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(54) **ANTI-CD3 ANTIBODIES, BISPECIFIC ANTIGEN-BINDING MOLECULES THAT BIND CD3 AND CD20, AND USES THEREOF**

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(60) Provisional application No. 61/704,029, filed on Sep. 21, 2012, provisional application No. 61/753,461, filed on Jan. 17, 2013, provisional application No. 61/763,110, filed on Feb. 11, 2013, provisional application No. 61/827,098, filed on May 24, 2013.

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(57) **ABSTRACT**

The present invention provides antibodies that bind to CD3 and methods of using the same. According to certain embodiments, the antibodies of the invention bind human CD3 with high affinity and induce human T cell proliferation. The invention includes antibodies that bind CD3 and induce T cell-mediated killing of tumor cells. According to certain embodiments, the present invention provides bispecific antigen-binding molecules comprising a first antigen-binding domain that specifically binds human CD3, and a second antigen-binding molecule that specifically binds human CD20. In certain embodiments, the bispecific antigen-binding molecules of the present invention are capable of inhibiting the growth of B-cell tumors expressing CD20. The antibodies and bispecific antigen-binding molecules of the invention are useful for the treatment of diseases and disorders in which an upregulated or induced targeted immune response is desired and/or therapeutically beneficial. For example, the antibodies of the invention are useful for the treatment of various cancers as well as other CD20-related diseases and disorders.

Specification includes a Sequence Listing.

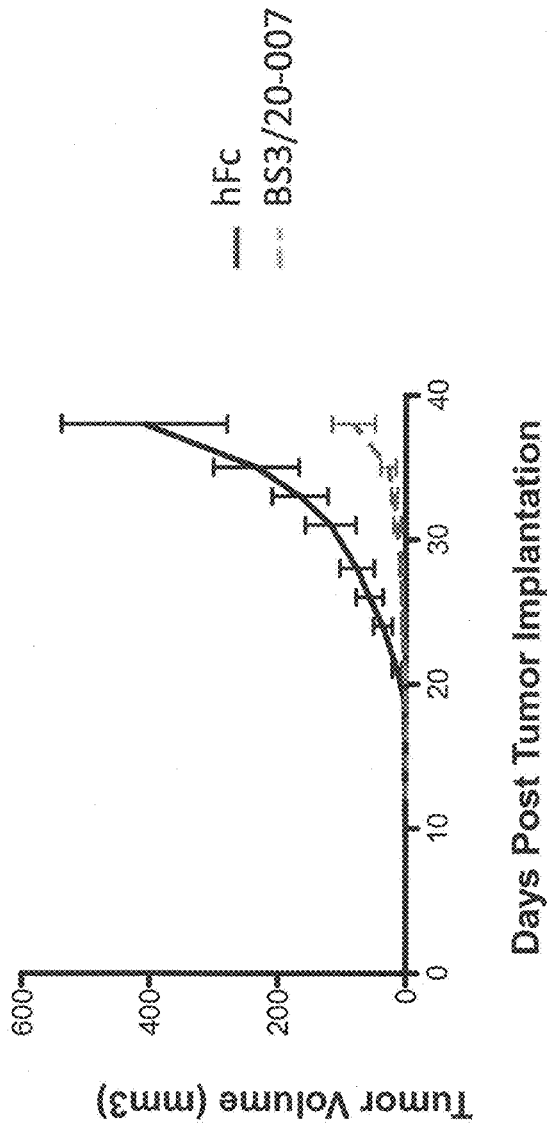
hFc
BS3/20-007
Tumor Volume (mm3)
600
400
200
0
0
10
20
30
40
Days Post Tumor Implantation

Figure 1

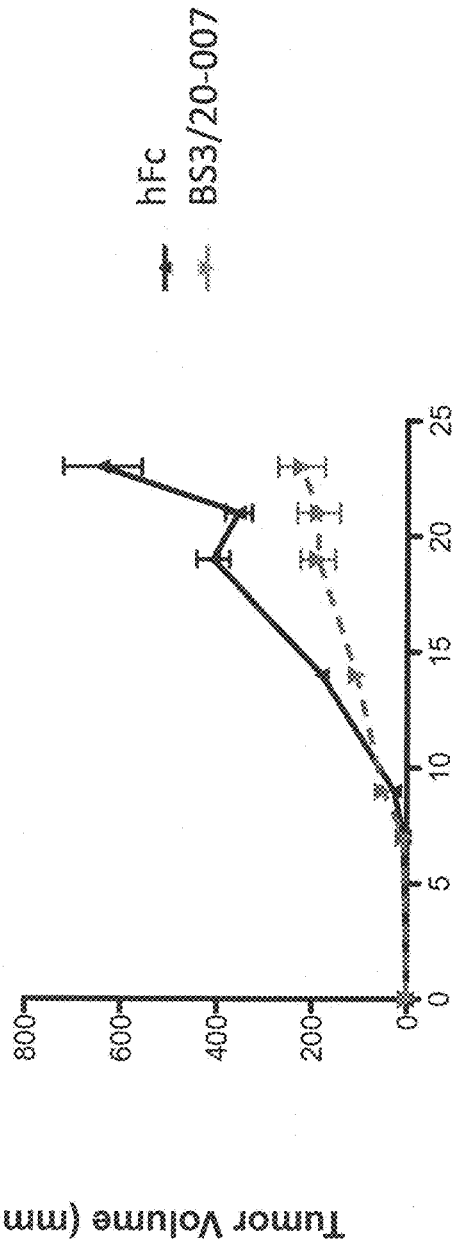
hFc
BS3/20-007
Tumor Volume (mm3)
800
600
400
200
0
0
5
10
15
20
25
Days Post Tumor Implantation

