT was measured in mouse plasma samples to provide exposure data in support of several acute and chronic efficacy studies as well as PK assessment.

While the assay format for mouse dAbs was quite similar to that for human dAbs in monkey samples, there were a few differences. The mouse plasma matrix was diluted to 1:10 (10%) in assay diluent, and all subsequent dilutions of test samples were made using 10% mouse matrix. Likewise, all standards and QCs were also incubated on ELISA plates in 10% mouse plasma. The concentration of BMS-2m-126-24-CT in test samples from mice was measured using mouse CD40L to capture the analyte. As the mouse dAb has Vk framework, all test samples, QCs, and the standards were detected with affinity purified rabbit anti-kappa (Vk) domain polyclonal antibody (Covance Research Products, Denver, PA) diluted to a concentration of 0.5 $\mu\text{g/mL}$ in PTB. The rest of the assay and analysis procedure was similar to the procedure for the analysis of human CD40L dAbs. Acceptance criteria for back-calculated concentrations of standards and QCs were also similar to those for human CD40L dAbs. The quantitative range

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of BMS-2m-126-24-CT as determined from the standard curve was 12.5 to 600 ng/mL in neat sample matrix.

Nonclinical Pharmacokinetics

TABLE 13 summarizes the PK parameters for BMS-986004, BMS-986003, and BMS-2m-126-24-CT in nonclinical animal species.

TABLE 13
Single-dose PK Parameters (mean $\pm$ SD) from Two Nonclinical Animal Species

Species	dAb	Route	Dose (mg/kg)	Cmax (μ M)	Tmax (h)	AUC _{0-inf} (μ M.h)	T1/2 (h)	CLTp (mL/h/kg)	Vss (L/kg)	F (%)
Mouse	BMS-2m-126-24-CT	IV	1 (N=3)	-	-	6.9	101	1.85	0.26	-
		SC	1 (N=3)	0.063	24	10	100	-	-	100
			10 (N=3)	0.68	24	114	120	-	-	100
Monkey	BMS-986003	IV	2 (N=2)	-	-	40	106	0.67	0.067	-
		SC	0.2 (N=4)	0.019 $\pm$ 0.004	60 $\pm$ 72	4.0 $\pm$ 2.7	85 $\pm$ 29	-	-	88
			2 (N=4)	0.22 $\pm$ 0.075	33 $\pm$ 43	29.7 $\pm$ 4.9	68 $\pm$ 11	-	-	74
			20 (N=4)	1.48 $\pm$ 0.34	11 $\pm$ 9	175 $\pm$ 27	105 $\pm$ 18	-	-	44
	BMS-986004	IV	11 (N=4)	-	-	241 $\pm$ 18	124 $\pm$ 12	0.59 $\pm$ 0.04	0.098 $\pm$ 0.01	-
	5c8-IgG1	IV	20 (N=4)	-	-	1800 $\pm$ 74	400	0.074	0.042	

BMS-986004 and BMS-986003 exhibited comparable PK profiles in monkeys (FIG. 11A and FIG. 11B). After IV administration, the plasma concentrations of BMS-986004 and BMS-986003 exhibited a bi-exponential decline up to 504 and 408 h, respectively. Accelerated

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clearance was observed afterward in 50% of monkeys enrolled in both studies. Immunogenicity testing of the plasma samples collected at 38 d after BMS-986004 treatment suggested that all monkeys developed anti-drug antibody (ADA); and that the monkeys with higher ADA levels showed faster clearance. Although no immunogenicity test was conducted for the IV PK study with BMS-986003, a similar level of immunogenicity was observed in monkeys after subcutaneous dosing with BMS-986003 in the PK/PD study, suggesting both proteins were immunogenic in monkeys. The terminal half-life ($T_{1/2}$) of 124 and 106 h for BMS-986004 and BMS-986003 was, therefore, determined using the exposures collected up to two weeks (336 h) only. The steady-state volume of distribution (V_{ss}) of BMS-986004 and BMS-986003 was 0.098 and 0.074 L/kg, respectively. The values are greater than the plasma volume (0.06 L/kg) but less than the volume of extracellular fluid (0.2 L/kg), suggesting that the proteins largely reside in the extracellular space. The total body plasma clearance (CL_{Tp}) of BMS-986004 and BMS-986003 was 0.59 and 0.65 mL/h/kg, respectively.

The PK parameters of BMS-986004 in monkeys were compared to those of abatacept, a similar size protein (78.5 vs 78-kDa BMS-986004, based on amino acid sequence), with the same modified human IgG1 Fc format. As expected, the parameters of BMS-986004 were nearly identical with those of abatacept (CL_{Tp} of 0.6 mL/h/kg, V_{ss} of 0.087 L/kg, $T_{1/2}$ of 5 d), suggesting the humans PK of BMS-986004 and abatacept is likely to be similar.

The absorption of BMS-986003 after subcutaneous (SC) administration was evaluated in the monkey PK/PD study. The monkeys were administered with BMS-986003 as single subcutaneous doses of 0 (vehicle control), 0.2, 2 and 20 mg/kg, at 24 h prior to the immunization with keyhole limpet hemocyanin (KLH), a T cell-dependent antigen. After dosing, BMS-986003 was slowly absorbed, with a T_{max} ranging from 6-96 h (FIG. 12). The exposure of BMS-986003 appeared to be less than dose-proportional across all dose levels. With a dose ratio of 1:10:100, the average C_{max} and AUC_{0-inf} ratios were 1:12:80 and 1:7:44, respectively. With the exposure following the IV dose (2 mg/kg) as reference, and assuming linear PK after IV dosing, the SC bioavailability of BMS-986003 was 88%, 74%, and 44% at 0.2, 2, and 20 mg/kg, respectively. The terminal $T_{1/2}$ was confounded by the immunogenicity observed with most of the monkeys at 2 to 5 weeks after dosing. Therefore, the $T_{1/2}$ was estimated to be 85, 66, and 105 h at 0.2, 2 and 20 mg/kg, respectively.

The PK of 5c8-IgG1, an anti-human CD40L monoclonal antibody used as a positive control in the PK/PD study, was evaluated after IV administration at 20 mg/kg (FIG. 12). 5c8-IgG1 exhibited 10-fold higher plasma exposures and 4-fold longer T_{1/2} when compared to BMS-986003 given SC at the same dose (TABLE 13).

The PK of the mouse surrogate dAb-Fc fusion protein, BMS-2m-126-24-CT, was evaluated in mice following single IV and SC administration (TABLE 13). After a single IV (1 mg/kg), the plasma concentrations followed a mono-exponential decline with a terminal T_{1/2} of 101 h (FIG. 13). The CL_{TP} was 1.85 mL/h/kg; and the V_{ss} was at 0.26 L/kg, indicating extracellular distribution. After single SC doses of 1 and 10 mg/kg, BMS-2m-126-24-CT was slowly absorbed with a T_{max} of 24 h. The systemic exposures increased in a dose-proportional manner. With a dose ratio of 1:10, the C_{max} and AUC_{0-inf} increased in the proportion of 1:11. The terminal T_{1/2} was 100 and 120 h at 1 and 10 mg/kg, respectively. The ratio of the dose-adjusted exposure (AUC_{0-inf}) after SC and IV administration was greater than 1, suggesting complete absorption after SC administration.

Pharmacokinetic / Pharmacodynamic Modeling

The PD of BMS-986003 was measured as the suppression of anti-KLH antibody response in the PK/PD study. BMS-986003 suppressed 70% the antibody response to KLH (% response

suppressed = $(1 - \frac{AUEC_{0-1008h} \text{ IgG titers}^{\text{treated group}}}{AUEC_{0-1008h} \text{ IgG titers}^{\text{vehicle group}}}) * 100$) at the highest dose of 20 mg/kg. Marginal (15%) and no suppression of the antibody response occurred at 2 and 0.2 mg/kg. In comparison, 5c8-IgG1 exhibited 10-fold higher plasma exposures and 4-fold longer T_{1/2} than BMS-986003 at the same dose level (20 mg/kg). As a result, 5c8-IgG1 suppressed 97% anti-KLH antibody response. In order to compare the in vivo potency between BMS-986003 and 5c8-IgG1, PK/PD modeling was performed using SAAM II (version 1.2.1, Seattle, WA). The plasma concentrations of BMS-986003 following SC administration were described using a first-order absorption kinetics coupled with a 2-compartment model, where the elimination occurred in both central and peripheral compartments. Because of complications from immunogenicity and possible nonlinear absorption, the PK data were fitted individually at each dose.

For 5c8-IgG1, a two-compartment model with central elimination was used. The anti-KLH antibody response, expressed as the average value of IgG titers, was modeled using a 6-

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compartment signal transduction model. The kinetics of KLH in the body was assumed to be a 1-compartment model. The inhibition of the IgG production by BMS-986003 and 5c8-IgG1 was described using an Imax model, with a maximum inhibition equal to 100%. As shown in FIG. 14, the model-fitted curves were able to describe both the PK and PD profile. The plasma IC50 of BMS-986003 and 5c8-IgG1 for the suppression of KLH-induced IgG production was estimated to be 74 ± 14 and 60 ± 18 nM, respectively. These results demonstrated that the potency of these two molecules was comparable *in vivo*.

The CD40L receptor occupancy (RO) of BMS-986004 was measured in the IV PK study. Following IV administration of 11 mg/kg, the RO of BMS-986004 on the peripheral-blood mononuclear cells (PBMC) was time- and concentration-dependent. PK/PD modeling was performed to estimate an RO EC50. The plasma concentrations were modeled using a modified two-compartment model with an additional ADA-mediated first order elimination constant introduced at 504 h after dosing; and the RO was modeled using an Emax model

($RO\% = \frac{E_{max} * Cp^\gamma}{EC50^\gamma + Cp^\gamma}$). As shown in FIG. 15, the fitted curves were able to describe both exposure and RO, with an estimated RO EC50 of 3.4 ± 0.3 nM and the γ (hill factor) of 3.1 ± 0.1 . In comparison, the RO EC50 was ~22-fold lower than the anti-KLH antibody response IC50 of 74 ± 14 nM, suggesting that >95% RO is required in order to achieve appreciable (>50%) anti-KLH antibody suppression.

Example 11

Nonclinical Toxicology Single-dose PK/PD Study

The objectives of this study were to 1) determine the tolerability of BMS-986003, including its potential immunogenicity, when given subcutaneously as a single dose to monkeys; 2) evaluate its PD (e.g., inhibition of the antibody response to T-cell-dependent antigen) and PK profiles; 3) evaluate the receptor occupancy of BMS-986003 and peripheral T-cell counts following subcutaneous dosing; and 4) aid dose selection for renal transplant studies and first-in-human dosing.

BMS-986003 was administered s.c. in the posterior thorax as single doses of 0 (vehicle control), 0.2, 2, or 20 mg/kg to groups of 2 cynomolgus monkeys per sex. An additional two

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monkeys/sex received a single intravenous dose of 20 mg/kg 5c8-IgG1, a monoclonal antibody to human CD40L that was used as a positive control in this study. All doses were administered at 2 mL/kg in the vehicle (PBS; pH 7.2). To assess the effects on the T-cell dependent antibody response, animals were immunized at approximately 24 hours after dosing with test article or immediately after dosing the positive control with 10 mg of KLH by intramuscular injection (posterior quadriceps or caudal thigh). Criteria for evaluation included survival, PK, immunogenicity, PD (inhibition of the antibody response to the T-cell-dependent antigen, KLH), clinical signs, body weights, food consumption, peripheral-blood immunophenotyping, receptor occupancy, and clinical-pathology evaluations (hematology, serum chemistry, and coagulation). Animals were returned to stock following a 6-week post-dose observation period.

At doses $\leq$ 20 mg/kg, BMS-986003 was slowly absorbed (T_{max} = 6-96 h) and C_{max} and AUC_{tot} values increased in a less than dose-proportional manner across all dose groups and there were no apparent gender differences. The $T_{1/2}$ values estimated ranged from 69-104 h across all doses. BMS-986003 was substantially immunogenic; all monkeys developed a positive anti-drug antibody (ADA) response during the 6-week post-dose period. At 0.2 and 2 mg/kg, the mean group total ADA response peaked at Day 22 at mean group end point titers (EPT) of 4203 and 6469, respectively. At 20 mg/kg, the ADA response, while positive, was somewhat delayed and partially suppressed, consistent with target pharmacology, peaking at Day 36 at a mean group EPT of 1828. Further characterization of the antibodies demonstrated the majority of binding to the dAb (non-Fc) portion of the molecule and these antibodies were shown to block the binding of BMS-986003 to CD40L in 2 different immunoassay formats suggesting that the ADA were neutralizing. In addition, the formation of ADA appeared to accelerate the elimination of BMS-986003 in several monkeys.

Mean PK parameters for BMS-986003 are presented in TABLE 14.

TABLE 14

Pharmacokinetic Summary

Mean Parameter	BMS-986003			5C8-IgG1
	SC			IV
	0.2 mg/kg (N = 4)	2 mg/kg (N = 4)	20 mg/kg (N = 4)	20 mg/kg (N = 4)
Gender	Male/Female	Male/Female	Male/Female	Male/Female
AUC(0-inf) μg·h/mL	219/407	2165/2477	14195/13114	267750/272250
CLTp mL/h/kg	Not applicable	Not applicable	Not applicable	ND/0.074
T1/2 h	69/101	68/69	107/104	ND/400
Cmax μg/mL	69/101	45/49	88/91	Not applicable
Tmax h	24/96	51/15	6/15	Not applicable

Molecular weight used for conversion was 78104 Da for BMS-986003, 150000 Da for 5c8-IgG1 mAb. ND = not determined,; AUCextra for males was above 20%, therefore the T1/2 was not reported.

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There were no BMS-986003- or 5c8-IgG1-related clinical observations or effects on body weights or clinical pathology parameters except 1 male treated with 5c8-IgG1 had decreased red blood cells ($0.74 \times$ control), hemoglobin ($0.73 \times$ predose), and hematocrit ($0.75 \times$ predose) on Day 8, and 3 of 4 monkeys receiving 5c8-IgG1 had decreased lymphocytes ($0.53 \times$ to $0.65 \times$ predose) on Day 8, suggestive of lymphocyte depletion.

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CD40L receptor occupancy was generally time- and dose-dependent and more sustained following administration of 20 mg/kg BMS-986003, consistent with higher and more sustained exposures at this dose and PD activity. For BMS-986003, mean peak receptor occupancy on peripheral-blood mononuclear cells (PBMC) was achieved at 24 hrs (97%), 6 hrs (99%) or 48 hrs (99%) post-dose, decreasing to $<90\%$ occupancy at 240, 360, or 696 hrs and to $<50\%$ occupancy at 360, 696, or 1032 hrs, at 0.2, 2, or 20 mg/kg, respectively. In comparison, for 5c8-IgG1 at 20 mg/kg, mean peak receptor occupancy on PBMC was achieved at 48 hours ($\geq 100\%$), and was sustained at $\geq 97\%$ for the entire study (1032 hr or through Day 44).

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BMS-986003 suppressed the antibody response to KLH only at the high dose of 20 mg/kg. On Days 8-30 at 20 mg/kg, there was a 69 to 83% suppression of the geometric group mean antibody response to KLH, relative to the control group, with a peak suppression of 83% occurring on Day 16. No suppression of the antibody response occurred at 0.2 or 2 mg/kg BMS-986003. These data demonstrate that BMS-986003 at a sustained receptor occupancy of >90% for at least 1 month and at sustained plasma concentrations above ~10 µg/mL through Day 11 is able to inhibit a T-cell dependent antibody response in cynomolgus monkeys. For the positive control antibody, 5c8-IgG1, suppression of 74-97% of the geometric group mean antibody response to KLH occurred on Days 8-30, with peak suppression of 97% by Day 16 which was generally sustained through Day 30.

No biologically relevant BMS-986003 related changes in absolute numbers of B cells (CD45+, CD20+, CD3-), total T (CD45+, CD3+) cells, helper T (CD45+, CD3+, CD4+, CD8-) cells, cytotoxic T (CD45+, CD3+, CD4-, CD8+) cells, or natural killer (CD45+, CD3-, CD16+) cells occurred during the study, which confirmed lack of any Fc effector function. However, on Day 8, 3 of 4 monkeys treated with 20 mg/kg 5c8-IgG1 had decreased T-lymphocytes (0.53×-0.66× predose), both helper T-cell (0.64× to 0.77× predose) and cytotoxic (0.40× to 0.61× predose) T-cell populations, suggestive of depletion.

In conclusion, BMS-986003 administered as single SC doses of 0.2, 2, or 20 mg/kg (AUC ≤ 14195 µg*hr/mL) was well tolerated in cynomolgus monkeys with no adverse drug-related effects. The positive control, 5c8-IgG1, at a dose of 20 mg/kg, resulted in complete, sustained inhibition of the antibody response to KLH and sustained receptor occupancy of nearly 100% through 30 days post-dose. Mild depletion of T-cells was also noted by Day 8 in monkeys receiving 5c8-IgG1 (0.40x to 0.77x predose), which was not observed with BMS-986003. BMS-986003 was able to suppress an antibody response to KLH at 20 mg/kg (peak suppression of 83%) following KLH immunization on Day 1 and had sustained receptor occupancy of ≥ 90% through Day 22 and ≥ 50% through Day 29. Similar dampening of the immunogenicity to BMS-986003 occurred at 20 mg/kg. However, lower BMS-986003 doses of 0.2 and 2 mg/kg did not suppress the antibody response to KLH or the anti-drug antibody response. The lack of pharmacology at the lower doses also correlated with decreasing receptor occupancy (i.e., <90% by Day 11 [0.2 mg/kg] or 16 [2 mg/kg]; <50% by Day 16 [0.2 mg/kg] or 30 [2 mg/kg]) and

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accelerated clearance, presumably due to the formation of ADA. The inhibition of TDAR is consistent with the mechanism of action of this compound and was not considered adverse.

Example 12

Evaluation of the Risk for TE / Thrombosis

It has been hypothesized that the TE associated with administration of the anti-CD40L monoclonal antibodies is mediated by anti-CD40L mAb-CD40L immune complex (IC)-mediated cross linking of platelets, facilitated by IC binding to FcγRIIa, an IgG Fc receptor, causing activation and aggregation (FIG. 10). Blocking the interaction of Fc moiety of IgG with FcγRIIa is, therefore, expected to mitigate platelet cross linking and thrombosis. The following methods and approaches were designed to evaluate the risk of TE and/or thrombosis.

In vitro platelet activation assays

Several in vitro assays were conducted to test the hypothesis that platelets are activated by CD40L mAb/sCD40L IC in a FcγRIIa-dependent manner. The positive control 5c8-IgG1 was used to validate the assays prior to testing BMS-986003 and BMS-986004. Blood from human donors or mice expressing hFcγRIIa receptor on platelets were used for these studies. Platelet activation was detected by flow cytometry using antibodies against the well-validated platelet activation markers P-selectin (CD62P) and PAC-1 (activated GPIIb/IIIa). Briefly, blood was diluted 1:25 in modified Tyrodes-HEPES containing 1mM CaCl₂ to which detection antibodies and test reagents was added, incubated, and analyzed for platelet activation. Initial experiments determined that sCD40L or 5c8IgG1 alone did not activate platelets, but different immune complex ratios of 1:1 to 1:8 of 5c8:sCD40L significantly activated platelets. Subsequent experiments used 5c8-IgG1 or 5c8-mIgG2a IC, mostly at a 1:3 molar ratio of 5c8:sCD40L.

Platelet activation by 5c8/sCD40L IC can be blocked by anti-FcγRIIa antibody

Studies were conducted with the FcγRIIa blocking antibody IV.3 to test whether activation of platelets by 5c8/sCD40L IC was indeed FcγRIIa-mediated. Blood from human donors was pre-incubated with 0.5μg/μl of the FcγRIIa blocking antibody IV.3 prior to dilution and incubation with detection antibodies as described above. Adenosine diphosphate (ADP), a

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platelet activator via a different mechanism, was used as a positive control. As illustrated in FIG. 16, platelet activation by 5c8/sCD40 IC was completely blocked by IV.3, while activation by ADP was not inhibited by the blocking antibody, indicating that activation by the IC is FcgRIIa-mediated.

5 *Selection of inert Fc tails*

A requirement for potential candidate molecules was absence of binding to FcgRIIa to prevent potential platelet activation. Several 5c8 constructs containing different mutations derived from IgG1 (e.g 5c8-CT and N297Q) or IgG4 (e.g., 5c8-S228P) were expressed and screened for Fc tails that did not activate platelets using different molar ratios of sCD40L to mAbs. Wild-type and most mutated constructs activated platelets except for 5c8-CT and 5c8-N297Q (FIG. 17). Absence of Fc (5c8-Fab2) also did not activate platelets further confirming that IC-platelet activation is Fc-mediated. The CT tail was chosen to format the dAb candidates BMS-986003 and BMS-986004.

5 *Effect of FcgRIIa polymorphism on platelet activation*

The gene for FcgRIIa is variable at codon 131, resulting in His-Arg (CAT/CGT) polymorphism. The genotype distribution in approximately 100 individuals with about equal distribution of Caucasians and African Americans was A/A (His homozygous; 14%), A/G (His/Arg heterozygous; 60%), and G/G (Arginine homozygous; 26%) for Caucasian Americans and A/A (30%), A/G (51%), and G/G (19%) for African-Americans. Reilly et al., *Clin. Diagn. Lab. Immunol.* 1: 640-644 (1994). Fc-dependent platelet aggregation was noted in samples from R131 individuals when treated with anti-CD9 in mIgG2 or mIgG1 Fc format, while platelets from H131 individuals aggregated only with anti-CD9 as mIgG2 format; this suggests that Fc-dependent aggregation with an IgG1 mAb could potentially segregate a patient population into low and high responders, which has previously been reported with this polymorphism. Tomiyama et al., *Blood* 80: 2261-2268 (1992). To address any potential differences in platelet activation with the IgG1 and CT Fc tail, 19 donors were genotyped for hFcgRIIa polymorphism and samples tested for platelet activation. The donor pool polymorphism (RR; 42%, HH; 21%, HR; 37%) was sufficient to evaluate any potential differences in platelet activation to the IgG1 format. Representative of literature reports, platelet activation with 5c8-IgG1/sCD40L IC was

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similar across all genotyped individuals. No activation was found with 5c8-CT/sCD40L IC (FIG. 18), suggesting no or minimal risk of increased TE in a patient population with an antibody formatted with the CT tail.

BMS-986004: Platelet activation in human blood donors

The experiments described above using 5c8, supported selection of the CT-tail as the best format for BMS-986004 (also called BMS2h-572-633-CT-L2). Blood obtained from 6 donors was treated with 5c8-IgG1, 5c8-CT, F(ab)₂, and BMS-986004. Platelets were activated by 5c8-IgG1 but not by any of the other constructs, including BMS-986004 (FIG. 19), suggesting that this dAb has no or low risk for causing platelet activation and TE in clinical studies.

BMS-986003: Platelet activation in blood from mice expressing hFcγRIIa

To further confirm that activation of platelets by anti-CD40L antibodies was mediated by FcγRIIa receptor, blood from transgenic mice expressing the human receptor (R131 genotype) was treated with 5c8-IgG1, 5c8-IgG2a, dAb-IgG1, 5c8-CT, and BMS-986003 (also called BMS-2h572-633-CT). Platelets were specifically activated by 5c8-IgG1, 5c8-IgG2a, and dAb-IgG1/sCD40L IC in blood from mice expressing hFcγRIIa, but not wild-type littermates. 5c8-CT and BMS-986003 did not activate platelets, further confirming a low risk for TE with the presently disclosed antibodies (FIG. 20).

Example 13

Epitope Binding Experiments

FIG. 25 shows SPR sensorgram data for experiments designed to test whether or not monovalent dAb molecules BMS2h-503-1, BMS2h-572-6, BMS2h-719-17, and the monovalent anti-CD40L 5c8 Fab fragment compete with each other for binding to CD40L. Experiments were performed using biotinylated CD40L (biot-IZ-hCD40L) that was captured on a streptavidin sensor chip surface. The tests involved the sequential injection of a specified molecule (phase “a”), immediately followed by injection of the same molecule in the presence of a second specified molecule (phase “b”), followed by dissociation (phase “c”). Competition for binding is identified as a reduction (blocking) of the binding signal for the second molecule in the presence

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of the first, with the level of blocking being governed by the association and dissociation kinetics of each molecule. For each pair of molecules tested, the binding of the second molecule was shown to be reduced when the first molecule was present. These result suggest that BMS2h-503-1, BMS2h-572-6, BMS2h-719-17, and 5c8 Fab compete with each other for binding to biot-IZ-hCD40L.

FIG. 26 shows SPR sensorgram data for binding of the indicated dAb-CT-long and the 5c8-CT-long molecules to either human CD40L monomer (triple CD40L mutant (T211E, S222Y, H224K, [108-261])) or to CD40L trimer (IZ-hCD40L). The dAb-CT-long and the 5c8-CT-long molecules were captured via their "CT-long" Fc-domain on an immobilized anti-human IgG Fc (Biacore, GE Healthcare) antibody sensor chip surface. The data in the top 3 panels show that human CD40L monomer binds specifically to BMS2h-719-202-CT-long and 5c8-CT-long, but does not bind to any of the indicated dAb-CT-long molecules that contain dAbs from the BMS2h-572-6 lineage.. In contrast, the bottom 3 panels show that CD40L trimer (IZ-hCD40L) binds strongly to all the tested dAb-CT-long molecules from the BMS2h-572-6 lineage, as well as to BMS2h-719-202-CT-long and 5c8-CT-long. These results suggest that the molecules from the BMS2h-572-6xx-CT-long lineage are specific for an epitope that is only present on the CD40L trimer and not present on monomeric human CD40L, whereas BMS2h-719-202-CT-long and 5c8-CT-long bind to an epitope that is present on both the CD40L monomer and trimer.

Although the present embodiments have been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of these embodiments, and would be readily known to the skilled artisan.

The term "comprising" as used in this specification and claims means "consisting at least in part of". When interpreting statements in this specification and claims which include "comprising", other features besides the features prefaced by this term in each statement can also be present. Related terms such as "comprise" and "comprised" are to be interpreted in similar manner.

In this specification where reference has been made to patent specifications, other external documents, or other sources of information, this is generally for the purpose of

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providing a context for discussing the features of the invention. Unless specifically stated otherwise, reference to such external documents is not to be construed as an admission that such documents, or such sources of information, in any jurisdiction, are prior art, or form any part of the common general knowledge in the art.

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What is Claimed Is:

1. An isolated antibody polypeptide comprising a first variable domain that specifically binds human CD40L, wherein CD40L comprises the amino acid sequence of SEQ ID NO: 1, wherein the amino acid sequence of the first variable domain comprises:

- (a) a CDR1 region having a sequence Trp-X₁-Leu-Met-Gly (SEQ ID NO: 2), wherein X₁ is Glu or Gln;
- (b) a CDR2 region having a sequence Gly-Ile-Glu-Gly-Pro-Gly-Asp-Val-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (SEQ ID NO: 3); and
- (c) a CDR3 region having a sequence Lys-X₂-Y₂-Z₂-Ser-Asp-Tyr (SEQ ID NO: 4), wherein X₂ is Asp or Glu, Y₂ is Ala or Ser, and Z₂ is Lys, Asn, or Arg.

2. The antibody polypeptide of claim 1, wherein the first variable domain comprises the amino acid sequence of BMS2h-572-633 (SEQ ID NO: 274).

3. The antibody polypeptide of claim 1, wherein the first variable domain comprises the amino acid sequence of: BMS2h-572-10 (SEQ ID NO: 225), BMS2h-572-11 (SEQ ID NO: 226), BMS2h-572-12 (SEQ ID NO: 227), BMS2h-572-14 (SEQ ID NO: 229), BMS2h-572-15 (SEQ ID NO: 230), BMS2h-572-22 (SEQ ID NO: 237), BMS2h-572-23 (SEQ ID NO: 238), BMS2h-572-6 (SEQ ID NO: 243), BMS2h-572-603 (SEQ ID NO: 246), BMS2h-572-604 (SEQ ID NO: 247), BMS2h-572-607 (SEQ ID NO: 250), BMS2h-572-608 (SEQ ID NO: 251), BMS2h-572-609 (SEQ ID NO: 252), BMS2h-572-610 (SEQ ID NO: 253), BMS2h-572-611 (SEQ ID NO: 254), BMS2h-572-612 (SEQ ID NO: 255), BMS2h-572-613 (SEQ ID NO: 256), BMS2h-572-614 (SEQ ID NO: 257), BMS2h-572-616 (SEQ ID NO: 259), BMS2h-572-619 (SEQ ID NO: 262), BMS2h-572-630 (SEQ ID NO: 271), BMS2h-572-631 (SEQ ID NO: 272), BMS2h-572-632 (SEQ ID NO: 273), BMS2h-572-634 (SEQ ID NO: 275), BMS2h-572-635 (SEQ ID NO: 276), BMS2h-572-8 (SEQ ID NO: 278), or BMS2h-572-9 (SEQ ID NO: 279).

4. The antibody polypeptide of any of claims 1-3, wherein the antibody polypeptide is a domain antibody (dAb).

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5. The antibody polypeptide of any of claims 1-3, wherein the antibody polypeptide is a fusion polypeptide comprising the first variable domain and an Fc domain.

6. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises an IgG4 Fc domain.

7. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises an IgG1 Fc domain.

8. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises a CT-Long domain (amino acids 139 to 370 of SEQ ID NO: 1362).

9. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises a CT-short domain (amino acids 138 to 362 of SEQ ID NO: 1363).

10. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises a N297Q Long Fc domain (amino acids 139 to 370 of SEQ ID NO: 1364).

11. The fusion polypeptide of claim 5, wherein the fusion polypeptide comprises a N297Q Short Fc domain (amino acids 138 to 362 of SEQ ID NO: 1365).

12. The antibody polypeptide of claim 5, wherein the antibody polypeptide comprises the amino acid sequence of SEQ ID NO: 1355.

13. The antibody polypeptide of claim 5, wherein the antibody polypeptide consists of the amino acid sequence of SEQ ID NO: 1355.

14. The antibody polypeptide of any of claims 1-3, wherein the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, wherein the second antigen is an antigen other than human CD40L.

15. The antibody polypeptide of claim 14, wherein the second antigen is a cluster of differentiation (CD) molecule, a Major Histocompatibility Complex (MHC) Class II molecule, or a serum albumin (SA).

16. An isolated nucleic acid encoding the antibody polypeptide of any one of claims 1-15.

17. A vector comprising the nucleic acid of claim 16.

18. An isolated host cell comprising the vector of claim 17.

19. A pharmaceutical composition comprising a therapeutically-effective amount of the antibody polypeptide of any one of claims 1 to 15 and a pharmaceutically acceptable carrier.

20. The pharmaceutical composition of claim 19, further comprising an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

21. Use of the isolated antibody polypeptide according to any one of claims 1-15 for the preparation of a medicament for the treatment of a patient, wherein the patient has or is at risk of having an immune disease.

22. The use of claim 21, in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

23. The use of claim 21, wherein the immune disease is an autoimmune disease or a graft-related disease.

24. The use of claim 21, wherein the immune disease is a graft-related disease.

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25. The use of claim 24, wherein the graft-related disease is selected from the group consisting of solid organ, tissue and/or cell transplant rejection, graft versus host disease (GVHD), an acute transplant rejection, and a chronic transplant rejection.

26. The use of claim 22, wherein the immunosuppressive/immunomodulatory and/or anti-inflammatory agent is a CTLA4 mutant molecule.

27. The use of claim 26, wherein the CTLA4 mutant molecule is L104EA29Y-Ig (belatacept).

28. The use of claim 21, wherein the immune disease is selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, autism, epilepsy, Arthus's phenomenon, anaphylaxis, and drug addiction.

29. The use of claim 21, wherein the immune disease is idiopathic thrombocytopenic purpura.

30. A method of treating a patient having or at risk of having an immune disease, the method comprising administering to the patient the isolated antibody polypeptide according to any one of claims 1-15.

31. The method of claim 30, further comprising administration of an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

32. The method of claim 30, wherein the immune disease is an autoimmune disease or a graft-related disease.

33. The method of claim 30, wherein the immune disease is a graft-related disease.

34. The method of claim 33, wherein the graft-related disease is selected from the group consisting of solid organ, tissue and/or cell transplant rejection, graft versus host disease (GVHD), an acute transplant rejection, and a chronic transplant rejection.

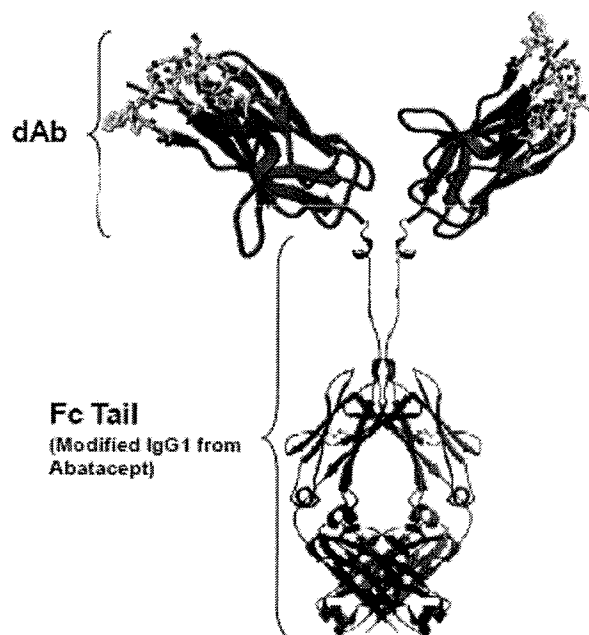
35. The method of claim 31, wherein the immunosuppressive/immunomodulatory and/or anti-inflammatory agent is a CTLA4 mutant molecule.

36. The method of claim 35, wherein the CTLA4 mutant molecule is L104EA29Y-Ig (belatacept).

37. The method of claim 30, wherein the immune disease is selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, epilepsy, Arthus's phenomenon, anaphylaxis, and drug addiction.

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38. The method of claim 30, wherein the immune disease is idiopathic thrombocytopenic purpura.

FIG. 1A**FIG. 1B**

EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVITYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYY
 CVKVGKDAKSDYRGQGLTVVSSASTEPKSSDKTHTSPSPAPPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
 PENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
 (MW=77,984 daltons)

dAb

Linker

Modified IgG1 Fc from Abatacept (Cys→Ser; Pro→Ser)

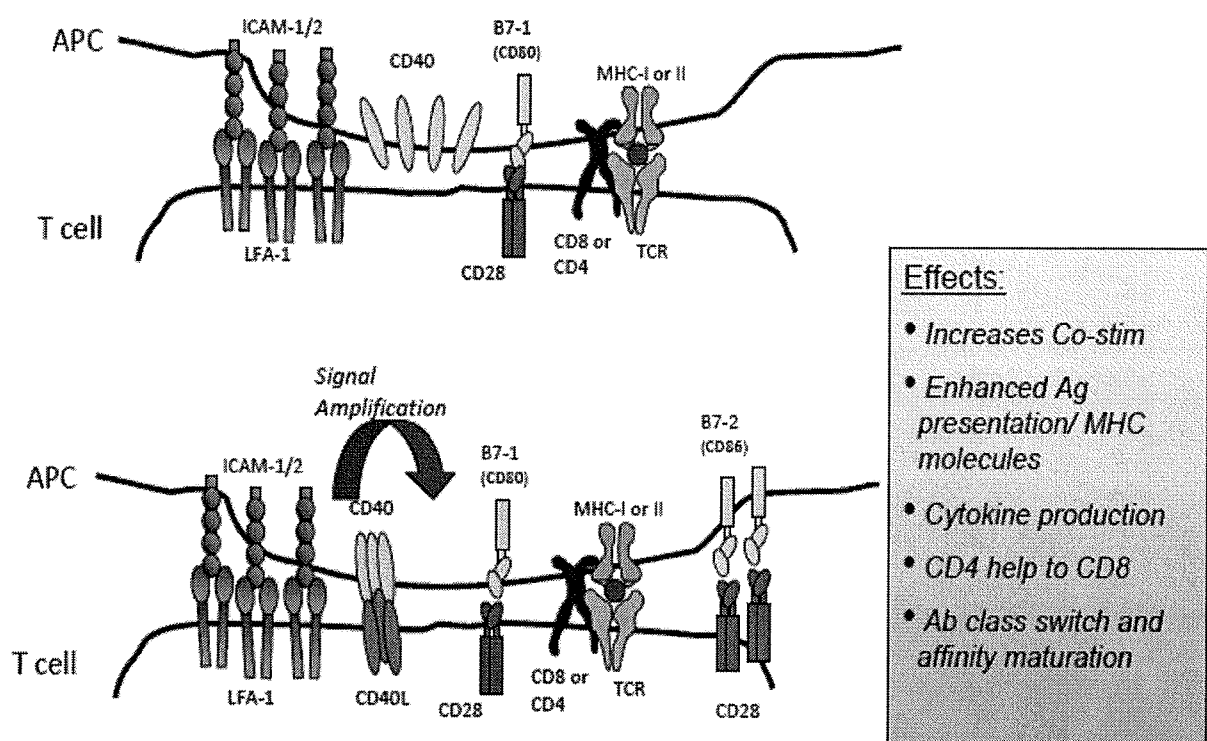
FIG. 2

FIG. 3

Fc

Domain antibody-AS-THTCPPCP...

CT-long

Domain antibody-AST-EPKSSDKTHTSPPSP ...

CT-short

Domain antibody-AS-THTSPPSP...

N297Qlong Fc

Domain antibody-AST-EPKSSDKTHTSPPSP...

N297Qshort Fc

Domain antibody-AS-THTSPPSP...