Figure 2

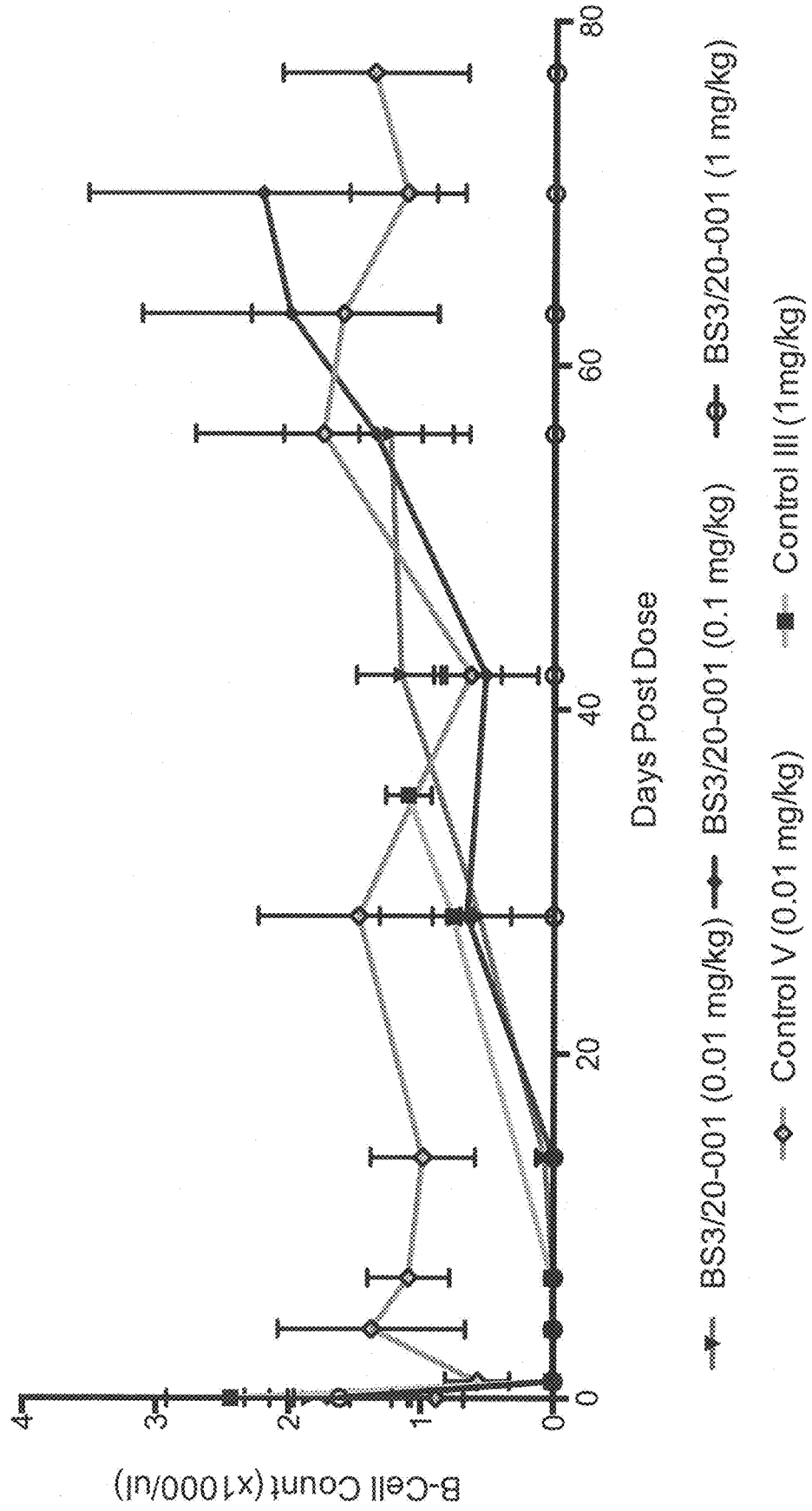
B-Cell Count (x1000/ul)
0
1
2
3
4
0
20
40
60
80
Days Post Dose
BS3/20-001 (0.01 mg/kg)
BS3/20-001 (0.1 mg/kg)
BS3/20-001 (1 mg/kg)
Control V (0.01 mg/kg)
Control III (1mg/kg)

Figure 3

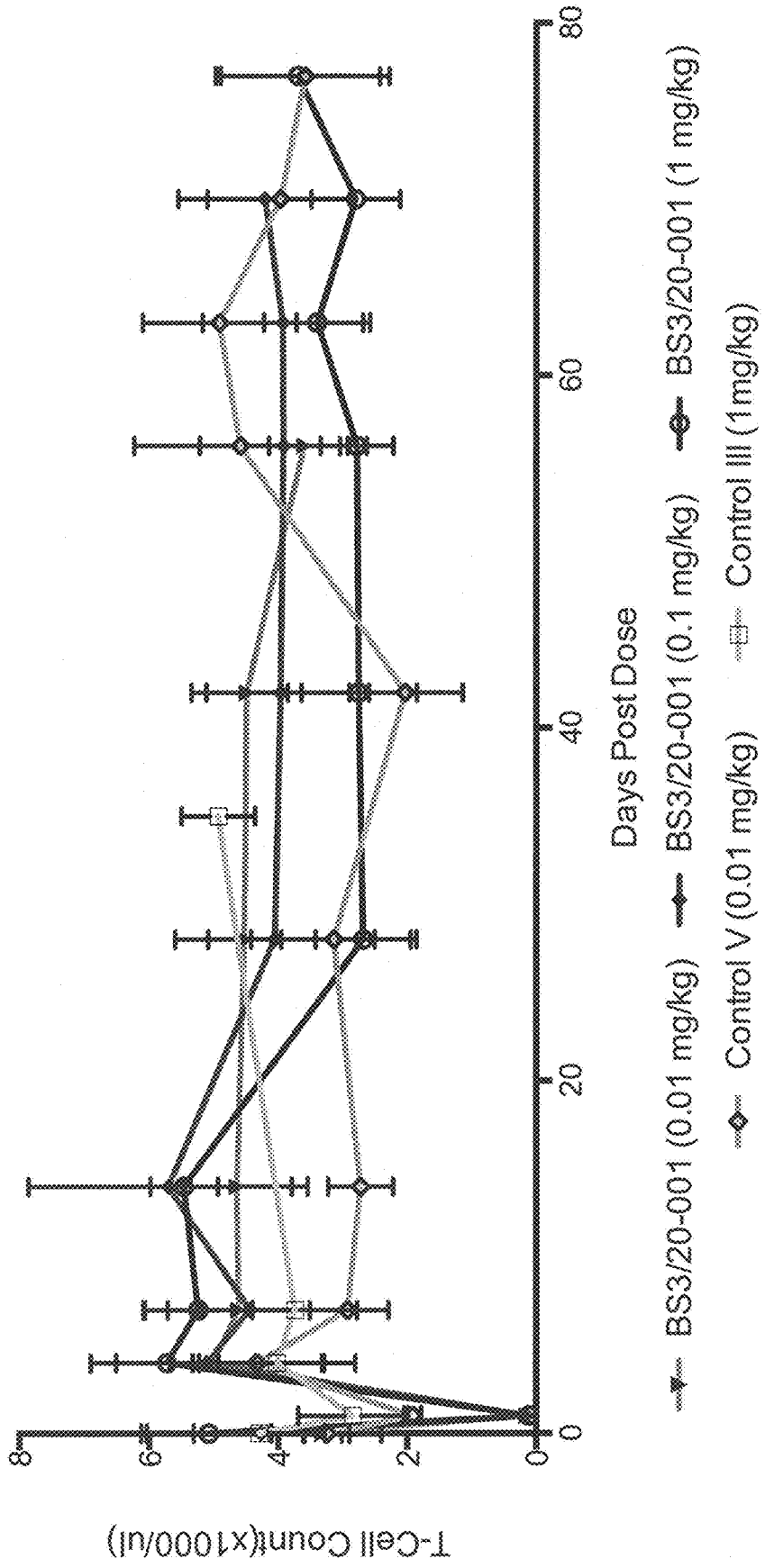
T-Cell Count(x1000/ul)
0
2
4
6
8
0
20
40
60
80
Days Post Dose
BS3/20-001 (0.01 mg/kg)
BS3/20-001 (0.1 mg/kg)
BS3/20-001 (1 mg/kg)
Control V (0.01 mg/kg)
Control III (1mg/kg)

Figure 4

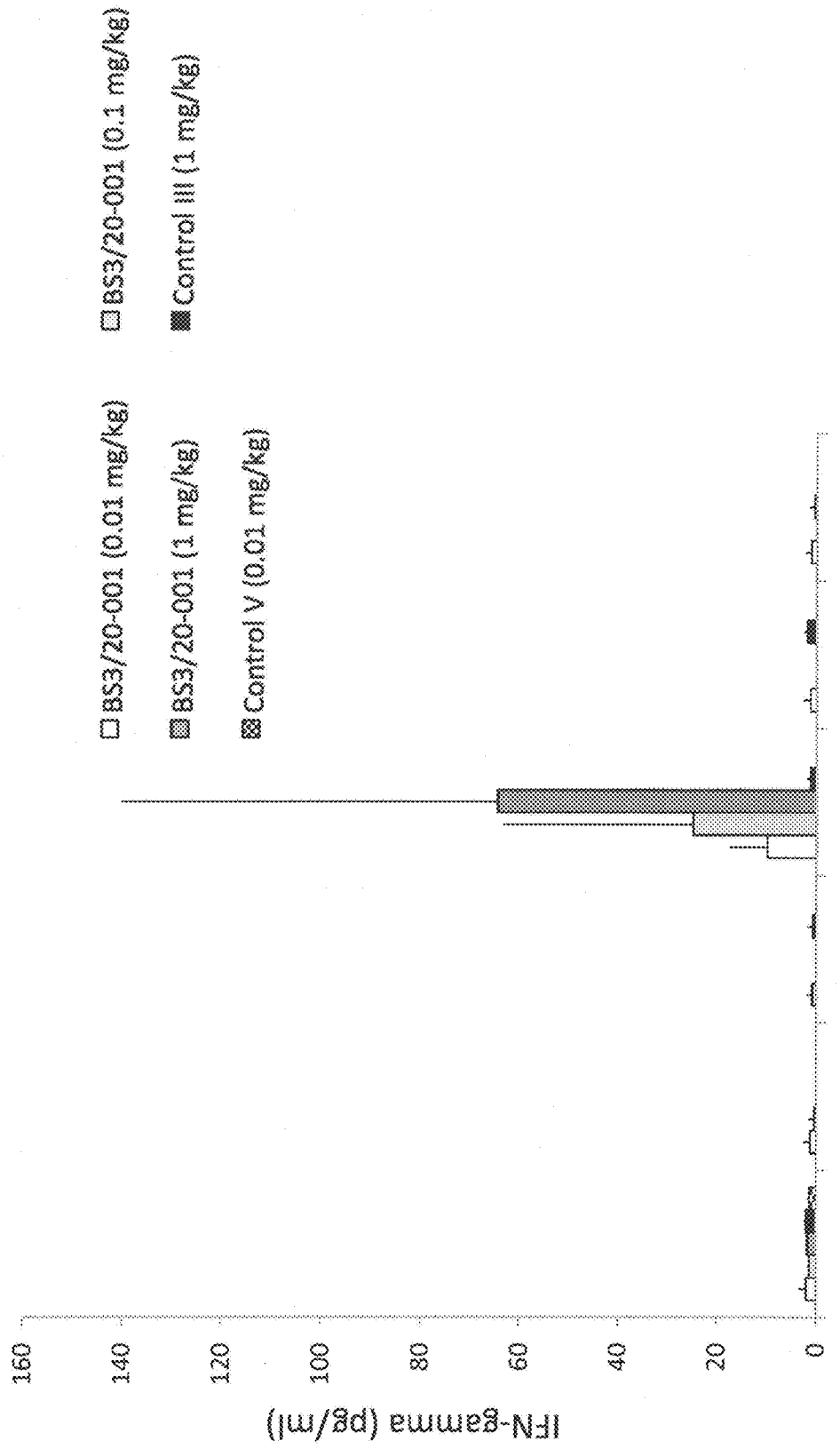
BS3/20-001 (0.01 mg/kg)
BS3/20-001 (0.1 mg/kg)
BS3/20-001 (1 mg/kg)
Control III (1 mg/kg)
Control V (0.01 mg/kg)
IFN-gamma (pg/ml)
0
20
40
60
80
100
120
140
160
Pre
0
5'
5hr
24hr
96hr
Time

Figure 5A

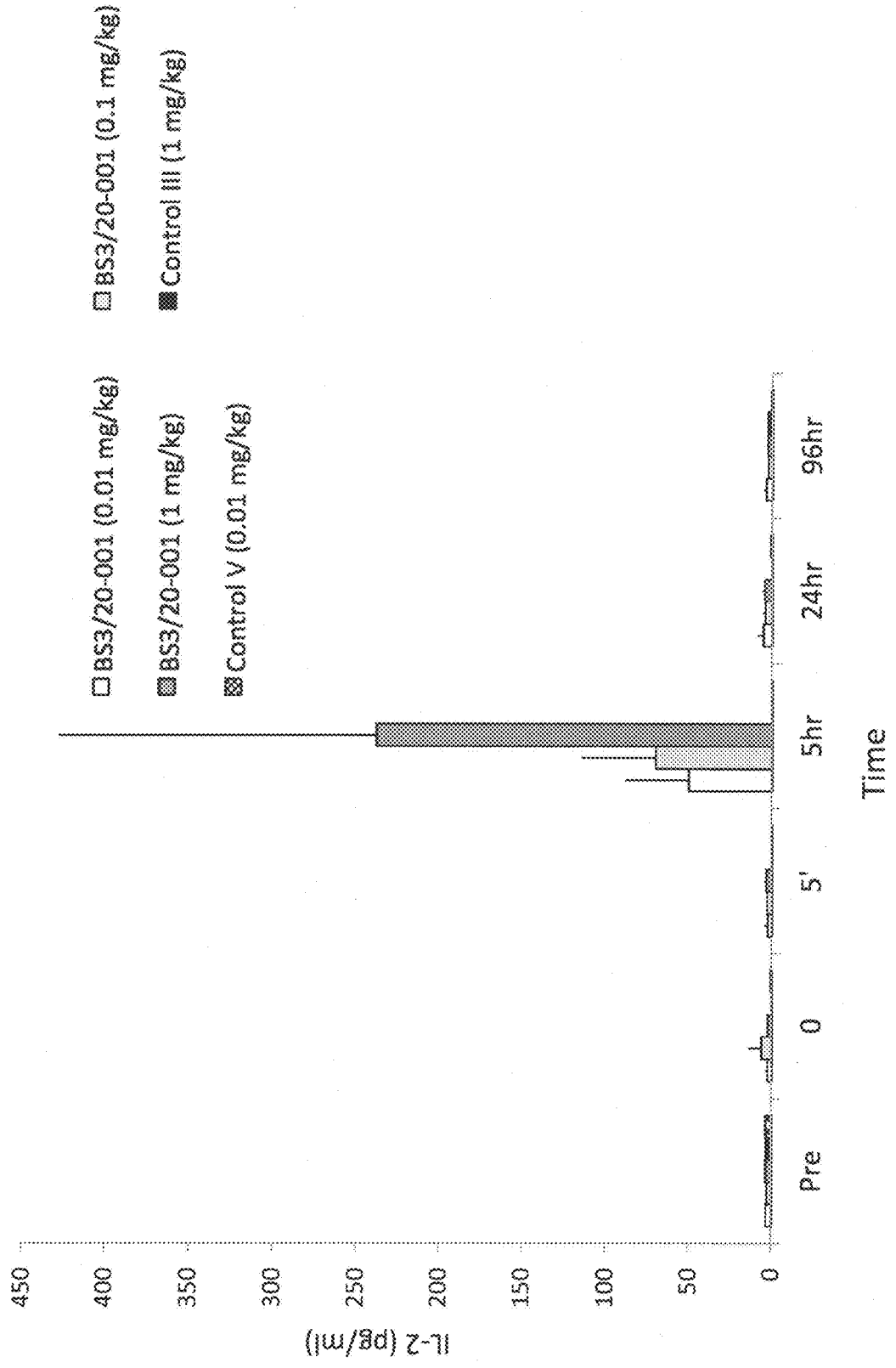
BS3/20-001 (0.1 mg/kg)
Control III (1 mg/kg)
BS3/20-001 (0.01 mg/kg)
BS3/20-001 (1 mg/kg)
Control V (0.01 mg/kg)
IL-2 (pg/ml)
450
400
350
300
250
200
150
100
50
0
Pre
0
5'
5hr
24hr
96hr
Time