Osteonectin signal peptide sequence:

MRAWIFFLLCLAGRALA ^ EVQLLES...(start of Domain antibody)

FIG. 4

BMS2h-572-633-CT-L2

MRAWIFFLLCLAGRALA[^]EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLE
WVSGIEGPGDVTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVKVGKDAKSDYRGQ
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BMS2h-572-633-CT-S1

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WYVDGVEVHNAKTKPREEQY[N]STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSF
FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

BMS2h-572-633-N297^Q long Fc

MRAWIFFLLCLAGRALA[^]EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLE
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GTLVTVSS[AS]TEPKSSDKTHT[CPP]CPAPELLGG[PSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQY[Q]STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP
VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

BMS2h-572-633-N297^Q short Fc

MRAWIFFLLCLAGRALA[^]EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLE
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GTLVTVSS[AS]THT[CPP]CPAPELLGG[PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQY[Q]STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSF
FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

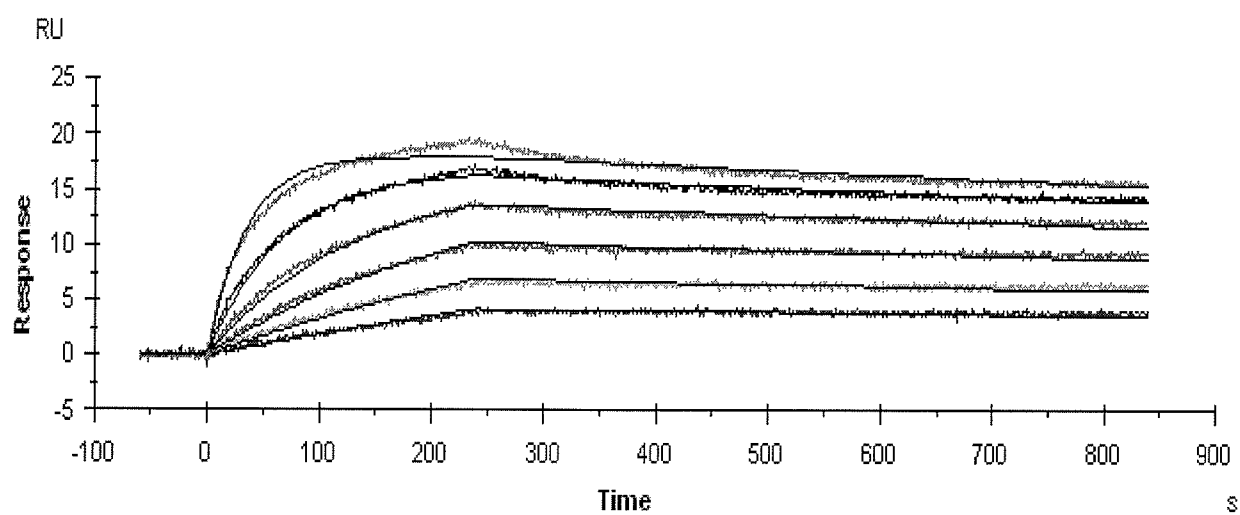
FIG. 5

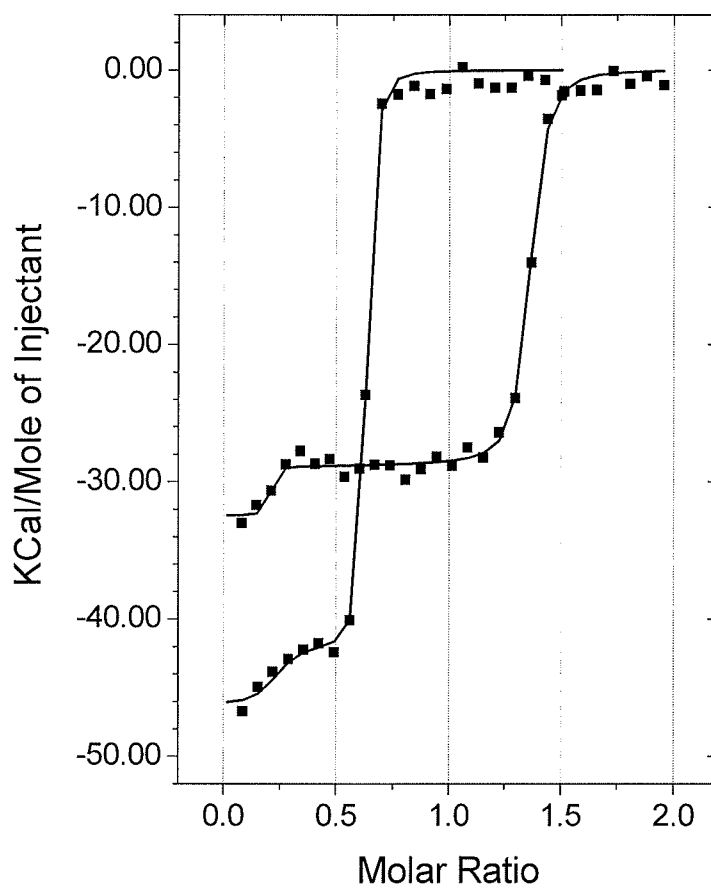
FIG. 6

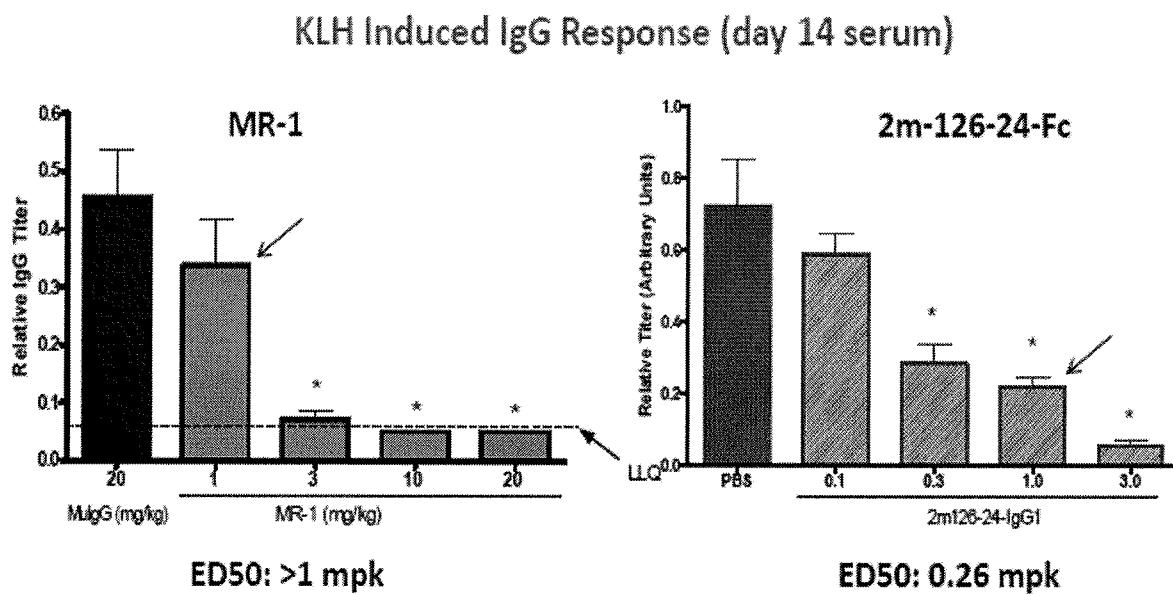
FIG. 7

FIG. 8

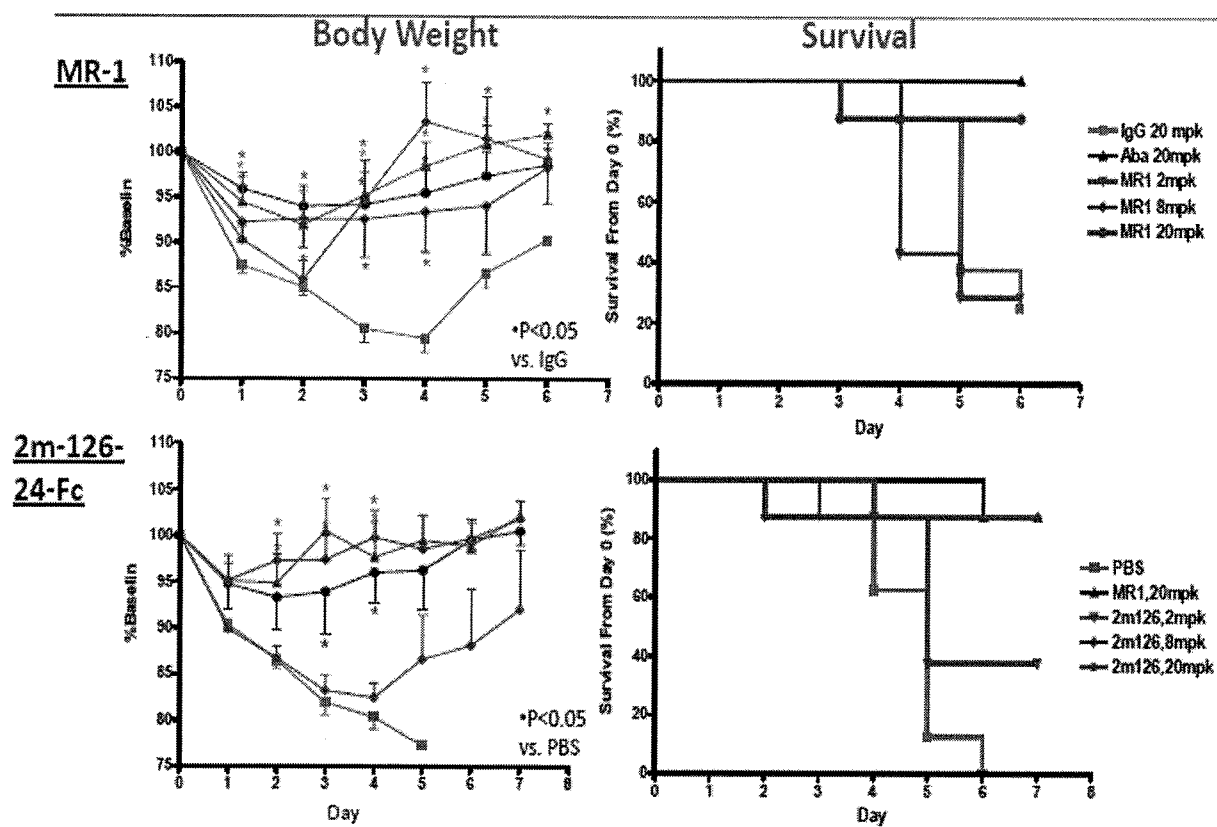
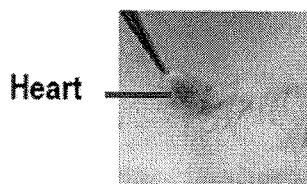


FIG. 9

- Insert heart from neonatal C57Bl/6 mice into the pinnae of adult BALB/c mouse ear.

- dosing: 2m126-24-Fc s.c. 1x/wk; CTLA4Ig i.p. 2x/wk

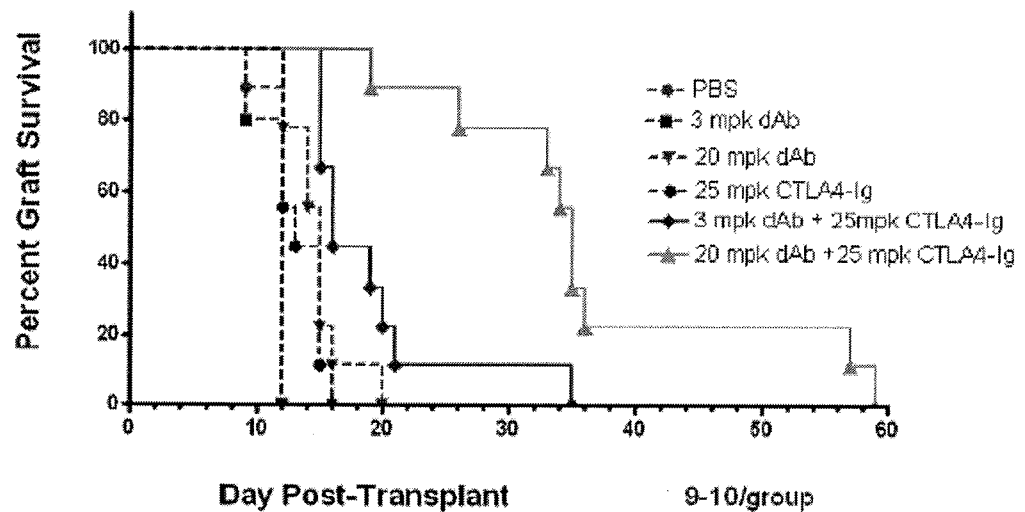
Graft Survival

FIG. 10

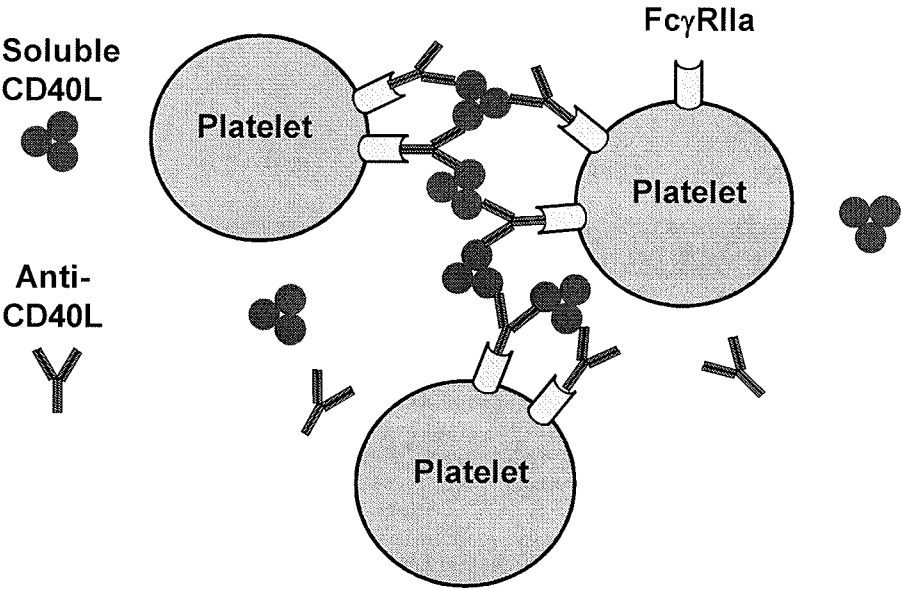


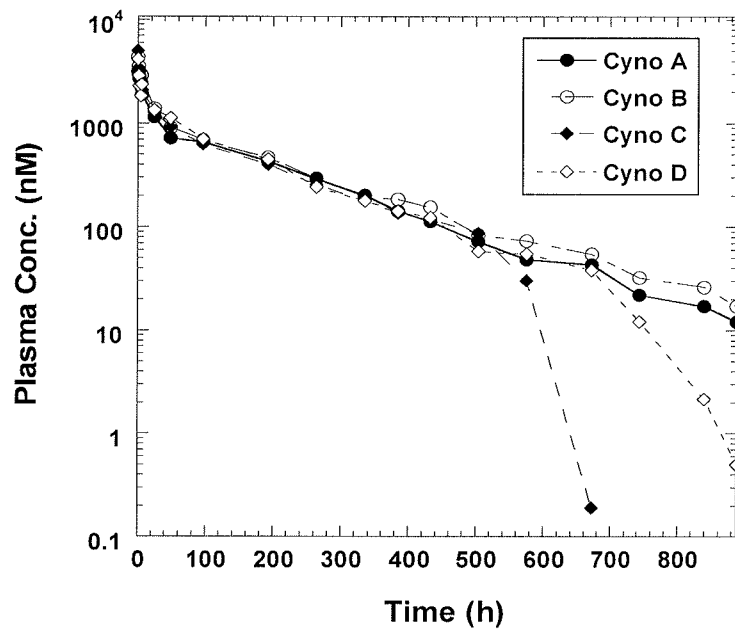
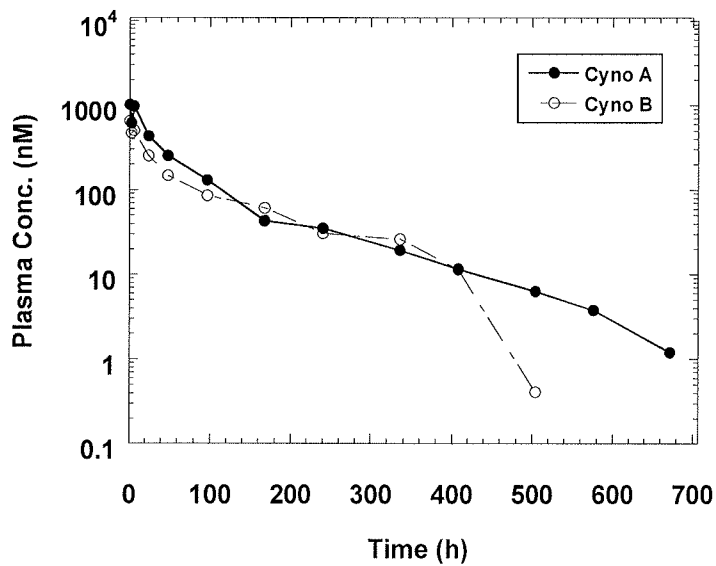
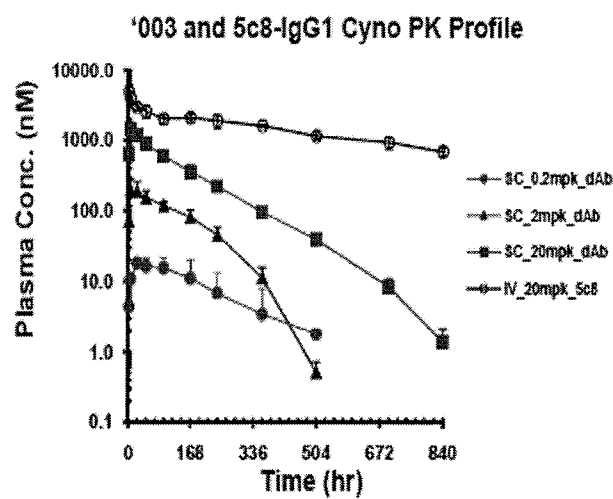
FIG. 11A**FIG. 11B**

FIG. 12



Ave. PK Para	BMS-986003_SC			5c8-IgG1_IV
	0.2mpk	2mpk	20mpk	20mpk
AUC _{tot} (μM·h)	4.0	30	175	1800
T _{1/2, 0-336h} (h)	85	66	105	~400

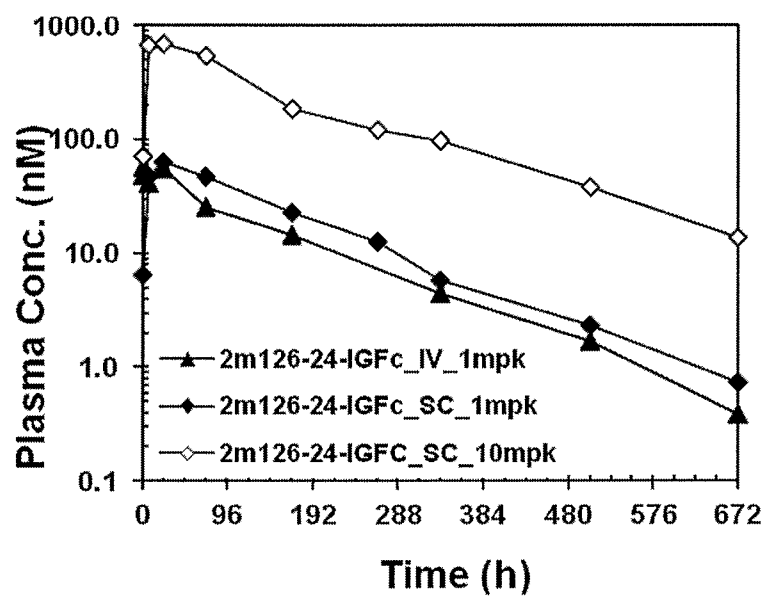
FIG. 13

FIG. 14

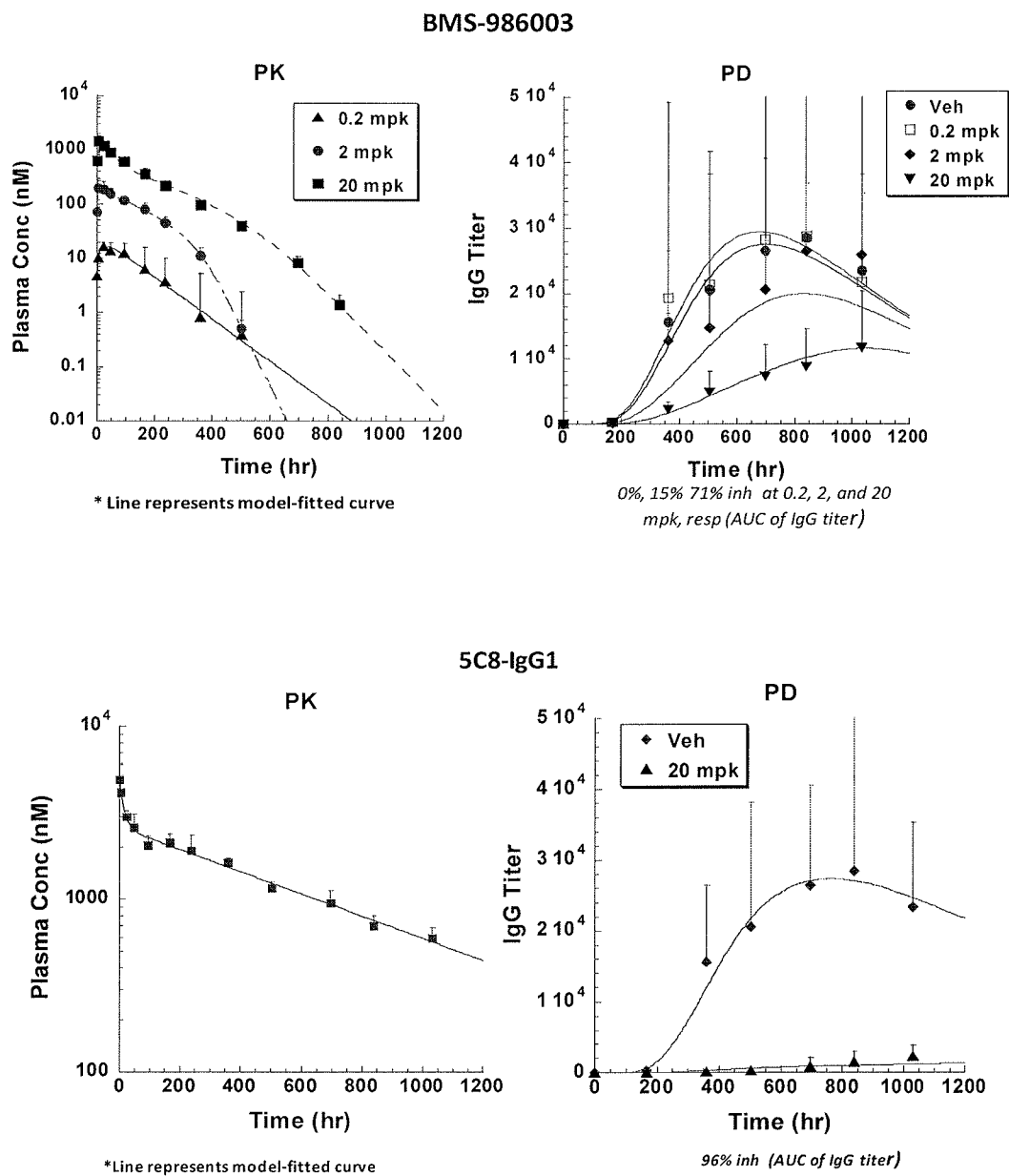


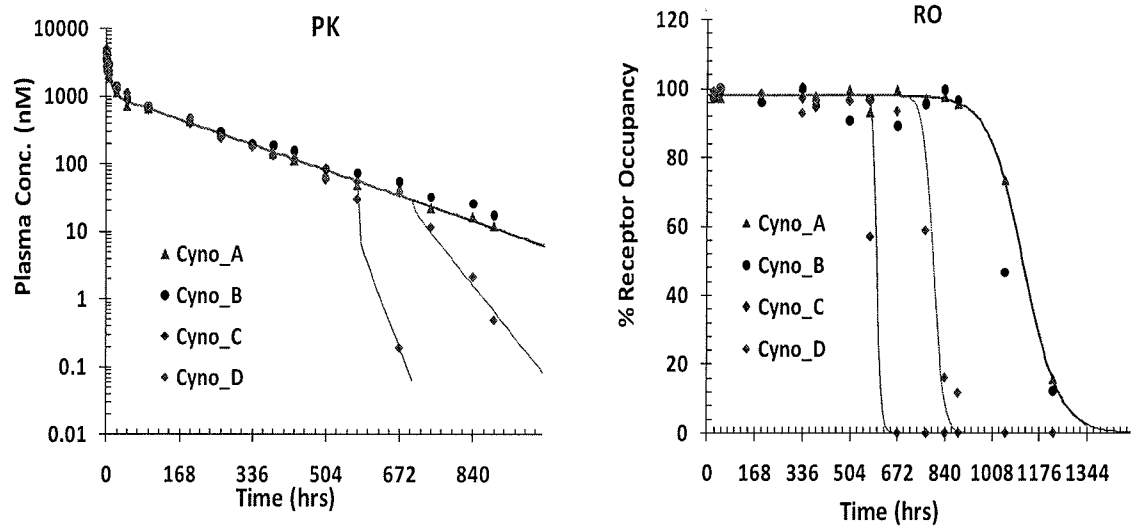
FIG. 15

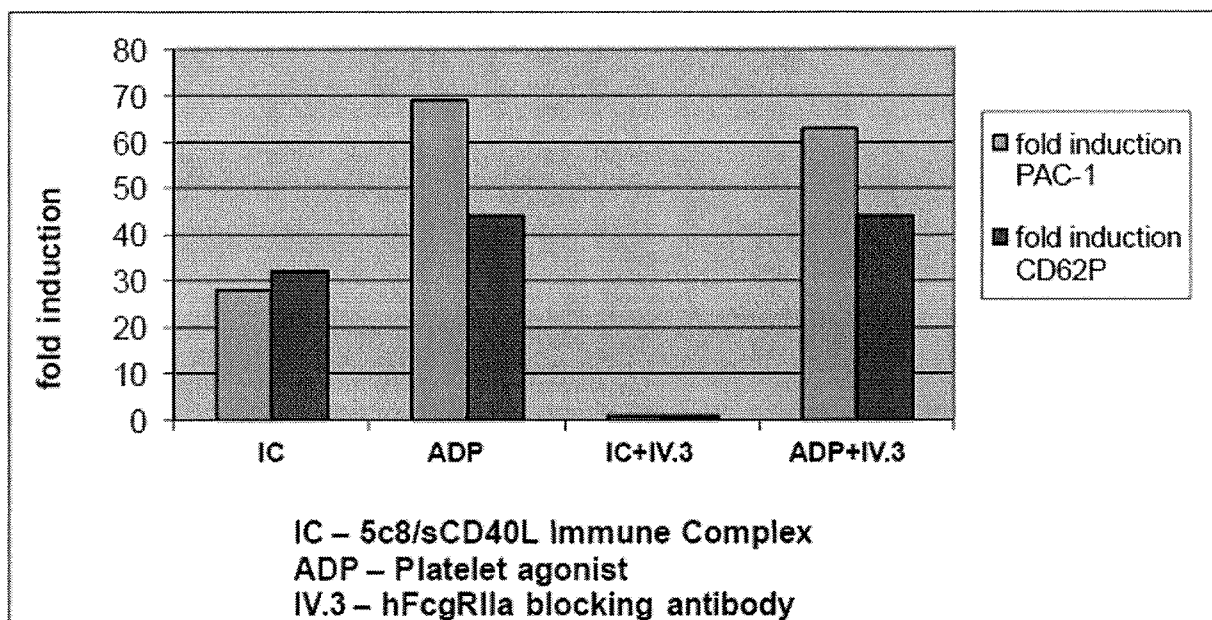
FIG. 16

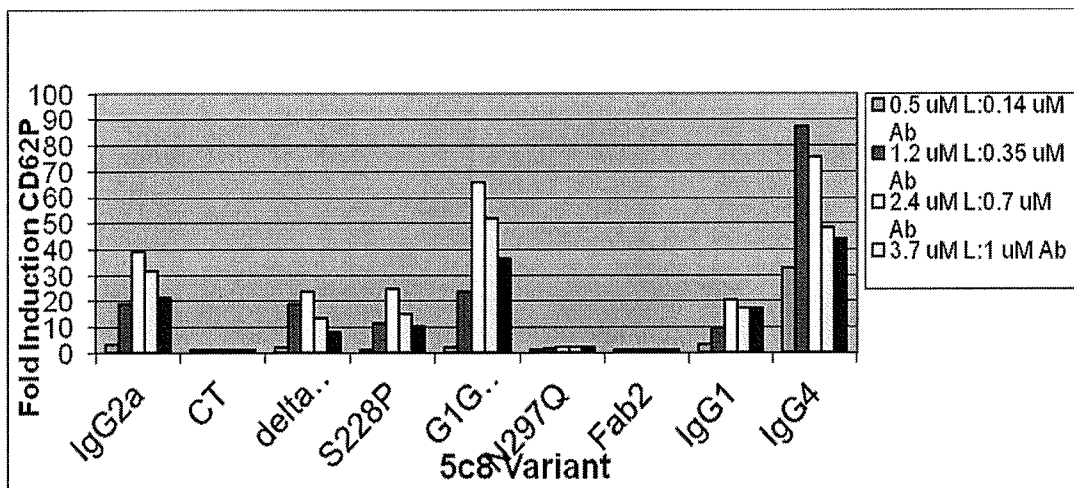
FIG. 17

FIG. 18

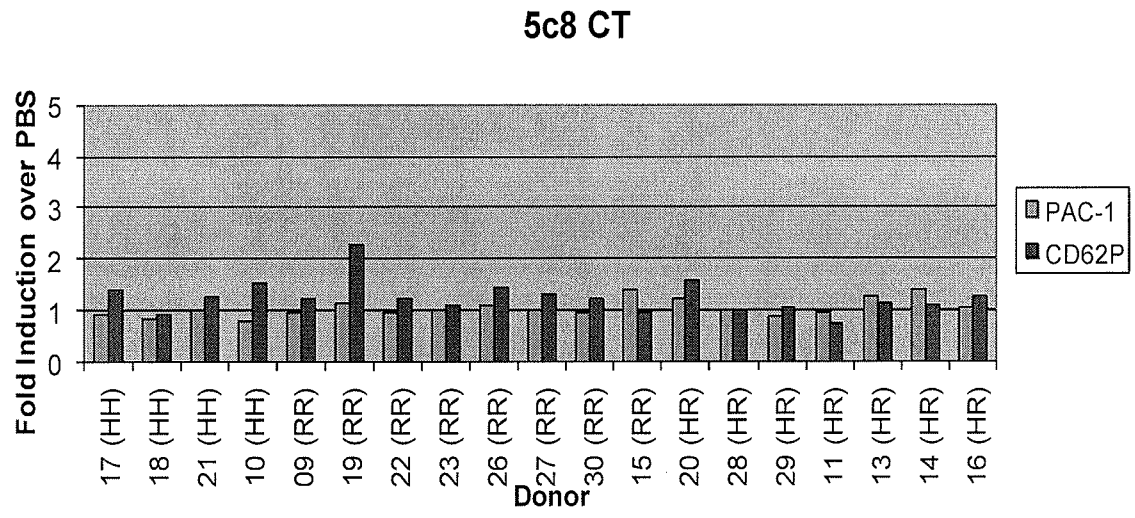


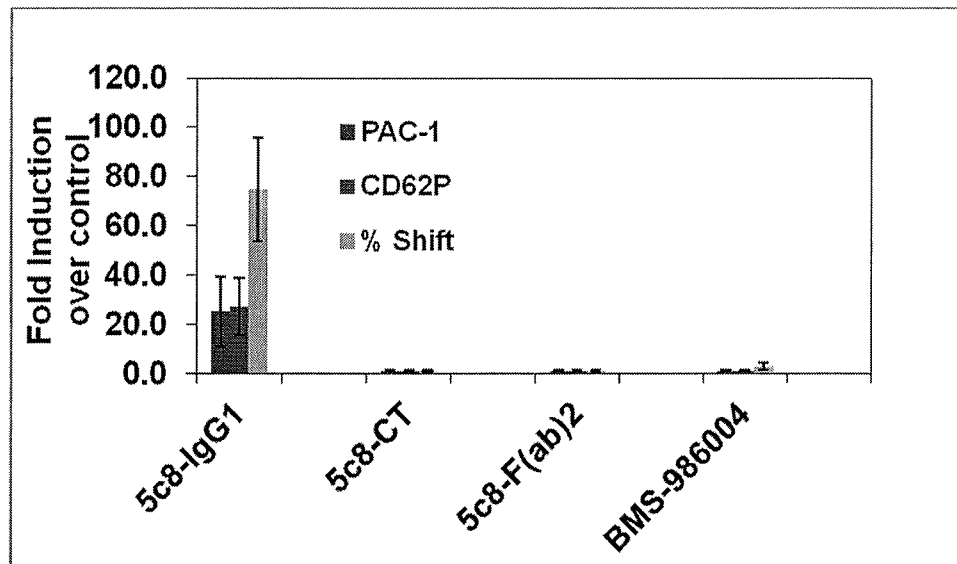
FIG. 19

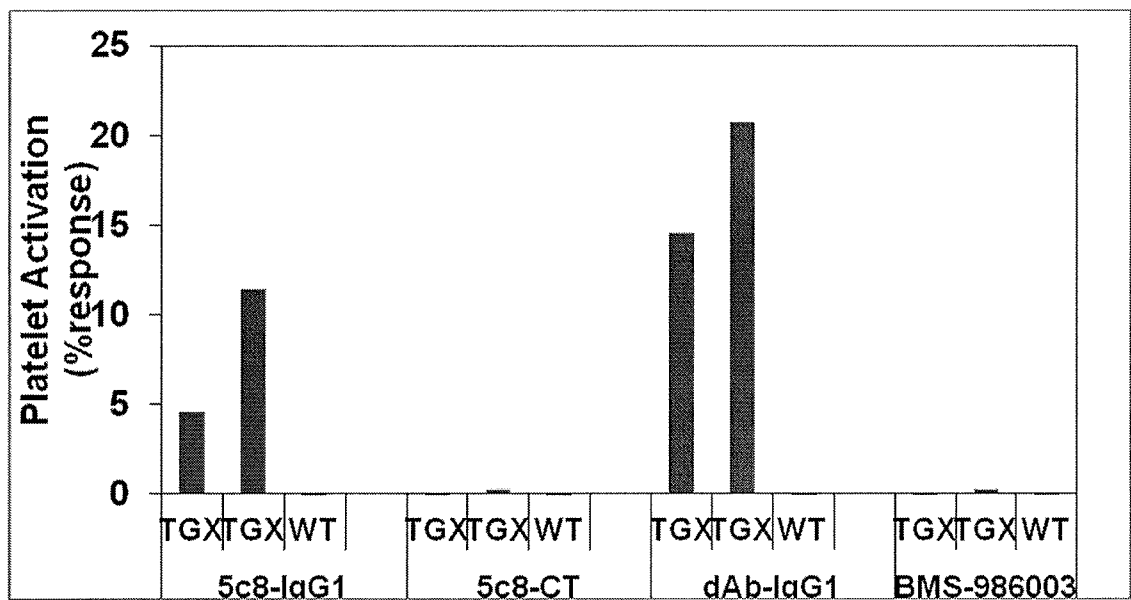
FIG. 20

FIG. 21

	CDR1	CDR2
BMS2h-572-6	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWQIMGWVRQAPGKGLEWVSGIEGPGDVTYY	60
BMS2h-572-608	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY	60
BMS2h-572-614	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWQIMGWVRQAPGKGLEWVSGIEGPGDVTYY	60
BMS2h-572-619	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWQIMGWVRQAPGKGLEWVSGIEGPGDVTYY	60
BMS2h-572-633	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY	60
BMS2h-572-634	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY	60
BMS2h-572-635	EVQLLESGGGLVQPGGSLRLSCAASGFTFNWELMGWARQAPGKGLEWVSGIEGPGDVTYY	60
	*****	*****
	CDR2	
	*****	*****
	CDR3	
	*****	*****
BMS2h-572-6	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKESNSDYRGQGT LVTVSS	118
BMS2h-572-608	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKESNSDYRGQGT LVTVSS	118
BMS2h-572-614	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKDAKSDYRGQGT LVTVSS	118
BMS2h-572-619	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKDSRSDYRGQGT LVTVSS	118
BMS2h-572-633	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKDAKSDYRGQGT LVTVSS	118
BMS2h-572-634	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKDSRSDYRGQGT LVTVSS	118
BMS2h-572-635	ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCVKVGKDSKSDYRGQGT LVTVSS	118
	*****	*****

	CDR1	CDR2
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
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96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

CDR2

BMS2h-719-2	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCAEPFTEFDYWGHTLVT	116
BMS2h-719-202	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCAEPFTEFDYWGHTLVT	116
BMS2h-719-203	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCAEPFTEFDYWGHTLVT	116
BMS2h-719-213	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCADPTEMDYWGHTLVT	116
BMS2h-719-214	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCADPTEFDYWGHTLVT	116
BMS2h-719-215	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCAEPFTELDYWGHTLVT	116
BMS2h-719-218	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCAEPFTEFDYWGHTLVT	116
BMS2h-719-225	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCAEPFTEFDYWGHTLVT	116

FIG. 23

BMS2h-503-1	DIQMTQSPSSLSASVGDRVTTITCRASHHIQRYLSWYQQKPGKAPKLLILWGSQLQSGVPS	60
BMS2h-503-2	DIQMTQSPSSLSASVGDRVTTITCRASHDIQRYLSWYQQKPGKAPKLLILWGSQLQSGVPS	60
	*****	*****
BMS2h-503-1	RFSGSGSGTDFTLTISSLQPEDEATYCGQWWAPPQTFGQGTKVEIKR	108
BMS2h-503-2	RFSGSGSGTDFTLTISSLQPEDEATYCGQWWAPPQTFGQGTKVEIKR	108
	*****	*****

FIG. 24

BMS2h-116-1312	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYQTSILRSGVPS	60
BMS2h-116-1313	DIQMTQSPSSLSASVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYQTSILRSGVPS	60
BMS2h-116-1320	DIQMTQSPSSLSAYVGDRVTITCRASQPIGPDLLWYQQKPGKAPKLLIYQTSILRSGVPS	60

BMS2h-116-1312	RFSGSGSETDFTLTISNLPEDLATYYCQQYWAFFVTFGKGTKVVIKR	108
BMS2h-116-1313	RFSGSGSETDFTLTISNLPEDFATYYCQQYWAFFVTFGRGTKVVIKR	108
BMS2h-116-1320	RFSGSGSETDFTLTISNLPEDFAKYCQQYWAFFVTFGQGTKVVIKR	108

FIG. 25

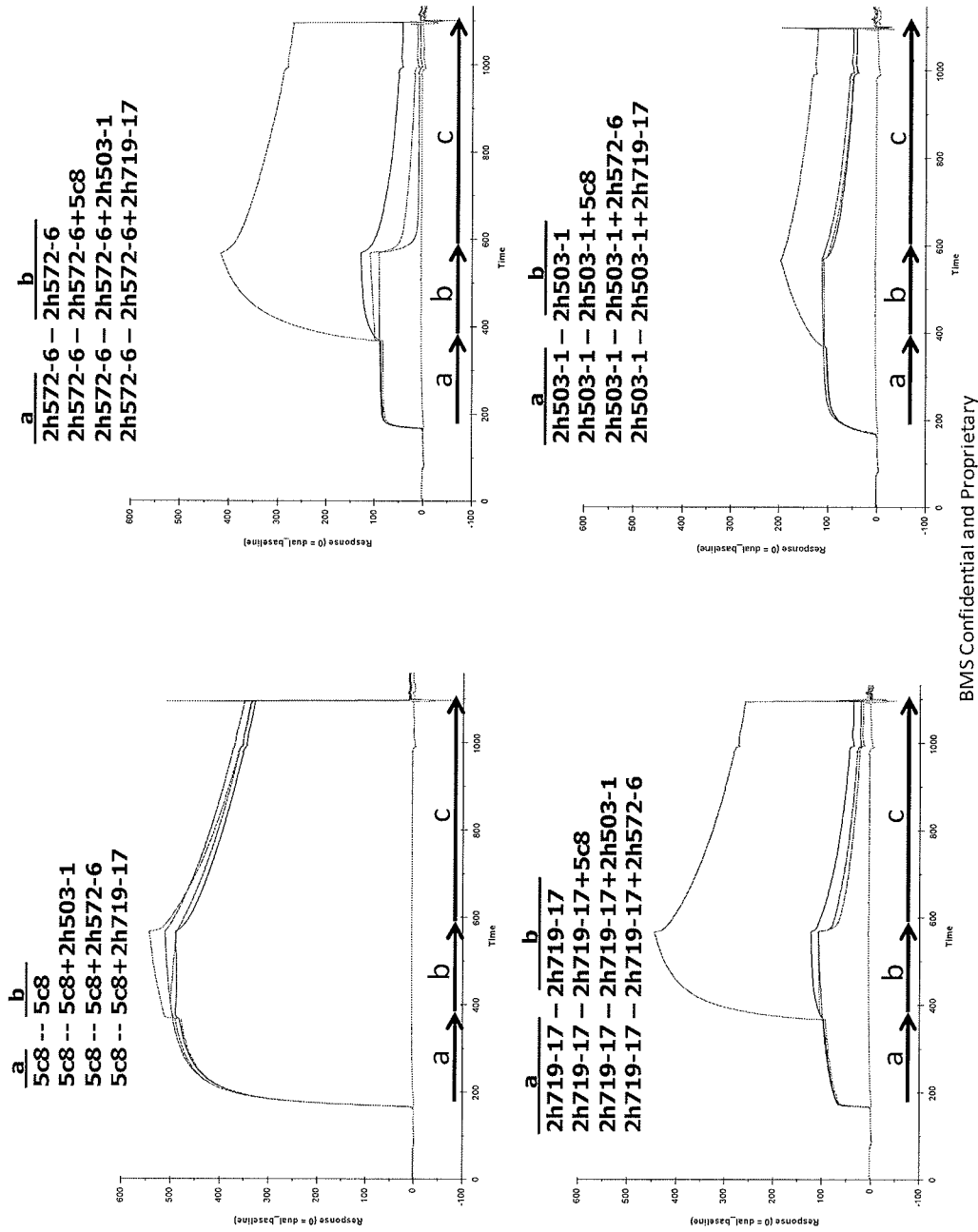
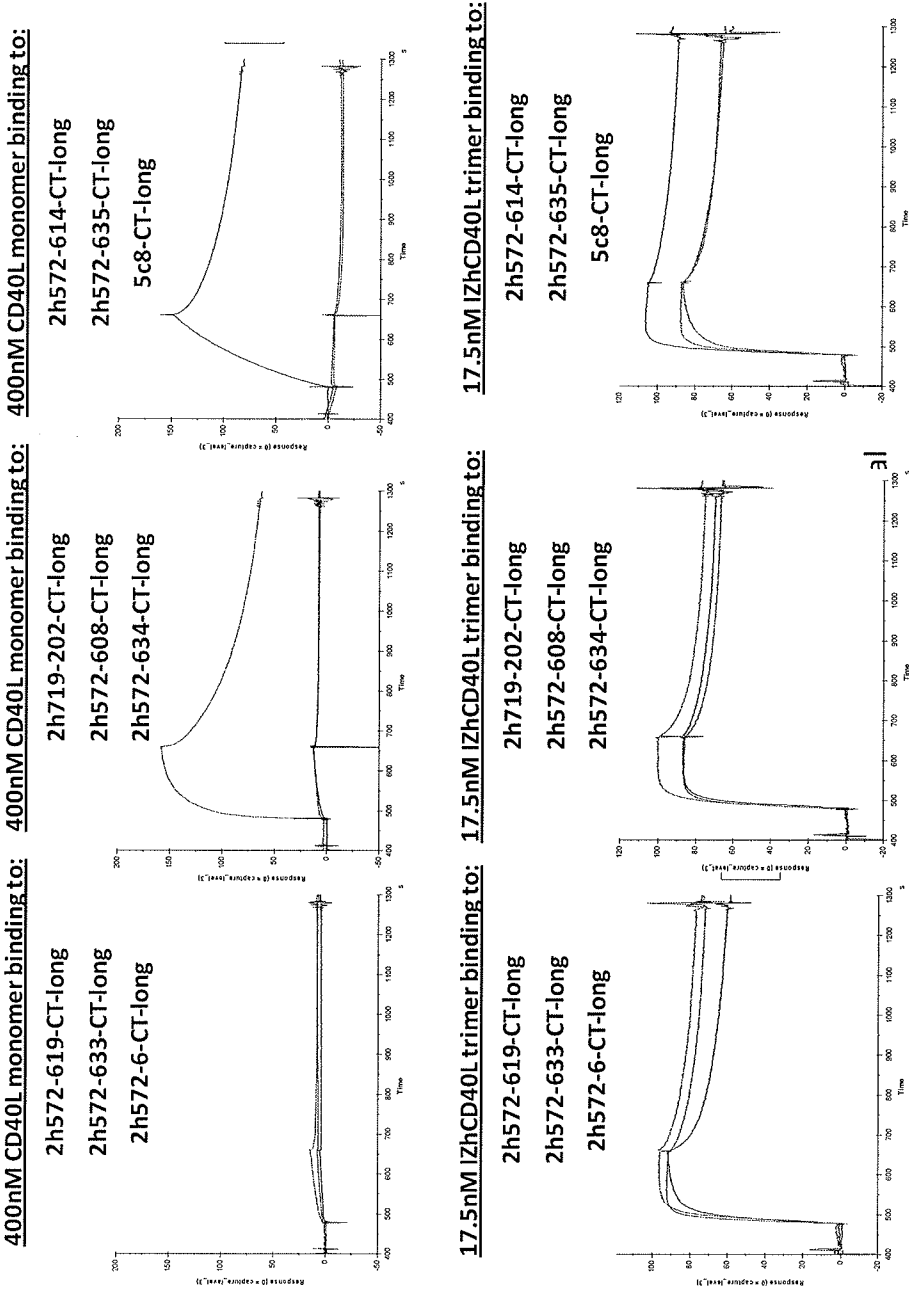