Figure 5B

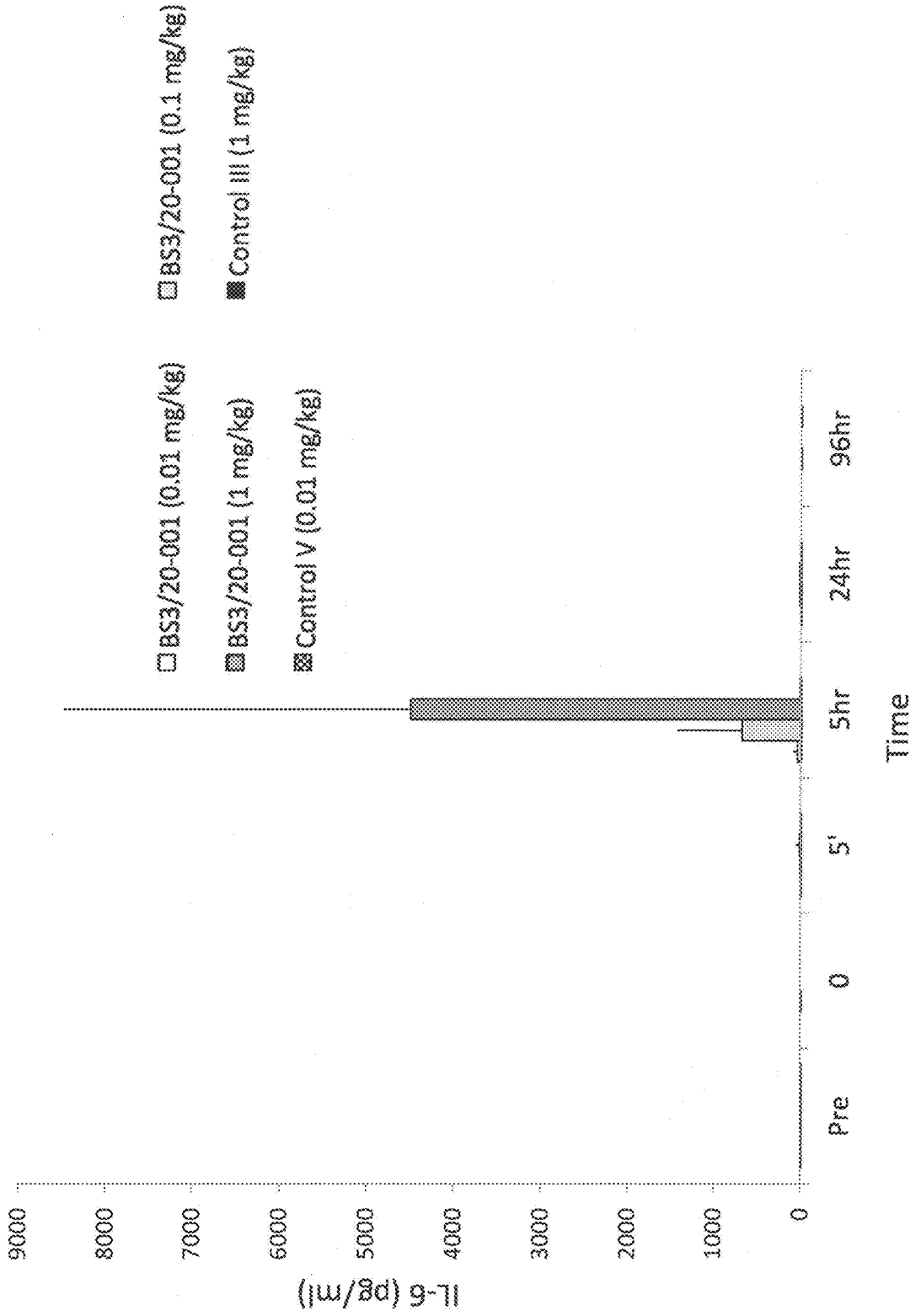
BS3/20-001 (0.1 mg/kg)
Control III (1 mg/kg)
BS3/20-001 (0.01 mg/kg)
BS3/20-001 (1 mg/kg)
Control V (0.01 mg/kg)
IL-6 (pg/ml)
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
Pre
0
5'
5hr
24hr
96hr
Time