FIG. 26



20089600.txt
SEQUENCE LISTING

<110> BRISTOL-MYERS SQUIBB COMPANY
DOMANTIS LIMITED

<120> ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40L

<130> 200896-0005-W0 (489826)

<140>

<141>

<150> 61/655,110

<151> 2012-06-04

<150> 61/546,800

<151> 2011-10-13

<160> 1365

<170> PatentIn version 3.5

<210> 1

<211> 261

<212> PRT

<213> Homo sapiens

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1 5 10 15

Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
50 55 60

Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
85 90 95

Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
100 105 110

Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
115 120 125

Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
130 135 140

Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145 150 155 160

20089600.txt

Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
165 170 175

Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
180 185 190

Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205

Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220

Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
225 230 235 240

Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
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Gly Leu Leu Lys Leu
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<223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

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Trp Glu Leu Met Gly
1 5

<210> 3
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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

Gly

<210> 4
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<220>
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<220>
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 Lys Asp Ala Lys Ser Asp Tyr
 1 5

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

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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 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 Asn
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<220>
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 <223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

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

<210> 7
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<220>
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 Arg Thr Phe Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Lys
 20 25 30

Val Gly

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 <211> 11
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 1 5 10

<210> 9
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<222> (103)..(103)
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with respect to those in the annotations for said position"

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1          5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr

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20

25

30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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
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Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
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Thr Val Ser Ser
 115

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

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

Leu Trp Gly Ser Gln 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 Gly Gln Trp Trp Ala Pro Pro Gln
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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<210> 11
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 <213> Artificial Sequence

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 <221> misc_feature
 <222> (85)..(85)
 <223> /note="Residue given in the sequence has no preference with respect to the annotation for said position"

<220>
 <221> VARIANT
 <222> (100)..(100)
 <223> /replace="Arg" or "Gln"

<220>
 <221> misc_feature
 <222> (100)..(100)
 <223> /note="Residue given in the sequence has no preference with respect to those in the annotations for said position"

<400> 11
 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 Pro Ile Gly Pro Asp
 20 25 30

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

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

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

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

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

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
 <221> VARIANT
 <222> (6)..(25)
 <223> /replace=" "

<220>
 <221> misc_feature
 <222> (6)..(25)
 <223> /note="Residues given in the sequence have no preference with respect to the annotation for said positions"

<220>
 <221> misc_feature
 <222> (1)..(25)
 <223> /note="This sequence may encompass 1 to 5 'Gly Gly Gly Gly Ser' repeating units"

<400> 12
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25

<210> 13
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 13
 Thr Val Ala Ala Pro Ser
 1 5

<210> 14
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 14
 Ala Ser Thr Ser Gly Pro Ser
 1 5

<210> 15
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 15
 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 Ile Ala Tyr
 20 25 30

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

Ser Trp Ile Asp Glu Trp Gly Leu Gln Thr 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 Lys Lys Thr Pro Glu Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 16
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 16
 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 Gly Asp Tyr
 20 25 30

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

Ser Gly Ile Asp Gly Glu Gly Ser Asp Thr 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 Lys Pro Gly Arg Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 17
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 17
 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 Glu Arg Tyr
 20 25 30

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

Ser Thr Ile His Gly Ser Gly Ser Ala Thr 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 Lys Gly Pro Tyr Thr Ser Arg His Asn Ser Leu Gly His Phe Asp
100 105 110

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

<210> 18

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 18

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 Met Asp Tyr
20 25 30

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

Ser Ser Ile Gly Pro Val Gly Met Ser Thr 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 Lys Tyr Gly Gly Thr Ser Gly Arg His Asn Thr Lys Phe Asp Tyr
100 105 110

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

<210> 19

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 19

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 Thr Glu Tyr
20 25 30

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

Ser Val Ile Ser Pro Leu Gly Phe Thr Thr 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 Lys Trp Thr Gly Gly Ser Gly Ile Leu Asn Ser Ser Phe Asp Tyr
100 105 110

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

<210> 20

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20

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 Arg Val Ser Asn Tyr
20 25 30

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

Ser Thr Ile Ser Ala Thr Asn 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 Thr Leu Tyr
65 70 75 80

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

Ala Ala Val Thr Trp Trp Leu Leu Arg His Asn Asp Asn Leu Gly Phe
 100 105 110

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

<210> 21
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 21
 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 Ser Ile Ser Tyr Lys
 20 25 30

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 22
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 22
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 23
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 23
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 Arg Ser Tyr
20 25 30

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

Ser Ser Ile Asn Pro Met Gly Tyr Gln Thr 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 Lys His Gly Val Gly Lys Gly Thr Lys Pro His Asn Phe Asp Tyr
100 105 110

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

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 24
 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 Glu Leu Tyr
 20 25 30

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

Ser Glu Ile Ser Gly Ser Gly Phe Pro Thr 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 Lys Ser Leu His Asp Lys Thr Gln His His Gln Glu Phe Asp Tyr
 100 105 110

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

<210> 25
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 25
 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 Ile Glu Tyr
 20 25 30

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

Ser Leu Ile Ser Pro Ser Gly Val Phe Thr 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 Lys Gly Asp Glu Ser Ser Thr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 26

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 26

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 Lys Arg Tyr
20 25 30

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

Ser Thr Ile Gly Ser Ser Gly Tyr Pro Thr 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 Glu Arg Met Pro Gly Tyr Phe Pro Gly Phe Ala Arg Gln Phe Asp
100 105 110

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

<210> 27

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 27

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 Trp Arg Tyr
20 25 30

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

Ser Thr Ile Asn Asp Glu Gly Arg Glu Thr 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 Lys Lys Arg Val Ser Ser Ser Val Asn Ala Pro Tyr Glu Phe Asp
100 105 110

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

<210> 28

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 28

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 Ala Asn Tyr
20 25 30

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

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

Ala Lys Val Leu Ala Asp Leu Ile Ala Gly His Ala Glu Phe Asp Tyr
100 105 110

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

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<210> 29
<211> 124
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 29
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 Pro Ser Tyr
20 25 30

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

Ser Gly Ile Ser Arg Ser Gly Ser Met Thr 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 Lys Gly Val Asp Ala His Val Tyr Tyr Met Glu Pro Phe Phe Asp
100 105 110

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

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<210> 30
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 30

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 Glu Arg Tyr
20 25 30

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

Ser Thr Ile Ser Ser Asp Gly Gly Gly Thr 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 Lys Pro Gly Thr Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 31

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 31

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 Pro Lys Tyr
20 25 30

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

Ser Ser Ile Asp Gly Asp Gly Lys Ser Thr 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 Lys Pro Asp Gln Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 32
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 32
 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 Tyr Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp 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 Tyr Gly Glu Thr Ser Gly Pro Ile Ser Glu Asn Phe Asp Tyr
 100 105 110

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

<210> 33
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 33
 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 Thr Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

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

Ser Ser Ile Thr Asn Glu Gly Val Ser Thr 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 Lys Pro Gly Lys Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 34

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 34

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 Gly Glu Tyr
20 25 30

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

Ser Ser Ile Thr Ser Asp Gly Leu Ser Thr 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 Lys Pro Gly Ile Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 35
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 35
 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 Ala Asp Tyr
 20 25 30

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

Ser Gly Ile Val Asp Asp Gly Leu Met Thr 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 Lys Pro Asp Val Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Asn
 115

<210> 36
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 36
 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 Ile Gly Tyr
 20 25 30

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

Ser Ser Ile Gly Pro Leu Gly Ala Thr Thr Tyr Tyr Ala Asp Ser Val
 Page 22

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 Lys Leu Pro Ala Gly Thr Ser Ser His Ser Val Asp Phe Asp Tyr
 100 105 110

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

<210> 37

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 37

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 Ala Asp Tyr
 20 25 30

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

Ser Ser Ile Thr Ser Asp Gly Val Ser Thr 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 Lys Pro Ser Val Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 38

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 38

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 Arg Arg Tyr
 20 25 30

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

Ser Trp Ile Glu Ala Asp Gly Arg Thr Thr 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 Lys Gly Leu Thr Asp Gln His Val Ile Glu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 39

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 39

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 Asp Gly Tyr
 20 25 30

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

Ser Ser Ile Ala Pro Asp Gly Asn Tyr Thr 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 Lys Phe Trp Gly Met Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 40
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 40
 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 Ala Ser Tyr
 20 25 30

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

Ser Ser Ile Gly Pro Ile Gly Phe Thr Thr 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 Glu Met Lys Ser Pro Tyr Lys Pro Gln Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 41
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 41
 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 Leu Ala Tyr
20 25 30

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

Ser Ser Ile Ser Pro Ser Gly Thr His Thr 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 Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 42
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 42
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 Asn Tyr
20 25 30

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

Ser Val Ile Ser Glu Val Gly Ser Leu Thr 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 Lys Pro His Asp Ser Ser Ile Gly Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 43
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 43
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 Trp Ser Tyr
20 25 30

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

Ser Ser Ile Met Ala Ser Gly Asp Asp Thr 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 Lys Trp Asp Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 44
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 44
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 Glu Glu Tyr
20 25 30

Val Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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Ser Thr Ile Ser Pro Ile Gly Leu Thr Thr 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 Glu Phe Pro Leu Ile Ile Leu Pro Asp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 45

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 45

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 Met Glu Tyr
 20 25 30

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

Ser Ile Ile Ser Pro Leu Gly Leu Ser Thr 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 Lys Tyr Gln Asp Ser Ser Asp Ser Gln Tyr Thr Asn Phe Asp Tyr
 100 105 110

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

<210> 46

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 46

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 Glu Asp Tyr
 20 25 30

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

Ser Ser Ile Gly Pro Leu Gly Leu Trp Thr Tyr Tyr Ala Asp Ser Ala
 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 Lys Ser Pro Leu Glu Gly Leu Ile Thr Asn Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 47

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 47

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 Asp Ala Tyr
 20 25 30

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

Ser Ile Ile Asp Trp Asp Gly Asn Ser Thr 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 Lys Pro Gly Asp Asn Val Gly Ile Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 48

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 48

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 Asn Tyr
 20 25 30

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

Ser Ala Ile Asp Glu Trp Gly Phe Ala Thr 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 Lys His Trp Glu Phe Thr Ser Asp Thr Ser Arg Phe Asp Tyr Trp
 100 105 110

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

<210> 49

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 49

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 Glu Asp Phe
 20 25 30

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

Ser Ser Ile Asn Asp Gln Gly Ser Leu Thr 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 Lys Pro Asp Gln Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 50

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 50

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 Ala Tyr
 20 25 30

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

Ser Arg Ile Ser Pro Gln Gly Gln Arg Thr 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 Lys Ile Arg Gly Gln Ser Arg Ile Pro Met Arg Phe Asp Tyr Trp
 100 105 110

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

<210> 51
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 51
 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 Pro Glu Tyr
 20 25 30

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

Ser Tyr Ile Ser Ser Asp Gly Tyr Ser Thr 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 Lys Pro His Gly Ser Pro Arg Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 52
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 52
 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 Thr Asp Tyr
 Page 32

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30

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

Ser Thr Ile Thr Ser Leu Gly Glu Ser Thr 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 Lys Pro Gly Arg Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 53

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 53

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 Ala Phe Tyr
 20 25 30

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

Ser Trp Ile Asp Ala Thr Gly Thr Arg Thr 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 Glu Gly Asn Tyr Gly Ser Ser Tyr Thr Met Gly Val Phe Asp Tyr
 100 105 110

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

<210> 54
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 54
 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 Asp Glu Tyr
 20 25 30

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

Ser Ser Ile Gly Pro Ser Gly Pro Asn Thr 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 Lys Ser Pro Tyr Phe Asp Val Ile Pro Ser Tyr Phe Asp Tyr Trp
 100 105 110

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

<210> 55
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 55
 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 Ala Asp Tyr
 20 25 30

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

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Ser Ser Ile Gln Ser Ser Gly Leu Arg Thr 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 Lys Arg Ala Asn Ser Arg Arg Gly Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 56

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 56

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 Asp Tyr
20 25 30

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

Ser Ser Ile Thr Ser His 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 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 Pro Asp Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 57

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 57

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 Ala His Tyr
 20 25 30

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

Ser Ser Ile Gly Arg Leu Gly Asn Arg Thr 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 Lys Arg Ala Thr Pro Val Pro Ile Lys Gly Leu Phe Asp Tyr Trp
 100 105 110

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

<210> 58

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 58

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 Leu Thr Phe Gly Arg Tyr
 20 25 30

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

Ser Ser Ile Asp Ser Asp Gly Trp Val Thr 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 Gln Pro Asp Ser Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 59
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 59
 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

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

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

Val Thr Val Ser Ser
 115

<210> 60
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 60
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15
Ser	Leu Arg 20	Ser Cys Ala Ala 25	Gly Phe Thr Phe Thr Arg Tyr 30
Arg Met	Ser Trp Val Arg Gln 35	Ala Pro Gly Lys Gly Leu Glu Trp Val 40	
Ser Gly Ile Ser Arg Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val 50	55		
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 Gly Met Thr Ala Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100	105	110	
Val Thr Val Ser Ser 115			

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<210> 61
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 61
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 Gln Met Tyr
20 25 30

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

Ser Met Ile Glu Pro Ala Gly Asp Leu Thr 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 Lys Tyr Gln Glu Gln Pro Trp Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 62
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 62
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 Pro Phe Pro Gln Tyr
20 25 30

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

Ser Met Ile Thr Ser Asp Gly Leu Asp Thr 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 Lys Pro Glu Pro Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 63
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 63
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 Met Tyr
20 25 30

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

Ser Thr Ile Leu Ser Asp Gly Thr Asp Thr 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 Lys Tyr Gly Ala Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 64
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 64
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 Lys Leu Tyr
20 25 30

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

Ser Ser Ile Asp Ala Gly Gly His Glu Thr 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 Lys Asp Trp Trp Asp Tyr Leu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 65

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 65
 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 Arg Tyr
 20 25 30
 Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Asn Arg Ser Gly Met Arg Thr 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 Glu Gly His Gln Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

<210> 66
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 66
 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 Thr Gly Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Thr Ile Asn Ala Asn Gly Ile Arg Thr 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 Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Gly Val Trp Arg Trp Gly Thr Gly His Lys Phe Asp Tyr
100 105 110

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

<210> 67

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 67

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 Lys Gln Tyr
20 25 30

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

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

Leu Val Thr Val Ser Ser
115

<210> 68

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 68

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 Gly Thr Tyr
 20 25 30

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

Ser Arg Ile Asn Trp Gln Gly Asp Arg Thr 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 Lys Ala Gly Phe Gly His Tyr Val Asp Gly Leu Gly Phe Asp Tyr
 100 105 110

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

<210> 69

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 69

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 Gly Tyr
 20 25 30

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

Ser Ser Ile Thr Asp Met Gly Asp Ser Thr 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 Lys Pro Gly Thr Ala Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 70
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 70
 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 Ala Lys Tyr
 20 25 30

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

Ser Ser Ile Thr Pro Lys Gly His Ser Thr 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 Lys Arg Pro Met Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 71
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 71
 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 Glu Arg Tyr
20 25 30

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

Ser Ser Ile Arg Pro Arg Gly Gly Lys Thr 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 Lys Trp Arg Arg Glu Gly Tyr Thr Gly Ser Lys Phe Asp Tyr Trp
100 105 110

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

<210> 72

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 72

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 Glu Arg Tyr
20 25 30

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

Ser Ser Ile Trp Pro Arg Gly Gln Lys Thr 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 Lys Gly Asn Ser Arg Tyr Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser

115

<210> 73
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 73
 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 Asp Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Phe 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 Ser Gly Arg Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 74
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 74
 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 Gly Tyr
 20 25 30

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

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Ser Gly Ile Ser Ser Glu Gly Leu Thr Thr 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 Lys Leu Gly Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 75
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 75
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 Thr Asn Tyr
20 25 30

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

Ser Thr Ile Arg Pro Asn Gly Thr Lys Thr 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 Lys Arg Ser Ser Ala His Leu Gln Arg Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 76
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 76

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 Gly Asn Tyr
 20 25 30

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

Ser Ser Ile Gly Arg His Gly Gly Arg Thr 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 Lys Lys Gly Ser Thr Tyr Pro Arg Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 77

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 77

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 Thr Ala Ser Gly Phe Thr Phe Ser His Tyr
 20 25 30

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

Ser Ser Ile Glu Pro Phe Gly Gly Gly Thr 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 Lys Val Tyr Pro Gln Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
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<210> 78
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 78
 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 Asn Tyr
 20 25 30

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

Ser Ser Ile Arg Pro Asp Gly Lys Ile Thr 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 Glu Val Tyr Ser Ser Cys Ala Met Cys Thr Pro Leu Leu Phe Asp
 100 105 110

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

<210> 79
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 79

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 Lys Arg Tyr
 20 25 30

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

Ser Asp Ile Gly Pro Arg Gly Phe Ser Thr 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 Lys Val Gly Arg Gly Gln Arg Asp Thr Ser Gln Pro Phe Asp Tyr
 100 105 110

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

<210> 80

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 80

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 Ala Ser Tyr
 20 25 30

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

Ser Gly Ile Thr Ser Gly Gly Leu Ser Thr 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 Lys Pro Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 Page 50

100

105

110

Thr Val Ser Ser
115

<210> 81
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 81
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 Ala Ser Tyr
20 25 30

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

Ser Gly Ile Ser Ser Asp Gly Leu Ser Thr 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 Lys Pro Gly Val Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 82
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 82
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 Asp Lys Tyr
20 25 30

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

Ser Gly Ile Glu Pro Leu Gly Asp Val Thr 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 Lys Glu Ala Ser Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 83

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 83

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 Thr Glu Tyr
20 25 30

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

Ser Ser Ile Asp Asn Val Gly Ser Ser Thr 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 Lys Pro Gly Lys Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 84
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 84
 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 Ala Asp Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Arg Gln Gly Phe Ala Thr 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 Lys Asp Leu Glu Arg Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 85
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 85
 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 Ala Asn Tyr
 20 25 30
 Glu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Ser Glu Trp Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Ala
 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 Lys Leu Val Gly Gly Thr Gln Tyr Glu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 86

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 86

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 His Asn Tyr
20 25 30

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

Ser Ser Ile Ser Ser Gly Gly Ser Ser Thr 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 Lys Pro Gly Val Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 87

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 87

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 Gly Leu Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg 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 Ala Gly Arg Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 88

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 88

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 Asn Tyr
20 25 30

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

Ser Ser Ile Thr Ser Glu 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 Thr Leu Tyr
65 70 75 80

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

Ala Lys Pro Gly Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 89
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 89
 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 Asp Tyr
 20 25 30

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

Ser Ser Ile Thr Ser Glu 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 Thr Val 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 Pro Gly Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 90
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 90
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Thr Ile Thr Ser Gln Gly Thr Ser Thr 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 Lys Pro Asp Arg Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 91
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 91
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 Arg Ser Tyr
20 25 30

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

Ser Ser Ile Thr Ser Asp Gly Gly Thr Thr 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 Lys Pro Asp Lys Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 92
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 92
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 Asn Leu Tyr
20 25 30

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

Ser Ser Ile Thr Ser Asp Gly Val Ser Thr 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 Lys Pro Asp Ser Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 93
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 93
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 Gly His Tyr
20 25 30

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

Ser Thr Ile Ser Asp Asn Gly Asn Gly Thr 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 Lys Pro Gly Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 94

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 94

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 Gly Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Gly Gly Thr 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 Lys Pro Gly Arg Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 95

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 95

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 Ala Arg Tyr
20 25 30

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

Ser Thr Ile Ser Asp Asp Gly Asp Ser Thr 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 Lys Leu Asp Lys Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 96

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 96

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 Asp Asn Asp
20 25 30

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

Ser Ala Ile Asp Thr Thr Gly Gly Gln Thr 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
Page 60

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 Pro Gly Lys Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

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<210> 97
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 97
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 Gly Glu Ser
20 25 30

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

Ser Ser Ile Leu Asp Glu Gly Ser Gly Thr 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 Lys Pro Asp Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

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<210> 98
<211> 117
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 98

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 Gly Glu Glu
20 25 30

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

Ser Ala Ile Thr Asp Asp Gly Asp Asp Thr 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 Lys Pro Asn Ala Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 99

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 99

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 Glu Val Tyr
20 25 30

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

Ser Gly Ile Val Asn Asp Gly Ser Ser Thr 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 Lys Pro Asp Lys Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 100
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 100
 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 Gly Asn Thr
 20 25 30

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

Ser Ser Ile Ala Asp Asp Gly Ser Ser Thr 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 Lys Pro Gly Gln Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 101
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 101
 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 Glu Glu Tyr
 20 25 30

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

Ser Thr Ile Ser Asp Asp Gly Ser Ser Thr 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 Lys Pro Asp Leu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 102

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 102

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 Glu Val Tyr
20 25 30

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

Ser Phe Ile Val Pro Gly Gly Asp Leu Thr 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 Glu Thr Trp Pro Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 103
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 103
 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 Asp Asn Tyr
 20 25 30

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

Ser Ser Ile Thr Ser Asp Gly Thr Ser Thr 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 Lys Pro Asn Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 104
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 104
 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 Lys Ala Tyr
 20 25 30

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

Ser Gln Ile Gly Arg Asp Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
 Page 65

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 Lys Pro Arg Arg Tyr Ala Ile Phe Thr Phe Asp Arg Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 105

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 105

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 Lys Gln Tyr
 20 25 30

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 106

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 106

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 Phe Asn Tyr
 20 25 30

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

Ser Ala Ile Ser Gly Ser 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 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 Val Phe Val Trp Ser Ala Asp Ile Asp Phe Asp Phe Asp Tyr
 100 105 110

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

<210> 107

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 107

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 Trp Tyr
 20 25 30

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

Ser His Ile Ala Ser Trp Gly Gly Lys Thr 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

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

Ala Lys Val Thr Val Lys Asp Gly Gly Tyr Leu Met Asp Phe Asp Tyr
100 105 110

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

<210> 108

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 108

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 Ala Glu Tyr
20 25 30

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

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

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

<210> 109

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 109

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 Gln Ala Tyr
20 25 30

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

Ser Thr Ile Ser Pro Asn Gly Leu Phe Thr 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 Lys Trp Leu Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 110

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 110

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 Ala Met Tyr
20 25 30

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

Ser Gly Ile Ser Pro Arg Gly Val Glu Thr 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 Lys Thr Asn Trp Asn Gly Val Asp Leu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 111
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 111
 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 Pro Thr Tyr
 20 25 30

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

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

Thr Leu Val Thr Val Ser Ser
 115

<210> 112
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 112
 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 Glu Gly Tyr
 20 25 30

Ser Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

Ser Ser Ile Asn Ala Ser Gly Thr Leu Thr 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 Lys Asp Gly Asn Arg Ser Glu Val Phe Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 113

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 113

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 Phe Glu Tyr
 20 25 30

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

Ser Ser Ile Ala Asn Asp Gly Ser Thr Thr 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 Lys Pro Asp Arg Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 114

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 114

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 Gln Asp Tyr
 20 25 30

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

Ser Glu Ile Asn Gln Asp Gly Thr Val Thr 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 Glu Ser Ser Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 115

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 115

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 Asp Asn Tyr
 20 25 30

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

Ser Ser Ile Ser Arg Asp Gly His Val Thr 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

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

<210> 116

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 116

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 Ala Val
20 25 30

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

Ser Ala Ile Thr Asp Asp Gly Leu Arg Thr 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 Lys Gly His Ile Tyr Gly Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 117

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 117

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 Glu Leu Tyr
 20 25 30

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

Ser Ala Ile Ser Ser Asp Gly Asp Thr Thr 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 Glu His Trp Leu Gly Thr Thr Leu Ser Leu Arg Asp Phe Asp Tyr
 100 105 110

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

<210> 118

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 118

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 Tyr Arg Tyr
 20 25 30

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

Ser Gln Ile Ser Pro Arg Gly Asn Ile Thr 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 Lys Ser Gly Val Ala Gly Ala Glu Ser Pro Glu Tyr Phe Asp Tyr
 100 105 110

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

<210> 119
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 119
 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 Leu Gly Tyr
 20 25 30

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

Ser Thr Ile Gly Pro Ile Gly Gly Gly Thr 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 Lys Ser Gln Asn Ile Tyr Gly Pro Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 120
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 120
 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 Glu Gln Tyr

20

25

30

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

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

Thr Val Ser Ser
 115

<210> 121

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 121

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 Pro Gln Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Leu Gly Ser Ser Thr 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 Lys Met Ser Lys Leu Leu Leu Ser Arg Glu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 122
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 122
 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 Ala Met Tyr
 20 25 30

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

Ser Gly Ile Ser Pro Arg Gly Val Glu Thr 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 Lys Thr Asn Trp Asn Gly Val Asp Leu Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 123
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 123
 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 Thr Arg His
 20 25 30

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

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Ser Thr Ile Thr Pro Thr Gly Asn Thr Thr 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 Lys Asp Ala His Asp Glu Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 124

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 124

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 Gly Pro Tyr
20 25 30

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

Ser Ser Ile Val Gly Asp Gly Leu Asp Thr 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 Lys Pro Asp Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 125

<211> 114

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 125

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 Gly Ser Thr
 20 25 30

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

Ser Glu Ile Arg Asp Thr Gly Leu Ala Thr 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 Ser Val Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110

Ser Ser

<210> 126

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 126

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 His Leu Gly
 20 25 30

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

Ser Ser Ile Ser Gly Thr Gly His Thr Thr 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 Lys Pro Met Asn Asp Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 127
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 127
 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 Met Asp Glu
 20 25 30

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

Ser Arg Ile Asn Ser Leu Gly Thr His Thr 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 Lys Ser Phe Met Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 128
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 128
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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<210> 129
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 129
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 Thr Asn Ala
20 25 30

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

Ser Ser Ile Ser Gly Ser 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 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 Gly Tyr Leu Thr Ser His Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 130
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 130
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 Arg Asp Tyr
20 25 30

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

Ser Thr Ile Thr Pro Ser Gly Leu Thr Thr 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 Glu Trp Ser Gln Ala Val Thr Arg Ser Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 131
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 131
Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Glu Ile Asn Gln Gln Gly Ser Ala Thr 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 Lys Thr Ile Gly Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 132

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 132

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 Thr Asp Gln
20 25 30

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

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

Lys Gly Arg Phe Thr Val 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 Trp Phe Asp Ile Ile Ala Trp Asp Pro Phe Ser Phe Asp Tyr
100 105 110

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

<210> 133

<211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 133
 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 Asn Gln Tyr
 20 25 30

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

Ser Ser Ile Thr Pro Ser Gly Phe Leu Thr 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 Glu Trp Asn Pro Phe Ile Thr Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 134
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 134
 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 Gly His Gln
 20 25 30

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

Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr 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 Lys Phe Asp Tyr Ser Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 135

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 135

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 Ala Ser Tyr
20 25 30

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

Ser Ser Ile Gly Ser Asp Gly Gly Pro Thr 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 Ser Ala Val Tyr Tyr Cys
85 90 95

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

Thr Val Ser Ser
115

<210> 136

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 136

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 Ala Glu
 20 25 30

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

Ser Thr Ile Thr Pro His Gly Asp Ser Thr 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 Lys Trp Arg Thr Leu Val Asp Trp Pro Thr Ser Glu Ser Phe Asp
 100 105 110

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

<210> 137

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 137

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 Thr Ser Tyr
 20 25 30

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

Ser Ser Ile Glu Pro Thr Gly Ile Thr Thr 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 Lys Pro His Phe Thr Glu Leu Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 138
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 138
 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 Glu Gly Glu
 20 25 30

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

Ser Thr Ile Thr Leu Pro Gly Pro Tyr Thr Phe 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 Lys Gly Asn Gly Thr Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 139
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 139
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Lys Ile Gly Ala Gln Gly Leu His Thr Tyr Tyr Ala Gly 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 Lys Gln Thr Thr Met Asp Tyr Glu Arg Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 140

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 140

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 Asp Glu Val
20 25 30

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

Ser Ala Ile Gly Asn Asn Gly Leu Lys Thr 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 Lys Ser Ala Leu Ser Tyr Arg Pro Pro Val Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 141
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 141
 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 Gln Asp Asp
 20 25 30

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

Ser Thr Ile Thr Leu Lys Gly Pro Ser Thr 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 Lys Ser Arg Asp Gly Leu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 142
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 142
 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 Ala Ser Ser
 20 25 30

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

20089600.txt

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

Leu Val Thr Val Ser Ser
115

<210> 143
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 143
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 Thr Asp Tyr
20 25 30

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

Ser Thr Ile Val Ser His Gly Gly Thr Thr 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 Lys Gly Lys Gly Tyr Asn Ala Gln Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 144
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 144

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 Gly His Gln
 20 25 30

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

Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr 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 Lys Phe Asp Tyr Ser Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 145

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 145

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 Asn Asp Tyr
 20 25 30

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

Ser Thr Ile Ser Ser His Gly Asp Ser Thr 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 Lys Gly Asp Val Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 146
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 146
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 Gly His Gln
20 25 30

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

Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr 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 Glu Trp Ser Asp Ser Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 147
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 147

20089600.txt

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 Ala Asp Tyr
20 25 30

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 148

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 148

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 Gly Val Glu
20 25 30

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

Ser Asn Ile Gly Arg Asp Gly Ser Met Thr 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 Lys Leu Gly Lys His Gly Thr Phe Asp Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser
115

<210> 149
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 149
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 Pro Glu Tyr
20 25 30

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

Ser Trp Ile Asp Glu Arg Gly Ser Leu Thr 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 Lys Arg Arg Lys Gly Thr Lys Gln Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 150
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 150
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 Glu Leu Tyr
20 25 30

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

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

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

<210> 151
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 151
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 Gly His Gln
20 25 30

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

Ser Thr Ile Thr Pro Asn Gly Tyr Tyr Thr 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 Lys Trp Ser Val Glu Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 152
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 152
 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 Asn Ser Tyr
 20 25 30
 Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Asn Pro Trp Gly Ser Arg Thr 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 Lys Gly Leu Val Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 153
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 153
 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 Asp Gly Asp
 20 25 30
 Met Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Thr Gln Leu Gly Ser Arg Thr 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 Lys Gln Asn Trp Arg Thr Leu Thr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 154

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 154

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 Asn Ala Tyr
20 25 30

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

Ser Ser Ile Leu Ser Asp Gly Val Ile Thr 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 Lys Ser Ala Arg Gly Ala Asn Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 155

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 155

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 Gly His Tyr
20 25 30

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

Ser Ser Ile Thr Pro His Gly Thr Ser Thr 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 Glu Phe Asn Ala Ile Phe Ser Glu Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 156

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 156

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 Arg Asp Tyr
20 25 30

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

Ser Thr Ile Thr Pro Ser Gly Leu Thr Thr 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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 157

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 157

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 Asp Leu Tyr
 20 25 30

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

Ser Met Ile Gly Arg Asp Gly Arg Phe Thr 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 Lys Leu Ala Gly Ser Leu Arg Gly Arg Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 158

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 158

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

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

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

Ser Thr Ile Thr Pro His Gly Ser Ser Thr 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 Lys Gln Arg Trp Gly Val Glu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 159

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 159

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 Gln Gly Tyr
20 25 30

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

Ser Ser Ile Ala Gly Arg Gly Gly Val Thr 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 Lys Gly Leu Tyr Ile Tyr His Ser Leu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 160
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 160
 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 Pro Gly Met
 20 25 30

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

Ser Ala Ile Thr Gly Thr Gly Ser Thr Thr 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 Lys Gly Tyr His Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 161
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 161
 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 Pro Met Val
 20 25 30

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

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

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

Val Thr Val Ser Ser
115

<210> 162
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 162
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 Gly His Gln
20 25 30

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

Ser Gly Ile Thr Asp Asp Gly Glu Ser Thr 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 Lys Gly Asp Tyr Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 163
<211> 117
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 163

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 Gly Glu Tyr
20 25 30

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

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

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

Val Thr Val Ser Ser
115

<210> 164

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 164

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 Asp Tyr
20 25 30

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

Ser Ser Ile Thr Pro Tyr Gly Ser Tyr Thr 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
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<210> 165
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 165
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 Asp Thr Tyr
20 25 30

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

Ser Thr Ile Thr Pro Tyr Gly Ser Ser Thr 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 Lys Trp Gly Leu Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

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<210> 166
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 166

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 Thr Thr Gly
20 25 30

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

Ser Ala Ile Gly Ile Gly Gly Asp Thr Thr 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 Lys Leu Thr Pro Ser Asn Gln Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 167

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 167

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 Lys Gln Tyr
20 25 30

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

Ser Ser Ile Thr Pro Ser Gly Phe Leu Thr 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 Glu Trp Asn Pro Phe Ile Ser Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 168
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 168
 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 Pro Asn Tyr
 20 25 30

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 169
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 169
 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 Lys Glu Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Ser Gly Met Asn Thr 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 Glu Trp Arg Ser Val Val Arg Pro Trp Pro Gly Val Phe Asp Tyr
100 105 110

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

<210> 170

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 170

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 Asp Asp Glu
20 25 30

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

Ser Ser Ile Thr Pro His Gly Thr Phe Thr 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 Lys Leu His Leu Lys Leu Tyr Glu Ser His Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 171
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 171
 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 Glu Gly Gly
 20 25 30

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

Ser Met Ile Pro Met Asp Gly Ser Ala Thr 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 Lys Ala Gly Ser Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 172
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 172
 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 Asp Phe Met
 20 25 30

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

Ser Ser Ile Gly Arg Asp Gly Ala Tyr Thr Tyr Tyr Ala Asp Ser Val
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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 Lys Leu Ala Ser Pro Ala Gln Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 173

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 173

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 Gly Asp Glu
 20 25 30

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 174

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 174

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 His Ala Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Arg Gly Ser Tyr Thr 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 Lys Trp Pro Pro Pro Ser Ser His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 175

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 175

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 Asp Gly Tyr
 20 25 30

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

Ser Ser Ile Thr Ser Asp Gly Thr Ser Thr 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 Lys Pro Gly Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 176
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 176
 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 Glu Gly Tyr
 20 25 30

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

Ser Ser Ile Ser Pro Gln Gly His Phe Thr 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 Glu Leu Arg Glu Leu Pro Arg Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 177
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 177
 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 Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Asp Ala Ser Gly Gly Pro Thr 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 Lys Ala Asn Gly Lys Lys Phe Pro Phe Thr Lys Tyr Phe Asp Tyr
100 105 110

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

<210> 178

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 178

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 Pro Ser Val
20 25 30

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

Ser Gly Ile Asn Leu Thr Gly Val Asp Thr 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 Lys Ser Ala Thr Thr Arg Gln Ala His Pro Leu Tyr Phe Asp Tyr
100 105 110

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

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<210> 179
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 179
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 Lys Glu Gly
20 25 30

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

Ser Thr Ile Ser Thr Asn Gly Leu Thr Thr 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 Lys Ser Thr Arg Asp Leu Gly Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 180
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 180
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 Glu Glu Tyr
20 25 30

Glu Met Ala Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
Page 113

35

40

45

Ser Phe Ile Ser Pro Arg Gly His Phe Thr 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 Lys Pro Ala Lys Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 181

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 181

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 Asp Thr Tyr
 20 25 30

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

Ser Arg Ile Ser Val Asp Gly Ser Ile Thr 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 Lys Thr Arg Met Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 182

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 182

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 Asn Ile Ser Arg Asp Gly Ser Lys Thr 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 Glu Ala Gln Ser Gly Gly Leu Arg Ser Gly Leu Thr Thr Phe Asp
 100 105 110

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

<210> 183

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 183

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

Ala Lys Ala Gly Pro Lys Gly Ile Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 184

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 184

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 Pro His
20 25 30

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

Ser Gly Ile Asp Gly Gly Gly Ser Met Thr 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 Lys Ser Asp Pro Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 185

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 185

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 His Ala Gly
 20 25 30

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

Ser Ser Ile Thr Leu Pro Gly Asp Met Thr 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 Lys Pro Asn Thr Gly Tyr Thr Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 186

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 186

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 Gly Asn Tyr
 20 25 30

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

Ser Ser Ile Ser Trp Asp Gly Ser Leu Thr 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 Gln Asn Thr Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 187
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 187
 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 His Asp Ala
 20 25 30

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

Ser Gly Ile Leu Ser Pro Gly Glu Asp Thr 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 Lys Phe Gly Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 188
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 188
 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 Arg Thr Asp
 Page 118

20

25

30

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

Ser Ser Ile Ser Pro Ser Gly Ala Tyr Thr 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 Lys Gly Leu Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 189

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 189

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 Ile Phe Glu Gln Tyr
 20 25 30

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

Ser Trp Ile Ser Pro Asp Gly Thr His Thr 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 Lys Phe Ser Leu Arg Lys Met Glu Lys Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 190
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 190
 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 Gln Asp Glu
 20 25 30

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

Ser Ser Ile Ala Ser Asp Gly Met Ser Thr 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 Gln Pro Gly Lys Asn Phe Asp His Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 191
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 191
 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 Asp Tyr
 20 25 30

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

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Ser Ser Ile Thr Thr Gly Gly Glu Arg Thr 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 Lys Arg Trp Asn Leu Tyr Thr Glu Ser Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 192

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 192

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 Gly Gly Gln
20 25 30

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

Ser Ser Ile Ala Pro Asp Gly Ile His Thr 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 Lys Asn Leu Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 193

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 193

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 Glu Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Pro Ser Gly Thr Phe Thr 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 Glu Trp Lys Ala Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 194

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 194

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 Pro His Ser
 20 25 30

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

Ser Leu Ile Leu Pro Ser Gly Ser Arg Thr 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 Lys Phe Ser Asp Glu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<210> 195
<211> 117
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 195
Glu Val Gln Leu Ser 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 Gly Asp Gly
20 25 30

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

Ser Gly Ile Ser Ser Asp Gly Val Thr Thr 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 Lys Asp Arg Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<210> 196
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 196
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 Asp Asp Tyr
20 25 30

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

Ser Ser Ile Ser Pro His Gly Val Tyr Thr 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 Lys Trp Leu His Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 197
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 197
 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 Asn Tyr
20 25 30

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

Ser Phe Ile Ala Gly Pro Gly Asn Tyr Thr 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 Lys Pro Gly Ser Thr Ala Thr Tyr Asn Asn Gly Gln Phe Asp Tyr
100 105 110

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

<210> 198
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 198
 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 Thr Glu Tyr
 20 25 30

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

Ser Ser Ile Ser Gly Ser Gly Arg Val Thr 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 Lys Trp Leu Lys Leu Val Arg Ala Pro Asn Pro Phe Asp Tyr Trp
 100 105 110

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

<210> 199
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 199
 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 Asn Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg 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 Ala Ser His Ser Leu Gly Pro Leu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 200