Figure 5C

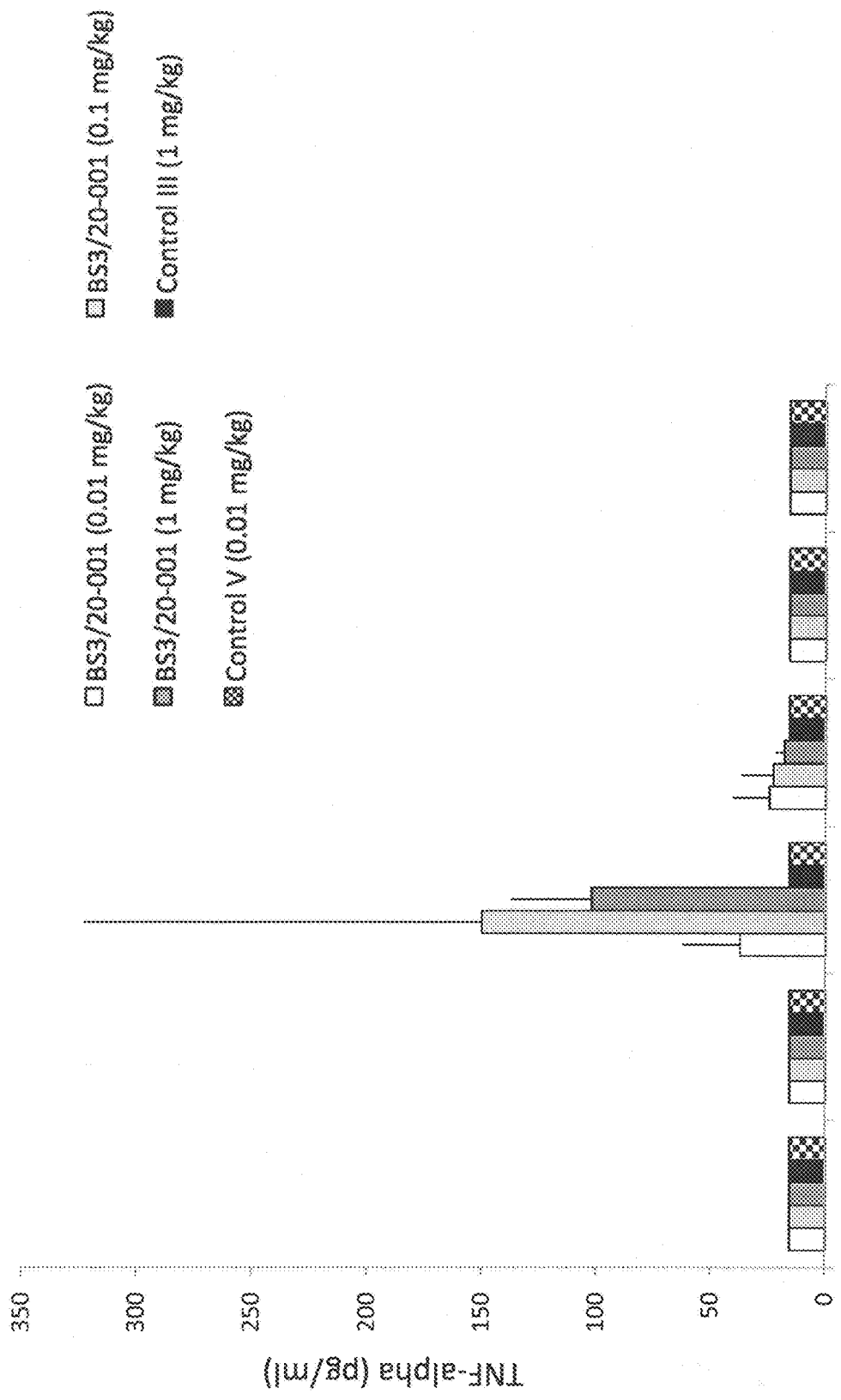
BS3/20-001 (0.01 mg/kg)
BS3/20-001 (1 mg/kg)
Control V (0.01 mg/kg)
BS3/20-001 (0.1 mg/kg)
Control III (1 mg/kg)
TNF-alpha (pg/ml)
350
300
250
200
150
100
50
0
Pre
0
5'
5hr
24hr
96hr
Time

Figure 5D

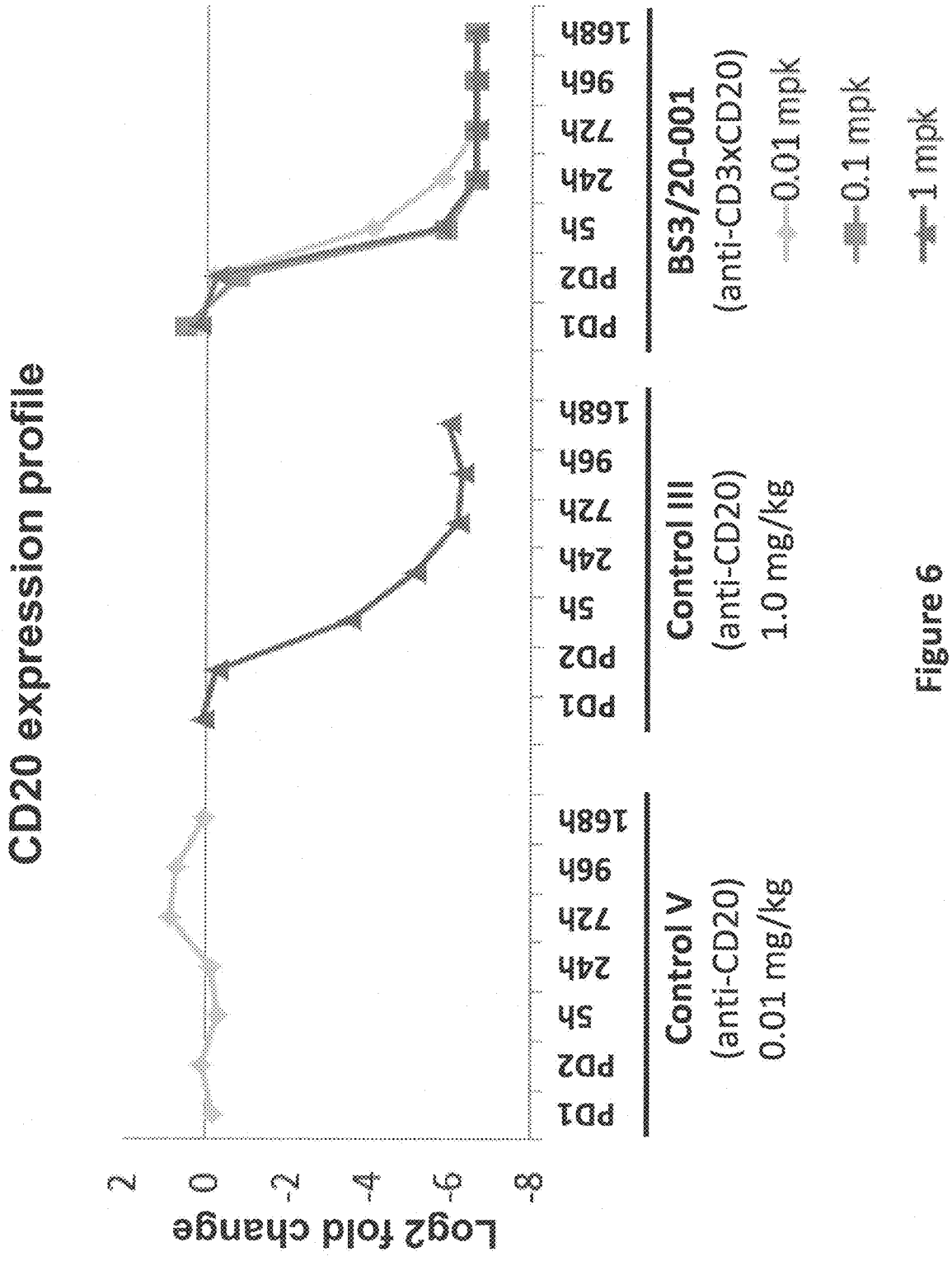
CD20 expression profile
Log2 fold change
2
0
-2
-4
-6
-8
PD1
PD2
5h
24h
72h
96h
168h
Control V
(anti-CD20)
0.01 mg/kg
Control III
(anti-CD20)
1.0 mg/kg
BS3/20-001
(anti-CD3xCD20)
0.01 mpk
0.1 mpk
1 mpk

Figure 6

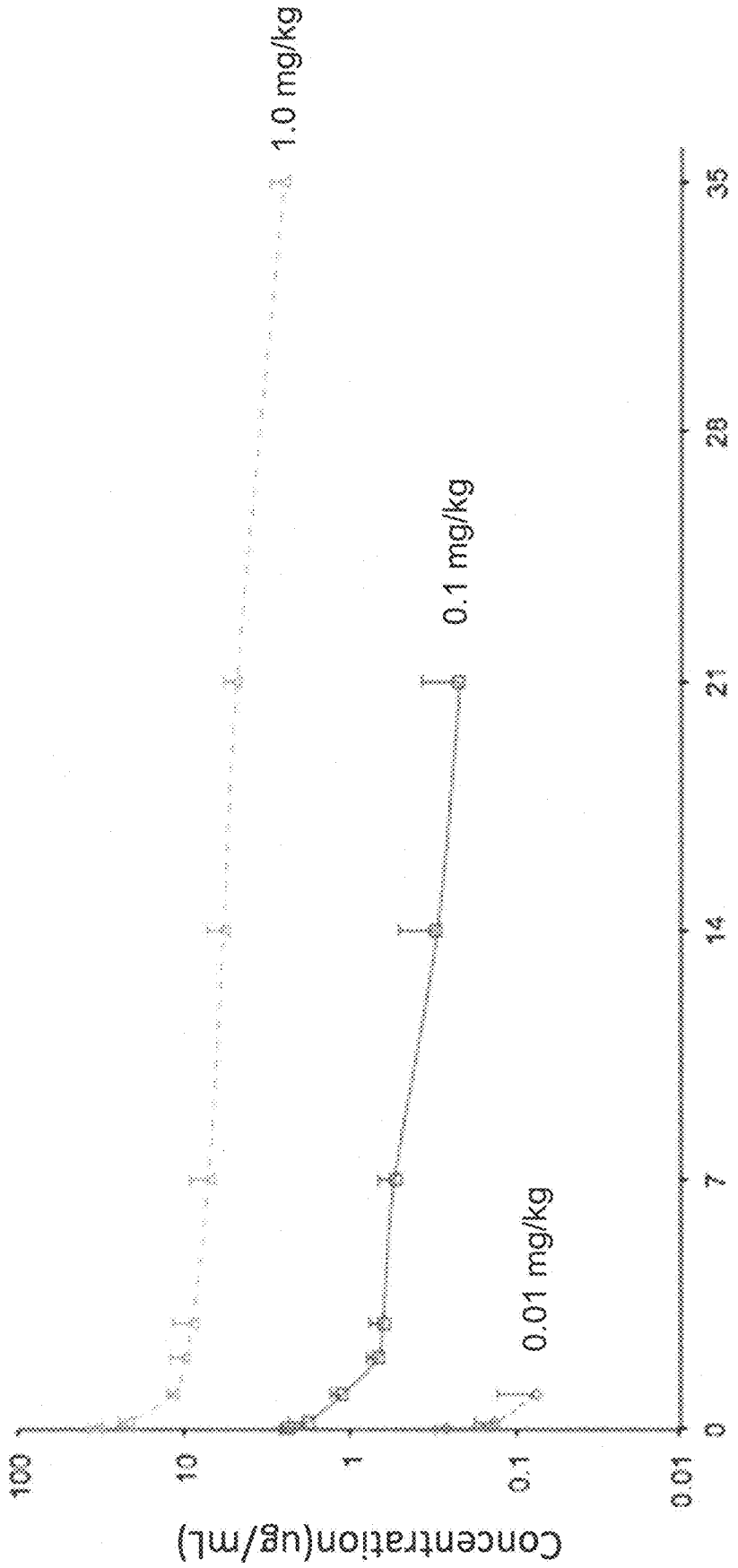
1.0 mg/kg
0.1 mg/kg
0.01 mg/kg
Concentration(ug/mL)
100
10
1
0.1
0.01
0
7
14
21
28
35
Time (Day)

Figure 7

ANTI-CD3 ANTIBODIES, BISPECIFIC ANTIGEN-BINDING MOLECULES THAT BIND CD3 AND CD20, AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a division of U.S. application Ser. No. 15/489,666, filed Apr. 17, 2017, which is a continuation of U.S. application Ser. No. 14/031,075, filed Sep. 19, 2013, now U.S. Pat. No. 9,657,102, which claims the benefit under 35 USC § 119(e) of U.S. Provisional Application No. 61/704,029, filed on Sep. 21, 2012; 61/753,461, filed on Jan. 17, 2013; 61/763,110, filed on Feb. 11, 2013; and 61/827,098, filed on May 24, 2013, the disclosures of which are herein incorporated by reference in their entireties.

REFERENCE TO A SEQUENCE LISTING

[0002] This application includes an electronic sequence listing in a file named "9250U504-Sequence.txt", created on Jun. 23, 2021 and containing 466,774 bytes, which is hereby incorporated by reference in its entirety for all purposes.

FIELD OF THE INVENTION

[0003] The present invention relates to antibodies, and antigen-binding fragments thereof, which are specific for CD3, and methods of use thereof. The present invention also relates to bispecific antigen-binding molecules that bind CD3 and a target molecule such as CD20, and methods of use thereof.

BACKGROUND

[0004] CD3 is a homodimeric or heterodimeric antigen expressed on T cells in association with the T cell receptor complex (TCR) and is required for T cell activation. Functional CD3 is formed from the dimeric association of two of four different chains: epsilon, zeta, delta and gamma. The CD3 dimeric arrangements include gamma/epsilon, delta/epsilon and zeta/zeta. Antibodies against CD3 have been shown to cluster CD3 on T cells, thereby causing T cell activation in a manner similar to the engagement of the TCR by peptide-loaded MHC molecules. Thus, anti-CD3 antibodies have been proposed for therapeutic purposes involving the activation of T cells. In addition, bispecific antibodies that are capable of binding CD3 and a target antigen have been proposed for therapeutic uses involving targeting T cell immune responses to tissues and cells expressing the target antigen.

[0005] CD20 is a non-glycosylated phosphoprotein expressed on the cell membranes of mature B cells. CD20 is considered a B cell tumor-associated antigen because it is expressed by more than 95% of B-cell non-Hodgkin lymphomas (NHLs) and other B-cell malignancies, but it is absent on precursor B-cells, dendritic cells and plasma cells. Methods for treating cancer by targeting CD20 are known in the art. For example, the chimeric anti-CD20 monoclonal antibody rituximab has been used or suggested for use in treating cancers such as NHL, chronic lymphocytic leukemia (CLL) and small lymphocytic lymphoma (SLL). CD20 is believed to kill CD20-expressing tumor cells by complement dependent cytotoxicity (CDC), antibody-dependent cell mediated cytotoxicity (ADCC) and/or induction of apoptosis and sensitization to chemotherapy. Although anti-CD20 tumor targeting strategies have shown great promise in clinical settings, not all patients respond to anti-CD20 therapy, and some patients have been shown to develop resistance to or exhibit incomplete responses to anti-CD20 therapy (e.g., resistance to rituximab).

[0006] Bispecific antigen-binding molecules that bind both CD3 and a target antigen (such as CD20) would be useful in therapeutic settings in which specific targeting and T cell-mediated killing of cells that express the target antigen is desired.

BRIEF SUMMARY OF THE INVENTION

[0007] In a first aspect, the present invention provides antibodies and antigen-binding fragments thereof that bind human CD3. The antibodies according to this aspect of the invention are useful, inter alia, for targeting T cells expressing CD3, and for stimulating T cell activation, e.g., under circumstances where T cell-mediated killing is beneficial or desirable. The anti-CD3 antibodies of the invention, or antigen-binding portions thereof, may be included as part of a bispecific antibody that directs CD3-mediated T cell activation to specific cell types such as tumor cells or infectious agents.