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 200

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 Thr Ala Tyr
20 25 30

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

Ser Trp Ile Ser Pro Ser Gly Ser Gly Thr 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 Lys Thr Leu Thr Asp Ser Pro Ser Gly His Tyr Glu Phe Asp Tyr
100 105 110

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

<210> 201

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 201
 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 Ala Arg Tyr
 20 25 30

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

Ser Arg Ile Thr Ala Gln Gly Leu Gly Thr 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 Lys Tyr Leu Thr Asp Phe Ser Ser Gly His Gln Glu Phe Asp Tyr
 100 105 110

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

<210> 202
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<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 Asp Asp Tyr
 20 25 30

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

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

20089600.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 Tyr Trp Pro Ser Thr Ser Trp Glu Thr Asp Phe Asp Tyr Trp
100 105 110

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

<210> 203

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 203

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

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

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

Ser Ser Ile Glu Met Gln Gly Lys Asn Thr 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 Lys Asp Arg Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 204

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
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polypeptide"

<400> 204

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 Gly Glu Glu
 20 25 30

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

Ser Cys Ile Asp Asn Leu Gly Ser Pro Thr 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 Ala Ala Val Tyr Tyr Cys
 85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 205

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 205

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 Gly Glu Glu
 20 25 30

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

Ser Ser Ile Asp Glu Gly Gly Arg Trp Thr 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 Lys Trp Thr Pro His Lys Gln Leu Ser Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 206
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 206
 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 Ser Phe Ala Asp Glu
 20 25 30

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

Ser Glu Ile Asp Pro Leu Gly Thr Gly Thr 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 Lys Tyr Gly Thr Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 207
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 207
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

20089600.txt

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

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

Ser Ser Ile Ser Asp Asp Gly Ile Ser Thr 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 Lys Pro Asp Met Ser Leu Ile Glu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 208

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 208

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 Asp Gly Thr
20 25 30

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

Ser Gly Ile Ser Gly Asp Gly Arg Asn Thr 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 Glu Pro Tyr Ala Leu Thr Ser Ser Lys Pro Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 209
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 209
 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 Asn Asp Tyr
 20 25 30

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

Ser Trp Ile His Gly Thr Gly Gly Gln Thr 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 Lys Ala Leu Ala Asp Arg Ser Gly Gly Val Val Glu Phe Asp Tyr
 100 105 110

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

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 210
 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 Glu Ala Glu
 20 25 30

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

20089600.txt

Ser Cys Ile Ser Asn Asp Gly Asn Thr Thr 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 Lys Glu Ser Leu Ile Ser Pro Gly Leu Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 211
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 211
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 Thr Gly Glu
20 25 30

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

Ser Thr Ile Asn Glu Thr Gly Tyr Met Thr 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 Lys Leu Ser Thr Arg Gly Val Pro Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 212

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 Arg Ser Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Met Gly Val Phe Thr 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 Lys Ser Asn Gln His Ala His Asp Pro Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 213

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 213

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 Asp Tyr
 20 25 30

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

Ser Ser Ile Ser Pro Met Gly Thr Phe Thr 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 Lys Ala Ala Leu Thr Glu Pro Met Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 214
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 214
 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 Arg Asp Tyr
 20 25 30

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

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

Lys Gly Arg Ser 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 Ala Glu Glu Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 215
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 215

20089600.txt

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 Ala Phe Pro Arg Tyr
20 25 30

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

Ser Asn Ile Asp Gln Phe Gly Met Lys Thr 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 Glu Glu Tyr Ala Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 216

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 216

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 Asp Lys Tyr
20 25 30

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

Ser Thr Ile Ser Pro Met Gly Val Phe Thr 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 Lys Gly Arg Gly Asn Thr Ser Asp Phe Asp Tyr Trp Gly Gln Gly
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105

110

Thr Leu Val Thr Val Ser Ser
115

<210> 217
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 217
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 Asn Tyr
20 25 30

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

Ser Thr Ile Ser Gly Ala Gly His Phe Thr 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 Lys Ser Phe Pro Arg Asp Glu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 218
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 218
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 Pro Lys Tyr
20 25 30

20089600.txt

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

Ser Glu Ile Gly Leu Asp Gly Ser Pro Thr 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 Lys Leu Gly Asp Pro Asn Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 219
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 219
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 Pro Thr Ser
20 25 30

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

Ser Gly Ile Gly Pro Asp Gly Leu Thr Thr 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 Lys His Ala Asp Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 220
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 220
 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 Glu Tyr
 20 25 30

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

Ser Trp Ile Asp Thr Asp Gly Gly Asp Thr 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 Lys Pro Gly Leu Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 221
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 221
 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 Thr Ala Ser Gly Phe Thr Phe Glu Asn Ala
 20 25 30

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

Ser Ser Ile Glu Gly Gln Gly Asn Ala Thr 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 Lys Ser Ser Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 222
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 222
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 Thr Arg Asn
20 25 30

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 223
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 223

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 224

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 224

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 225
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 225
 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val 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 Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 226
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 226
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Gln Val Thr Val Ser Ser
115

<210> 227
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 227
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 228
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 228
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 229
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 229
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 230

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 230

Glu Val Arg 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 Asn Phe Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 231

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 231

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

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 232

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 232

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

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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
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65 70 75 80

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

Val Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly His Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 233
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 233
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 234
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 234

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr 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 Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 235

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 235

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Lys Phe Asp Tyr Leu Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 236
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 236
 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Glu 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 Lys Val Gly Lys Glu Ser Asn Leu Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 237
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 237
 Glu Val Gln Leu Phe Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 238
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 238
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ile 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 Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 239
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 239
 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Thr 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 Val Gly Lys Glu Ser Glu Phe Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 240
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 240
 Glu Val Arg 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
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50

55

60

Lys Gly Arg Phe Thr Ile Thr 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

Val Lys Val Gly Lys Glu Ser Asn Leu Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 241

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 241

Glu Val Gln Leu Leu Val 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 242

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 242

Glu Val Gln Leu Leu Val 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 243

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 243

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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 244
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 244
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 Lys Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Pro 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 245
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 245
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 Lys Trp His
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Ser Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 246
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 246
 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 Asn Trp His
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
115

<210> 247
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 247
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 Lys Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 248
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 248
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 Lys Trp Gln
20 25 30

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

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45

Ser Gly Ile Glu Gly Pro Gly Asp Ile Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 249

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 249

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 Asn Trp His
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 250

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 250

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 Lys Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 251

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 251

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 Asn Trp Glu
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 252

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 252

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 253

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 253

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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 254

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 254

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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 255
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 255
 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 256
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 256
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ala Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp Gln
 Page 161

20

25

30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 257

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 257

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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 258
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 258
 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Lys Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 259
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 259
 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 Asn Trp Gln
 20 25 30

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

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Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 260

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 260

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Arg Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 261

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 261

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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Tyr Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 262

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 262

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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Arg Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 263
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 263
 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 Asn Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Asp Ser Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 264
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 264
 Glu Val Gln Leu Leu Glu Phe Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Arg Asp Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> 265
<211> 118
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 265
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Thr Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 266
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 266
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Glu Ser Ser Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 267
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 267
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Phe 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

Val Lys Val Gly Lys Asp Ser Ala Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 268

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 268

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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Asn Asp Ser Tyr Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 269

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 269
 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 Asn Trp Gln
 20 25 30
 Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Lys Val Gly Lys Asp Ser Ser Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 270
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 270
 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 Asn Trp Gln
 20 25 30
 Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Ile Tyr Tyr Cys
85 90 95

Val Lys Val Gly Lys Asp Ser Ala Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 271
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 271
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 Lys Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 272
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 272

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 Lys Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Arg Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 273

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 273

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 Lys Trp Gln
 20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 274
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 274
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 Asn Trp Glu
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 275
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 275
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Arg Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 276

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 276

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 Asn Trp Glu
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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

Val Lys Val Gly Lys Asp Ser Lys Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser

115

<210> 277
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 277
 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 Asn Trp Gln
 20 25 30
 Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Val Gly Lys Glu Ser Asn Phe Asp Tyr Leu Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 278
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 278
 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 Val Ala Ser Gly Phe Thr Phe Asn Trp Gln
 20 25 30
 Leu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

20089600.txt

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 279
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 279
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 Asn Trp Gln
20 25 30

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

Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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 Lys Val Gly Lys Glu Ser Asn Ser Asp Tyr Arg Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 280
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 280

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 Gly Trp
 20 25 30

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

Ser Ser Ile Asp Glu Ser Gly Leu Asn Thr 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 Glu Gly Ala Pro Gln Tyr Gln Ile Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 281

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 281

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 Pro Asn Tyr
 20 25 30

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

Ser Tyr Ile Ser Arg Arg Gly Leu Leu Thr 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 Lys Thr Ser His Tyr Met Asn Asn Gly Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 282
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 282
 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 Val Asp Tyr
 20 25 30

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

Ser Ser Ile Ser Pro Ile Gly Thr Phe Thr 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 Lys Asp Pro Tyr Gly Met Glu Asp Gly Leu Thr Trp Phe Asp Tyr
 100 105 110

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

<210> 283
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 283

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 Asp Ala Tyr
 20 25 30

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

Ser Thr Ile Thr Ser Glu Gly Leu Ser Thr 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 Lys Pro Ser Asp Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 284

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 284

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 Asp Gly Tyr
 20 25 30

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

Ser Thr Ile Ser Arg Gly Gly Trp Phe Thr 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 Lys Gly Thr Ser Gln Ser Ser Thr Gly Ser Phe Asp Tyr Trp Gly
 Page 179

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 285
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 285
 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 Arg Arg Tyr
 20 25 30

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

Ser Glu Ile Ser Pro Thr Gly Ala Leu Thr 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 Lys Leu Gly Ser Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 286
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 286
 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 Phe Pro Tyr
 20 25 30

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 287
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 287
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 Glu Val Tyr
20 25 30

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

Ser Thr Ile Asp Glu Ser Gly Arg Asp Thr 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 Lys Pro Gly Val Trp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 288
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 288
 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 Ala Phe Tyr
 20 25 30

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

Ser Thr Ile Thr Pro Lys Gly His His Thr 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 Lys Val Phe Lys Gly Lys Gly Trp Thr Arg Pro Ser Gly Phe Asp
 100 105 110

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

<210> 289
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 289
 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 Asn Glu Tyr
 20 25 30

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

Ser Ser Ile Gly Arg Arg Gly Trp Leu Thr 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 Lys Ala Val Leu Leu Asp Ser Thr Lys Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 290

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 290

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 Asp Glu Tyr
20 25 30

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

Ser Thr Ile Ser Ala Arg Gly Pro Phe Thr 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 Lys Gly Arg His Trp Leu Arg Asn Gly Arg Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 291

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 291

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 Gly Met Gln
20 25 30

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

Ser Ser Ile Thr Asp Asp Gly Thr Ser Thr 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 Lys Pro Asp Arg Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 292

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 292

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 Gly Ala Ala
20 25 30

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

Ser Leu Ile Thr Asn Asp Gly Ile Ser Thr 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

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

Thr Val Ser Ser
 115

<210> 293
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 293
 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 Asn Lys Tyr
 20 25 30

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

Ser Ser Ile Asp Ser Ser Gly Glu Leu Thr 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 Glu Glu Val Pro Met Gly Asn Gln Thr Phe Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 294
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 294
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 295
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 295
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 Glu Asp Tyr
20 25 30

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

Ser Cys Ile Gly Pro Gly Gly Lys Pro Thr 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 Lys Val Asp Gly His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 296
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 296
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 Gln Tyr
20 25 30

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

Ser Thr Ile Ser Ser Arg Gly Trp Leu Thr 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 Lys Gly Pro Gly Gly Arg Arg Arg Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 297
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 297
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 Leu Asp Tyr
20 25 30

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

Ser Thr Ile Ser Pro Met Gly Met Gly Thr 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 Lys Ser Ser Ala Ile Ser Phe Thr Ser Asp Ile Ser Asn Phe Asp
100 105 110

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

<210> 298

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 298

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 Asp Tyr
20 25 30

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

Ser Ser Ile Ser Trp Ser Gly Phe Gln Thr 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 Lys Pro Gly Val Ala Arg Met Pro Thr Gly Ile Ala Phe Asp Tyr
100 105 110

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

<210> 299

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 299

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 Ala Tyr
20 25 30

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

Ser Ser Ile Asp Ser Ala Gly Thr Phe Thr 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 Glu Pro Phe Gly Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 300

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 300

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 Glu Tyr
20 25 30

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

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

Ala Lys Thr Val Arg Arg Gly Leu Pro Arg Pro Ser Arg Tyr Phe Asp
100 105 110

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

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<210> 301
<211> 121
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 301
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 Asp Tyr
20 25 30

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

Ser Ser Ile Ser Pro Met Gly Thr Phe Thr 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 Lys Gly Leu Ser Val Tyr Ser Gly Leu Asp Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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<210> 302
<211> 123
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 302

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 His Tyr
20 25 30

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

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

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

<210> 303

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 303

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 Ala Arg Tyr
20 25 30

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

Ser Thr Ile Ser Pro Thr Gly Val Leu Thr 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 Lys Gly Phe Glu Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 304
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 304
 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 Glu Ala Tyr
 20 25 30

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

Ser Leu Ile Ser His Thr Gly His Ala Thr 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 Lys Gly His Trp Pro Phe Asp Tyr Arg Gly Gln Gly Thr Leu Ile
 100 105 110

Thr Val Ser Ser
 115

<210> 305
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 305
 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 Glu Asp Glu
 20 25 30

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

Ser Asp Ile Ser Pro Gly Gly Trp Thr Thr 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 Lys Gly Tyr Arg Pro Phe Asp Glu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 306

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 306

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 Val Thr Phe Asp Ala Ile
20 25 30

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

Ser Ser Ile Ser Arg His Gly Glu Tyr Thr 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 Glu Asp Ala Trp Ser Arg His Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 307
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 307
 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 Asp Ser Thr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met 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 Gly Ala Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 308
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 308
 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 Gly Arg Gln
 20 25 30

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

Ser Ser Ile Asp Asp Asp Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val
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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 Lys Gly Asp Pro Trp Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 309

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 309

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 Thr Ala Ser Gly Phe Thr Phe Ser Asp Thr
 20 25 30

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

Ser Gly Ile Asp Asp Gly Gly Val Ser Thr 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 Lys Pro Asp Arg His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 310

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 310

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 Gly Ser Thr
 20 25 30

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

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

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

Leu Val Thr Val Ser Ser
 115

<210> 311

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 311

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 Arg Ser Gly
 20 25 30

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

Ser Thr Ile Thr Asn Asp Gly Thr Ser Thr 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 Lys Ser Asp Ser Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 312
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 312
 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 Ala Ala Tyr
 20 25 30

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

Ser Tyr Ile Ser Pro Asn Gly Thr Ala Thr 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 Glu Tyr Val Gly Met Arg Trp Asn Ser Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 313
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 313
 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

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

Ser Ser Ile Thr Ser Leu Gly Thr Ser Thr 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 Lys Pro Gly Arg Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 314
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 314
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 Asn Glu Tyr
20 25 30

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

Ser Thr Ile Thr Ser Glu Gly Ser Gly Thr 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 Lys Pro Asn Gly Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 315
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 315
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 Asp Tyr
20 25 30

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

Ser Thr Ile Thr Ser Glu Gly His Ser Thr 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 Lys Pro Gly Thr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 316
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 316
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 Asp Tyr
20 25 30

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

40

45

Ser Thr Ile Asp Ser Asp Gly Ser Phe Thr 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 Lys Pro Gly Val Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 317

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 317

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 Lys Asp Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Thr Gly Gln Ser Thr 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 Lys Pro Gly Asn Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 318

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 318

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 Leu Asp Tyr
 20 25 30

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

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

Lys Ser 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 Val Arg Val Gly Arg Gly Val His Pro Pro Lys Phe Asp
 100 105 110

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

<210> 319

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 319

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 Asn Leu Tyr
 20 25 30

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

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

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

Thr Val Ser Ser
115

<210> 320

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 320

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 Glu Asn Tyr
20 25 30

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

Ser Thr Ile Ala Pro Leu Gly Val Pro Thr 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 Lys Lys Lys Val Gly Ala Trp Leu Gln Ser Arg Ser Phe Asp Tyr
100 105 110

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

<210> 321

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 321

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 Met Asp Tyr
 20 25 30

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

Ser Thr Ile Gly Ala Ser Gly His Tyr Thr 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 Lys Tyr Leu Asp Met Leu Leu Phe Gly Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 322

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 322

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 Ala Glu Tyr
 20 25 30

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

Ser Arg Ile Ala Gly Asn Gly Ser Arg Thr 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 Ile Met Leu Ser His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 323
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 323
 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 Tyr Asn Tyr
 20 25 30

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

Ser Gly Ile Asp Ser Met Gly Leu Val Thr 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 Lys Gly Ser Asn Ala Ser Asp Trp Val Val Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 324
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 324
 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 Ala Ser Tyr
 100 105 110

20

25

30

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

Ser Ser Ile Ala Asp Thr Gly Asp Arg Thr 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 Lys Leu Arg Gly Met Ala Arg Val Trp Gly Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 325

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 325

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 Tyr Tyr
 20 25 30

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

Ser Ser Ile Ser Asp Arg Gly Leu Gln Thr 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 Lys Phe Thr Glu Ile Pro Leu Asp Trp Leu Glu Val Phe Asp Tyr
 100 105 110

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

<210> 326
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 326
 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 Gly Ser Tyr
 20 25 30

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

Ser Ser Ile Thr Asn Ser Gly Thr Glu Thr 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 Lys Ser Met Tyr Pro Asp Leu Glu Ile Val His Phe Asp Tyr Trp
 100 105 110

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

<210> 327
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 327
 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 Glu Thr Tyr
 20 25 30

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

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Ser Ala Ile Asp Gln Glu Gly Ser Ala Thr 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 Lys Asn Ser Gly Thr Arg Pro Gly Leu Arg Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 328

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 328

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

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

Ser Arg Ile Asp Ala Ser Gly Tyr Phe Thr 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 Gln Leu Leu Lys Leu Ser Leu Asn Pro Asn Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 329

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 329

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 Ser Ile His Asn Thr Gly Leu Ser Thr 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 Lys Gly Thr Gln His Arg Phe Val Val Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 330

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 330

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 Glu Gly Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Leu Gly Pro Asp Thr 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 Lys Leu Leu Met Gly Glu Tyr Leu Asn Ser Arg Thr Phe Asp Tyr
100 105 110

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

<210> 331
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 331
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 Asn Thr Tyr
20 25 30

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

Ser Trp Ile Asp Ala Asp Gly Trp Val Thr 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 Gln Thr Gly His Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 332
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 332
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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<210> 333
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 333
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 Pro Glu Tyr
20 25 30

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

Ser Thr Ile Thr Pro Ser Gly Gly His Thr 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 Ala Ala Val Tyr Tyr Cys
85 90 95

Ala Ile Pro Leu Ser Ser Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 334
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 334
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 Asn Tyr
20 25 30

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

Ser Leu Ile Asn Gly Ala Gly Asp Met Thr 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 Glu Gly Gly Ala Arg Ser Phe Gly Val Pro Pro Asn Phe Asp Tyr
100 105 110

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

<210> 335
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 335
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 Thr Asp Gly
20 25 30

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

Ser Arg Ile Val Asp Pro Gly Asp Ser Thr 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 Lys Ala Gly Asp Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 336

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 336

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

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

Ser Val Ile Ser Ser Lys Gly Asp Ser Thr 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 Gln Thr Ser Ser Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 337

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 337
 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 Glu Ala Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met 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 Ser Ala Val His Pro Ser Tyr Arg Ala Glu Leu Phe Asp Tyr
 100 105 110

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

<210> 338
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 338
 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

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

Ser Arg Ile Glu Pro Asp Gly Ser Asn Thr 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 Lys Gly Pro Asp Asn Phe Thr Met Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 339

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 339

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 Asn Lys Tyr
20 25 30

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

Ser Ser Ile Asp Ser Leu Gly His Tyr Thr 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 Glu Ala Glu Phe Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 340

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 340

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 Lys Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 341

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 341

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

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

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser
115

<210> 342
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 342
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Met Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 343
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 343
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala 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 Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 344

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 344

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 Lys Arg Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Val 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 Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 345
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 345
 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 Lys Arg Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr 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 Asp Pro Phe Thr Glu Leu Asp Tyr Trp Gly His Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 346
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 346
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
 1 5 10 15

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

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

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Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Phe Cys
85 90 95

Ala Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 347
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 347
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 Ala Phe Lys Arg Tyr
20 25 30

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

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

Ala Asp Pro Phe Thr Glu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 348
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 348

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 Pro Phe Lys Arg Tyr
 20 25 30

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

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

Thr Val Ser Ser
 115

<210> 349

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 349

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 Lys Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Ile Asp Tyr Trp Gly Gln Gly Thr Gln Val
100 105 110

Thr Val Ser Ser
115

<210> 350
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 350
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

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

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Gly Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 351
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 351

Glu Val Gln Leu Leu 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 Lys Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 352

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 352

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 Lys Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
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100

105

110

Thr Val Ser Ser
115

<210> 353
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 353
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 Lys Arg Tyr
20 25 30

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

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

Thr Val Ser Ser
115

<210> 354
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 354
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 Lys Lys Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 355
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 355
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 Asn Ser Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 356
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 356
 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 Lys Arg Tyr
 20 25 30
 Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 357
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 357
 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 Lys Arg Tyr
 20 25 30
 Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Met Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 358

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 358

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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 359

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 359

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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Leu Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 360

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 360

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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr Tyr Tyr Ala Glu 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

Ala Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 361
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 361
 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 Asn Thr Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 362
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 362
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 363

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 363

Glu Val Gln Leu Ser 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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 364
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 364
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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 365
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 365
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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Met Asn Ser Met Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Pro Phe Thr Glu Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 366

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 366

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 Lys Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val
 100 105 110

Thr Val Ser Ser
 115

<210> 367

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 367

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 Asn Phe Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Asp Pro Phe Thr Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 368

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 368

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

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

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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
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<210> 369
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 369
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 Lys Arg Tyr
20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Ser Phe Thr 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 Glu Pro Phe Thr Glu Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

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<210> 370
<211> 124
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 370

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 Glu Ala Tyr
20 25 30

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

Ser Ser Ile Ser Pro Leu Gly Leu Trp Thr 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 Lys Leu Ser Ala Gly Ala Glu Thr His Val Tyr Arg Leu Phe Asp
100 105 110

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

<210> 371

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 371

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 Gly Asn Tyr
20 25 30

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

Ser Ser Ile Gly Val Leu Gly His Thr Thr 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 Lys Leu Met Ser Leu Arg Thr Phe Glu Asn Leu Phe Asp Tyr Trp
 100 105 110

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

<210> 372
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 372
 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 Thr Lys Tyr
 20 25 30

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

Ser Gly Ile Asp Ala Asn Gly Asn Arg Thr 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 Glu Gly Thr Trp Arg Arg His Phe Ala Ile Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 373
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 373
 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 Asp Leu Tyr
 20 25 30

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

Ser Ser Ile Ser Asp Leu Gly Thr Leu Thr 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 Lys Asn Gly Phe Arg Val Thr Ser Asn Asp Arg Arg Phe Asp Tyr
100 105 110

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

<210> 374

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 374

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 Thr Gly Gly
20 25 30

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

Ser Met Ile Glu Gly Gly Gly Val Thr Thr 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 Glu Leu Asp Leu Arg Thr Gly Gln Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 375
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 375
 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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 376
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 376
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Phe Cys
 85 90 95

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

Leu Val Thr Val Ser Ser
 115

<210> 377

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 377

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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 378

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 378

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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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

Leu Val Thr Val Ser Ser
 115

<210> 379

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 379

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 Pro Ala Tyr
 20 25 30

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

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

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

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

Ala Glu Pro Ser Asp Pro Thr Met Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 380

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 380

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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Met Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 381

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 381

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 Ala Tyr
20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Asp Pro Ser Asp Pro Thr Met Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 382

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 382

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

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

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

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

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

Leu Val Thr Val Ser Ser
115

<210> 383
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 383
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 Ala Tyr
20 25 30

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

Thr Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Met Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 384
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 384
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 Thr Ala Tyr
20 25 30

Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
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35

40

45

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Lys Leu Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 385

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 385

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

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

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 386

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 386

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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 387

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 387

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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Pro Val Thr Val Ser Ser
 115

<210> 388

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 388

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

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

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

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

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

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

Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr Gln
 100 105 110

Val Thr Val Ser Ser
 115

<210> 389

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 389

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 Ala Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Phe 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 Asp Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 390

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 390

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Arg Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 391
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 391
 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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Lys Phe Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 392
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 392
 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 Ala Tyr
 Page 247

20

25

30

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

Ser Leu Ile Gly Asp Arg Gly Thr Trp Thr Tyr Tyr Ala Asp Pro 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 Asp Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 393

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 393

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 Ala Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Val 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 Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 394
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 394
 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 Ala Tyr
 20 25 30

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

Ser Leu Ile Gly Asp Arg Gly Ser Trp Thr 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 Glu Pro Ser Asp Pro Thr Lys Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 395
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 395
 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 Asp Asn Tyr
 20 25 30

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

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

Thr Val Ser Ser
115

<210> 396

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 396

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 Ala Ser Tyr
20 25 30

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

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

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

<210> 397

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 397

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 Glu Arg Tyr
 20 25 30

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

Ser Arg Ile Ser His Ser Gly Arg Thr Thr 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 Gln Leu Asp Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 398

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 398

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 Lys Arg Tyr
 20 25 30

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

Ser Arg Ile Asn His Asn Gly Ser Val Thr 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 Lys Met Pro Gln Gly Thr Ser Asp Trp Tyr Tyr Phe Asp Tyr Trp
 100 105 110

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

<210> 399
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 399
 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 Lys Tyr
 20 25 30

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

Ser Thr Ile Leu Glu Asp Gly Leu Thr Thr 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 Lys Pro Gly Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 400
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 400
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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<210> 401
<211> 116
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 401
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 Glu Gly Gly
20 25 30

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

Ser Met Ile Pro Met Asp Gly Ser Ala Thr 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 Lys Ala Gly Glu Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 402
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 402
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 Arg Glu Tyr
20 25 30

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

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

Thr Val Ser Ser
115

<210> 403
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 403
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 Arg Asp Tyr
20 25 30

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 404

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 404

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 Lys Glu His
20 25 30

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

Ser Gly Ile Gly Ala Glu Gly Val Trp Thr 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 Glu Pro Thr Met Ser Asn Gly Ser Gln Ser Arg Phe Asp Tyr Trp
100 105 110

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

<210> 405

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 405
 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 Asp Asn Thr
 20 25 30

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

Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 406
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 406
 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 Asp Asn Thr
 20 25 30

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

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 407

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 407

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 Asp Asn Thr
20 25 30

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

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

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 408

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 408

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 Asp Asn Thr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Phe 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 409

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 409

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 Asp Asn Thr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
 100 105 110

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

<210> 410
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 410
 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 Asp Asn Thr
 20 25 30

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

Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 411
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 411
 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 Asp Asn Thr
20 25 30

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

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 412

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 412

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 Asp Asn Thr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ala 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

Trp Gly Leu Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 413
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 413
 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 Asp Asn Thr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
 100 105 110

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

<210> 414
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 414
 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 Asp Asn Thr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Arg 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 415
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 415
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 Asp Asn Thr
20 25 30

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

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr 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 His Cys
85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 416
<211> 123
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 416

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

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

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

Ser Gly Ile Ile Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 417

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 417

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 Asp Asn Thr
 20 25 30

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

Ser Gly Ile Ser Glu Asp Gly Asn Arg Thr 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 Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
 100 105 110

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

<210> 418
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 418
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
 1 5 10 15

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

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

Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr 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 Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 419
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 419

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 Asp Asn Thr
20 25 30

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

Ser Gly Ile Ser Glu Asp Gly Asn Arg Thr 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 His Cys
85 90 95

Ala Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 420

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 420

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 Asp Asn Thr
20 25 30

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

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

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asn
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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
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110

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

<210> 421
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 421
 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 Asp Asn Thr
 20 25 30

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

Ser Gly Val Thr Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 422
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 422
 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 Glu Ala Ser Gly Phe Thr Phe Asp Asn Thr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 423

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 423

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 Asp Asn Thr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser 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 Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 424
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 424
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Thr
 20 25 30
 Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Glu Asp Gly Asn Arg Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Val Tyr
 100 105 110
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 425
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 425
 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 Gly Ser Ala
 20 25 30
 Glu Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Arg Pro Gly Gln Val Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
100 105 110

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

<210> 426
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 426
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 Asp Asp Gly
20 25 30

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

Ser Leu Ile Leu Pro Ser Gly Ser Arg Thr 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 Lys His Ser Leu Thr Asn Arg Pro Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 427
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 427

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 Lys Tyr
20 25 30

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

Ser Asp Ile Asp Ala Val Gly Thr Arg Thr 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 Ile Pro Gly Gly Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 428

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 428

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 Glu Met Tyr
20 25 30

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

Ser Ser Ile Glu Gly Ala Gly His Ala Thr 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

Ala Ile Val Leu Gly Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 429
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 429
 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 Leu Gln Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Val Gly Leu Thr Thr 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 Lys Leu Phe Glu Gly Ser Arg Ile Gln Arg Asp Val Gly Phe Asp
 100 105 110

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

<210> 430
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 430
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Ser Ile Arg Gly Ser Gly Leu Val Thr 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 Lys Val His Thr Thr Leu His Thr Glu Val Ile Gly Phe Asp Tyr
100 105 110

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

<210> 431
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 431
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 Gln Tyr
20 25 30

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

Ser Glu Ile Ser His Ser Gly Ser Asn Thr 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 Ile Ser Gly Leu His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 432
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 432
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 Asp Tyr
20 25 30

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

Ser Arg Ile Gly Val Glu Gly Gly Asp Thr 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 Lys Leu Leu Arg Leu Tyr Arg Leu Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 433
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 433
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 Ala Lys Tyr
20 25 30

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

Ser Lys Ile Asn Ser Asp Gly Gly Leu Thr 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 Lys Gly Leu His Gly Arg Gly Phe Val Ile Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 434

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 434

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 Arg Tyr
 20 25 30

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

Ser Arg Ile Asn Ser Met Gly Leu Ala Thr 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 Lys Asp Tyr Ser Val Ala Pro His Gly Tyr Pro Leu Gly Phe Asp
 100 105 110

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

<210> 435

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 435

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 Lys Asp Tyr
20 25 30

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

Ser Thr Ile Thr Asp Asn Gly Thr Ser Thr 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 Lys His Met Ser Leu Ala Thr Tyr Leu Gln Phe Phe Asp Tyr Trp
100 105 110

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

<210> 436

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 436

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 Met Glu Tyr
20 25 30

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

Ser Arg Ile Ser Ser Asp Gly Leu Trp Thr 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
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65              70              75              80
Leu Gln Met Asn Ser 85 Leu Arg Ala Glu Asp 90 Thr Ala Val Tyr Tyr 95 Cys
Ala Lys Gly Val 100 Ser Ala Leu Ala Pro 105 Phe Asp Ile Gly Phe 110 Asp Tyr
Trp Gly Gln Gly Thr Leu Val Thr 120 Val Ser Ser
<210> 437
<211> 121
<212> PRT
<213> Artificial Sequence
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
<400> 437
Glu Val Gln Leu 5 Leu Glu Ser Gly Gly Gly 10 Leu Val Gln Pro Gly 15 Gly
Ser Leu Arg Leu 20 Ser Cys Ala Ala Ser 25 Gly Phe Thr Phe Lys 30 Glu Tyr
Asn Met Ala Trp Val Arg Gln Ala 40 Pro Gly Lys Gly Leu 45 Glu Trp Val
Ser Ser Ile Asn Phe Ala Gly 55 Arg Thr Thr Tyr Tyr 60 Ala Asp Ser Val
Lys Gly Arg Phe Thr Ile 70 Ser Arg Asp Asn Ser 75 Lys Asn Thr Leu Tyr 80
Leu Gln Met Asn Ser 85 Leu Arg Ala Glu Asp 90 Thr Ala Val Tyr Tyr 95 Cys
Ala Lys Leu Ser 100 Leu Pro Leu Asp Ile 105 Phe Ser Phe Asp Tyr 110 Trp Gly
Gln Gly Thr Leu Val Thr Val Ser Ser 120

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<210> 438
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 438

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 Gly Asp Tyr
20 25 30

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

Ser His Ile Ser Ser Asn Gly Arg Phe Thr 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 Glu Thr Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 439

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 439

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 Gly Asp Tyr
20 25 30

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

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

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

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

Ala Glu Thr Ser Gly Tyr Tyr Glu Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 440
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 440
 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 Gly Asp Tyr
 20 25 30

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

Ser His Ile Ser Ser Asn Gly Arg Phe Thr 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 Glu Thr Ser Gly Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 441
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 441
 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 Gly Asp Tyr
 20 25 30

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

Ser His Ile Ser Ser Asn Gly Arg Phe Thr 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 Glu Thr Ser Ser Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 442

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 442

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 Gly Asp Tyr
20 25 30

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

Ser His Ile Ser Ser Asn Gly Arg Phe Thr Tyr 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 Glu Thr Ser Gly Tyr Tyr Glu Tyr Trp Gly His Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 443
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 443
 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 Ala Phe Gly Asp Tyr
 20 25 30

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

Ser His Ile Ser Ser Asn Gly Arg Phe Thr 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 Glu Thr Ser Gly Tyr Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 444
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 444
 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 Gly Asp Tyr
 20 25 30

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

Ser His Ile Ser Ser Asn Gly Arg Phe Ile Tyr Tyr Ala Asp Ser Val
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50

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

Thr Val Ser Ser
 115

<210> 445

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 445

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 Arg Glu Tyr
 20 25 30

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

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

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

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

Ala Ile Gln Leu Pro Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 446

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 446

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 Gly Asn Asp
 20 25 30

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

Ser Phe Ile Asn Val Asp Gly Arg Glu Thr 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 Glu Trp Ser Pro Gly Arg Val Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 447

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 447

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 Gly Gly Trp
 20 25 30

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

Ser Ser Ile Ala His Glu Gly Gly Glu Thr 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 Lys Tyr Val Pro Gly Ser Pro Leu Phe Asp Tyr Trp Gly Gln Arg
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 448
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 448
 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 Asp Gln Gly
 20 25 30

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

Ser Gly Ile Gly Ser Asn Gly Pro Arg Thr Ser 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 Lys Ser Gly Glu Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 449
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 449
 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 Arg Gln Ser
20 25 30

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

Ser Val Ile Gly Asn Asn Gly Glu Phe Thr 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 Lys Asp Asn Trp Leu Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 450
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 450
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 Asp Leu Ser
20 25 30

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

Ser Thr Ile Gly Gly Asp Gly Ser His Thr 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 Glu Gly Thr Gln Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 451
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 451
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 Ala Tyr
20 25 30

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

Ser Ser Ile Gly Val Thr Gly Tyr Asp Thr 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 Lys Gly Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 452
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 452
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 Gly Asp Tyr
20 25 30

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

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

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

<210> 453

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 453

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 Phe His Tyr
 20 25 30

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

Ser Ser Ile Gly Pro Val Gly Arg Glu Thr 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 Lys Met Ile Gln Ser Pro Leu Phe Lys Asp Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 454

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 454

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 Glu Trp Tyr
 20 25 30

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

Ser Arg Ile Asp Ser Gly Gly Asn Gln Thr 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 Glu Ala Ser Leu Trp Lys Trp Arg Leu Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 455

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 455

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 Glu Glu Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Leu Gly Ile Ser Thr 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 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Ala Thr Ser Gln Glu Ser Leu Arg Ser Phe Asp Tyr Trp
100 105 110

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

<210> 456

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 456

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 Lys Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser 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 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 Gly Pro Leu Pro Asp Ala Phe Trp Thr Arg Gly Phe Asp Tyr
100 105 110

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

<210> 457

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

20089600.txt

<400> 457

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 Gly Thr Tyr
20 25 30

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

Ser Thr Ile Asp Arg His Gly Leu Ala Thr 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 Lys Thr Pro Gly Ser Ser Trp Gln Thr Val Phe Gly Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 458

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 458

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 Glu Ser Tyr
20 25 30

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

Ser Ser Ile Asp His His Gly His Ser Thr Tyr Tyr Ala Asp Ser Ala
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 Lys Leu Leu Arg Val Ser Met Ile Phe Gly Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 459
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 459
 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 Val Gln Tyr
 20 25 30

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

Ser Trp Ile Ser Ser Ser Gly Thr Tyr Thr 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 Glu Thr Ser Arg Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 460
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 460
 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 Arg Glu Tyr
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Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Leu Ile Ser Pro Pro Gly Arg Thr Thr 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 Lys Val Val Ile Leu Gly Tyr Thr Asn Arg Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 461

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 461

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 Pro Asn Tyr
 20 25 30

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

Ser Ser Ile Asn Ser Ser Gly Met Glu Thr 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 Lys Phe Phe Arg Leu Asn Asp His Asn Ser Val Phe Gly Phe Asp
 100 105 110

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

<210> 462
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 462
 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 Lys Asp Tyr
 20 25 30

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

Ser Ser Ile Val Gly Ser Gly Ser Met Thr 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 Lys Gly Pro Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 463
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 463
 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 His Asn Tyr
 20 25 30

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

20089600.txt

Ser Ser Ile Asp Glu His Gly Thr Ile Thr 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 Lys Asp Ser Leu Asp Arg Val Trp Ile Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 464

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 464

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 Ala Asp Tyr
20 25 30

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

Ser Ser Ile Tyr Ser Ala Gly Ser Pro Thr 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 Lys Leu Tyr His Arg Glu Pro Ile Leu Phe Gly Phe Asp Tyr Trp
100 105 110

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

<210> 465

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 465

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 Glu Arg Tyr
 20 25 30

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

Ser Thr Ile Ser Ser Asp Gly Gly Gly Thr 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 Lys Pro Gly His Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 466

<211> 119

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 466

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 Gly Ser Tyr
 20 25 30

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

Ser Glu Ile Asp Arg Thr Gly Glu Arg Thr 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 Glu Pro Gly Phe Ala Ser Leu Pro Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 467
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 467
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 Thr Asp Tyr
20 25 30

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

Ser Lys Ile Ser Pro Ser Gly Arg Ser Thr 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 Lys Asp Pro Phe Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 468
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 468
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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<210> 469
<211> 121
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 469
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 Arg Asp Tyr
20 25 30

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

Ser Thr Ile Ser Pro Leu Gly His Phe Thr 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 Lys Ser Gly Phe His Glu Tyr Thr Glu Gly Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 470
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 470
 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 Asp Arg Ala
 20 25 30

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

Ser Leu Ile Gly Arg Gly Gly Asp Ile Thr 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 Lys Ile Arg Asn Leu His Trp Asp Val Gly Arg Gln Phe Asp Tyr
 100 105 110

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

<210> 471
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 471
 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 Gly Arg Tyr
 20 25 30

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

Ser Ser Ile Ser Ser Asp Gly Gly Gly Thr 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 Lys Pro Ser Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 472

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 472

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

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

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

Ser Ser Ile Ser Pro Val Gly Phe Leu Thr 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 Lys Gly His Glu Gly Ser Tyr Thr Pro Arg Ser Ala Phe Asp Tyr
100 105 110

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

<210> 473

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

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 473
 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 Val Ala Tyr
 20 25 30

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

Ser Thr Ile Ala Pro Leu Gly Gly Asn Thr 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 Lys Arg Pro Glu Gly Leu Gln Ile Asp Ser Gln Asn Phe Asp Tyr
 100 105 110

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

<210> 474
 <211> 116
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 474
 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 Ala Leu Tyr
 20 25 30

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

Ser Ser Ile Asp Ser Ser Gly Ser Asp Thr 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 Lys Pro Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 475
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 475
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 Arg Gln Tyr
20 25 30

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

Ser Thr Ile Ala Ser Asp Gly Val Ser Thr 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 Lys Val Gly Arg Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 476
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 476

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 Glu Gln Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg 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 Gly Met Asp Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 477

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 477

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 Val Asp Tyr
 20 25 30

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

Ser Thr Ile Ser Thr Gly Gly Phe Ser Thr 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 Lys Ala Arg Tyr Tyr Tyr Leu Ser Gln Ile Lys Asn Phe Asp Tyr
 100 105 110

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

<210> 478
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 478
 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 Asp Ile Tyr
 20 25 30

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

Ser Ser Ile Ser Pro Leu Gly Leu Val Thr Tyr Tyr Ala Asp Pro 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 Lys Leu Lys Glu His Gly Asp Val Pro Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 479
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 479
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

Ser Thr Ile Ser Pro Thr Gly Leu Leu Thr 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 Lys Phe Lys Arg Ser Gly Lys Thr Asp Asp Thr Asn Phe Asp Tyr
100 105 110

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

<210> 480

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 480

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 Arg Glu Tyr
20 25 30

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

Ser Thr Ile Val Gly Asp Gly Asn Gly Thr 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 Lys Gln Asp Arg Gln Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 481
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 481
 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 Glu Glu Tyr
 20 25 30

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

Ser Thr Ile Ser Pro Ile Gly Val Thr Thr 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 Lys Asn Ala Tyr Asp Arg Lys Ser Asn Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 482
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 482
 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 Asp Arg Tyr
 20 25 30