[0008] Exemplary anti-CD3 antibodies of the present invention are listed in Tables 1 and 2 herein. Table 1 sets forth the amino acid sequence identifiers of the heavy chain variable regions (HCVRs) and light chain variable regions (LCVRs), as well as heavy chain complementarity determining regions (HCDR1, HCDR2 and HCDR3), and light chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) of the exemplary anti-CD3 antibodies. Table 2 sets forth the sequence identifiers of the nucleic acid molecules encoding the HCVRs, LCVRs, HCDR1, HCDR2 HCDR3, LCDR1, LCDR2 and LCDR3 of the exemplary anti-CD3 antibodies.

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

[0010] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising an LCVR comprising an amino acid sequence selected from any of the LCVR amino acid sequences listed in Table 1, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0011] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising an HCVR and an LCVR amino acid sequence pair (HCVR/LCVR) comprising any of the HCVR amino acid sequences listed in Table 1 paired with any of the LCVR amino acid sequences listed in Table 1. According to certain embodiments, the present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCVR/LCVR amino acid sequence pair contained within any of the exemplary anti-CD3 antibodies listed in Table 1. In certain embodiments, the HCVR/LCVR amino acid sequence pair is selected from the group consisting of SEQ ID NOs: 2/10 (e.g., H1H2712N); 114/122 (e.g., H2M2609N); 514/522 (e.g., H2M3563N); 770/778 (e.g., H1H5778P); 1050/1234 (e.g., H1H7195B); and 1090/1234 (e.g., H1H7208B).

[0012] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a heavy chain CDR1 (HCDR1) comprising an amino acid sequence selected from any of the HCDR1 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0013] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a heavy chain CDR2 (HCDR2) comprising an amino acid sequence selected from any of the HCDR2 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0014] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a heavy chain CDR3 (HCDR3) comprising an amino acid sequence selected from any of the HCDR3 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0015] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a light chain CDR1 (LCDR1) comprising an amino acid sequence selected from any of the LCDR1 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0016] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a light chain CDR2 (LCDR2) comprising an amino acid sequence selected from any of the LCDR2 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0017] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a light chain CDR3 (LCDR3) comprising an amino acid sequence selected from any of the LCDR3 amino acid sequences listed in Table 1 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0018] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising an HCDR3 and an LCDR3 amino acid sequence pair (HCDR3/LCDR3) comprising any of the HCDR3 amino acid sequences listed in Table 1 paired with any of the LCDR3 amino acid sequences listed in Table 1. According to certain embodiments, the present invention provides antibodies, or antigen-binding fragments thereof, comprising an HCDR3/LCDR3 amino acid sequence pair contained within any of the exemplary anti-CD3 antibodies listed in Table 1. In certain embodiments, the HCDR3/LCDR3 amino acid sequence pair is selected from the group consisting of SEQ ID NOs: 8/16 (e.g., H1H2712N); 120/128 (e.g., H2M2609N); 520/528 (e.g., H2M3563N); 776/784 (e.g., H1H5778P); 1056/1240 (e.g., H1H7195B); and 1096/1240 (e.g., H1H7208B).

[0019] The present invention also provides antibodies, or antigen-binding fragments thereof, comprising a set of six CDRs HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3) contained within any of the exemplary anti-CD3 antibodies listed in Table 1. In certain embodiments, the HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences set is selected from the group consisting of SEQ ID NOs: 4-6-8-12-14-16 (e.g., H1H2712N); 116-118-120-124-126-128 (e.g., H2M2609N); 516-518-520-524-526-528 (e.g., H2M3563N); 772-774-776-780-782-784 (e.g., H1H5778P); 1052-1054-1056-1236-1238-1240 (e.g., H1H7195B); and 1092-1094-1096-1236-1238-1240 (e.g., H1H7208B).

[0020] In a related embodiment, the present invention provides antibodies, or antigen-binding fragments thereof, comprising a set of six CDRs HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3) contained within an HCVR/LCVR amino acid sequence pair as defined by any of the exemplary anti-CD3 antibodies listed in Table 1. For example, the present invention includes antibodies, or antigen-binding fragments thereof, comprising the HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences set contained within an HCVR/LCVR amino acid sequence pair selected from the group consisting of SEQ ID NOs: 2/10 (e.g., H1H2712N); 114/122 (e.g., H2M2609N); 514/522 (e.g., H2M3563N); 770/778 (e.g., H1H5778P); 1050/1234 (e.g., H1H7195B); and 1090/1234 (e.g., H1H7208B). Methods and techniques for identifying CDRs within HCVR and LCVR amino acid sequences are well known in the art and can be used to identify CDRs within the specified HCVR and/or LCVR amino acid sequences disclosed herein. Exemplary conventions that can be used to identify the boundaries of CDRs include, e.g., the Kabat definition, the Chothia definition, and the AbM definition. In general terms, the Kabat definition is based on sequence variability, the Chothia definition is based on the location of the structural loop regions, and the AbM definition is a compromise between the Kabat and Chothia approaches. See, e.g., Kabat, "Sequences of Proteins of Immunological Interest," National Institutes of Health, Bethesda, Md. (1991); Al-Lazikani et al., *J. Mol. Biol.* 273:927-948 (1997); and Martin et al., *Proc. Natl. Acad. Sci. USA* 86:9268-9272 (1989). Public databases are also available for identifying CDR sequences within an antibody.

[0021] The present invention also provides nucleic acid molecules encoding anti-CD3 antibodies or portions thereof. For example, the present invention provides nucleic acid molecules encoding any of the HCVR amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

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

[0023] The present invention also provides nucleic acid molecules encoding any of the HCDR1 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR1 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0024] The present invention also provides nucleic acid molecules encoding any of the HCDR2 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR2 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0025] The present invention also provides nucleic acid molecules encoding any of the HCDR3 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCDR3 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0026] The present invention also provides nucleic acid molecules encoding any of the LCDR1 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR1 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0027] The present invention also provides nucleic acid molecules encoding any of the LCDR2 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR2 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0028] The present invention also provides nucleic acid molecules encoding any of the LCDR3 amino acid sequences listed in Table 1; in certain embodiments the nucleic acid molecule comprises a polynucleotide sequence selected from any of the LCDR3 nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto.

[0029] The present invention also provides nucleic acid molecules encoding an HCVR, wherein the HCVR comprises a set of three CDRs (i.e., HCDR1-HCDR2-HCDR3), wherein the HCDR1-HCDR2-HCDR3 amino acid sequence set is as defined by any of the exemplary anti-CD3 antibodies listed in Table 1.

[0030] The present invention also provides nucleic acid molecules encoding an LCVR, wherein the LCVR comprises a set of three CDRs (i.e., LCDR1-LCDR2-LCDR3), wherein the LCDR1-LCDR2-LCDR3 amino acid sequence set is as defined by any of the exemplary anti-CD3 antibodies listed in Table 1.