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

20089600.txt

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asp 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 Val Leu Gly Arg His Phe Asp Pro Leu Leu Pro Ser Phe Asp
100 105 110

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

<210> 483
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 483
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 Glu Asp Tyr
20 25 30

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

Ser Thr Ile Thr Pro Gly Gly Phe Trp Thr 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 Lys Thr Ser Ser Gly Glu Leu Gln Leu Val Glu Asp Phe Asp Tyr
100 105 110

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

<210> 484
<211> 351
<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 484

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gaggtgcagc tggttgagtc tgggggaggc ttagtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttatt gcttatgata tgagttgggt ccgccaggct      120
ccagggaagg gtctggagtg ggtctcatgg attgatgagt ggggtctgca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagcgtgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagacg      300
cctgaggagt ttgactactg gggtcaggga accctggtca ccgtctcgag c                351

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<210> 485

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 485

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt gattatgaga tgagttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaggg attgatggtg agggttctga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagcgtgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaccgggg      300
aggagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                348

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<210> 486

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 486

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag cgttatccta tgacgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaacg attcatggtt ctggtagtgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagcgtgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggccg      300
tatactagtc ggcataatag tcttgggcat tttgactact ggggtcaggg aaccctggtc      360
accgtctcga gc                372

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<210> 487
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 487
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttatg gattatccta tgggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attgggcctg ttggtatgag tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatggg 300
 gggactagtg gtaggcataa tactaagttt gactactggg gtcaggggaac cctggtcacc 360
 gtctcgagc 369

<210> 488
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 488
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttact gagtatccta tgagttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagtt atttctcctc ttggttttac gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggact 300
 ggtgggagtg gtattttgaa ttcttctttt gactactggg gtcaggggaac cctggtcacc 360
 gtctcgagc 369

<210> 489
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 489
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt tagggttagc aattacgatt tgacctgggt ccgccaggct 120

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ccaggggaagg gtctagagtg ggtatcaacc attagtgccaa caaacggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attattgcgc ggcagtgacg      300
tggtggttgt tgcgtcataa cgacaacttg gggttttggg gtcaggggaac cctggtcacc      360
gtctcgagc                                          369

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<210> 490
<211> 363
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 490
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt tagcattagc tataagaata tggcctgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtatcagcc attaaggcgg caaacggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attattgcgc gacagggagt      300
cagaagaagc ggacctacac gttcgacttt tggggtcagg gaaccctggt caccgtctcg      360
agc                                          363

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<210> 491
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 491
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagg ttgtatgaga tggcgtgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcaggg attgatattt tgggttcgag gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatctg      300
tcgtggcagg gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc          354

```

```

<210> 492
<211> 369
<212> DNA
<213> Artificial Sequence

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```

<220>

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<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 492

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagg tcttatacga tgggttgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcatct attaatccta tgggttatca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacatggg      300
gtgggaagg gtactaagcc gcataatttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369

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<210> 493

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 493

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag ctgtatagga tgtcttgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcagag attagtggta gtggttttcc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtctg      300
catgataaga ctcagcatca tcaggagttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369

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<210> 494

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 494

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttatt gagtatccta tgcggtgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcactt atttctccgt ctggtgtgtt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggat      300
gagtctagta cttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagc          354

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<210> 495
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 495
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag cggtatgata tggattgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg attgggagtt cgggttatcc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaaggatg 300
 cctggttatt ttctggggtt tgctcggcag tttgactact ggggtcaggg aaccctggtc 360
 accgtctcga gc 372

<210> 496
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 496
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttg cggtatgcta tggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg attaattgatg agggtcggga gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagcgg 300
 gtgtctagtt ctgtgaatgc tccgtatgag tttgactact ggggtcaggg aaccctggtc 360
 accgtctcga gc 372

<210> 497
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 497
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgcg aattatagta tgagttgggt ccgccaggcc 120

20089600.txt

ccaggggaagg gtctagagtg ggtctcatcg attgatcgtc ttggtacgca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa tacgctgtat	240
ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagtgtg	300
gctgatctta ttgctgggca tgcggagttt gactactggg gtcaggggaa cctgggtcacc	360
gtctcgagc	369

<210> 498
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 498	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttccg tcgtatgata tggcgtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaggg atttcgaggt ctgggttctat gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ttgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtgtt	300
gatgcgcatg tttattatat ggagcctttt tttgactact ggggtcaggg aaccctggtc	360
accgtctcga gc	372

<210> 499
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 499	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgag aggtatcaga tggcgtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaacg attagtcttg atggtggggg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt	300
actgtttttg actactgggg tcaggaacc ctgggtcaccg tctcgagc	348

<210> 500
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 500

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgctgtctc      60
tcctgtgcag cctccggatt cacatttccg aagtatgaga tggcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attgatgggt atggttaagtc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaccggat      300
cagttttttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

```

<210> 501

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 501

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgctgtctc      60
tcctgtgcag cctccggatt caccttttct tattattcga tgtattgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg atttcgcctt ttggttgggg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagga cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatggg      300
gagacgagtg gtccgatttc tgagaatttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc      369

```

<210> 502

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 502

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgctgtctc      60
tcctgtacag cctccggatt caccttttgc ggttatcaga tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attactaatg aggggtgtttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300
aagtattttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 503
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 503
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttggg gagtatgaga tgggtgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcatct attacgtcgg atggtctgag tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gaaaccgggt 300
 attcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 504
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 504
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttgct gattatgata tggcttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaggt attgttgatg atggtcttat gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat 300
 gttgcttttg actactgggg tcaggggacc ctggtcaccg tctcgaac 348

<210> 505
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 505
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttatt ggttatgcta tggcgtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaagt attggtcctt tgggtgagac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgcct 300

gctggtacga gtagtcatag tgtggatttt gactactggg gtcaggaac cctggtcacc 360
gtctcgagc 369

<210> 506
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 506
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgcg gattatgaga tgacttgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcatct attactagt atggtgtttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaaccgtcg 300
gttcagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 507
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 507
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttcgt aggtatgtta tggggtgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcatgg attgaggctg atggtcgtac gacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaagggctt 300
acggatcagc atgttattga gtttgactac tggggtcagg gaaccctggg caccgtctcg 360
agc 363

<210> 508
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 508
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

20089600.txt

tcctgtgcag cctccggatt cacctttgat ggttatcgta tggggtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcatcg attgctccgg atggttaatta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattttgg	300
gggatgcagt ttgactactg gggtcaggga accctgggtca ccgtctcgag c	351

<210> 509
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 509	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct tcgtatccga tgggttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaagt attggtccta ttggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaatgaag	300
tcgccttata agccgcagtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc	360

<210> 510
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 510	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttttg gcttattgga tgggttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcatct atttctccgt cgggtacgca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctcaggac accgcggtat attactgtgc gaaatatact	300
gagccggggg tgggttcttt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc	360

<210> 511
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 511
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg aattatgaga tgggggtgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcagtg atttctgagg tgggttctct gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctcat      300
gatagttcga ttgggtttga ctactggggg cagggaaacc tggtcaccgt ctcgagc          357

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```

<210> 512
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 512
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttgg tcttatgata tgacgtgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcatct attatggctt cgggtgatga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatgggat      300
cgggattttg actactgggg tcagggaaacc ctggtcaccg tctcgagc          348

```

```

<210> 513
<211> 360
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 513
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gagtatgtta tgtcgtgggt ccgccaggct      120
ccaggggaagg gtctggagtg ggtctcaact atttctccta ttggtctgac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatttcct      300
ttgattattc ttctgattt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360

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```

<210> 514
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 514

gaggtgcagc tggttgagtc tgggggaggc ctggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttatg gagtatgcga tgatttgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaatt atttctccgc ttggtttgtc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcag	300
gattcgtctg atagtcagta tacgaatttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 515

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 515

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag gattatggga tggggtgggc cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaagt attggtcctc tgggtctttg gacatactac	180
gcagactccg cgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctccg	300
cttgaggggtt tgattacgaa ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 516

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 516

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat gcgtatgaga tggggtgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaatt attgattggg atggtaattc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggg	300

gataatgttg gtatttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> 517
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 517
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttagt aattattata tgggtgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagcg attgatgagt ggggttttgc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacattgg 300
 gagtttacgt ctgatacgtc gcgttttgac tactgggggc agggaaacct ggtcaccgtc 360
 tcgagc 366

<210> 518
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 518
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag gattttgata tggcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attaatgac agggttctct gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat 300
 cagttttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 519
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 519
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttagt gcttatgata tgatgtgggt ccgccaggct 120

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ccaggggaagg gtctagagtg ggtctcacgg attagtcctc agggtcagcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt      300
gggcagtcgc ggattcctat gaggtttgac tactggggtc agggaaccct ggtcaccgtc      360
tcgagc                                          366

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```

<210> 520
<211> 357
<212> DNA
<213> Artificial Sequence

```

```

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 520
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcct gagtatgata tgacgtgggt ccgccaggct      120
ccaggggaagg gtctggagtg ggtctcatat attagttctg atgggttattc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgcat      300
gggagtcgcg gggagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc      357

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<210> 521
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 521
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ccaggggaagg gtctagagtg ggtctcaacg attactagtt tgggtgagag tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt      300
cgtatTTTTT actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 522
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

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polynucleotide"

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccaggaagg gtctagagtg ggtctcatgg attgatgcta cgggtacgag gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggtaat      300
tatgggagtt cgtatactat gggggttttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                369

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<210> 523
<211> 366
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 523
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccaggaagg gtctagagtg ggtctcatcg attggtcctt ctggtccgaa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctccg      300
tattttgatg ttattcctag ttattttgac tactgggggc agggaaccct ggtcaccgtc      360
tcgagc                                366

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<210> 524
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 524
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccaggaagg gtctagagtg ggtctcatct attcagtcgt cgggtttgcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacgggct      300
aattctcgta ggggttttga ctactggggg caggaaccc tggtcaccgt ctcgagc      357

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<210> 525
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
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<400> 525
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 ccaggaagg gtctagagtg ggtctcatct attactagtc atggtggggtc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
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 aaggattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 526
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 526
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 ccaggaagg gtctagagtg ggtctcatcg attggtaggc tgggtaatcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtgct 300
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 tcgagc 366

<210> 527
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 527
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 ccaggaagg gtctagagtg ggtctcaagt attgattcgg atggttgggt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

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<210> 528
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 528
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 ccaggaagg gtctagagt ggtctcaggt attaatcggg gtggtactcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttgg 300
 aggagggggg ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 529
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 529
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 ccaggaagg gtctggagt ggtctcaggg atttcgaggg atggttatcg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtatg 300
 actgcgtcgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 530
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 530
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 tcctgtgcag cctccggatt cacctttcag atgtatccga tgggggtgggt ccgccaggct 120

20089600.txt

ccagggaagg gtctagagtg ggtctcaatg attgagccgg ctggtgatct tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcag	300
gagcagcctt ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 531
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cccctttccg cagtatcaga tggcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaatg attacttctg atggtcttga tacatattac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctgag	300
cctctttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 532
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 532	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt atgtatgata tgcattgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaacg attttgtctg atggtacgga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatggg	300
gctatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 533
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

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<400> 533
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
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ccagggaagg gtctagagtg ggtctcatct attgatgcgg ggggtcatga gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagattgg      300
tgggattatc tgtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage          354
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<210> 534
<211> 351
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt caccttttcg cggtatccga tgagttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcatct attaatcggt cgggtatgcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggcat      300
caggcgccgt ttgactactg gggtcagggg accctggtca ccgtctcgag c              351
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<210> 535
<211> 369
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 535
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt caccttttac gggatatgcta tgtcttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact attaatgcga atggtattcg gacatactac      180
gccgactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acggcctgcg tgccgaggac accgcggtat attactgtgc gaaagggggg      300
gtttggaggt gggggactgg gcataagttt gactactggg gtcaggggaa cctggtcacc      360
gtctcgagc                                369
```

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<210> 536
<211> 354
<212> DNA
<213> Artificial Sequence
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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 536

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag cagtatgata tgcggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaacg atttcgcaga atggtactaa gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgagg	300
actggtaggt attttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 537

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 537

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg acttatgata tggggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaagg attaattggc agggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg	300
tttggtcatt atgttgatgg tcttgggttt gactactggg gtcaggggaac cctggtcacc	360
gtctcgagc	369

<210> 538

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 538

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tcctgtgcag cctccggatt cacctttagt gggatgaga tggcgtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcatct attactgata tgggtgattc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggg	300
actgcgtttg actactgggg tccgggaacc ctggtcaccg tctcgagc	348

<210> 539
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 539
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 ccagggaagg gtctagagtg ggtctcaagt attactccga agggtcattc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
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<210> 540
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 540
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 tcctgtgcag cctccggatt cacctttgag cggtataata tgtcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attcgccgc ggggtgggaa gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggcgg 300
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 tcgagc 366

<210> 541
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 541
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 tcctgtgcag cctccggatt cacctttgag aggtatggta tgacttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcaagt atttggccga ggggtcagaa gacatactac 180

20089600.txt

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggaat	300
agtcggtatg tttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 542
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 542	
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ccaggggaagg gtctagagtg ggtctcaact attacttcgg atggtatttc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
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aggttttttg actactgggg tcaggggaacc ctggtcaccg tctcgagc	348

<210> 543
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 543	
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ccaggggaagg gtctagagtg ggtctcaggt attagttcgg agggctttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
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cgtaggtttg actactgggg tcaggggaacc ctggtcaccg tctcgagc	348

<210> 544
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 544	
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tcctgtgcag cctccggatt cacctttact aattatagta tgggttgggt ccgccaggct      120
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gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacggtcg      300
tctgcgcac ttcagagggt tgactactgg ggtcaggga cctgggtcac cgtctcgagc      360

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<210> 545
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 545
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ccaggaagg gtctagagt ggtctcatcg attggtcgtc atggtgggcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagggg      300
agtacttatc ctagggttga ctactggggt caggaaccc tggtcaccgt ctcgagc      357

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<210> 546
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 546
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ccaggaagg gtctagagt ggtctcaagt attgagcctt ttggtggtgg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagtgtat      300
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<210> 547
<211> 372
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

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polynucleotide"

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<400> 547
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccaggaagg gtctagagtg ggtctcatct attcggcctg atggttaagat tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagtttat      300
tcttcgtgtg cgatgtgtac tccgcttttg ttgactact ggggtcaggg aaccctggtc      360
accgtctcga gc                                                              372

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<210> 548
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 548
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ccaggaagg gtctagagtg ggtctcagat attgggccga ggggtttttc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgggt      300
cgtggtcagc gtgatactag tcagccgttt gactactggg gtcagggaac cctggtcacc      360
gtctcgagc                                                                369

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<210> 549
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 549
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct tcttatcaga tggcttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggg attacttcgg gtggtcttag tacgtactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300
aggggttttg actactgggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 550
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 550
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggtgggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgct tcttatgaga tgacttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaggg atttcttctg atggtctgtc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300
 gtgtgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 551
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 551
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctctggatt cacctttgat aagtatttga tgtcgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcaggg attgagcctc tgggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggct 300
 tcgggggatt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 552
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 552
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccgggtt cacctttact gagtatgaga tgtcttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaagt attgataatg tgggtagtag tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggg 300

aagctttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 553
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 553
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgct gattatgaga tgtgggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagcg atttctaggc agggttttgc tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatctg 300
 gagcgggatg attttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 554
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 554
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgct aattatgaga tgggggtgggc ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagtt atttctgagt ggggttattc tacatactac 180
 gcagactccg cgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttgtg 300
 ggtgggactc agtatgagtt tgactactgg ggtcaggga cctgggtcac cgtctcgagc 360

<210> 555
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 555
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcat aattatgaga tgtcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagt atttcttcgg gtgggttcttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300
 gttaagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 556
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 556
 gaggtgcagc tggttgagtc cgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttggg ctgtatgaga tgacgtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcaagt attacgggtg atggtatttc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggg 300
 aggaagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 557
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 557
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttagt aattatcaga tggcgtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcaagt attactagt aggggtgggtc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacactgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300
 aagaattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 558
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 558
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

20089600.txt

tcctgtgcag cctccggatt cacctttagt gattatcaga tggcgtgggt tcgccaggct	120
ccaggaagg gactagagt ggtctcaagt attactagt aggggtgggtc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacagtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt	300
aagaatttcg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 559
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 559	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aattatgaga tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaact attacgtcgc aggttactag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat	300
cggtcttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 560
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 560	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgt agttatgaga tgacttgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcatct attacgtcgc atggtggtac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat	300
aagacgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 561
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 561
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaat ttgtatgaga tgacttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcatct attactagtg atggtgtttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat      300
tctccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348

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<210> 562
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 562
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg cattatgata tggcttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact attagtata atggtaatgg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300
cgtgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348

```

```

<210> 563
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 563
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt cgttatcaga tggcttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcatct atttcttctg atggtggggg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggg      300
cgggcgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348

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```

<210> 564
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 564

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgcg aggtatcaga tggcttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcaact atttctgatg atggtgattc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactggat	300
aagttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 565

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 565

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatgatgaga tgacgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attgatacga cgggtgggca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt	300
aaggagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 566

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 566

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg gagagtgaga tgagttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaagt attcttgatg agggttctgg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat	300
aaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 567
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 567
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttggg gaggaggaga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcagcg attactgatg atggtgatga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctaata 300
 gcgggtgctt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 568
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 568
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttgag gtgtatgata tggcttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcaggg attgttaatg atggttcttc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300
 aaggattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 569
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 569
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttggt aatacggaga tgacttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatcg attgcggatg atggttctag tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt 300

caggcttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 570
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 570
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag gagtatcaga tggcgtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaacg atttcgatg atggttcttc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300
 cttatttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 571
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 571
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag gtgtatcaga tgggttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcattt attgtgcctg ggggtgattt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaacgtgg 300
 ccggagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 572
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 572
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat aattatgaga tgacgtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatct attacgagt atggtacttc gacatactac 180

20089600.txt

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctaata	300
ccgccgtttg actactgggg tcaggggaacc ctggtcaccg tctcgagc	348

<210> 573
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 573	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttaag gcgtatgata tgggttggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcacag attgggaggg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctcgt	300
cggtatgcta tttttacttt tgatcggggg caggggaacc tggtcaccgt ctcgagc	357

<210> 574
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 574	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttaag cagtatccga tgggttggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaacg atttctacta atggtgtgag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggacg	300
gatattatct cgtcttcgga gtttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 575
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

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<400> 575
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttttt aattatgata tgtcttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttttt      300
gtgtggtcgg ctgatattga ttttgatttt gactactggg gtcagggaac cctggtcacc      360
gtctcgagc                                     369
```

```
<210> 576
<211> 369
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
```

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<400> 576
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg tggtatgata tgagttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcacat attgcgagtt ggggtggtaa gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgcg      300
gtgaaggatg gggggatatc gatggatttt gactactggg gtcagggaac cctggtcacc      360
gtctcgagc                                     369
```

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<210> 577
<211> 366
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 577
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttgc gagtatgcta tggcgtgggt ccgccaggct      120
ccagggaagg gtctggagtg ggtctcaagt attgggcggg atggtgcggt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggaag      300
gcggcgagg agcgggggtc ttggtttgac tactgggggc aggaaccct ggtcaccgct      360
tcgagc                                     366
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<210> 578
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 578
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttcag gcttatcaga tgcagtgggt ccgccaggct 120
 ccaggaagg gtcttgagtg ggtctcaact attagtccta atggtctttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggttg 300
 agttcttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 579
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 579
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttgct atgtattcga tggcttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaggt atttcgcctc gtggtgttga gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactaat 300
 tggaatggtg tggatctgtt tgactactgg ggtcaggga ccttggtcac cgtctcgagc 360

<210> 580
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 580
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttcct acgtatatga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaact attaatacga atggtcgtga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggat 300

agtaatatgt cgttttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> 581
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 581
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag ggttattcga tgacgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attaatgcgt cgggtactct gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaagatggg 300
 aatagggtctg aggttttttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 582
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 582
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttttt gaggatgaga tgacgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attgcgaatg atggttcgac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaacctgat 300
 cggcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 583
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 583
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcag gattatttga tggcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagag attaatcagg atgggtactgt tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaagttct	300
ccgtattttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 584
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 584	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgat aattatgcga tgcgtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcatct attagtcggg atggcatgt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactttct	300
tctaaggggg ggacgtttgc tagttctttt gactactggg gtcaggaac cctggtcacc	360
gtctcgagc	369

<210> 585
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 585	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttagt gctgttccga tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcagcg attacgatg atggctttcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcat	300
atttatgggg attattttga ctactggggg caggaaccc tggtcaccgt ctcgagc	357

<210> 586
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 586
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag ctttatagga tgatgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtagtg atggtgatac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacattgg      300
ttgggtacta cgttgtcttt gagggatttt gactactggg gtcagggaac cctggtcacc      360
gtctcgagc                                     369
```

```
<210> 587
<211> 369
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
```

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<400> 587
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttat cgttatacga tggcgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcacag atttcgccta ggggtaatat tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtggg      300
gtggcggggg cggagtcgcc tgagtatttt gactactggg gtcagggaac cctggtcacc      360
gtctcgagc                                     369
```

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<210> 588
<211> 357
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 588
gaggtgcagc tggttgagtc tgggggaggt ttggtgcagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttttg ggttattata tgagttggat ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaacg attgggccga ttggtggtgg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctcag      300
aatatttatg gtccttttga ctactggggg cagggaaacc tggtcaccgt ctcgagc       357
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<210> 589
<211> 348
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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 589
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag cagtatgata tggcttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagag attagtcgtg atggtgggcg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagagtat 300
ccttattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 590
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 590
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttccg cagtatagta tgggtgtgggt ccgccaggct 120
ccagggaagg gtcttgagtg ggtctcaact atttcgcctc tgggttcttc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaatgagt 300
aagttgttgc tgtcgaggga gtttgactac tggggtcagg gaaccctggt caccgtctcg 360
agc 363

<210> 591
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 591
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgct atgtattcga tggcttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt atttcgcctc gtggtgttga gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactaat 300

tggaatggtg tggatctgtt tgactactgg ggtcagggaa ccttgggtcac cgtctcgagc 360

<210> 592
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 592
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttacg cgtcatggta tggcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg attacgccta ctggtaatat tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatgct 300
 catgatgagg ggtattttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 593
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 593
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt ccgtatgaga tgacttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatcg attgttgggt atggtctgga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat 300
 cgggtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 594
 <211> 342
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 594
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt agtacgccta tgatgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagag attagggata cgggtctggc tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gagtgtttcg 300
 ttgactact ggggtcaggg aaccctggtc accgtctcga gc 342

<210> 595
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 595
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttcat ctgggggata tgcatgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatcg attagtggga cgggtcatac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctatg 300
 aatgatcagg ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 596
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 596
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttatg gatgaggata tgttgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagg attaattcgc tgggtactca tacatactac 180
 gcagactccg tgaagggccg attcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatcgttt 300
 atgatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 597
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 597
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttcgt aattatcaga tgcattgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaggt attgatgcga ctggtcgggc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gagatctact	300
aggtcatttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 598
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 598	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttacg aatgcggata tgggtgtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaagt attagtggta gtgggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtat	300
ttgacttcgc attttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc	354

<210> 599
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 599	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagg gattattcta tggcttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaact attactccgt cgggtcttac gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggtct	300
caggcgggta ctcggtcttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 600
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 600
gaggtgcagc tgttggagtc tgggggagac ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttct gatgagggtg tgatgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagag attaatcagc agggttcggc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgatt      300
gggatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 601
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 601
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact gatcagccga tgggtgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg attggggcgc gtgggtgggccc tacatactac      180
gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggttt      300
gatattattg cttgggatcc ttttagtttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                369

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<210> 602
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 602
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaat cagtatccta tgatgtgggt tcgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attactcctt ctgggtttttt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggaat      300
ccttttatta ctacgtttga ctactggggg caggaacccc tggtgaccgt ctcgagc          357

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<210> 603
<211> 354

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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 603
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttgat 300
tattcgcttc gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 604
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 604
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgct tcttatgaga tggcgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatcg attggtagtg atgggtgggc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac tccgcggtat attactgtgc gaaacctgat 300
agggcttttg actactgggg tcagggaacc ctgggtcaccg tctcgagc 348

<210> 605
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 605
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttct gcggagcaga tgacttgggc ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaact attactccgc atgggtgattc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggcgg 300
actttgggtg attggcctac gaggtagtcg tttgactact ggggtcaggg aaccctgggc 360

accgtctcga gc

372

<210> 606
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 606
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttacg tcttatgaga tgggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attgagccta ctggtattac gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaacctcat 300
 ttactgagc ttggttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 607
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 607
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag ggggagcaga tggcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg attacgctgc ctggtccgta tacattctac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaagggagt 300
 gggacgtttt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 608
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 608
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt aattatgcga tggcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaaag attggggcgc aggtcttca tacatactac 180

20089600.txt

gcaggctccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagacg	300
acgatggatt atgagagggt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 609
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 609	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat gaggttgata tgtcgtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcagct attggttaata atggtcttaa gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcggct	300
ctgtcgtata ggcctcctgt ttttgactac tggggtcagg gaaccctggc caccgtctcg	360
agc	363

<210> 610
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 610	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcag gatgatacta tgtcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaacg attacgctta aggggtccgtc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgagg	300
gatgggttgt attttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 611
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

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<400> 611
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct tcgtctccga tggcttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaagt attggtcggg atggtagtac gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccttcg      300
ccttatcggc ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg          354
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<210> 612
<211> 360
<212> DNA
<213> Artificial Sequence
```

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
```

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<400> 612
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact gattattcga tggtttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact attgtgagtc atggttggtac tacatactac      180
gcagactccg tgaagggccg attcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttaag      300
ggttataatg cgcagtatct tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc      360
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<210> 613
<211> 354
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 613
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttgat      300
tattcgcttc gttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg          354
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<210> 614
<211> 348
<212> DNA
<213> Artificial Sequence
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<220>
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<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 614

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60

tcctgtgcag cctccggatt cacctttaat gattatgata tgatttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaact attagttcgc atggtgatag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtgat 300

gttttttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 615

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 615

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60

tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaatggctg 300

gattcttttg actacagggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 616

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 616

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60

tcctgtgcag cctccggatt cacctttgct gattatgaga tggcttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaggg attcagtcta atggtaatat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcta 300

tctcagggtt agtattttga ctactggggg caggaaccc tggtcaccgt ctcgagc 357

<210> 617

<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 617
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggg gtggagccta tgtcttggtt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaaatt attggtcgtg atgggttcgat gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgggg 300
aagcatggta cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 618
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 618
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttccg gaggatcgga tgatgtgggt ccgccaggct 120
ccagggaagg gtctggagtg ggtctcatgg attgatgagc ggggttcgct tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaggcgg 300
aaggggtacta agcagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 619
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 619
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag ttgtatgcta tggcgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attggtgctg tgggtgagac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggct 300
aataatcttt ctgataatct tgtgtttgac tactgggggc agggaaccct gggtcaccgtc 360

tcgagc

366

<210> 620
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 620
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg catcagcaga tggcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact attactccga atggttatta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaatggctc 300
 gttgagtggg ttgactactg gggtcaggga accctgggtc ccgtctcgag c 351

<210> 621
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 621
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat agttatacga tgaattgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagt attaatacctt ggggtagtcg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggat accgcggtat attactgtgc gaaaggtctg 300
 gtgctgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 622
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 622
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat ggtgatatga tgtcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatcg attactcagc ttggtagtag gacatactac 180

20089600.txt

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagaat	300
tggcggactc ttacttttga ctactgggggt cagggaaaccc tggtcaccgt ctcgagc	357

<210> 623
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 623	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccgatt cacctttaat gcttatggga tgatgtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcatct attctttctg atggtgttat tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtgc	300
cgggggtgcga atttttttga ctactgggggt cagggaaaccc tggtcaccgt ctcgagc	357

<210> 624
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 624	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttggg cattatatga tgggtgtgggt ccgccaggct	120
ccagggaaagg gtctggagtg ggtctcatct attacgcctc atggtacgag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatttaaat	300
gctattttta gtgaggcgtt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 625
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 625	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60

20089600.txt

tcctgtgcag cctccggatt cacctttagg gattattcta tggcttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaact attactccgt cgggtcttac gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggtct	300
caggcgggta ctcggtcttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 626
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 626	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat ctttatgcga tggcttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaatg attgggaggg atggtcgttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattggct	300
ggttcgctga ggggtcgttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 627
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 627	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat aaggctagta tgggttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaact attacgcctc atggttcgtc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagcgg	300
tggggtgttg agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc	354

<210> 628
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 628
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcag gggatatagta tgggttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attgctgggc gtggtggtgt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtttg      300
tatatttatc atagtctgtt tgactactgg ggtcaggga ccttggtcac cgtctcgagc      360

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<210> 629
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 629
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcct ggtatggaga tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagct attactggga ctggtagtac gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttat      300
catccgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 630
<211> 351
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 630
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttccg atggtggcta tgtcttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attgctcggg atggtaatgt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagtttcg      300
ccgactgggt ttgactactg gggtcaggga accctggtca ccgtctcgag c      351

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<210> 631
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 631

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg catcaggata tgcgtgggt cgcaggct      120
ccagggaagg gtctagagtg ggtctcaggg attacgatg atggtgagag tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtgat      300
tatgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348

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<210> 632

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 632

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg gagtataata tgatgtgggt cgcaggct      120
ccagggaagg gtctagagtg ggtctcacag attacgaggg atggttctag gacatactac      180
gcagactccg tgaggggccc gttcaccatc tccgcgaca attccaggaa cagctgtat      240
ctgcaaatga acagcctgcg tgccgaggac tccgcggtat attactgtgc gaaactgtcg      300
aatattgggt ttgactactg gggtcaggga accctggtca ccgtctcgag c      351

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<210> 633

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 633

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gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt gattattcta tgatttgggc cgcaggct      120
ccagggaagg gtctagagtg ggtctcatcg attacgccgt atggttctta tacatactac      180
gcagactccg tgaagggccc gttcaccatc tccgcgaca attccaagaa cagctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaactgat      300
tatttgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348

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<210> 634
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 634
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat acgtatagta tgatgtgggt ccgccaggct 120
 ccaggaagg gtcttgagtg ggtctcaact attactcctt atggtagttc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggggt 300
 ctggtgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 635
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 635
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgactc 60
 tcctgtgcag cctccggatt cacctttact acgggtccta tgatgtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcagcg attggtattg ggggtgatac gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtct attactgtgc gaaattgact 300
 ccgtctaata agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 636
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 636
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag cagtatcaga tgatgtgggt tcgccaggct 120
 ccaggaagg gtctagagtg ggtctcaagt attactcctt ctgggtttttt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggaat 300

ccttttatta gtacgtttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> 637
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 637
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcct aattatgata tggtttgggt ccgccaggct 120
 ccagggaaagg gtctagagtg ggtctcatcg atttctgctt tgggtaatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaacga acagcctgcg tgccgaggac actgcggtat attactgtgc gaaatggcgt 300
 agtgctatta ctggttaatt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 638
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 638
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag gagtatcaga tgtcttgggt ccgccaggct 120
 ccagggaaagg gtctagagtg ggtctcaact atttcgccgt cgggtatgaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatggcgg 300
 tcggttggtc gtccttggcc ggggtgtgtt gactactggg gtcagggaaac cctgggtcacc 360
 gtctcgagc 369

<210> 639
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 639
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat gatgagagta tggcgtgggt ccgccaggct 120

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ccaggggaagg gtctagagtg ggtctcatcg attactcctc atggtacttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttcat	300
cttaagttgt atgagtctca ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 640
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 640	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgag ggtggtgaga tgggttggt cgcaggct	120
ccaggggaagg gtctagagtg ggtctcaatg attccgatgg atggtagtgc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg	300
agtacgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 641
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 641	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgat tttatgccga tggcgtgggt cgcaggct	120
ccaggggaagg gtctagagtg ggtctcatct attgggaggg atggtgctta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttgct	300
tcgccggcgc agtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc	354

<210> 642
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 642
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt gatgagccta tgctgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attgggggta cgggtacgac gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtaat      300
cagggtgatt ttattaatcg gtttcactac tggggtcagg gaaccctggt caccgtctcg      360
agc                                                                    363

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<210> 643
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 643
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcat gcgtataata tggcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaacg atttctccgc ggggttctta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggccg      300
ccgccttcgt ctcatcttga ctactggggg caggaaccc tggtcaccgt ctcgagc      357

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<210> 644
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 644
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgat gggatatgaga tggcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attacgagtg atggtacgag tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg      300
ctgcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 645
<211> 357

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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 645
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag ggttatatga tgtattgggt ccaccaggct 120
ccggggaagg gtctagagtg ggtctcatct atttctctc agggtcattt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacttcgt 300
gagcttcctc gtctgtttga ctactggggg caggaaccc tggtcaccgt ctcgagc 357

<210> 646
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 646
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttagt agttatgcta tgggttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatcg attgatgcga gtggtgggtcc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgaat 300
gggaagaagt ttccttttac taagtatttt gactactggg gtcagggaac cctggtcacc 360
gtctcgagc 369

<210> 647
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 647
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcct agtgtgcata tggcgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggg attaactctga cgggtgttga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtgtc 300

actactaggc aggcgcattcc gttgtatttt gactactggg gtcagggaac cctggtcacc 360
gtctcgagc 369

<210> 648
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 648
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaag gagggtgaga tgtattgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaacg atttcgacta atggtcttac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctact 300
cgtgatctgg gttttgccta ctgggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 649
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 649
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag gaggatgaga tgggttgggc ccgccaggct 120
ccaggaagg gtctagagtg ggtctcattt atttctctc gtggtcattt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggct 300
aagacttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 650
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 650
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat acgtatgaga tgctttgggt ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcacgt atttctgttg atggtagtat tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaacgcgg	300
atgcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 651
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 651 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt tcgtatgcta tgcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaa atttctcgtg atggttcgaa gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcgcag	300
tctggggggc ttcggtcggg tttgactacg tttgactact ggggtcaggg aaccctggtc	360
accgtctcga gc	372

<210> 652
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 652 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag actccggatt cacctttagc agctatgcc a tgagctgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatct attgggaggg atggtgctta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg	300
ccgaagggta ttgcgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 653
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 653
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt ccgcatgcta tggcttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcaggt attgatgggg ggggttcgat gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcggat      300
cctccgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 654
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 654
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttcat gcgggggaga tgcattgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg attacgtgc ctggtgatat gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgaat      300
actgggtata cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc      354

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<210> 655
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 655
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg aattatggta tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt atttcgtggg atggttctct tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaaatacg      300
cggctttttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 656
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 656

gaggtgcagc	tggttgagtc	tgggggaggc	ttggtacagc	ctgggggggc	cctgcgctctc	60
tcctgtgcag	cctccggatt	cacctttcat	gatgcggata	tgctgtgggt	ccgccaggct	120
ccagggaagg	gtctagagtg	ggtctcaggt	atthttgtctc	cgggtgagga	tacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tcccgcgaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgcg	tgccgaggac	accgcggtat	attactgtgc	gaaatttggt	300
ctgccgtttg	actactgggg	tcagggaacc	ctggtcaccg	tctcgagc		348

<210> 657

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 657

gaggtgcagc	tggttgagtc	tgggggaggc	ttggtacagc	ctgggggggc	cctgcgctctc	60
tcctgtgcag	cctccggatt	cacctttcgt	actgatcaga	tgaattgggt	ccgccaggct	120
ccagggaagg	gtctagagtg	ggtctcaagt	atthttccta	gtggtgcgta	tacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tcccgcgaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgcg	tgccgaggat	accgcggtat	attactgtgc	gaaaggtctt	300
ggtgcttttg	actactgggg	tcagggaacc	ctggtcaccg	tctcgagc		348

<210> 658

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 658

gaggtgcagc	tggttgagtc	tgggggaggc	ttggtacagc	ctgggggggc	cctgcgctctc	60
tcctgtgcag	cctccggatt	catctttgag	cagtatcaga	tggtttgggt	ccgccaggct	120
ccagggaagg	gtctagagtg	ggtctcatgg	atthtcgctg	atggtacgca	tacatactac	180
gcagactccg	tgaagggccg	gttcaccatc	tcccgcgaca	attccaagaa	cacgctgtat	240
ctgcaaatga	acagcctgcg	tgccgaggac	accgcggtat	attactgtgc	gaaatttagt	300
ttgcgtaaga	tggagaagtt	tgactactgg	ggtcagggaa	ccctgggtcac	cgtctcgagc	360

<210> 659
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 659
 gaggtgcagc tggttgaatc tgggggaggc ttggtacagc ctgggggggtc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttcag gatgagcaga tggcgtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcaagt attgctgtctg atggtatgtc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga atagcctgcg tgccgaggac accgcggtat attactgtgc gcaacctggg 300
 aagaattttg accactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 660
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 660
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttagt gattatgcga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatcg attactactg ggggtgagcg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgttgg 300
 aatctgtata cggagtcttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 661
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 661
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttggg ggtcagccga tggattgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatct attgctcctg atggtattca tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatttg 300

ggtcagggtt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 662
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 662
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag cggtatcaga tgacgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagt atttctccta gtggtacggt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc ggaatggaag 300
 gcgctttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 663
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 663
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcct cattcgacta tgtattgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcactt attttgccgt cgggtagtcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaattttct 300
 gatgagcgtt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 664
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 664
 gaggtgcagc gtgcggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt gatgggaata tggattgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaggt atttctagt atggtgtgac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagg 300
 ggtcaggggt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 665
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 665
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cttccggatt cacctttgat gattatatga tgtggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attagtccgc atggtgttta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggttg 300
 catacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 666
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 666
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cttccggatt caccttttcg aattatacga tggcgtgggg ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcattt attgctggtc cgggtaatta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300
 agtactgcga cgtataataa tggtcagttt gactactggg gtcagggaac cctggtcacc 360
 gtctcgagc 369

<210> 667
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 667
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttacg gagtatagta tgggtgtgggt ccgccaggct      120
ccagggaagg gtctggagtg ggtctcatct attagtggga gtggtcgtgt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggctt      300
aagctggtta gggctcctaa tccgtttgac tactgggggc aggaaccct ggtcaccgtc      360
tcgagc                                     366
```

```
<210> 668
<211> 360
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
```

```
<400> 668
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttagt aattatcaga tggcgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaggt atttctaaga ctggtcattc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcttcg      300
cattcgttgg ggcctctttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc      360
```

```
<210> 669
<211> 369
<212> DNA
<213> Artificial Sequence
```

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 669
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttacg gcgtatagga tggcttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcatgg atttcgctt ctggttcggg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactttg      300
acggattcgc cgtcggggca ttatgagttt gactactggg gtcaggggaa cctgggtcacc      360
gtctcgagc                                     369
```

```
<210> 670
<211> 369
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<212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 670
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgcg cggtatgaga tggggtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcacgg attactgctc agggctcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca actccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatctt 300
 actgatttta gtagtgggca tcaggagttt gactactggg gtcaggaac cctggtcacc 360
 gtctcgagc 369

<210> 671
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 671
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat gattatggta tgtcgtgggt ccgccagggt 120
 ccaggaagg gtctggagt ggtctcaggt attagtcata atggatgtt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatattgg 300
 ccgtctacta gttgggagac tgattttgac tactggggtc aggaaccct ggtcaccgctc 360
 tcgagc 366

<210> 672
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 672
 gaggtgcagc tgttggagtc tgggggaggc tcggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg aatgagccta tggcttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcaagt attgagatgc agggtaagaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagg 300
 ggtcaggggt ttgactactg gggtcagggga accctgggtca ccgtctcgag c 351

<210> 673
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 673
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg gaggaggaga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatgt attgataatc tgggtagtcc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaaacgatt 300
 tctcatcagt atgataggtt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 674
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 674
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg gaggaggaga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatcg attgatgagg ggggtcggtg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggacg 300
 ccgcataagc agttgtcgtt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 675
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 675
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cagctttgct gatgagtata tggtttgggc ccgccaggct 120

```

ccaggggaagg gtctagagtg ggtctcagag attgatccgt tgggtactgg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatggg      300
acggcttttg actactgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 676
<211> 357
<212> DNA
<213> Artificial Sequence

```

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 676
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgcctc      60
tcctgtgcag cctccggatt caccttttct acgcatgata tgatgtgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcatcg atttctgatg atggtattag tacatactac      180
gcagactccg tgaagggccg gttcaccatt tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctgat      300
atgtctctta ttgagtttga ctactggggg caggaaccc tggtcaccgt ctcgagc          357

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<210> 677
<211> 363
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 677
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgat ggtactccga tggtttgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcaggg attagtgggt atggtaggaa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccttat      300
gcgcttactt cgtctaagcc ttttgactac tggggtcagg gaaccctggg caccgtctcg      360
agc                                                                363

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<210> 678
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

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polynucleotide"

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<400> 678
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttaat gattatacta tgggttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatgg attcatggga ctggtggtca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctttg      300
gctgatagga gtgggggggt tgttgagttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369

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```

<210> 679
<211> 360
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 679
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttgag gcggagacga tggcttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatgt attagtaatg atggttaatac gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagtct      300
ctgattagtc ctgggtcttt tgactactgg ggtcaggga cctggtcac cgtctcgagc      360

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```

<210> 680
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 680
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttact ggtgagtata tgaattgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaact attaatgaga ctggttatat gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga atagcctgcg tgccgaggac accgcggtat attactgtgc gaaactttct      300
acgagggggg tgccttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc      357

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<210> 681
<211> 360

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<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 681

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagg tcgtatgata tgggttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaacg atttcgccta tgggtgtttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctaata	300
cagcatgctc atgatccttt tgactactgg ggtcaggga ccttggtcac cgtctcgagc	360

<210> 682

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 682

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt gattatgata tgggttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcaagt atttcgccta tgggtacggt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgct	300
ttgactgagc ctatgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 683

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 683

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgt gattatgata tgggttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaact atttctcctc ttggtcattt tacatactac	180
gcagactccg tgaagggccg gtccaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagctgag	300
gaggcttttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 684
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 684
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgcttc 60
 tcctgtgcag cctccggatt cgcctttcct aggtatggta tgacgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaaatt attgatcagt ttggtatgaa gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagagtat 300
 gcttcgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 685
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 685
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgcttc 60
 tcctgtgcag cctccggatt cacctttgat aagtatgata tgggttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg atttcgccta tgggtgtttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgg 300
 ggtaataactt cggattttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 686
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 686
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgcttc 60
 tcctgtgcag cctccggatt cacctttagt aattatgata tggcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact atttctgggg cgggtcattt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtttt 300
 ccgcgtgatg agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 687
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 687
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttccg aagtatgaga tgaggtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcagag attggtctgg atggttcgcc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgggg 300
 gatccgaatg gttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 688
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 688
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttccg actagtgaga tggattgggt ccgccaggct 120
 ccaggaagg gtctggagt ggtctcaggt attgggcctg atggtttgac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatgag 300
 gattggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 689
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 689
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttct gaggatgata tgtattgggt ccgccaggct 120

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ccaggggaagg gtctagagtg ggtctcatgg attgatactg atggtgggga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt	300
ctgaagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 690
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 690 gaggtgcagc tggtggagtc tgggggaggc ctggtacagc ctgggggggc cctgcgtctc	60
tcctgtacag cctccggatt cacctttgag aatgcttcta tgcagtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcatct attgaggggc agggtaatgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagttcg	300
tcttggtctt ttgactactg gggtcaggga accctggtca ccgtctcgag c	351

<210> 691
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 691 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttacg cgtaatgaga tggggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaact attacgccga ctggtacggt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacggat	300
cctggtaata ggtattttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 692
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

<400> 692
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 693
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 693
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attttgacta ccgggggtcag gggaccctgg tcaccgtctc gagg 354

<210> 694
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 694
gaggtgcagc tggttgagtc tgggtgaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccgctc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 695
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 695

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctcaggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagattccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggagc accgcggtat attactgtgt gaaagttggg 300

aaggagagta attctgacta ccgggggtcag ggaaccagg tcaccgtctc gagg 354

<210> 696

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 696

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctccgatt cacctttaat tggcagctga tgggttgggc ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggagc accgcggtat attactgtgc gaaagttggg 300

aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 697

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 697

gaggtgcagt tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctccgatt cacctttaat tggcagctga tgggttgggc ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180

gcagactccg tgaaggaccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgctaata acagcctgcg tgccaggagc accgcggtat attactgtgc gaaagtaggg 300

aaggagagta attttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 698

<211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 698
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggt cgcaggct 120
ccagggaagg gtctagagtg ggtctcaggc attgagggtc ctggtgatgt tacatactac 180
gcagactcag tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cagctgtat 240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 699
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 699
gaggtgcggc tatttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caactttaat tggcagctga tgggttggt cgcaggct 120
ccagggaagg gtctagagtg ggtctcaggc attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat 240
ctgcaaatga acagcctgcg tgccaggac accgcagtat attactgtgc gaaagttggg 300
aaggagagta attctgacta ccggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 700
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 700
gaggtgcagc tggttgagtc tgggggaggc ttggtacggc ctggggggtc actgcgtctc 60
tcctgtgtag cctccggatt cacctttaat tggcagctga tgggttggt cgcaggct 120
ccagggaagg gtctagagtg ggtctcaggc attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat 240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attttgacta ccggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 701
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 701
 gaggtgcagc tgttggagtc tgggggaggc ttggtacaga ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctataat tggcagctga tgggttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgatgac accgcggtat attactgtgt gaaagttggg 300
 aaggagagta attttgacta ccgggggtcac ggaaccctgg tcaccgtctc gaggc 354

<210> 702
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 702
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgcaaggct 120
 cctgggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
 aaggagagta attttgacta ccgggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 703
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 703
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggcc 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca ataccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 704
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 704
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgcttc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120
ccaggaagg gtcttgagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta agtttgacta cctgggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 705
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 705
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgctcttc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagaatccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta atcttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 706
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 706
gaggtgcagc tgtttgagtc tgggggaggc tcggtacagc ctgggggggtc cctgctcttc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120

20089600.txt

ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg	300
aaggagagta attctgacta ccgggggtcag gggaccctgg tcaccgtctc gagg	354

<210> 707
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 707	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
acctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcgggt attgagggtc ctggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcatcatc tcccgcgaca attccaagaa cacgctatat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg	300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 708
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 708	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac	180
gcggactccg tgaagggccg gttcaccatc tcccgcgaca attccacgaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg	300
aaggagagtg aatttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 709
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

<400> 709
gaggtgcggc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc acccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta atcttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 710
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 710
gaggtgcagc tggttggtgc tgggggaggc ctggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 711
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 711
gaggtgcagc tggttggtgc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240
ctgcaaatga acggcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
aaggagagta attttgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 712
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 712
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120
 ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
 aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 713
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 713
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag tggcagctca tggggtgggc ccggcaggct 120
 ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
 aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 714
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 714
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag tggcacctga tggggtgggt ccggcaggct 120
 ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
 aaggagagta gttctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 715
 <211> 354

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 715
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaac tggcacctga tggcctgggc ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 716
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 716
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct 120
ccagggaagg gtctcagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 717
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 717
gaggtgcagc tggttgagtc tgggggaggc ttggtgcagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaag tggcagctga tggcctgggc ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatat tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 718
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 718
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaac tggcacttga tgggctgggc ccggcaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
 aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gaggc 354

<210> 719
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 719
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag tggcagctca tggggtgggc ccggcaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
 aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gaggc 354

<210> 720
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 720
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 721
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 721
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaac tggcagctca tgggctgggc ccggcaggct 120
ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggatgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagttggg 300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 722
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 722
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120
ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggatgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc 300
aaggacagca agtccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 723
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 723
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcgggct 120

20089600.txt

ccaggggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtcggg	300
aaggacagca agtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc	354

<210> 724
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 724	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtcggg	300
aaggacagca actcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc	354

<210> 725
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 725	
gaggtgcagc tggttgagtc tgggggaggc ttggcacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc	300
aaggacagca agtccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagc	354

<210> 726
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 726
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc cagggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300
aaggacgcca agtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 727
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 727
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc cagggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300
aaggacaaga actcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 728
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 728
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc cagggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300
aaggagagca agtccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 729
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 729

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggat accgcggtat attactgtgt gaaagtgggg 300

agggacagca agtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gaggc 354

<210> 730

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 730

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcggactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggat accgcggtat attactgtgt gaaagtcggg 300

aagtacagca actcggacta ccgggggtcag ggaaccctgg tcaccgtatc gaggc 354

<210> 731

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 731

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120

ccaggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgt gaaagtgggc 300

aaggacagca ggtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gaggc 354

<210> 732

<211> 354

<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 732

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct	120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg	300
aaggacgaca gctcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagg	354

<210> 733

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 733

gaggtgcagc tggttgagtt tgggggaggc ttggtacagc ctggggggtc cttgcgtttt	60
tcctgtgcag cttccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct	120
ccagggaagg gtttagagtg ggtttcaggt attgagggtc caggtgatgt tacatattac	180
gcagattccg tgaagggccg gttcaccatt tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcttgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg	300
agggacagca attccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg	354

<210> 734

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 734

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct	120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg	300
aaggacagca cctcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagg	354

<210> 735
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 735
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg 300
 aaggagagca gtcgggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 736
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 736
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc ttccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggc 300
 aaggacagcg cgtccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 737
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 737
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttgggt ccggcaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtcggc 300
aacgacagct actcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 738
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 738
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctctggatt cacctttaat tggcagctga tgggttggtt ccggcaggct 120
ccaggaagg gtctagagt ggtctcaggt attgagggtc caggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acggcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg 300
aaggacagca gtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 739
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 739
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat tggcagctga tgggttggtt ccggcaggct 120
ccaggaagg gtctagagt ggtctcaggt attgagggtc caggtgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcgatat attactgtgt gaaagtgggg 300
aaggacagcg cgtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc 354

<210> 740
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 740
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct 120

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ccaggggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg	300
aaggacgcca agtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc	354

<210> 741
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 741	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc	300
aaggacagca ggtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagc	354

<210> 742
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 742	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag tggcagctga tgggctgggt ccggcaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attgagggtc caggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggc	300
aaggacagca agtccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagc	354

<210> 743
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

<400> 743
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggatgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgt gaaagtgggg 300
aaggacgcca agtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 744
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 744
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggatgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg 300
aaggacagca ggtcggacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 745
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 745
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaac tgggagctga tgggctgggc ccggcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgagggtc caggatgatgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgt gaaagtgggg 300
aaggacagca agtccgacta ccgggggtcag ggaaccctgg tcaccgtatc gagg 354

<210> 746
<211> 354
<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 746

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccgatt cacctttaat tggcagctga tgggatgggc ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac	180
gcagactccg tgaagggtcg gttcaccatc tccgcgaca attccaagaa cacgctgtat	240
ctacaaatga acagcctgcg tgccaggac tccgcggtat attactgtgc gaaagttggg	300
aaggagagta attttgacta cctgggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 747

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 747

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgtag cctccgatt cacctttaat tggcagctga tgggttgggt ccgccaggcg	120
ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaagtcggg	300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtttc gagg	354

<210> 748

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 748

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccgatt cacctttaat tggcagctga tgggttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaggt attgagggtc ctggtgatgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaagttggg	300
aaggagagta attctgacta ccgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 749

<211> 360

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 749
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttagt ggggtgggaga tgggttggtt cgcgccaggct 120
ccagggaagg gtctagagtg ggtctcatct attgatgagt ctggtcttaa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggtgcg 300
ccgcagtatc agattacatt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 750
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 750
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcct aattatggga tgtattgggt cgcgccaggct 120
ccagggaagg gtctagagtg ggtctcatat atttcgcgga ggggtttggt gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgtcg 300
cattatatga ataatgggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 751
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 751
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtg gattatacga tggcttggtt cgcgccaggct 120
ccagggaagg gtctggagtg ggtctcatct attagtccga ttggtacttt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcct 300
tatgggatgg aggatgggtc gacgtgggtt gactactggg gtcaggggaa ccctggtcacc 360

gtctcgagc

369

<210> 752
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 752
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat gcgtatgata tgcagtgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcaacg attacgtcgg agggctcttc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctagt 300
 gatttggttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 753
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 753
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat gggatgata tgggttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact atttctcgtg ggggttgggt cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggacg 300
 agtcagtcgt ctacggggag ttttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 754
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 754
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgt cggtatgata tgctttgggc ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcagag atttcgccta cgggtgctct tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttggt	300
tcgacttttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 755
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 755	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttttt ccgtattata tgagttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatct atttcgggta cgggtgggct tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgacg	300
cagaatgcga cgctttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 756
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 756	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag gtttatacta tggcgtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcaacg attgatgagt ctggtcgtga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt	300
gtttggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 757
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 757
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttgcg ttttataaga tgggggtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaacg attactccta agggatcatca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttttt 300
aagggttaagg gttggactcg tccgagtggg tttgactact ggggtcaggg aaccctggtc 360
accgtctcga gc 372

<210> 758
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 758
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttaat gagtatagta tgatgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatct attgggaggc gtggttggtt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgtg 300
ctgctggatt ctactaagtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 759
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 759
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttgat gagtatccga tgacttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaact atttctgcgc gtggttccttt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg 300
cattggcttc gtaatggtcg ttttgactac tggggtcagg gaaccctggg caccgtctcg 360
agc 363

<210> 760
<211> 348

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 760
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggt atgcagtcga tgcagtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaagt attactgatg atggtactag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgat 300
cgggtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 761
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 761
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggg gcggctgata tgcagtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcactg attactaatg atggtatttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt 300
gatcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 762
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 762
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat aagtatagga tgcagtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaagt attgatagtt ctggtgagct gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagaggtt 300
ccgatgggga atcagacttt ttttgactac tggggtcagg gaacctgggt caccgtctcg 360

agc

363

<210> 763
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 763
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttact gattatacta tgggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatcg attacgtctc aggggtgcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaagctacg 300
 ggtacggatt cgtcgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 764
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 764
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag gattatgaga tgtcttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcatgt attgggcccgg ggggtaagcc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggac accgcggtat attactgtgc gaaagtggat 300
 gggcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 765
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 765
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttagt cagtatgata tgggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg atttcttcga ggggttggct tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtccg	300
gggggtcgtc ggcggtttga ctactggggg caggggaaccc tggtcaccgt ctcgagc	357

<210> 766
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 766	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttctg gattatgcga tgggttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcaact atttctccga tgggtatggg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgagt	300
gctatttcgt ttacttctga tatttctaata tttgactact ggggtcaggg aaccctggtc	360
accgtctcga gc	372

<210> 767
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 767	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttagt gattatccga tgtcttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaagt atttcttgggt ctggttttca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacctggt	300
gttgcgagga tgcctactgg gattgctttt gactactggg gtcaggggaac cctggtcacc	360
gtctcgagc	369

<210> 768
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 768
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt gcttatgaga tgcagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attgatagtg ctggtacttt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtct attactgtgc ggaacctttt      300
gggatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 769
<211> 372
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 769
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg gagtatccga tgaagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaacg attgatcggc agggtgatcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgggtg      300
cggagggggtc ttctcgtcc gagtcgttat tttgactact ggggtcaggg aaccctggtc      360
accgtctcga gc                                                              372

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<210> 770
<211> 363
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 770
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt gattatgata tgggttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcaagt atttcgccta tgggtacggt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtctg      300
agtgtgtatt cgggtcttga ttttgactac tggggtcagg gaaccctgggt caccgtctcg      360
agc                                                                      363

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<210> 771
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 771
 gaggtgcagc tggtggagtc tgggggaggc ctggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttct cattatgata tgggttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcagat attgattata ttggttaagac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tctcgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcttcg 300
 gatgaggtgg gtgttaatac ttccaagttt gactactggg gtcaggggaac cctggtcacc 360
 gtctcgagc 369

<210> 772
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 772
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttgc cggtatgata tggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact atttctccta ctggtgtgtt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggttt 300
 gaggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 773
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 773
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag gcttatccga tgagttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcactg atttctcata cgggtcatgc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcat 300
 tggccttttg actaccgggg tcaggaacc ctgatcaccg tctcgagc 348

<210> 774
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 774
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc cagggggggtc cctgcgcttc 60
 tcctgtgcag cctccggatt cacctttgag gatgagtgga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcagat attagcccg gtggttggaac tacatactac 180
 gccgactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttat 300
 cgtccgtttg atgagtttga ctactggggt caggaaccc tggtcaccgt ctcgagc 357

<210> 775
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 775
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgcttc 60
 tcctgtgcag cctccggagt cacctttgat gctattgaga tgtcttgggt ccgccaggct 120
 ccaggaagg gtctggagt ggtctcatcg atttcgctc atggtgagta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagatgct 300
 tggctctcggc attttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 776
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 776
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgcttc 60
 tcctgtgcag cctccggatt cacctttgat agtacggata tgagttgggt ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcaggt attttggata atggtagtaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat	240
ctgcaaatga atagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggggag	300
agggattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 777
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 777	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cttccggatt cacctttggt aggcagagta tgcagtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaagt attgatgatg atggtttttc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggat	300
ccgtgggggtt ttgactactg gggtcaggga accctgggtca ccgtctcgag c	351

<210> 778
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 778	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtacag cctccggatt cacctttagt gatacgaga tggcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attgatgatg ggggtgtgag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccggat	300
cgtcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 779
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

20089600.txt

<400> 779
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttggg agtacgacga tggggtgggt ccgccaggct 120
ccagggaagg gtctggagtg ggtctcagtg atttcggatg atggtggttt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttgat 300
ggttatggtg tttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 780
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 780
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttcgg agtggggata tgaattgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaact attacgaatg atggtacgtc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa tacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctgat 300
tctgattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 781
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 781
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttgct gcttatgcta tgacgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatat attagtccga atggtacggc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaatatgtg 300
gggatgctgtt ggaattcttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 782
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 782
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttcg agttatgaga tggcttgggc cgcgcaggct 120
 ccaggaagg gtctagagtg ggtctcatct attacagtc ttggtacttc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300
 aggaagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 783
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 783
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat gaggatgaga tgacgtgggt cgcgcaggct 120
 ccaggaagg gtctagagtg ggtctcaacg attactagtg agggtagtgg gacatactac 180
 gcagactccg taaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctaata 300
 ggtaagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 784
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 784
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttct gattatgaga tggttggggt cgcgcaggct 120
 ccaggaagg gtctggagtg ggtctcaact attactagtg agggtcattc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggg 300
 acttcgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 785
 <211> 348

<212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 785
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttagt gattatgaga tgagttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg attgattctg atggtagttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300
 gtgaagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 786
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 786
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttaag gattatgaga tgacttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct atttcttcta ctggtcagtc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300
 aataagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 787
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 787
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttctt gattatggta tggcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagct atttgcctc ttggtcttag tacatactac 180
 gcagactccg tgaagagccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagggtg 300
 aggggtgggta ggggtgttca tcctccgaag tttgactact ggggtcaggg aaccctgggc 360

accgtctcga gc

372

<210> 788
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 788
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat ttgtatgaga tgacttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attactagtg atggtgtttc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggg 300
 gtgatttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 789
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 789
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag aattatgcta tgcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaacg attgctccgc tgggtgttcc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaagaag 300
 gttggggcgt ggctgcagtc gcggagtttt gactactggg gtcagggaac cctggtcacc 360
 gtctcgagc 369

<210> 790
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 790
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttatg gattatgaga tgcattgggt ccgccaggct 120

20089600.txt

ccaggggaagg gtctagagtg ggtctcaacg attggtgctt ctggtcatta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatctt	300
gatatgctgc tgtttgggtt tgactactgg ggtcagggaa ccttggtcac cgtctcgagc	360

<210> 791
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 791	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct gagtatgaga tgatgtgggc ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcacgt attgctggta atggttctcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gataatgctt	300
tctcattttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 792
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 792	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttat aattatgata tgagttgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attgattcga tgggtcttgt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggctt	300
aatgcgagtg attgggttgt ttttgactac tggggtcagg gaaccctggg caccgtctcg	360
agc	363

<210> 793
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 793
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgcg tcgtatcata tgacttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg attgcggata cgggtgatcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaata acagcctgcg tgccgaggac actgcggtat attactgtgc gaaattgcgt      300
gggatggctc gggtttgggg gtttgactac tggggtcagg gaaccctggg caccgtctcg      360
agc                                                                    363

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<210> 794
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 794
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt tattatgata tgatgtgggt ccgccaggct      120
ccaggaagg gtctagagtg gatctcatct atttcggatc gtggtcttca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatttacg      300
gagattccgt tggattgggt ggaggtgttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                                                369

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<210> 795
<211> 366
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 795
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg agttataaga tgttgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg attactaatt ctggtactga gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgatg      300
tatccggatt tggagattgt gcattttgac tactgggggc aggaaccct ggtcaccgtc      360
tcgagc                                                                    366

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<210> 796
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 796
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
 tcctgtgcag cctccggatt cacctttgag acttatcgta tgagttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagct attgatcagg agggttctgc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatagt 300
 gggacgaggc cggggcttcg gtttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 797
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 797
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgccctc 60
 tcctgtgcag cctccggatt cacctttagt agttatgata tgctttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcacgg attgatgcga gtggttattt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaattgttg 300
 aagctgtcgt tgaatcctaa ttttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 798
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 798
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
 tcctgtgcag cctccggatt cacctttagc agctatgcca tgagctgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcatcg attcataata ctggtttgtc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggact	300
cagcatcggtt ttgttggttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 799
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 799	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag ggttatccta tgtcgtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaact attagtcctt tgggtcctga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaactgttg	300
atggggggagt atttgaattc taggacgttt gactactggg gtcagggaac cctgggtcacc	360
gtctcgagc	369

<210> 800
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 800	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat acgtatagta tgtcttgggt ccgccaggct	120
ccaggggaagg gtctggagtg ggtctcatgg attgatgctg atggttgggt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactggg	300
catacgtttg actactgggg tcaggaacc ctgggtcacc tctcgagc	348

<210> 801
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 801
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttacg gatggggaga tgggttgggc ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagg attgtggatc ctggtgattc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt      300
gatcagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 802
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 802
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttcct gagtatgaga tgaagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaact attactccgt cgggtgggtca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gatacctctt      300
tctagttttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348

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<210> 803
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 803
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt caccttttct aattatgtga tgatttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcactt attaatggtg ctggtgatat gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggggggt      300
gcgcgttcgt ttgggggttc gcctaatttt gactactggg gtcaggggaac cctggtcacc      360
gtctcgagc      369

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<210> 804
<211> 348

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<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 804
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttacg gatggggaga tgggttgggc ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaagg attgtggatc ctggtgattc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt 300
gatcagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 805
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 805
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgtag cctccggatt cacctttacg ctgtataata tgtcttgggt ccgccaggct 120
ccagggaagg gtctggagtg ggtctcagtt atttctagta agggtgatag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaacgagt 300
agtgtttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 806
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 806
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag gcgtattata tgagttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggt attgttaata atggtttgtt gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcggct 300
gttcacccctt cgtatagggc ggagttgttc gactactggg gtcagggaac cctggtcacc 360

gtctcgagc

369

<210> 807
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 807
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttagt tcgtatgaga tggcgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcacgt attgagcctg atggtagtaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtccg 300
 gataatttta ctatgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 808
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 808
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat aagtatatga tgggggtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attgatagtc ttggtcatta tacatactac 180
 gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcggag 300
 tttccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 809
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 809
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag aggtatgaga tgacgtgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
 actgagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 810
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 810
 gaggtgcagc tggttgagtc tgggggaggc atggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
 actgagtttg actactgggg tcaggaacc caggtcaccg tctcgagc 348

<210> 811
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 811
 gaggtgcagc tggttgagtc tgggggaggc atggtgcagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
 actgagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 812
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 812
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgcaaggct	120
ccaggaagg gtctggagt ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccgagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt	300
actgagtttg actattgggg tcagggtacc ctggtcaccg tctcgagc	348

<210> 813
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 813	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaccggttt	300
actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 814
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 814	
gaggtgcagc tggtggagtc ggggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcgtgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat	240
ctacagatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaccggttt	300
actgagcttg actactgggg tcatggaacc ctggtcaccg tctcgagc	348

<210> 815
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 815
gaggtgcagc tgttggagtc tgggggaggc ttggtacggc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat atttctgtgc agatccgttt      300
actgagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 816
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 816
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cgcctttaag aggtatgaga tgacatgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcatatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt      300
actgagattg actactgggg tcaggaacc ctggtcaccg tctcgagc      348

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<210> 817
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 817
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cccctttaag aggtatgaga tgacgtgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt      300
actgagtttg actaccgggc tcaggaacc ctggtcaccg tctcgagc      348

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<210> 818
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 818

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttaag aggtatgaga tgcgtgggt ccgccaggct	120
ccagggaagg gtctggagt ggtctcttct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt	300
actgagattg actactgggg tcagggaacc caggtcaccg tctcgagc	348

<210> 819

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 819

gaggtgcagc tggttgagtc tgggggaggc ttggtacatc ctgggggggc cctgcgtctc	60
tcctgtgcag cttccgatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct	120
ccagggaagg gtctggagt ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgacgaggat accgcggtat attactgtgc ggaaccgttt	300
actgagtttg actacggggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 820

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 820

gaggtgcagc tggttgagtc tgggggaggc tgggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag ctcaggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct	120
ccagggaagg gtctggagt ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt	300
actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 821
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 821
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atgggtcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
 actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 822
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 822
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttaag aggtatgaga tgacgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atgggtcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cactctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
 actgagattg actaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 823
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 823
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt cacctttaag aagtatgaga tgatgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atgggtcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300

actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 824
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 824
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaac agctatgaga tgatgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
 actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 825
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 825
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgag tgccgaggat accgcggtat attactgtgc ggatccattt 300
 actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 826
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 826
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggacccgttc 300
 acggagatgg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 827
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 827
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggacccgttc 300
 acggagtctg actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 828
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 828
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta 60
 tcctgtgcag cctccgatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggagccgttc 300
 acggagttag actactgggg tcatggaacc ctggtcaccg tctcgagc 348

<210> 829
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 829
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggcc	120
ccaggaagg gtctggagt ggtctcatcg atttcgtccg acggttcctt cacgtactac	180
gccgagtcgg tcaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt	300
actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc	348

<210> 830
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 830	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaac acgtatgaga tgcagtgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcatct atttcgtcgg atggttcctt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt	300
actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc	348

<210> 831
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 831	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaac aagtatgaga tgatgtgggc ccgccaggct	120
ccaggaagg gtctggagt ggtctcatct atttcgtcgg atggttcctt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt	300
actgagtttg actactgggg tcatggaacc ctggtcaccg tctcgagc	348

<210> 832
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 832
gaggtgcagc tgtcggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct      120
ccaggggaagg gtctggagtg ggtctcatct atttcgtcgg atgggttcttt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa tacgctgtat      240
ctgcaaataga acagcctgcg tgccgaggat accgcggtat attactgtgc ggatccgttt      300
actgagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 833
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 833
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccagact      120
ccaggggaagg gtctggagtg ggtctcatct atttcgtcgg atgggttcttt tacatactac      180
gcagactccg tgaaggggagc gttcaccatc tcccgcgaca attccaagaa cagcgtgtat      240
ctgcaaataga acagcctgcg tgccgaggat accgcagtat attactgtgc ggaaccgttt      300
actgagtttg actactgggg tcaggaacc ctggtcaccg tctcaagc                      348

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<210> 834
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 834
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct      120
ccaggggaagg gtctggagtg ggtctcatct atttcgtcgg atgggttcttt tacatactac      180
gcagactccg tgaaggggagc gttcaccatc tcccgcgaca attccaagaa cagcgtgtat      240
ctggaaataga acagcatgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt      300
actgagtttg acaactgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 835
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 835

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc agaaccgttt	300
actgagtttg actactgggg tcagggaacc caggtcaccg tctcgagc	348

<210> 836

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 836

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt caactttaag aggtatgaga tgacgtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc agaccgttt	300
actgagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 837

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 837

gaggtgcagc tggttgagtc tgggggagac ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgatgtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatct atttcgtcgg atggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcacgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt	300
actgagtttg actacagggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 838
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 838
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttaag aggtatgaga tgtcgtgggt ccgccaggct 120
ccaggaagg gtctggagtg ggtctcatct atttcgtcgg atgggttcttt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaccgttt 300
actgagtttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 839
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 839
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttgag gcgtatccta tgtcgtgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaagt atttcccctc ttggttttgtg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttagt 300
gctggggcgg agactcatgt ttatcggtt tttgactact ggggtcaggg aaccctggtc 360
accgtctcga gc 372

<210> 840
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 840
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttggt aattatgaga tgatgtgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcatct attggggtgt tgggtcatac gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

20089600.txt

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttatg	300
tcgttgagga cgtttgagaa tctttttgac tactgggggtc agggaaccct ggtcaccgtc	360
tcgagc	366

<210> 841
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 841	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttacg aagtatccta tggcttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attgatgcta atggtaatag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggact	300
tggcgtaggc attttgcgat ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 842
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 842	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat ctgtatgata tgatgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatct atttctgacg tgggtacgct tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatggt	300
tttaggggta cgagtaatga tcgtaggttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 843
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 843
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact ggtggggata tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaatg attgaggggtg gtggtgtgac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacttgat      300
cttcggacgg gtcagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc      357

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<210> 844
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 844
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg      300
gacctaacta agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc      354

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<210> 845
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 845
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcatctc      60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat atttctgtgc ggatccgtcg      300
gacctaacta agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc      354

```

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<210> 846
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 846

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc	60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttggtt cgcaggct	120
ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgtaga attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgctc	300
gacctaacta agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 847

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 847

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc	60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttggtt cgcaggct	120
ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgtaga attccaagaa cagctgtat	240
ctgcaaatga gcagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgctc	300
gacctaacta agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 848

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 848

gaggtgcagc tggttgagtc tgggggtggc ttggtacagc ctgggggggc cctgcgctctc	60
tcctgtgcag cctccggatt caccttcccg gcttatacta tgggttggtt cgcaggct	120
ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgtaga attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg	300
gacctaacta tggttgacta ctgggggtcag ggaacccttg tcaccgtctc gagg	354

<210> 849
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 849
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt caccttttcg gcttatacta tgggctgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctctctt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300
 gatcctacta tgtttgtcta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 850
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 850
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag catccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgtaga attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtca 300
 gatcctacta tgtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 851
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 851
 gaggtgcagc tggttgagtc tggggggggc atggtacagc ctgggggggc cctgctcttc 60
 tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcatgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg 300

gaccta acttggacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 852
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 852
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtcacactt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg 300
 gaccta acttggacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 853
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 853
 gaggtgcagc tggtggagtc tgggggaggc ttggtgcagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttacg gcttatacta tgggttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacactgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgcgc ggaaccgtcg 300
 gaccta agttagacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 854
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 854
 gaggtgcagc gtctggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 acctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180

20089600.txt

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgtcg 300
 gatcctacta agtttgtcta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 855
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 855
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc agatccgtcg 300
 gatcctacta agtttgtcta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 856
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 856
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt caccttttcg gcttatacta tgggttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgcgc ggaaccgtcg 300
 gatcctacta agtttgtcta ctgggggtcag ggaaccccg tcaccgtctc gagg 354

<210> 857
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 857
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

20089600.txt

tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcgctt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa catgctgtat	240
ctgcaaatga aaagcctgcg tgccgaggac accgcggtat attactgcg ggatccgctcg	300
gacccacta agtttgtcta ctgggggtcaa ggaaccagg tcaccgtctc gagg	354

<210> 858
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 858	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcactt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc ttcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggatccgctcg	300
gacccacta agtttgtcta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 859
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 859	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg gattatacta tgggttgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcactt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgctcg	300
gacccacta agttcgacta ctgggggtcgg ggaaccctgg tcaccgtctc gagg	354

<210> 860
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 860
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcc      300
gacctaata agtttgtcta ctgggggtcag ggaaccctgg tcaccgtctc gagg          354

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<210> 861
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 861
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcactt attggggatc gtggtacttg gacatattac      180
gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacactgtat      240
ctgcaaatga acagcctgcg tgccgaggac actgcggtat attattgtgc ggatccgtcg      300
gacctaata agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg          354

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<210> 862
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 862
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac      180
gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg      300
gacctaata agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg          354

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<210> 863
<211> 354
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 863

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg gcttatacta tgggttgggt ccgccaggct	120
ccagggatgg gtctggagtg ggtctcactt attggggatc gtggttcttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgtcg	300
gacctaacta agtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 864

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 864

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc cgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aattataaga tgtattgggt ccgccaggct	120
ccaggggaagg gtctggagtg ggtctcaagt atttcggaga taggtaatct gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatagctctg	300
acgcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 865

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 865

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgcg agttatcgta tgtattgggt ccgccaggct	120
ccaggggaagg gtctggagtg ggtctcatat attgatccgc cgggtagtcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtttg	300
aatttgtcgt ttccttatat taattttgac tactgggggc aggaaccct ggtcaccgtc	360
tcgagc	366

<210> 866
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 866
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag cggtatgaga tgctgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcacgt atttctcatt cgggtcggac gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaattggat 300
 ggtccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 867
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 867
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag aggtattata tggattgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagg attaatacata atggttctgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaatgccg 300
 cagggacttt ctgattggta ttattttgac tactgggggc agggaaccct ggtcaccgtc 360
 tcgagc 366

<210> 868
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 868
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttct aagtatgata tgtcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact attctggagg atggtctgac tacatactac 180

20089600.txt

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggg 300
 cgtttgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 869
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 869
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt caccttttcg gattatccta tgacgtgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcaact attctgtctc cgggtacgga gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgag 300
 aaggattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 870
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 870
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttgag ggtggtgaga tgggttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaatg attccgatgg atggtagtgc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt 300
 gaggtgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 871
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 871
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccgatt cacctttagg gagtatacata tgaagtgggc ccgccaggct	120
ccaggaagg gtctagagt ggtctcagg attagtaggg atggtatgaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatacagctt	300
gctttgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 872
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 872	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgcctc	60
tcctgtgcag cctccgatt cacctttcgt gattatgaga tgctttgggc ccgccaggct	120
ccaggaagg gtctagagt ggtctcagg attcttccgt cgggtggggc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggt	300
tcggggaatg ggcctattct ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 873
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 873	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttaag gagcatgata tgttttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcagg attggggctg aggggtgtttg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaccgacg	300
atgtctaag gttctcagtc gcgttttgac tactgggggc aggaaccct ggtcaccgctc	360
tcgagc	366

<210> 874
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 874

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 875

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 875

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtttcaggt attactgagg atggtaatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 876

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 876

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc ccttcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagcgtgtat	240
ctgcaaatga acaacctgcg tgccgaagac accgcggtat attactgtgc gaaaattcgt	300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctgggtcacc 360
gtctcgagc 369

<210> 877
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 877
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct 120
ccaggaagg gtctagagt ggtctcaggt attactgagg atggtaatcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tccgcgaca atttcaagaa cacgctgtat 240
ctgcagatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctgggtcacc 360
gtctcgagc 369

<210> 878
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 878
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcaggt attactgagg atggtaatcg tacatactac 180
gcagattccg tgaagggccg gttcaccatc tccgcgaca atttcatgaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300
aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcaggggaac cctgggtcacc 360
gtctcgagc 369

<210> 879
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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```
<400> 879
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cttgcgtctc      60
tcctgtgcag cctccggatt cacctttgat aacactgaga tggcttggat ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt      300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
```

```
<210> 880
<211> 369
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 880
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccgggtt cacctttgat aatactgaga tggcttggat ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gaaaattcgt      300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
```

```
<210> 881
<211> 369
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
```

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<400> 881
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc cagggggggtc cctgcgtctc      60
tcctgtgcag cctctggatt cacctttgat aatactgaga tggcttggat ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cgcgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt      300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtctgggaac cctggtcacc      360
gtctcgagc                                     369
```

<210> 882
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 882
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120
 ccaggggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300
 aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcagggaac cctggtcacc 360
 gtctcgagc 369

<210> 883
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 883
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat aatactgaga tggcctggat ccgccaggct 120
 ccaggggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa caggctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300
 aatctgcatt gggatgtggg gaggcagttt gactactggg gtcagggcac cctggtcacc 360
 gtttcgagc 369

<210> 884
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 884
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120
 ccaggggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat atcactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctcgtcacc	360
gtctcgagc	369

<210> 885
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 885	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgagggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctggtcacc	360
gtctcgagc	369

<210> 886
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 886	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcaggt attagtgagg atggtaatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgcagaggac tccgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcaggggaac cctggtcacc	360
gtctcgagc	369

<210> 887
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 887

gaggtgcagc tgttggagtc tgggggaggc ttggtagagc ctgggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

cctgggaagg gtctcgagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga gcagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctggtcacc 360

gtctcgagc 369

<210> 888

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 888

gaggtgcagc tgttggagtc tgggggaggc ctggtacagc ctgggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcaggt attagtgagg atggtaatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat atcactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctggtcacc 360

gtctcgagc 369

<210> 889

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 889

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcaggt attactgagg atggtaatcg tacatactac 180

gctgactccg tgaagggccg gttcatcatc tcccgcgaca attccaagaa cacgctgaat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300

aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaac cctggtcacc 360

gtctcgagc

369

<210> 890
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 890
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct 120
 ccaggaggagg gtctagagtg ggtctcaggt gttactgagg atggtaatcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt 300
 aatctgcatt gggatgtggg gaggcaattt gactactggg gtcaggggaa cctgggtcacc 360
 gtctcgagc 369

<210> 891
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 891
 gaggtgcagc tggttgagtc agggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgaag cctccggatt cacctttgat aatactgaga tggcttggat ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaggt attattgagg atggtaatcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attattgtgc gaaaattcgt 300
 aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggggaa cctgggtcacc 360
 gtctcgagt 369

<210> 892
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 892
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttggat cgcaggct	120
ccaggaagg gtctagagt ggtctcagg attactgagg atggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagag ctgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggaac cctggtcacc	360
gtctccagc	369

<210> 893
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 893	
gaggtgcagc tggtggagtc tgggggaggc tcggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatactgaga tggcttgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcagg attactgagg atggtaatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cactctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gtctactggg gtcaggaac cctggtcacc	360
gtctcgagc	369

<210> 894
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 894	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg tcggtgaga tggggtgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcagg atttcaggc ctggtcagg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaattcgt	300
aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggaac cctggtcacc	360
gtctcgagc	369

<210> 895
 <211> 357

<212> DNA
 <213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 895
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttgat gatggtacta tgggggtgggc ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcactt attttgccgt cgggtagtcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacattcg 300
 ctgactaatc gtccgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 896

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 896
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttagt aagtatgata tgcggtgggc ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagat attgatgctg ttggtactcg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gataccgggg 300
 gggacgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 897

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 897
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctgtctc 60
 tcctgtgcag cctccggatt cacctttgag atgtatggta tgatgtgggc ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct attgaggggtg cgggtcatgc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac actgcggtat attactgtgc gatagtgtctt 300
 ggtatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 898
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 898
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctcgggatt cacctttttg cagtatccga tgggttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact atttctcctg ttggtttgac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaattgttt 300
 gaggggtcga ggattcagcg tgatgtgggt tttgactact ggggtcaggg aaccctggtc 360
 accgtctcga gc 372

<210> 899
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 899
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag aagtatcaga tgggttgggc ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatcg attcgggggt ctggtcttgt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgc 300
 actacgctgc atacggaggt gattgggttt gactactggg gtcaggggaac cctggtcacc 360
 gtctcgagc 369

<210> 900
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 900
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc cggggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttagt cagtatacga tgtattgggc ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcagag atttctcata gtggttctaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatcgggg	300
ctgcattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 901
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 901 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg gattatgcga tggcttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcacgt attggtgtgg aggggtgggga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgttg	300
cggctttatc gtctgggggt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 902
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 902 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct aagtatgata tgacgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaaag attaatcttg atggttgtct tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg	300
catggtaggg ggtttggtat ttttgactac tggggtcagg gaaccctggg caccgtctcg	360
agc	363

<210> 903
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 903
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg cggtatgata tgggtgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcacgg attaattcta tgggtctggc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagattat      300
tcggttgcg cgcatgggta tcctttgggt ttgactact ggggtcaggg aaccctggtc      360
accgtctcga gc                                                              372

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<210> 904
<211> 366
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 904
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaag gattattcga tgatgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaacg attactgata atggtacgtc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatatg      300
tcgcttgcta cttatctgca gttttttgac tactgggggc agggaaccct ggtcaccgtc      360
tcgagc                                                                      366

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<210> 905
<211> 369
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 905
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttatg gagtatgata tgctttgggt ccgccaggct      120
ccaggaagg ctctagagtg ggtctcacgt atttcgctcg atggtctttg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg      300
agtgcgcttg ctcttttga tattggtttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                                                  369

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<210> 906
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 906
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag gagtataata tggcttgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcaagt attaattttg ctggtcggac gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactgtct 300
 cttccttttg atattttttc ttttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 907
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 907
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300
 ggattattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 908
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 908
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct 120
 ccagggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240
 ctgcgaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300
 gggtattatg aatactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 909
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 909
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60
 tcctgtgcag cctccgatt cacctttggt gattatggta tgaattgggt ccgccaggct 120
 ccaggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300
 gggtattttg aatactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 910
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 910
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccgatt cacctttggt gattatggta tgaattgggt ccgccaggcc 120
 ccaggaagg gtctggagtg ggtctcacat atttcttcta atggtcgttt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt 300
 agttattttg aatactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 911
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 911
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tcctgtgcag cctccgggtt cacctttggt gattatggta tgaattgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcacat atttcttcta atggtcgttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgttt	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt	300
ggttattatg agtactgggg tcatggaacc ctggtcaccg tctcgagc	348

<210> 912
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 912	
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgcgtctc	60
tcctgtgctg cctccggatt cgcctttggt gattatggta tgaattgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcacat atttcttcta atggtcgttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt	300
ggttattttg aatactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 913
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 913	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggt gattatggta tgaattgggt ccgccaggct	120
ccaggaagg gtctggagt ggtctcacat atttcttcta atggtcgttt tatatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaactagt	300
ggttactttg aatactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 914
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 914
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagg gagtatgtta tgggggtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact attaatgggt tgggtaatgt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca ataccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggag accgcggtat attactgtgc gatacagctg      300
cctaattttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348

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<210> 915
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 915
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt aatgatggga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcattt attaatgttg atggtaggga gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaatggtct      300
cctgggcggg ttcagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc        357

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<210> 916
<211> 357
<212> DNA
<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

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<400> 916
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt ggttgggata tggcgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaagt attgctcatg aggggtggtga gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatgtt      300
cctgggtctc ctctgtttga ctactggggg cagagaaccc tggtcaccgt ctcgagc        357

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<210> 917
<211> 348
<212> DNA
<213> Artificial Sequence

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<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 917

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat cagggttgga tgtattgggt cgcaggct	120
ccagggaagg gtctagagtg ggtctcagg attggttcga atggctctcg gacatcctac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgggg	300
gagtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 918

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 918

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagg cagagtata tgtggtgggt cgcaggct	120
ccagggaagg gtctagagtg ggtctcagtt attggttaata atggtgagtt tacatactac	180
gcagactcgg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagataat	300
tggctgttgt ttgactactg gggtcaggga accctggtca ccgtctcgag c	351

<210> 919

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 919

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat ctagtacta tgtattgggt cgcaggct	120
ccagggaagg gtctagagtg ggtctcaact attggtgggg atggtagtca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc ggaaggtagc	300
cagtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 920
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 920
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttcg gcgtatacga tggagtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaagt attggggtta cgggttatga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaaggtggt 300
 cagggttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 921
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 921
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg gattatggga tgtcttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatat attgatcctc tgggtcgtct tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc ggaagatttg 300
 tcgtcgtgc agtatgggt gtcgcctaatt ttgactact ggggtcaggg aaccctggtc 360
 accgtctcga gc 372

<210> 922
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 922
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttttt cattattcta tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatct attggtccgg ttggtcggga gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaatgatt	300
cagtcgccgt tgtttaagga ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 923
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 923	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag tggtatgata tgtattgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcacgt attgatagtg ggggtaatca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga atagcctgcg tgccgaggac accgcggtat attactgtgc ggaagcgtcg	300
ctttggaagt ggaggttggt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 924
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 924	
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag gagtatggta tggcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaact atttctccgc tgggtatttc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatgct	300
acgtctcagg agtctttgcg gtcttttgac tactggggtc agggaaccct ggtcaccgtc	360
tcgagc	366

<210> 925
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 925
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttagt aagtatgaga tgatgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggctct      300
ctgcctgatg cgttttggac taggggtttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
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<210> 926
<211> 363
<212> DNA
<213> Artificial Sequence
```

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 926
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttggt acttattcta tggcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaact attgatcggc atggtttggc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactcct      300
ggttcttctt ggagactgt ttttggctac tggggtcagg gaaccctggt caccgtctcg      360
agc                                     363
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<210> 927
<211> 363
<212> DNA
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"
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<400> 927
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgctctc      60
tcctgtgcag cctccggatt cacctttgag tcgtatccta tgggttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attgatcatc atggtcattc gacatactac      180
gcagactccg cgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgctt      300
agggtttcga tgatttttgg ttttgactac tggggtcagg gaaccctggt caccgtctcg      360
agc                                     363
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<210> 928
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 928
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgtg cagtatggga tgagttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatgg attagtagta gtggtacgta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctacg tgccgaggac accgcggtat attactgtgc ggaaacgtct 300
 aggatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 929
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 929
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcgg cctccggatt cacctttcgg gagtatgata tgggttggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcactt atttcgcctc ctggtcgtac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagttgtg 300
 attctgggtt atacgaatag gtttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 930
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 930
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcct aattacggga tggttggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatcg attaattctt cgggtatgga gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatttttt 300
 cgtctgaatg atcataattc tgtgttttgg tttgactact ggggtcaggg aaccctggtc 360
 accgtctcga gc 372

<210> 931
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 931
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaag gattataaga tgatgtggat ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatcg attgttgggt ctggttcgat gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcct 300
 gggtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 932
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 932
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcat aattatgcta tgggggtgggt ccgccgggct 120
 ccagggaagg gtctagagtg ggtctcaagt attgatgagc atggtactat tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagt 300
 ctggatcggg tttggatttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 933
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 933
 gaggtgcagc tgttggagtc tggggggggc ttggtacagc ctggggggtc cctgcgtctc 60

20089600.txt

tcctgtgcag cctccggatt cacctttgct gattatccga tgacttgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcaagt atttattctg cgggttctcc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaactttat	300
catcgggagc cgattctttt tgggtttgac tactgggggc agggaaccct ggtcaccgct	360
tcgagc	366

<210> 934
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 934	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag aggtatcaga tggcgtgggt cgcaggct	120
ccgggaagg gtctagagt ggtctcaacg attagttctg atggtggggg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctggt	300
catcggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 935
 <211> 357
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 935	
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggt tcttatacta tgatgtgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcagag attgatcgga cgggtgagcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacctggg	300
tttgcttctc ttccttttga ctactggggg caggaaccc tggtcaccgt ctcgagc	357

<210> 936
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 936

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccgatt cacctttacg gattatacta tgtattgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaaag atttctccga gtggctgttc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccaggat accgcggtat attactgtgc gaaagatccg	300
tttgggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 937

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 937

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccgatt cacctttgat gatgcggaga tgttttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcatct attgatgtc gtggtttgac gacatactac	180
gcagaccccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc ggaagcgacg	300
tcggctatgt atccttttga ctactggggg caggaaccc tggtcaccgt ctcgagc	357

<210> 938

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 938

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccgatt cacctttcgt gattatgata tgggttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaact atttctctc ttggtcattt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccaggat accgcggtat attactgtgc gaaatctggg	300
tttcatgagt atactgaggg gtttgactac tggggtcagg gaaccctggg caccgtctcg	360
agc	363

<210> 939
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 939
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat cgtgcgggta tggggtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcactg attgggcgtg gtggtgatat tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaaattcgt 300
 aatctgcatt gggatgtggg gaggcagttt gactactggg gtcaggaac cctggtcacc 360
 gtctcgagc 369

<210> 940
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 940
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt cgttatcaga tggcttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatct atttcttctg atggtggggg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaaccgtct 300
 cgtcggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 941
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 941
 gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtt cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag ttgtatccga tggcgtgggt ccgccaggct 120
 ccaggaagg gtctggagt ggtctcatcg atttctccgg ttggttttct gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggcat	300
gaggggtcgt atactccgcg gtcggctttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 942
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 942	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgtg gcgtatccta tggcgtgggt ccgccaggct	120
ccaggggaagg gtctggagtg ggtctcaact attgcgcctc tgggtggtaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacggccg	300
gaggggctgc agattgattc tcagaatttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 943
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 943	
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgcg ttgtatcaga tggcttgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcatcg attgattctt ctggtagtga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctgag	300
cgtgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 944
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 944
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgctctc 60
tcctgtgcag cctccggatt caccttttagg cagtaccaga tgggttgggc ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaacg attgcgctcg atggtgtttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggt 300
cgtgattttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 945
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 945
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttgag cagtatgata tgaggtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatgg attgatgagg cgggtcatga gacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg 300
gatgggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 946
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 946
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgctctc 60
tcctgtgcag cctccggatt cacctttggt gattatccga tgggttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaacg atttctacgg ggggtttttc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgcg 300
tattattatc ttagtcagat taagaatttt gactactggg gtcagggaac cctggtcacc 360
gtctcgagc 369

<210> 947
<211> 360
<212> DNA
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 947

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc	60
tcctgtgcag cctccggatt cacctttgat atttatggga tgacttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcaagt atttcgcctc ttggtcttgt tacatactac	180
gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaactgaag	300
gagcatgggg atgttccttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc	360

<210> 948

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 948

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc	60
tcctgtgcag cctccggatt cacctttgag ctttatccga tgagttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaact atttctccta cgggtttggt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttaag	300
aggagtggga agactgatga tactaatttt gactactggg gtcagggaac cctgggtcacc	360
gtctcgagc	369

<210> 949

<211> 348

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 949

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctcttc	60
tcctgtgcag cctccggatt cacctttcgg gagtatgata tgctgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaacg attgtggggg atggtaatgg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacaggat	300
cgtcagtttg actactgggg tcagggaacc ctgggtcacc tctcgagc	348

<210> 950
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 950
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gagtatggta tgagttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaacg atttcgccta ttggtgttac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatgct      300
tatgatcgga agtctaattt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc      360
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<210> 951
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 951
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgat cggtatgtga tgggtgtgggt ccgccaggct      120
ccagggaagg atctagagtg ggtctcaggt attactccga gtggtaggag gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagga cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgttg      300
gggcgtcatt ttgatcctct tctgccttcg tttgactact ggggtcaggg aaccctggtc      360
accgtctcga gc                                                                372
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<210> 952
 <211> 369
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 952
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gattatgcta tgagttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact attactccgg gtggtttttg gacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaataa acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaacgtct 300
 agtggggagt tgcagttggt tgaggatttt gactactggg gtcaggggaac cctggtcacc 360
 gtctcgagc 369

<210> 953
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 953
 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 Lys His Ser
 20 25 30

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

Tyr His Arg Ser Gln 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 Val Arg His Arg Pro Tyr
 85 90 95

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

<210> 954
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 954
 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 Ala Ile Gly His Arg
 20 25 30

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

Tyr His Arg Ser Lys 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 Val Ala Leu Phe Pro Tyr
85 90 95

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

<210> 955

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 955

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 His Ile Gly His His
20 25 30

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

Tyr His Arg Ser His 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 Ser Ala Thr Tyr Tyr Cys Gln Gln Trp Asp Arg Pro Pro Tyr
85 90 95

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

<210> 956

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 956

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 Ala Ile Gly His Arg
 20 25 30

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

Tyr His Arg Ser Lys 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 Val Arg Ala Val Pro Tyr
 85 90 95

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

<210> 957

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 957

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 Ala Ile Gly His Arg
 20 25 30

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

Tyr His Arg Ser Lys 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 Val Arg Phe Ser Pro Tyr
 85 90 95

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

<210> 958
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 958
 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 Ala Ile Gly His Arg
 20 25 30
 Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr His Arg Ser Lys 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 Ala Arg Pro Val
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 959
 <211> 108
 <212> PRT
 <213> Artificial Sequence

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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 Asn His Arg
 20 25 30
 Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr His Arg Ser Arg 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
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65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Lys Val Arg Pro Asn

85 90 95

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

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<210> 960
<211> 108
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<220>  
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polypeptide"
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<400> 960
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 Ala Ile Gly His Arg
20 25 30

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

Tyr His Arg Ser Lys 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 Ser Pro His
85 90 95

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

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<210> 961
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>  
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<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 961
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 Ala Ile Gly His Arg
20 25 30

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

Tyr His Arg Ser Lys 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 Arg Ala Val Arg Pro Phe
85 90 95

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

<210> 962
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 962
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 Ala Ile Gly His Arg
20 25 30

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

Tyr His Arg Ser Lys 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 Tyr Arg Pro Leu
85 90 95

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

<210> 963
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 963

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

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

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

Tyr Ala Gly Ser Ile 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 Ser Ile Arg Pro Tyr
 85 90 95

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

<210> 964

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
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<400> 964

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 Pro Ile Gly Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile 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 Tyr Trp Ala Phe Pro Val
 85 90 95

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

<210> 965
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 965
 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 Pro Ile Gly Pro Asp
 20 25 30

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

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

Ser Glu 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 Trp Ala Phe Pro Val
 85 90 95

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

<210> 966
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 966
 Asp Ile Gln Ile 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 Pro Ile Gly Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile Leu Arg 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 Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
85 90 95

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

<210> 967

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 967

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 Pro Ile Gly Pro Asp
20 25 30

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

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

Arg 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 Trp Ala Phe Pro Val
85 90 95

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

<210> 968

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 968

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 Pro Ile Gly Pro Asp
20 25 30

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

Tyr Gln Thr Ser Ile Leu Arg 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 Tyr Trp Thr Phe Pro Val
 85 90 95

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

<210> 969
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 969
 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 Pro Ile Gly Pro Asp
 20 25 30

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

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

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

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

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

<210> 970
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 970

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 Pro Ile Gly Pro Asp
20 25 30

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

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

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

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

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

<210> 971

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 971

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 Pro Ile Gly Pro Asp
20 25 30

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

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

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

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

Thr Phe Gly Arg Gly Thr Lys Val Val Ile Lys Arg
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<210> 972
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 972
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 Pro Ile Gly Pro Asp
20 25 30

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

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

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

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

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

<210> 973
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 973
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 Pro Ile Gly Pro Asp
20 25 30

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

Tyr Gln Thr Ser Ile Met Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 974
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 974
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Tyr Val Gly
1 5 10 15

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

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

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

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

Glu Asp Phe Ala Lys Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
85 90 95

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

<210> 975
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 975
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 Pro Ile Gly Pro Asp
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20

25

30

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

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

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

Val Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
 85 90 95

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

<210> 976

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 976

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 Pro Ile Gly Pro Asp
 20 25 30

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

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

Ser Glu 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 Trp Ala Phe Pro Val
 85 90 95

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

<210> 977

<211> 108

<212> PRT

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 977

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 Pro Ile Gly Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile 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 Tyr Trp Thr Phe Pro Val
 85 90 95

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

<210> 978

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 978

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 Pro Ile Asp Pro Asp
 20 25 30

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

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

Ser Gly 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 Gln Gln Tyr Trp Ala Phe Pro Val
 85 90 95

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

<210> 979
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 979
 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 Pro Ile Gly Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile Leu Arg 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 Tyr Trp Ala Phe Pro Val
 85 90 95

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

<210> 980
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 980
 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 Pro Ile Glu Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile 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 Tyr Trp Ala Ser Pro Val
85 90 95

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

<210> 981
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 981
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 Pro Ile Gly Pro Asp
20 25 30

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

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

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

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

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

<210> 982
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 982
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 Arg Ala Ser Gln Pro Ile Gly Pro Asp
20 25 30

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

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

Ser Glu 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 Trp Ala Phe Pro Val
85 90 95

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

<210> 983
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 983
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

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

Tyr Gln Thr Ser Ile Leu Arg 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 Ser Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ala Phe Pro Val
85 90 95

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

<210> 984
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 984

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 Pro Ile Gly Pro Asp
 20 25 30

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

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

Ser Gly Ser Val 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 Trp Ala Phe Pro Val
 85 90 95

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

<210> 985

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 985

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 Pro Ile Asp Pro Asp
 20 25 30

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

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

Ser Gly Ser Arg 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 Trp Ala Phe Pro Val
 85 90 95

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

<210> 986
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
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<400> 986
 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 Pro Ile Gly Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile 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 Gln Tyr Trp Ala Phe Pro Val
 85 90 95

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

<210> 987
 <211> 108
 <212> PRT
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<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 987
 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 Met Pro Ile Gly Pro Asp
 20 25 30

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

Tyr Gln Thr Ser Ile Leu Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
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Ser Glu 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 Trp Ala Phe Pro Val
 85 90 95

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

<210> 988

<211> 108

<212> PRT

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

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

Tyr Gly Gly Ser Glu Leu Gln Ser Gly Val Pro Pro 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 Cys Ile Ser Ser Pro Cys
 85 90 95

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

<210> 989

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Ile Gly Asp Ser
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Phe Ser Ser Ile 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 Tyr His Thr Ser Pro Thr
85 90 95

Thr Phe Gly Arg Gly Thr Lys Val Lys Ile Lys Arg
100 105

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20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ser Ser Gln 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 Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr His Gly Tyr Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 991
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Met Ile Asp Gln Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asn Ala Ser Trp 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 Tyr His Gly Tyr Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

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 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

His Tyr Gly Ser Val 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 Ser Ala Thr Tyr Tyr Cys Gln Gln Val His Gln Ala Pro Thr
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Asp Ser
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gly Ile Ser Glu 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 Ser Ala Thr Tyr Tyr Cys Gln Leu Ser Ser Ser Met Pro His
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 994
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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Glu Ile Glu Thr Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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Tyr Asp Ser Ser His 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 Tyr His Gln Asn Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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20 25 30

Leu Val Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Thr Glu 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 Gln Ser Lys Gly Pro Leu
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20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Met Gly Ser Tyr 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 Ile Tyr Ser Phe Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Phe Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg 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 His His Thr Arg Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Met Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Tyr 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 Tyr His Lys Leu Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Trp 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 Tyr His Lys Leu Pro Val
Page 501

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Glu Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser His 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 Tyr Ser Ser Tyr Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Asp Glu Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Lys Leu Leu Ile
35 40 45

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Tyr Ser Ala Ser Tyr 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 Arg Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Leu Leu Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asn Glu Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asn Ala Ser Met 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

Lys Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr His Thr Asn Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Page 503

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Leu	Glu	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	Leu	Leu	Ile	
Tyr	His 50	Ser	Ser	Glu	Leu	Gln 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly	
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80	
Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90	Tyr	His	Met	Ser	Pro 95	Val	
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20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Met Leu Leu Ile
35 40 45

Tyr Ser Ser Ser Asp 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 Tyr His Ser Leu Pro Val
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asp Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asn Ser Ser Phe Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Ala 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 His Ser Leu Pro Val
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 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ser Ser Gln 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 Tyr His His Leu Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Gly Ser Trp 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 Tyr Arg Trp Ile Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Leu 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 Tyr Ser Ser Leu Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Thr Thr Ser
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Met 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 Tyr Trp Val Thr Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile His Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Gly Ser Met 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 Tyr Ser Ala Asn Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile His Thr Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Gly Ser Met 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 Tyr Ser Val Ser Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Gly Ser Leu 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 Tyr His Leu His Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Thr Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Arg Ser Thr 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 Tyr Asp Ser Tyr Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asn Ala Ser Glu 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 Arg Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Gln Trp Pro Thr
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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 20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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40

45

Tyr Leu Ser Ser Arg 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 Leu Lys Lys Pro Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Lys Ile Lys Asn Arg
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Glu Val Ser His 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 Gly Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Arg Gln Ser Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp Ile Gly Glu Glu
20 25 30

Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Thr Leu Gln Ser Glu 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 His
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr Glu Trp Pro Tyr
85 90 95

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Ser Gly Gly
20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Thr Ser Met 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 Leu Tyr Ser Ala Pro Tyr
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<400> 1019
 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 Asp Ile Asp Gln Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asn Val Ser Leu 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 Tyr Ser Met Asn Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1020
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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Gln
 20 25 30

Leu Lys Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gln Ala Ser Gly 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 Tyr Asp Leu Arg Pro Gln
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1021
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<220>
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 polypeptide"

<400> 1021
 Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Lys Ile Ser Thr Ser
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ser Ser Trp 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 Tyr Glu Tyr Asn Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1022
 <211> 108
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1022
 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 Thr Ile Gly Glu Ser
 20 25 30

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Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Phe Ala Ser Leu 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 His His Met Leu Pro Ser
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1023
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1023
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 Phe Ile Gly Asp Ser
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Phe Ser Ser Ile 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 Tyr Met Asp Ile Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1024
<211> 108
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<220>
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<400> 1024

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 Asp Ile Asp His Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ser Ser Met 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 Tyr His Ser Ile Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1025

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1025

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 Gln Ile Glu Thr Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Gly Ser Trp 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 Tyr His Ser Leu Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1026
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1026
 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 Asp Ile Gly Asn Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr His Gly Ser Trp 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 Tyr Asp Phe Asn Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1027
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1027
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Cys Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Gly Leu
 20 25 30

Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Gly Ser Gly 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
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1028
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<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 1028
Asp Ile Gln Met Thr Gln Thr 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 Gly His Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asn Val Ser Trp 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 Tyr Ser His Asn Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1029
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<213> Artificial Sequence
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<220>  
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<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 1029
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 His Ile Glu Asn Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser His 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 Tyr His Leu Gln Pro Thr
 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1030
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1030
 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 Val Ile Glu Gly Ser
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr His Arg Ser Ile Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Arg 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 Gln Leu Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1031
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 1031

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 Arg Pro Ile Asn Gly Lys
 20 25 30

Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ala Phe Ala Ser Ala 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 Val Gln Gln Ala Val Tyr Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1032

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1032

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 Ala Ile Glu Thr Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Arg 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 His Tyr Gln Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1033
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1033
 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 Asp Ile Glu His Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Gln 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 Tyr Gln Gln Gln Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1034
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 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1034
 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 Ser Gln Ile Glu Glu Ser
 20 25 30

Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ala Asp Val Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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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 Ala Gln Gly Val Val Glu Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1035

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1035

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 Tyr Ile Gly Leu Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Trp 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 Tyr Phe Arg Gln Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1036

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1036

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 Thr Pro Ile Gly Thr Met
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gly His Ser Ser Trp 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 Gly Gln His Val Arg Pro Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1037

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1037

Asp Ile Gln Leu Thr Gln Ser Pro Thr Ser Leu Ser Ala Thr Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Pro Ile Gly Thr Met
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gly His Ser Ser Trp 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 Gly Gln His Val Arg His Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1038

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1038

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 Thr Pro Ile Gly Thr Met
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly His Ser Ser Trp 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 Gly Gln His Val Arg Pro Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
100 105

<210> 1039

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1039

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 Val Ser Thr Pro Ile Gly Thr Met
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Pro 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 Gly Gln His Val Arg Pro Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
Page 524

<210> 1040
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1040
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 Thr Pro Ile Gly Thr Met
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Cys 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 Gly Gln His Val Arg Pro Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1041
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1041
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 Thr Pro Ile Gly Thr Met
20 25 30

Ile Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly His Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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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 Gly Gln His Val Arg Pro Pro Ala
85 90 95

Thr Phe Gly Lys Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1042
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1042
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 Tyr Ile Asp Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Gly Ser Gln Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gln Val Val Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1043
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1043
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
Page 526

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Val Asp Ser Ser Gly 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 Gly Gln Asp Arg Trp Ser Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1044
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1044
 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 Ser Arg Ile Gln His Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gly Gly His Ser Gly 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 Ala Gln Ser Cys Ala Trp Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1045
 <211> 108
 <212> PRT
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<220>

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<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1045

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 Arg Gly Ile Asp Gly Asp
20 25 30

Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Ala Asp Ser Ser Leu 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 Gly Gln Gly Ala Val Arg Pro Met
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1046

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1046

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 Arg Gly Ile Asp Thr Asp
20 25 30

Leu Trp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Ala Asp Ser Ser Leu 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 Gly Gln Gly Ala Val Arg Pro Met
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1047
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1047
 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 Tyr Thr Ile Pro Val Ala
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ala Asp Ala Ser Leu 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 Ala Gln Gly Trp Pro Gly Pro Gln
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1048
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1048
 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 Ala Thr Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Thr Ser Met 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 Tyr Ser Tyr Asn Pro Ser
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1049
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1049
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 Val Pro Ile Thr Glu Gly
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gln Ala Asn Ser Trp 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 Gly Gln Trp Glu His Val Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1050
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1050
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 Arg Ala Ser Ser Met Ile Leu Tyr Gly
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Gly Thr Ser Ala 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 Gly Gln Trp Glu Thr Val Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1051
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1051
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 Pro Ile Asn Gly Leu
20 25 30

Leu Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Met 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 Leu Ala Arg Ile Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Gly Ile Lys Arg
100 105

<210> 1052
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1052

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 Leu Ile Arg Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gln Ser Ser Gln 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 Tyr Asn Ser Tyr Pro Asp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1053

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1053

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 Trp Ile Gly Asp Ser
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Phe Gly Ser Tyr 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 Tyr Leu His Thr Pro Ser
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1054
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1054
 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 Asp Ile Glu Ala Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr His Ser Ser Glu 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 Tyr Gly Phe Asn Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1055
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1055
 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 Ser Pro Ile Glu Tyr Gly
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gly Gly Gly Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
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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 Gly Gln Trp Glu Val Gln Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1056

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1056

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 Asp Thr Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ser Ser Gln 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 Tyr His Ser Ala Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1057

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1057

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 Arg Ala Ser Gly Trp Ile Gly Met Ser
20 25 30

Leu Glu Trp His Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Arg Gly 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 Ser Gln Ser Arg Trp Pro Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1058
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1058
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 Arg Asn Ile Ser Asn Ala
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Leu Gly Ala Ser Trp 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 Thr Gln Val Trp Asp Arg Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1059
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1059

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 Asp Ile Met Ser Ala
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Thr Ser Ile 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 Val Tyr Leu Leu Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1060

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1060

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 Glu Ile Gly Ile Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ser
 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 Ala Ser Asn Pro Pro
 85 90 95

Thr Phe Gly Arg Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1061
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1061
 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 Met Ile Gly Asp Trp
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Ser Ser Glu 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 Leu Tyr Phe Trp Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1062
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1062
 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 Ala Ile Glu Leu Asn
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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Tyr Asp Ala Ser Met 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 Tyr Asp Val Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1063

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1063

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 Ala Ile Glu His Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Met 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 Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ala Tyr Pro Pro
85 90 95

Thr Tyr Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1064

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1064

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 Arg Ala Ile Glu Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Phe
35 40 45

Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Gly 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 Leu Gln Tyr Asp Val Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1065
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1065
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Thr Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Met 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 Tyr Asp Ala Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1066
<211> 108
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1066

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 Ala Ile Glu His Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Arg 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 Asp Ala Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1067

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1067

Asp Ile Gln Met Asn Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu His Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Met 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 Tyr Asp Ala Tyr Pro Pro
Page 540

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1068
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1068
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 Ala Ile Glu Ser Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Met 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 Tyr Asp Val Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1069
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1069
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 Ala Ile Glu His Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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Tyr Asp Ala Ser Met 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 Tyr Asp Ala Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1070
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1070
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 Asp Glu Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Ser Ser Ser Trp 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 Tyr Phe Gln Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1071
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1071
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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1              5              10              15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Glu Asp
      20              25              30
Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
      35              40              45
Tyr Ser Ser Ser Trp 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 Tyr Phe Gln Tyr Pro Pro
      85              90              95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
      100              105

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<210> 1072
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<400> 1072
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 Asp Glu Asp
      20              25              30
Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
      35              40              45
Tyr Ser Ser Ser Trp 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 Tyr Ser Gln Tyr Pro Pro
      85              90              95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
      100              105

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<210> 1073
 <211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1073

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 Glu Glu Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Ser Ser Ser Trp 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 Tyr Phe Gln Tyr Pro Pro
 85 90 95

Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1074

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1074

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 Asp Glu Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Ser Ser Ser Trp 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 Phe Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1075
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1075
 Glu Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Ser Ile Asp Lys Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Ser Ser Ser Trp 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 Arg Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
 85 90 95

Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1076
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1076
 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 Asp Glu Asp
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Ser Ser Ser Trp 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 Ile Ala Thr Tyr Tyr Cys Lys Gln Tyr Ser Gln Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1077
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1077
Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Lys Asp
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Ser Ser Ser Trp 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

Glu Asp Phe Ala Thr Tyr His Cys Gln Gln Tyr Phe Gln Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1078
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1078

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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 Glu Tyr Ile Asn Ala Glu
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ser Ser Gly 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 Leu Gln Asn Ala Met Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1079

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1079

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 Leu Asp Ile Asn Asn Gly
20 25 30

Leu Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Leu Gly Ala Ser Gly 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 Ser Gln Val Arg Ser Arg Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1080

<211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1080
 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 Asp Ile Leu Ser Ala
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Gly Ser Ser Val 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 Asn Tyr Ser Leu Pro Ile
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1081
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1081
 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 Ser Pro Ile Glu Ser Tyr
 20 25 30
 Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Arg Tyr Val Ser Val 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 Gly Gln Trp Phe Arg Ala Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1082
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1082
 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 Val Ser Glu Ser Ile Asn Ala Glu
 20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ser Gly Phe Ser Gly 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 Val Gln Phe Ala Met Trp Pro Phe
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1083
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1083
 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 Met Met Ile Arg Phe Gly
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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Gly Gly Gly 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 Gly Gln His Glu Arg Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1084

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1084

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 Gly Thr Leu
 20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Thr Ser Val 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 Met Val Tyr Arg Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1085

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

20089600.txt

<400> 1085

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 Thr Ile Glu Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ser Ser Gln 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 Tyr Asp Lys Val Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1086

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1086

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 His His Ile Gln Arg Tyr
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Leu Trp Gly Ser Gln 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 Gly Gln Trp Trp Ala Pro Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1087
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1087
 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 His His Ile Gln Arg Tyr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Trp Gly Ser Gln 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 Gly Gln Trp Trp Ala Pro Pro Gln
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1088
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1088
 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 His Asp Ile Gln Arg Tyr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Trp Gly Ser Gln 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 Gly Gln Trp Trp Ala Pro Pro Gln
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1089
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1089
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 Tyr Ile Asp Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Gly Ser Leu 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 Gly Gln Gly Ala Val Val Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1090
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1090
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 Asp Ile Ala Phe Asp
20 25 30

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Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser 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 Leu Gln Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1091
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1091
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 Ala Thr Leu
20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Gly Ser Met 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 Met Trp Gln Arg Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1092
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1092

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 Pro Ile Val Asp Glu
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu 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 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Trp Ser Thr Tyr Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1093

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1093

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

Asp Gly Val Ser Gly 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 Gly Gln Asp Trp Asp Trp Pro Arg
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1094
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1094
 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 Arg Asn Ile Arg Asp Trp
 20 25 30
 Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Asp Trp Gly Ser Val 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 Ala Gln Thr Trp Asp Asp Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1095
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1095
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Arg Asp Trp
 20 25 30
 Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Asp Trp Gly Ser Glu 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
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65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Thr Trp Tyr Asp Pro Leu

85 90 95

Thr Phe Gly His Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1096
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 1096
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 Ile Asp Ile His Gly Gly
20 25 30

Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Val Gly Val Ser Gly 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 Asn Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Val Trp Arg Arg Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1097
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 1097
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 Asp Ile Gly Ser Ser
20 25 30

20089600.txt

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ser Ser Leu 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 Ala Leu Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1098
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1098
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 Gln Ile Glu Thr Asn
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Gly Ser Trp 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 Tyr Lys Tyr Leu Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1099
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 1099

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 Asp Ile Gly Ser Ala
 20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Gly Ser Asp 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 Gln Tyr Phe Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1100

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1100

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 Ala Ile Tyr Gly Gly
 20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gly Glu Ser Met 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 His Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr His Lys Pro Phe
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1101
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1101
 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 Gly Val Trp
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Gly Ser Phe 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 Phe Ser Ser Pro Ser
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1102
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1102
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Pro Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Asp Glu
 20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ser Ser Thr 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 Phe Gln Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1103
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1103
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 Ser Asn Ile Thr Gly Pro
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Pro Gly Trp Ser Thr 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 Gly Gln Val Trp Gly Glu Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1104
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1104
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 Arg Ile Ala Tyr Gly
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Gly Gly Arg Ser Gly 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 Val Gln Pro Gly Met Pro Pro Asp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1105
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1105
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 Lys Gln Ile Val Gly Gly
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Arg His Ser Gly 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 Val Gln Gly Val Trp Ala Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1106
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1106

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 Pro Ala Ile Ala Ala Lys
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Ala Asp Ser Gly 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 Gly Gln Leu Trp Ala Gly Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1107

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1107

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 Arg Thr Ile Ala Asp Gly
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Ala Tyr Ser Gly 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 Gly Gln Leu Trp Glu Gly Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

<210> 1108
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1108
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 Tyr Gly Phe
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Val 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 Leu Ala Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1109
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1109
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 Asp Ile Arg Asp Trp
20 25 30

Leu Met Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Gly Ser Phe 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 Leu Tyr Asp Thr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1110
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1110
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 Asn Thr Gly
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ser Ser Ala 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 Ser Tyr Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1111
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1111
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 Lys Ile Phe Gly Trp
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30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gly Thr Ser Lys 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 Val Tyr Ser Leu Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1112

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1112

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 Ser Asn Ile Gly Ala Asp
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gly Gly Ala Ser Gly 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 Gly Gln Leu Trp Asn Gly Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1113

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1113

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 Ser Pro Ile Tyr Asp Gly
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ser Gly Ala Ser Trp 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 Gly Gln Leu Trp Leu Gly Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gln
 100 105

<210> 1114

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1114

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 Ser Arg Ile Tyr Asn Gly
 20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Gly Gly Arg Ser Gly 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 Ala Gln Val Gly Glu Ala Pro Ser
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1115
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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Phe Ile Asn Glu Glu
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ser Trp Ser Ser Trp 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 Val Gln Pro Gly Gly Gly Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1116
 <211> 108
 <212> PRT
 <213> Artificial Sequence

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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asp Ile Leu Asp Glu
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Gly Gly Gly Ser Gly 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 Gly Gln Leu Trp His Gly Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1117
<211> 108
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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Pro Ile Tyr Thr Gly
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Gly Arg Ser Gly 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 Met Gln Val Gly Thr Ala Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1118
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<212> PRT
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Asp Ile Arg 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 Arg Ala Ser Gln Asn Ile Ser Arg Arg
20 25 30

Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ser Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Gly 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 Tyr Pro His
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1119
<211> 108
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20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Val Gly Ile Ser Gln 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 Gly Gln Leu Trp Ser Ala Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1120
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Ile Asp Gly Met
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Pro Gly Phe Ser Gly 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 Gly Gln Ser Val Glu Ala Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1121

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Tyr Ile Ala His Pro
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Pro Gly Ser Ser Val 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 Gly Gln Ser Val Val Val Pro Trp
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1122
 <211> 108
 <212> PRT
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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 Arg Thr Ile Glu Gly Gly
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Met Gly Gly Ser Gly 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 Gly Gln Leu Trp Val Gly Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1123
 <211> 108
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 <223> /note="Description of Artificial Sequence: Synthetic
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<400> 1123
 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 Lys Phe Ile Arg Asp Glu
 20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Gly Gly Ser Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
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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 Gly Gln Leu Trp Arg Ala Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1124
 <211> 108
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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 Lys Pro Ile Tyr Gly Gly
 20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Gly Gly Gly Ser Val 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 Gly Gln Val Trp Gly Gly Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1125
 <211> 108
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 <223> /note="Description of Artificial Sequence: Synthetic
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<400> 1125
 Asp Ile Arg 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 Arg Ala Ser Arg Pro Ile Ser Gly Cys
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Asp Gly Ala Ser Gly 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 Gly Gln Trp Trp Glu Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1126
<211> 108
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20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

His Gly Val Ser Thr 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 Gly Gln Leu Glu Ala Ala Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1127
<211> 108
<212> PRT
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asp Ile Gly Asp Trp
 20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Val Trp Ala Ser Val 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 Ala Gln Trp Gly Thr Pro Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1128

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Asn Arg Ile Glu Tyr Gly
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Ser Gly Ser Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ser
 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 Gly Gln Leu Glu Ala Ala Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1129
 <211> 108
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<220>
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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Gly His Phe
 20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Gly Gly 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 Gly Gln Leu Val Glu Pro Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1130
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1130
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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Ile Tyr Ser Asp
 20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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Asp Gly Trp Ser Gly 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 Gly Gln Leu His Arg Ala Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1131
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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Phe Ile Thr Asp Arg
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Gly Val Ser Gly 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 Gly Gln Ser Ser Glu Leu Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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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 Arg Lys Ile Gly Ser Glu
20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Gly Arg Ser Arg 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 Gly Gln Leu Trp Glu Pro Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1133
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polypeptide"

<400> 1133
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 Arg Asn Ile Gly Asn Gly
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Gly Glu Gly Ser Arg 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 Gly Gln Leu Trp His Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1134
<211> 108
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<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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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 Arg Asn Ile Tyr Gly Trp
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Gly Gly Trp Ser Gly 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 Ala Gln Asp Tyr Thr Leu Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1135

<211> 108

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Lys Asp Trp
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Phe Ala Ser Gly 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 Ser Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr
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Thr Ser Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1136
<211> 108
<212> PRT
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Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Leu Ile Ser Ser His
20 25 30

Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
35 40 45

Tyr Asp Ala Ser Glu 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 His Arg Ser Leu Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1137
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

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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 Trp Ile Gly Gly Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

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Tyr Gln Ile Ser Val Leu Gln Ser Gly Ile 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 Tyr Ile Arg Ser Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1138

<211> 108

<212> PRT

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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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 Gly Ala Ala
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Leu 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 Leu Phe Arg Leu Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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<210> 1139

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1139

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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Leu	Val	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	Leu	Leu	Ile				
Tyr	Gly 50	Ser	Ser	Ile	Leu	Gln 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly				
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Gln	Pro 80				
Glu	Asp	Phe	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90	Tyr	Ala	Glu	Ala	Pro 95	Ile				
Thr	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys	Arg								

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<223> /note="Description of Artificial Sequence: Synthetic
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<400> 1140
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 Gly Ser Ser
20 25 30

Leu Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile
35 40 45

Tyr Tyr Ser Ser Lys 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 Leu Ser Ser Pro Tyr
85 90 95

Thr Val Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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$\langle 210 \rangle$ 1141
 $\langle 211 \rangle$ 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1141

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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Glu
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Thr Ser Asn 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 Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Leu Glu Thr Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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<210> 1142

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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1142

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 Lys Ile Trp Asp Ala
 20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Arg Gly Ser Ile 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 Phe Tyr Arg Trp Pro His
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1143
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 polypeptide"

<400> 1143
 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 His Ile Glu Asp Ser
 20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Gly Ser Val 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 Met Tyr Lys Phe Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1144
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 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Asn Ser Ser
 20 25 30

Leu Leu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Thr Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg 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 Ile Trp Gly Ser Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1145
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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Pro Val Gly
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Ser Gly Ser Thr 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 Asp Trp Tyr Tyr Pro Asn
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1146
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 1146

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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 Pro Ile Tyr Gly Trp
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Thr Ser Gly 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 Ile His Ser Ser Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1147

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1147

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 Phe Ile Asp Thr Ser
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Gly Ser His 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 Leu Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Val Leu Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1148

<211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1148
 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 Asp Ile Gly Asp Ala
 20 25 30

Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Ser Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Gly 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 Arg His Ser Thr Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1149
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1149
 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 Asp Ile Asp Glu Ser
 20 25 30

Leu Met Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Val Ser Tyr 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 Arg Trp Lys Ala Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1150
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1150
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 Glu Ile Val Glu Asp
20 25 30

Leu Tyr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Ala Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Trp 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 Arg Arg Arg Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

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<210> 1151
<211> 108
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<400> 1151
 Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Pro Met
20 25 30

Leu Arg Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
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35

40

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Tyr Ala Gly Ser Ile 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 Leu Val Thr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1152

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1152

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 Asp Ala
 20 25 30

Leu Phe Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Tyr Gly Ser Val 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 Arg Phe Gln Glu Pro Val
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1153

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1153

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 Gln Ile Ser Asp Glu
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Val Ser Ile 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 Trp Leu Ser Phe Pro Ser
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 1154

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1154

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gagcaagtca gaatattaag cattcggttac ggtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctatcat cgttcccagt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcaacag gttaggcatc gtccttatac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1155

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1155

gacatccaga tgaccagtc tccatcctct ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcat cggccaagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag gttgctttgt ttccttatac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1156
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1156
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcatattggt catcatttaa ggtggtacca gcagaaacca 120
 gggaaagccc ccaagctcct gatctatcat aggtcccatt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattctg ctacgtacta ctgtcaacag tgggataggc cgccttatac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1157
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1157
 gacatccaga tgaccagtc cccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatcat cggccaagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag gtgcgggctg tgccttatac gtttggccaa 300
 gggaccaagg tggaaattaa acgg 324

<210> 1158
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1158

20089600.txt

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcat cgggtccaagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag gttcgttttt ctccttatac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                           324
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<210> 1159
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1159
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcat cgggtccaagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tcttatgcta ggctgtgac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                           324
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<210> 1160
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1160
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca aagtattaat cataggttat attggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcat cgggtccaggt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaggattttg ctacgtacta ctgtcaacag tataaggtta ggcctaatac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                           324
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<210> 1161
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1161
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatttatcat cgggtccaagt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag acttattcgt ctcctcatac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1162
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1162
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatcat cgggtccaagt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctacaacct 240
gaagattttg ctacgtacta ctgtcaacag agggcggtga ggccttttac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1163
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1163
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggctattggg catcggttac gttggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatcat cgggtccaagt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag acttattatc gtcctcttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1164
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1164

gacatccaga tgaccagtc tccagcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattgat cctatgttaa ggtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgcg ggttccattt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag actagtatta ggccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1165

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1165

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattggt cctgatattac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1166

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1166

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattggt cctgatatac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccatct tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1167
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1167
gacatccaga taaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcag acgtccatat tgcgaagtgg agtcccatca      180
cgtttcagtg gcagtgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagatcttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
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<210> 1168
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1168
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca      120
gggaaagccc ctaagcttct gatctatcag acgtccattt tgcgaagtgg ggtcccatca      180
cgtttcagtg gcagaggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
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<210> 1169
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1169
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca acctattggt cctgatttac tgtggtacca gcagaaacca      120
gggaaagccc ctaagctctt gatctatcag acgtccattt tgcgaagtgg ggtcccatca      180
cgtttcagtg gcagcggatc tgggactgat ttcactctca ccatcagcag tctgcaacct      240
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gaagattttg ctacgtacta ctgtcaacag tattggactt ttcctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1170
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1170
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300
 gggaccaagg tggtaatcaa acgg 324

<210> 1171
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1171
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagatcttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggcaaa 300
 gggaccaagg tggtaatcaa acgg 324

<210> 1172
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1172
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccga 300
 gggaccaagg tggtaatcaa acgg 324

<210> 1173
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1173
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gagcaagtca gcctattggt cctgatttac tgtggtaccg gcagaaacca 120
 gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg tgtcccatca 180
 cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300
 gggaccaagg tggtaatcaa acgg 324

<210> 1174
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1174
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatcag acgtccatta tgcgaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattggactt ttcctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1175
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1175

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat atgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattggc cctgatttac tttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgagacagat ttcaccctca ccatcagcaa tctgcaacct	240
gaagattttg ctaagtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tggatgatcaa acgg	324

<210> 1176
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1176	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattggc cctgatttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgagacagat ttcactctca ccatcagcaa tctgcaacct	240
gtagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tagtaatcaa acgg	324

<210> 1177
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1177	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattggc cctgatttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1178
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1178
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gcctatcggc cctgatttac tgtggtaccg gcagaaacca 120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tattggactt ttcctgtgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1179
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1179
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gcctattgat cctgacttac tgtggtacca gcagaaacca 120
ggtaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagtt ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tattgggcat ttcctgtgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1180
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1180
gacatccaga tgaccagtc tccatcctcc ctgtctgcat cagtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaagcca 120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1181
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1181

gacatccaga tgaccagtc tccatcatcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattgaa cctgatttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1182

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1182

gacatccaga tgaccagtc accatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggctagtca gcctattggt cctgatttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca	180
cgtttcagcg gcagtgaatc cgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagatattg caacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaggg tggaaatcaa acgg	324

<210> 1183

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1183

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccttca	180
cgtttcagtg gcagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1184
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1184
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcgcc      60
atcacttgcc gggcaagtca gcctatttgt cctgatatac tgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattctg ctacgtacta ctgtcaacag tattgggctt ttctgtgac gttcgggtcaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1185
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1185
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcctatttgt cctgatttac tgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcgaagtgg ggtcccgtca      180
cgtttcagtg gcagtggatc tgtgacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tattgggctt ttctgtgac gttcgggcaa      300
gggaccaagg tggaatcaa gcgg                                           324
```

<210> 1186
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1186
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcctattgat cctgatttac tgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc taggacagat ttcactctca ccatcagcag tctgcaacct      240
```


gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1187
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1187
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcctattggt cctgatttac tgtggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatctatcag acgtccattt tgcaaagtgg ggtcccatca 180
 cgtttcagt gtagtgatc tgggacagat ttcactctca ccatcagcgg tctgcaacct 240
 gaagattttg ctacgtacta ctgtcagcag tattgggctt ttcctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1188
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1188
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtat gcctattggt cctgatttac tgtggtacca gcagaaacca 120
 gggaaggccc ctaagtcct gatctatcag acgtccattt tgcaagtgg ggtcccatca 180
 cgtttcagt gtagtgaatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattgggctt ttcctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1189
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1189
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gtggattggg gatacgtaa cgtggtacca gcagaaacta 120

gggaaagccc ctaagctcct gatctatggg ggttccgagt tgcaaagtgg ggtcccacca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tgtattagta gtccttgtac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1190
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1190
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gtttattggg gattctttat cttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatttt tcttccattt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatactt cgcctactac gttcggccga 300
 gggaccaagg tgaaaatcaa acgg 324

<210> 1191
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1191
 gacatccaga tgaccagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gactattgag actaatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat tcttcccagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct 240
 gaagatttag ctacgtacta ctgtcaacag tatcatgggt atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1192
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1192

20089600.txt

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gatgattgat caggatttag agtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctataat gcgtcctggt tgcaaagtgg ggtcccatca	180
cgtttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcatgggt atcctattac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1193
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1193	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gacgatttat acttcgttaa gttggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatccattat gggtccgtgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattctg ctacgtacta ctgtcaacag gttcatcagg ctctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1194
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1194	
gacatccgga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtggattggg gattcttttag cgtggtacca gcagaagcca	120
gggaaagccc ctaagctcct gatctatggt atttccgagt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattctg ctacgtacta ctgtcaactg tctagtagta tgcctcatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1195
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1195
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggagattgag acgaatttag agtggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgat tcgtcccatt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatcatcaga atcctccgac gttcggccaa 300
ggaaccaagg tggaaatcaa acgg 324

<210> 1196
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1196
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gtggattggg aggcagttag tttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctatggg gcgaccgagt tgcaaagtgg ggtcccatca 180
cgttttagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag cagtcgaagg gtcctcttac gttcggccat 300
gggaccaagg tggaaatcaa acgg 324

<210> 1197
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1197
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggggattggg actgatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatatg gggttcctatt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag atttattctt ttcctattac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1198
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1198

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattgag gagatgttac attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt ggttccctgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtagatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag catcatactc gtccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1199

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1199

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattggg atggatttag agtggtacca gcagatacca	120
gggaaagtcc ctaagctcct gatctatgat gcgtcctatt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcataagc ttcctgcgac gtttggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1200

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1200

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattatg gataatttag agtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgcg gcgtcctggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcataagt tgctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1201
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1201
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gagcaagtca gaatattggg gaggatttag agtggtacca gcagaaacca 120
 gggaatgccc ctaagctcct gatctatagt gcgtcccatt tgcaaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattctagtt atcctgttac gttcggccaa 300
 gggaccaagg tggaatcaa acgg 324

<210> 1202
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1202
 gacatccaga tgacccagtc tccatcctcc ctgtctgcat ccgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gccgattgat gaggatttag agtggtacca gcagaaacca 120
 gggaatgccc ctaagctcct gatctatagt gcgtcctatt tgcaaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag actgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatcttc tgctgtctac gttcggccaa 300
 gggaccaagg tggaatcaa acgg 324

<210> 1203
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1203
 gacatccaga tgatccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggaatattaat gaggatttag agtggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctataat gcttccatgt tgcaaagcgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

aaagattttg ctacgtacta ctgtcaacag tatcatacta atcctactac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1204
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1204
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattgag gcggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatcat tcttccgagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatatgt cgctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1205
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1205
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattgat agtgatttag agtggtacca gcagaaacca 120
 gggaaagccc ctatgtcctt gatctattct tcgtccgatt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatagtc tgctgtttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1206
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1206
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatatttcg gatgatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctataat tcgtcctttt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tggggcagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatagtt tgcctgttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1207
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1207
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattgag ggtaatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat tcgtcccagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatcatc ttcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1208
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1208
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gagtattgat acggatttag agtggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat gggtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcggtgga ttcctgttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1209
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1209

20089600.txt

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gagtattagt actgatttag agtggtacca gcagaaacta	120
gggaaagccc ctaagctcct gatctatgat gcttccttt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattcgagtc tgcctgttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1210
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1210	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctattacg acgtcttttag agtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat gcgtccatgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattgggcta cgctgttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1211
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1211	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacctgcc gggcaagtca gaatattcat acgaatttag agtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat ggttccatgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tattcggcta atcctgttac gttcggccaa	300
gggaccaagg tgggaatcaa acgg	324

<210> 1212
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1212
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gtggattcat acggatttag agtggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgat ggttccatgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatagtgtgt cgctgtttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1213
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1213
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gagtattgat aataatttag agtggtacca gcagaaacca 120
ggggaagccc ctaagctcct gatctatgat ggttcccttt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctta ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatcatcttc atcctgtttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1214
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1214
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggatattgat acgaatttag agtggtatca gcagaaacca 120
ggggaagccc ctaagctcct gatctatgat cgttccacgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatgattctt atcctgtgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1215
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1215

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtctattgag tctaatttag agtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctataat gcgtccgagt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcgacct	240
gaagattttg ctacgtacta ctgtcaacag tatgatcagt ggcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1216

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1216

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcact	60
atcacttgcc gggcaagtca ggctattggt aatactttac ggtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt agttccaggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag ctgaagaagc ctccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1217

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1217

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gaagattaag aatcggttag cgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgag gtttccatt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcggcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag aggaggcagt cgccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1218
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1218
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtga ggatattggg gaggagttaa tttggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctattcg gcgtccacgt tgcaaagtga ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacat      240
gaagattttg ctacgtacta ctgtcaacag gtttatgagt ggccttatac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1219
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1219
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcctatttct ggggggttaa ggtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctattct acttccatgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag ctttattctg ctcccttatac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1220
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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<400> 1220
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ggatattgat caggatttag agtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctataat gtttcctgtg tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
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gaagattttg ctacgtacta ctgtcaacag tattctatga atcctgttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1221
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1221
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattggg aatcagttaa agtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatcag gcttcgggt tgcaaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatgatttga ggcctcagac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1222
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1222
 gacatccaga tgaccagtc tccatccttc ctgtctgcat ctgtaggatga ccgtgtcacc 60
 atcacttgcc gggcgagtca gaagatttct acgtcttttag agtggtatca gcagaaacca 120
 gggaaagccc ctaggctcct gatctatgat tcttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatgagtata atcctattac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1223
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1223
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gacgattggg gagagtttac attggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctatddd gcttccctgt tgcaaagtgg ggtcccatcg 180
 cgtttcagtg gcagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct 240
 gaagatdddg ctacgtacta ctgtcaacag catcatatgc ttcctttctac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1224
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1224
 gacatccaaa tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gtttattggt gattctttat cttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatddd tcttccattd tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagatdddg ctacgtacta ctgtcaacag tatatggata ttcctattac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1225
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1225
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattgat cataattdtag agtggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat agttccatgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagatdddg ctacgtacta ctgtcaacag tatcattcta ttcctgttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1226
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1226

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtca gcagattgag acgaatttag agtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat gggtcctggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcatagtt tgcctgctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1227
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1227	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtca ggatattggt aataatttag agtggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatctatcat gggtcctggt tgcaaagtgg ggtcccatcg	180
cgtttcagtg gcagtggatc tgggacagat ttcactctta ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatgatttta atcctactac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1228
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1228	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ctgtgtcacc	60
atcacttgcc gggcaagtca gaattattgat ggtctgttat ggtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgag gggtccgggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag aaggcttttg agcctttttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1229
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1229
gacatccaga tgaccagac tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gagtattggt catgatttag agtggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctataat gtgtcctggt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat tttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatagtcata atcctcctac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1230
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1230
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcact 60
atcacttgcc gggcaagtca gcatattgag aatgatttag agtggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctattct gcttcccatt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatcatcttc agcctacgac gttcggccca 300
gggaccaagg tggaaatcaa acgg 324

<210> 1231
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1231
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcact 60
atcacttgcc gggcaagtca gggtattgag ggtagtttaa attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctatcat aggtccattt tgcaaagtgg ggtcccatca 180
cgtttcagt gccgtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag acttatcagc ttcctttgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1232
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1232

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg tcctattaat ggtaagttat tttggtacca gcagaaacca	120
ggcaaagccc ctaagctcct gatcgcgttt gcttccgctt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgtgcag caggctgtgt atcctattac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1233

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1233

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggctattgag acgaatttag agtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat gggtcctttt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagaggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcattatc agcctgcgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1234

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1234

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattgag catgatttag agtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctattcg gcgtcccagt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcagcagc agcctactac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1235
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1235
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtgc gcagattgag gagtctttat ggtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgcggt gtttcctgt tgcaaagtgg agtcccatca 180
 cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgctcag ggtgtggtgg agcctcgtac gttcggccaa 300
 gggaccaagg tggaatcaa acgg 324

<210> 1236
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1236
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gtatattggt ctggatttag agtggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattttcggc agcctattac gttcggccaa 300
 gggaccaagg tggaatcaa acgg 324

<210> 1237
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1237
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1238
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 1238
 gacatccagt tgaccagtc tccaacctcc ctgtctgcaa ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacct 120
 gggaaagccc ctaagtcctt gatcgggcag tcgtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggactgat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag catgtgcgtc atcctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa gcgg 324

<210> 1239
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 1239
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacca 120
 gggaaagccc ctaagtcctt gatcgggcag tcgtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggacag catgtgcgtc ctctgcgac gttcggccaa 300
 gggaccaagg tgggaatcaa acgg 324

<210> 1240
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 1240
 gacatccaga tgaccagtc tccgtcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggttaagtac gccgattggt actatgttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccacca 180
 cgtttcagtg gcagcggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1241
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1241
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtac gccgattggt actatgttag attggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gctgtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1242
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1242
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtac gccgattggt actatgatag attggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgggcat tcgtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag catgtgcgtc ctctgcgac gttcggcaaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1243
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1243

20089600.txt

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacatgcc gggcaagtca gtatatgtat actaathtag agtggtacca gcagaaacca	120
gggaaagccc ctaggtctct gatctatgat gggtcccagt tgcaaagtgg ggtcccatca	180
cgtttcagt gcaagtggatc tgggacagat ttcactctca tcatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatcagggtg tgcctgttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1244
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1244	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtacca gcagaaacca	120
gggaaagccc ctaggtctct gatcgtggat tcttccgggt tgcaaagtgg ggtcccatca	180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag gatcgttggc ctctgtctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1245
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1245	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagttc gcggattcag catatgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgggtgg cattccgggt tgcaaagtgg ggtcccatca	180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgcgcaa tcgtgtgcgt ggcctctgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1246
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1246
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtag gggattgat ggtgatttat ggtggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgcgat tcttcctgt tgcaaagtgg ggtcccatca 180
cgtttcagt gcatggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgggcag ggggctgttc ggcctatgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1247
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1247
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtag gggattgat actgatttat ggtggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgcgat tcttcctgt tgcaaagtgg ggtcccatca 180
cgtttcagt gcatggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgggcag ggggctgttc ggcctatgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1248
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1248
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtta tactattccg gttgcttttag attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgctgat gcgtccttgt tgcaaagtgg ggtcccatca 180
cgtttcagt gcatggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgctcag ggttgccgg ggcctcagac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1249
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1249

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gagtattgcg acggacttag agtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat acttccatgt tgcaaagcgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatagttata atccttcgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1250

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1250

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtgt gcctattact gagggtttat cgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccaggct aattcctggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag tgggagcatg ttcctgacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1251

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1251

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtag tatgattctt tatggtttag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcggtagt acttccgcgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag tgggagacgg ttcctgctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1252
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1252
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcctattaat gggcttttaa tttggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgcg atgtccagtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag ttggctcgga ttccttttac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1253
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1253
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gagcaagtca gctgattcgg acttatattag cgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatcag tcttctcagt tgcaaagtgg tgtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tataattctt atcctgatac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1254
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1254
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gtggattggg gattcggttaa gttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatatt ggttcctatt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
```


gaagattttg ctacgtacta ctgtcaacag tatttgcata ctccttcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1255
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1255
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattgag gcggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatctatcat tcttccgagt tgcaaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatggtttta atcctcctac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1256
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1256
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagttc tcctattgag tatggtttag attggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatcgggggg ggtccgcgt tgcaaagtgg ggtcccatca 180
 cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag tgggaggttc agcctgctac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1257
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1257
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcggattgat actgatttag agtggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat agttcacagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatcatagtg cgcctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1258
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1258
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtgg gtggattggt atgtctttag agtggcacca gcagaaacca 120
 gggaaagccc ctaagctcct gatccgtggg gcttcctctt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtagtcag tctcgggtggc cgcctgtgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1259
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1259
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtgcg taatatttcg aatgctttat cgtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatccttggg gcttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtactcag gtgtgggata ggcctttttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1260
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1260

20089600.txt

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattatg tcggctttat cttggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctattct acttccattt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag gtttatttgc tgcctgttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1261
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1261	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggagattggg attgatttag agtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgct gcttcttatt tgcaaagtgg ggtcccatca	180
cgtttcagta gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatgcttcta atcctcctac gttcggccga	300
gggaccaagg tggaaatcaa acgg	324

<210> 1262
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1262	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gatgattggg gattgggttaa attggtacca gcagaaacca	120
gggaaagccc ctaaactcct gatctatcgt agttccgagt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag ttgtattttt ggcctcgtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1263
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1263
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggcgattgag ctttaatttag agtggtacca gcagaaacca 120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tatgatgttt atcctcctac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1264
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1264
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggccagtca ggcgattgag cataatttag agtggtacca gcagaagcca 120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccattagcag tctccaacct 240
gaagatttag ctacgtacta ctgtcaacag tatgatgctt atcctcctac gtacggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1265
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1265
gacatccaga tgacacagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtgc ggcgatagag actaatttag agtggtacca gcagaaacca 120
gggaaggccc ctaagctcct gttctatgat gcttccatgt tgcaaagcgg ggtcccatca 180
cgtttcggtg gcaagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtctacag tatgatgttt atcctcctac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1266
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1266

gacatccaga tgaccagtc tccatcctcc ctgtctgcaa ctgtaggaga ccgtgtcacc	60
atcacttgtc gtgcaagtca ggcgattgag actaatcttag agtggtacca gcagaaacca	120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagac ttcactctca ccattagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1267

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1267

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggcgattgag cataacttag agtggtacca gcagaaacca	120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca	180
cgtttcagtg gcagaggatc tgggacagat ttcactctca ccattagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1268

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1268

gacatccaga tgaaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtctcc	60
atcacttgca gggcaagtca ggctattgag cataatttag agtggtacca gcagaaacca	120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1269
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1269
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ggcgattgag tctaatttag agtggtacca gcaaaaacca      120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tatgatgttt atcctcctac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1270
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1270
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gtgcaagtca ggcgattgag cataatttag agtggtacca gcagaaacca      120
gggaaggccc ctaagctcct gatctatgat gcttccatgt tgcaaagcgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccattagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tatgatgctt atcctcctac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1271
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1271
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gggatttgat gaggatttag agtggtacca gcagaaacca      120
gggaaagccc ctaggctcct gatctattct agttcctggg tgcaaagtgg ggtcccatca      180
cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
```

gaagattttg ctacgtacta ctgtcaacag tatttttcagt atcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1272
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1272
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagt ggagtgatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatttttcagt atcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1273
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1273
 gacatccaga tgaccagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60
 atcacttgca gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagt ggagtgatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tattctcagt atcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1274
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1274
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gagtattgaa gaggatttag agtggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagcgg ggtcccatca 180
 cgtttcagtg ggagtggctc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatttttcagt atcctccgac gttcggccat 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1275
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1275
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtactt ctgtcaacag tatttttcagt atcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1276
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1276
 gagatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atgacttgcc gggcaagtca gagtattgat aaggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagagg ggtcccatca 180
 cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcgacct 240
 gaagattttg ctacgtacta ctgtcaacag tatttttcagt atcctccgac gttgggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1277
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1277

20089600.txt

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
 atcacttgcc gggcaagtca gagtattgat gaggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcgg tctgcaacct 240
 gaagatatcg ctacgtacta ctgtaaacag tattctcagt atcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1278
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1278
 gacatccaga tgaccagtc cccaccctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gagtattgat aaggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctattct agttcctggt tgcaaagagg ggtcccatca 180
 cgtttcagtg ggagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacca ctgtcaacag tattttcagt atcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1279
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1279
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtga gtatattaat gctgagtttag cttggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatggg agttccgggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtctgcag aatgcgatgt ggcctattac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1280
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1280
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtct ggatattaat aatggtttaa tttggtacca gcagaaacca 120
gggaaagccc ctaggctcct gatcttgggt gcgtccggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgttcgcag gtgcgttctc ggccttttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1281
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1281
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggatattctg agtgcgttag cttggtatca gcagaaacca 120
gggaaagccc ctaagtcctt gatctatggg agttccgttt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc agggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag aattatagtc ttcctattac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1282
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1282
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagttc tcctattgag tcgtatttaa ggtggtacca gcagaaacca 120
gggaaagccc ctaagtcctt gatcaggtat gtgtccgtgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgggcag tggtttcggg cgcctgttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1283
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1283

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggtaagtga gtctattaat gctgagttac attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctctggg ttttccgggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgtgcag tttgcatgtt ggccttttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1284

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1284

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtat gatgattagg tttgggtag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcggtagt gggcctctt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag catgagcggg ggcctgctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1285

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1285

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gagtattggt actcttttac gttggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt acttccgttt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag atggtttatc gtccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1286
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1286
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gactattgag actaatntag agtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatctatgat tcttcccagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tatgataagg ttcttgcgac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1287
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1287
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca tcatattcag aggtatttat cgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcctttgg gggtcccagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgggcag tgggtgggctc ctctccgac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1288
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1288
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca tcatattcag aggtatttat cgtggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcctttgg gggtcccagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
```

gaagattttg ctacgtacta ctgtgggcag tgggtgggctc ctcctcagac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1289
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1289
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca tgatattcag aggtatttat cgtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcctttgg ggttcccagt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag tgggtgggctc ctcctcagac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1290
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1290
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacatgcc gggcaagtca gtatattgat actaatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgat ggttccctgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag ggggctgttg tgcctgttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1291
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1291
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattgct tttgatttag agtggtatca gcagaaacca 120

20089600.txt

```

gggaaagccc ctaagctcct gatctattcg gcgtccatgt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggtcagat ttcactctca ccatcagcag tctgcaacct    240
gaagattttg ctacgtacta ctgtcaacag tataatcttc agcctcctac gttcggccaa    300
gggaccaagg tggaaatcaa acgg                                           324

```

<210> 1292
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```

<400> 1292
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc    60
atcacttgcc gggcaagtca gaatattgct acgctgttac gttggtacca gcagaaacca    120
gggaaagccc ctaagctcct gatctatgct ggttccatgt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct    240
gaagattttg ctacgtacta ctgtcaacag atgtggcagc gtccttatac gttcggccaa    300
gggaccaagg tggaaatcaa acgg                                           324

```

<210> 1293
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```

<400> 1293
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc    60
atcacttgcc gggcaagtca gcctattggt gatgagttag attggtacca gcagaaacca    120
gggaaagccc ctaagctcct gatctatgct gcgtccatgt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct    240
gaagattttg ctacgtacta ctgtcatcag tgggtctactt atcctacgac gttcggccaa    300
gggaccaagg tggaaattaa acgg                                           324

```

<210> 1294
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1294

20089600.txt

gacatccaga tgaccaatc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtacca gcagaaacca	120
gggaaagccc ctaagctcct aatcgatggg gtttccgggt tgcaaagtgg ggtcccatca	180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag gattgggatt ggcctcgtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1295
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1295	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtag gaatattcgt gattgggttac ggtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgattgg ggggccgtgt tgcaaagtgg ggtcccatca	180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgctcag acgtgggatg atcctctgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1296
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1296	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ttgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtag gaatattcgt gattgggttac ggtggtacca acagaaacca	120
gggaaagccc ctaagctcct gatcgattgg ggggccgagt tgcaaagtgg ggtcccatca	180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgctcag acgtgggatg atcctctgac gttcggccac	300
gggaccaagg tggaaatcaa acgg	324

<210> 1297
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1297
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtat tgatattcat ggtgggttaa cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgtgggg gtttcgggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
gaagattttg ctacgtacta ctgtgcgag gtgtggcgta ggccttttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1298
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1298
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggatattggg agttcggtat cttggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct tcttcctgtg tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag acttatgctc ttcctgttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1299
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1299
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gcagattgag acgaatttag agtggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgat ggttcctggt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag tataagtatc tgcctgtgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1300
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1300

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggtga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattggg tctgcgttaa ggtggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatttg ggttccgatt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag acgcagtatt ttcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1301

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1301

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggcgatttat ggggggttac ggtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatggg gagtccatgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcatcct	240
gaagattttg ctacgtacta ctgtcaacag gtttatcata agccttttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1302

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1302

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacgtgcc gggcaagtca gcgtattggg gtgtgggttag attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat ggttcctttt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag actttttcga gtcctttctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1303
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1303
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcccc      60
atcacttgcc gggcaagtca gtggattggg gatgagttat attggtatca gcagaaacca      120
gggaaagccc ctaagtcct gatctatagt tcttcactt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tcgtttcagt ttccttatac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1304
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1304
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtag taatattacg gggccgttag agtggtacca gcagaaacca      120
gggaaagccc ctaagtcct gatccctggg tggtcactt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag gtgtgggggg agcctgttac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1305
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1305
gacatccaga tgaccagtc tccatcctcc ctgtctgcgt ctataggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gcgtattgct tatggtttac attggtacca gcagaaacca      120
gggaaagccc ctaggtcct gatcgggggg cggtcgggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
```

gaagattttg ctacgtacta ctgtgtgcag cctgggatgc cgcctgatac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1306
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1306
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gggcaagtaa gcagattgtt ggtggtttat cttggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatcgggctg cattctgggt tgcaaagtgg ggtcccatca 180
 cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgtgcag ggggtttggg ctctctgggac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1307
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1307
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gggcaagtcc tgctattgct gctaagttag attggtacca gcagaaacca 120
 gggaaagccc ctaagtcct gatcgggtgc gattccgggt tgcaaagtgg ggtcccatca 180
 cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ctgtgggcgg ggcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1308
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1308
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60
 atcacttgcc gggcaagtgc tactattgct gatggggttag attggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcggggcg tattccgggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ctttgggagg gtcctccgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1309
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1309
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gaggatttat gggtttttag attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatggg gtgtcctcgt tgcaaagtgg ggtcccatca 180
 cgtttttagt gcagcggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag actttggcgt ggccttttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1310
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1310
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggatattcgg gattggttaa tgtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctattgg ggttcctttt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag ctgtatgata ctccttatac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1311
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1311

20089600.txt

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gaatattaat acggggttag attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat agttccgctt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag acgtcgtatt atccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1312
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1312	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gaagattttt ggttggttag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatggg acttccaagt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag gtttattcgc ttccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1313
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1313	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagttc gaatattggg gcggatttag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgggggg gcgtccgggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag ctgtggaatg ggcctcctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1314
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1314
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtag tccgatttat gatggtttag attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctctggg gcttcctggg tgcaaagtgg ggtcccatca 180
cgcttcagt gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ttgtggttgg gtcctccgac gttcggccaa 300
gggaccaagg tggaaatcaa acag 324

<210> 1315
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1315
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagttc gcgtatttat aatggtttac attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgggtgg cggctccggg tgcaaagtgg ggtcccatca 180
cgtttcagt gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgctcag gtgggggagg ctccttctac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1316
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1316
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtag gtttattaat gaggagttag attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctcgtgg tcttcctggg tgcaaagtgg ggtcccatca 180
cgtttcagt gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgtgcag ccgggggggtg gtcctgggac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1317
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1317

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtag ggatattctg gatgagttag attggtacca gcagaaacca	120
gggaaagccc ctaggtcctt gatcgggtgg ggggccgggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ctgtggcatg ggcctccgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1318

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1318

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtag tcctatttat acggggtttac attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgggtgg cgggccgggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtatgcag gttgggacgg ctcttgctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1319

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1319

gacatccgga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gaatatttct aggcgggttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctattct tcttcccgggt tgcaaagtgg ggtcccatca	180
cgtttcggtg gcagtggatc tgggacggat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag acgtatagct atcctcatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1320
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1320
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtag tccgattccg caggatttat attggtacca gcagaaacca      120
gggaaagccc ctaagtcct gatcgttggg atttcccagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgggcag ttgtggagtg cgcttgctac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1321
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1321
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtaa gtctattgat gggatgttag attggtacca gcagaaacca      120
gggaaagccc ctaagtcct gatccctggg ttttccggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgggcag tcggttgagg cgcttggac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1322
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1322
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtcg gtatattgct catcctttag attggtacca gcagaaacca      120
gggaaagccc ctaagtcct gatcccgggt tcgtccgttt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
```


gaagattttg ctacgtacta ctgtgggtcag tcggttgtgg tgccttggac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1323
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1323
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtcg gacgattgag ggtgggttag attggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcatgggg ggttccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag ttgtgggtgg gtcctcctac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1324
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1324
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtaa gtttattagg gatgagttat attggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatcgggtgg tgcctcttgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag ctgtggcggg cgcttgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1325
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1325
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtaa gccgatttat ggtgggttag agtgggtacca gcagaaacca 120

gggaaagccc ctaggctcct gatcgggggg ggttccgtgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag gtgtgggggg gtcctgttac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1326
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1326
 gacatccgga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtcg gccgattagt ggttgtttag attggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgatggg gcttccgggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag tgggtgggagt atcctcctac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1327
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1327
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtaa gcctattgtg agggatttag agtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatccatggt gtgtccacgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggcag cttgaggcgg cgctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1328
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1328

20089600.txt

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg ggatattggg gattgggttat attggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatcgtttgg gcgtccgtgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgcgag tgggggactc ctcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1329
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1329	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtaa tcgtattgag tatggtttag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctcgggg tcttcccgtt tgcaaagtgg ggtcccatca	180
cgtttcagta gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag cttgaggcgg cgctgcgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1330
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1330	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg gaatattggg catttttttag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcttgggg gggtcctcgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag ttggtggagc ctcctgcgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1331
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1331
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagttc gagtatttat agtgatttat attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgatggg tgggccgggt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgggcag ctgcatcgtg ctctgcgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1332
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1332
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtag gtttattact gatcgtttag attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcggtggg gtttccgggt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgggcag agttcggagt tgccttggac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1333
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1333
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtcg taagattggg agtgagttat attggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcggtggg aggtcccggg tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgggcag ttgtgggagc ctctgcgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1334
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1334

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtag gaatattggt aatggtttag attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcggggag ggggccggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgggcag ctttggcata ctctcctac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1335

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1335

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg gaatatttat ggttggttat cgtggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatcgggtggg tgggccggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgcgag gattatacgt tgcctggtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1336

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1336

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattaag gattggttac attggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatatt gcgtccggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattctg ctacgtacta ctgtcaacag cattatagta cgccttatac gtccggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1337
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1337
gacatccaga tgaccagtc tccaccctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gttgatttct tctcatttag attggtacca gcagaaacca      120
gggaaagccc ctaagctcct ggtctatgat gcttccgagt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag catcgcagtc tgccttttac gttcggccaa      300
gggaccaagg tagaaatcaa acgg                                           324
```

<210> 1338
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1338
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gtggatttgt ggggcgttag cgtggtacca gcagaaacca      120
gggaaagccc ctaggctcct tatctatcag atttccgttt tgcaaagtgg gatcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcaacag tatattcggt ctctttttac gttcggccaa      300
gggaccaagg tggaatcaa acgg                                           324
```

<210> 1339
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

```
<400> 1339
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gaggattggg gcggcgtaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatggt ctgtcctctt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
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gaagattttg ctacgtacta ctgtcaacag ctgttttaggc ttcctttgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1340
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1340
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcctattggg ggtcgttttag tgtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatggg tcttccattt tgcaaagtgg ggtcccatca 180
 cgtttcagt gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tatgctgagg ctctattac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1341
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1341
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gaatattggg tctagtttaa tttggtacca gcagaaacca 120
 gggaaagccc ctacgtcctt gatctattat tctgtccaagt tgcaaagtgg ggtcccatca 180
 cgtttcagt gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tctttgtcga gtccttatac ggtcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1342
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1342
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gtggattggg agtgagtttag cgtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattgg acgtccaatt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag attctggaga ctcctttgac gtttggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1343
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1343
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gaagatttgg gatgctttat attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatcgt ggggccattt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag ttttatcggg ggcctcatal gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1344
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1344
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcatattgag gattctttac ggtggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatctattat ggttccgtgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag atgtataagt ttcctattac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1345
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1345

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gacatccaga cgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcggattaat tcttctttac tgtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgat acttccactt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtagatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagatttcg ctacgtacta ctgtcaacag atttgggggtt cgcctcctac gttcggccag	300
gggaccaagg tggaaatcaa acgg	324

<210> 1346
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1346	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtcgattcct gttggtttaa attggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatctattct ggggccactt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag gattggtatt atcctaatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1347
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1347	
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gcctatttat ggttggttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatttg acgtccgggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag attcatagtt ctccttttac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1348
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1348
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gtttattgat acgtcgttag agtggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgat ggggccatt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatttag ctacgtacta ctgtcaacag tattgggttc ttcctctgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1349
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1349
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggatattggg gatgctttat tttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatctattat tcttccatgt tgcaaagtgg ggtcccatca 180
cgtttcagt gcggtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaacag cggcatagta ctctgctac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1350
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1350
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggatattgat gagtctttaa tgtggtacca gcagaaacca 120
gggaaagccc ctaggtcctt gatctatggg gtgtcctatt tgcaaagtgg ggtcccatca 180
cgtttcagt gcaagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatttcg ctacgtacta ctgtcaacag cgggtggaagg ctctttttac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1351
<211> 324
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1351

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtggtacc	60
atcacttgcc gggcaagtca ggagattgtg gaggatttat attggtatca gcagaaacca	120
gggaaagccg ctaagctcct gatctatggt gcgtcctggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag acgcgtaggc gtccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1352

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1352

gacatccaga tgaccagtc tccagcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggatattgat cctatgttaa ggtggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatctatgcg ggttccattt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag acgctggtga ctccttatac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1353

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1353

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtcgatttcg gatgcgttat tttggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatctattat ggttccgttt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcaacag cgttttcagg agcctgtgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1354
 <211> 324
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 1354
 gacatccaga tgaccagtc tccatcctcc ctgtccgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gcagattagt gatgagttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagtcct gatctatgct gtgtccattt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaacag tggttgagtt ttccttcgac gtttggccaa 300
 gggaccaagg tggaatcaa acgg 324

<210> 1355
 <211> 353
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1355
 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 Asn Trp Glu
 20 25 30
 Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Glu Gly Pro Gly Asp Val Thr 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
 Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp Lys
 115 120 125

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Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser
 130 135 140

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 145 150 155 160

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 165 170 175

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 180 185 190

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 195 200 205

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 210 215 220

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 225 230 235 240

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 245 250 255

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 260 265 270

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 275 280 285

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 290 295 300

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 305 310 315 320

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 325 330 335

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 340 345 350

Lys

<210> 1356
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 1356

Ala	Ser	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
1				5				10	

<210> 1357

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1357

Ala	Ser	Thr	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro
1				5					10					15	

Ser Pro

<210> 1358

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1358

Ala	Ser	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro
1				5				10	

<210> 1359

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 1359

Ala	Ser	Thr	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro
1				5					10					15	

Ser Pro

<210> 1360

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

peptide"

<400> 1360

Ala Ser Thr His Thr Ser Pro Pro Ser Pro
 1 5 10

<210> 1361

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 peptide"

<400> 1361

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15

Ala Glu Val Gln Leu Leu Glu Ser
 20

<210> 1362

<211> 370

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 1362

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15

Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 20 25 30

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
 35 40 45

Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 50 55 60

Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
 65 70 75 80

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 85 90 95

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 100 105 110

Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
 115 120 125

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Thr Leu Val Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp
130 135 140

Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly
145 150 155 160

Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
165 170 175

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
180 185 190

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
195 200 205

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
210 215 220

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
225 230 235 240

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
245 250 255

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
260 265 270

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
275 280 285

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
290 295 300

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
305 310 315 320

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
325 330 335

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
340 345 350

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
355 360 365

Gly Lys
370

<210> 1363
<211> 362
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1363

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15

Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 20 25 30

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
 35 40 45

Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 50 55 60

Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
 65 70 75 80

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 85 90 95

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 100 105 110

Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
 115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr His Thr Ser Pro Pro Ser
 130 135 140

Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro
 145 150 155 160

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 165 170 175

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 180 185 190

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 195 200 205

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 210 215 220

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 225 230 235 240

20089600.txt

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
245 250 255

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
260 265 270

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
275 280 285

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
290 295 300

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
305 310 315 320

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
325 330 335

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
340 345 350

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
355 360

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<210> 1364
<211> 370
<212> PRT
<213> Artificial Sequence
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<220>  
<221> source  
<223> /note="Description of Artificial Sequence: Synthetic  
polypeptide"
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<400> 1364
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1 5 10 15

Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
20 25 30

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
35 40 45

Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
50 55 60

Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
65 70 75 80

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
85 90 95

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
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100

105

110

Cys Val Lys₁₁₅ Val Gly Lys Asp Ala₁₂₀ Lys Ser Asp Tyr Arg₁₂₅ Gly Gln Gly
 Thr Leu₁₃₀ Val Thr Val Ser Ser₁₃₅ Ala Ser Thr Glu Pro₁₄₀ Lys Ser Ser Asp
 Lys₁₄₅ Thr His Thr Cys Pro₁₅₀ Pro Cys Pro Ala Pro₁₅₅ Glu Leu Leu Gly Gly₁₆₀
 Pro Ser Val Phe Leu₁₆₅ Phe Pro Pro Lys Pro₁₇₀ Lys Asp Thr Leu Met₁₇₅ Ile
 Ser Arg Thr Pro₁₈₀ Glu Val Thr Cys Val₁₈₅ Val Val Asp Val Ser₁₉₀ His Glu
 Asp Pro Glu₁₉₅ Val Lys Phe Asn Trp₂₀₀ Tyr Val Asp Gly Val₂₀₅ Glu Val His
 Asn Ala₂₁₀ Lys Thr Lys Pro Arg₂₁₅ Glu Glu Gln Tyr Gln₂₂₀ Ser Thr Tyr Arg
 Val₂₂₅ Val Ser Val Leu Thr₂₃₀ Val Leu His Gln Asp₂₃₅ Trp Leu Asn Gly Lys₂₄₀
 Glu Tyr Lys Cys Lys₂₄₅ Val Ser Asn Lys Ala₂₅₀ Leu Pro Ala Pro Ile₂₅₅ Glu
 Lys Thr Ile Ser₂₆₀ Lys Ala Lys Gly Gln₂₆₅ Pro Arg Glu Pro Gln₂₇₀ Val Tyr
 Thr Leu Pro₂₇₅ Pro Ser Arg Asp Glu₂₈₀ Leu Thr Lys Asn Gln₂₈₅ Val Ser Leu
 Thr Cys₂₉₀ Leu Val Lys Gly Phe₂₉₅ Tyr Pro Ser Asp Ile₃₀₀ Ala Val Glu Trp
 Glu₃₀₅ Ser Asn Gly Gln Pro₃₁₀ Glu Asn Asn Tyr Lys₃₁₅ Thr Thr Pro Pro Val₃₂₀
 Leu Asp Ser Asp Gly₃₂₅ Ser Phe Phe Leu Tyr₃₃₀ Ser Lys Leu Thr Val₃₃₅ Asp
 Lys Ser Arg Trp₃₄₀ Gln Gln Gly Asn Val₃₄₅ Phe Ser Cys Ser Val₃₅₀ Met His
 Glu Ala Leu₃₅₅ His Asn His Tyr Thr₃₆₀ Gln Lys Ser Leu Ser₃₆₅ Leu Ser Pro

Gly Lys

370

<210> 1365
 <211> 362
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 1365
 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15

Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 20 25 30

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Trp
 35 40 45

Glu Leu Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 50 55 60

Val Ser Gly Ile Glu Gly Pro Gly Asp Val Thr Tyr Tyr Ala Asp Ser
 65 70 75 80

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 85 90 95

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 100 105 110

Cys Val Lys Val Gly Lys Asp Ala Lys Ser Asp Tyr Arg Gly Gln Gly
 115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr His Thr Cys Pro Pro Cys
 130 135 140

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 145 150 155 160

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 165 170 175

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 180 185 190

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 195 200 205

Glu Gln Tyr Gln Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 210 215 220

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 225 230 235 240
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 245 250 255
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 260 265 270
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 275 280 285
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 290 295 300
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 305 310 315 320
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 325 330 335
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 340 345 350
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 355 360