[0031] The present invention also provides nucleic acid molecules encoding both an HCVR and an LCVR, wherein the HCVR comprises an amino acid sequence of any of the HCVR amino acid sequences listed in Table 1, and wherein the LCVR comprises an amino acid sequence of any of the LCVR amino acid sequences listed in Table 1. In certain embodiments, the nucleic acid molecule comprises a polynucleotide sequence selected from any of the HCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto, and a polynucleotide sequence selected from any of the LCVR nucleic acid sequences listed in Table 2, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity thereto. In certain embodiments according to this aspect of the invention, the nucleic acid molecule encodes an HCVR and LCVR, wherein the HCVR and LCVR are both derived from the same anti-CD3 antibody listed in Table 1.

[0032] The present invention also provides recombinant expression vectors capable of expressing a polypeptide comprising a heavy or light chain variable region of an anti-CD3 antibody. For example, the present invention includes recombinant expression vectors comprising any of the nucleic acid molecules mentioned above, i.e., nucleic acid molecules encoding any of the HCVR, LCVR, and/or CDR sequences as set forth in Table 1. Also included within the scope of the present invention are host cells into which such vectors have been introduced, as well as methods of producing the antibodies or portions thereof by culturing the host cells under conditions permitting production of the antibodies or antibody fragments, and recovering the antibodies and antibody fragments so produced.

[0033] The present invention includes anti-CD3 antibodies having a modified glycosylation pattern. In some embodiments, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

[0034] In another aspect, the invention provides a pharmaceutical composition comprising a recombinant human antibody or fragment thereof which specifically binds CD3 and a pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of an anti-CD3 antibody and a second therapeutic agent. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with an anti-CD3 antibody. Exemplary agents that may be advantageously combined with an anti-CD3 antibody include, without limitation, other agents that bind and/or activate CD3 signaling (including other antibodies or antigen-binding fragments thereof, etc.) and/or agents which do not directly bind CD3 but nonetheless activate or stimulate immune cell activation. Additional combination therapies and co-formulations involving the anti-CD3 antibodies of the present invention are disclosed elsewhere herein.

[0035] In yet another aspect, the invention provides therapeutic methods for stimulating T cell activation using an anti-CD3 antibody or antigen-binding portion of an antibody of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an antibody or antigen-binding fragment of an antibody of the invention to a subject in need thereof. The disorder treated is any disease or condition which is improved, ameliorated, inhibited or prevented by stimulation of CD3 activity or signaling.

[0036] According to another aspect, the present invention provides bispecific antigen-binding molecules that bind CD3 and a target antigen. According to certain exemplary embodiments, the bispecific antigen-binding molecules bind CD3 and CD20; such bispecific antigen-binding molecules are also referred to herein as "anti-CD3/anti-CD20 bispecific molecules." The anti-CD20 portion of the anti-CD3/anti-

CD20 bispecific molecule is useful for targeting tumor cells that express CD20 (e.g., B-cell tumors), and the anti-CD3 portion of the bispecific molecule is useful for activating T-cells. The simultaneous binding of CD20 on a tumor cell and CD3 on a T-cell facilitates directed killing (cell lysis) of the targeted tumor cell by the activated T-cell. The anti-CD3/anti-CD20 bispecific molecules of the invention are therefore useful, inter alia, for treating diseases and disorders related to or caused by CD20-expressing tumors (e.g., lymphomas).

[0037] The bispecific antigen-binding molecules according to this aspect of the present invention comprise a first antigen-binding domain that specifically binds human CD3, and a second antigen-binding domain that specifically binds CD20. The present invention includes anti-CD3/anti-CD20 bispecific molecules (e.g., bispecific antibodies) wherein each antigen-binding domain comprises a heavy chain variable region (HCVR) paired with a light chain variable region (LCVR). In certain exemplary embodiments of the invention, the anti-CD3 antigen-binding domain and the anti-CD20 antigen binding domain each comprise different, distinct HCVRs paired with a common LCVR. For example, as illustrated in Example 7 herein, bispecific antibodies were constructed comprising a first antigen-binding domain that specifically binds CD3, wherein the first antigen-binding domain comprises an HCVR/LCVR pair derived from an anti-CD3 antibody; and a second antigen-binding domain that specifically binds CD20, wherein the second antigen-binding domain comprises an HCVR derived from an anti-CD20 antibody paired with an LCVR derived from an anti-CD3 antibody (e.g., the same LCVR that is included in the anti-CD3 antigen-binding domain). In other words, in the exemplary molecules disclosed herein, the pairing of an HCVR from an anti-CD20 antibody with an LCVR from an anti-CD3 antibody creates an antigen-binding domain that specifically binds CD20 (but does not bind CD3). In such embodiments, the first and second antigen-binding domains comprise distinct anti-CD3 and anti-CD20 HCVRs but share a common anti-CD3 LCVR.

[0038] The present invention provides anti-CD3/anti-CD20 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises any of the HCVR amino acid sequences as set forth in Table 1 or Table 18. The first antigen-binding domain that specifically binds CD3 may also comprise any of the LCVR amino acid sequences as set forth in Table 1 or Table 19. According to certain embodiments, the first antigen-binding domain that specifically binds CD3 comprises any of the HCVR/LCVR amino acid sequence pairs as set forth in Table 1 or Table 17. The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises any of the heavy chain CDR1-CDR2-CDR3 amino acid sequences as set forth in Table 1 or Table 18, and/or any of the light chain CDR1-CDR2-CDR3 amino acid sequences as set forth in Table 1 or Table 19.

[0039] According to certain embodiments, the present invention provides anti-CD3/anti-CD20 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a heavy chain variable region (HCVR) having an amino acid sequence selected from the group consisting of SEQ ID NOs:1250, 1266, 1282, 1298, 1314 and 1329 or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0040] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a light chain variable region (LCVR) having an amino acid sequence selected from the group consisting of SEQ ID NOs:1258, 1274, 1290, 1306, 1322 and 1333, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0041] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a HCVR and LCVR (HCVR/LCVR) amino acid sequence pair selected from the group consisting of SEQ ID NOs:1250/1258, 1266/1274, 1282/1290, 1298/1306, 1314/1322, and 1329/1333.

[0042] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a heavy chain CDR3 (HCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:1256, 1272, 1288, 1304, 1320 and 1332, or a substantially similar sequence thereto having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR3 (LCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:1264, 1280, 1296, 1312, 1328 and 1336, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0043] In certain embodiments, the first antigen-binding domain that specifically binds CD3 comprises a HCDR3/LCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOs: 1256/1264, 1272/1280, 1288/1296, 1304/1312, 1320/1328 and 1332/1336.

[0044] The present invention also provides anti-CD3/anti-CD20 bispecific antigen-binding molecules, wherein the first antigen-binding domain that specifically binds CD3 comprises a heavy chain CDR1 (HCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:1252, 1268, 1284, 1300, 1316 and 1330, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR2 (HCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:1254, 1270, 1286, 1302, 1318 and 1331, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR1 (LCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:1260, 1276, 1292, 1308, 1324 and 1334, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR2 (LCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs:1262, 1278, 1294, 1310, 1326 and 1335, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0045] Certain non-limiting, exemplary anti-CD3/anti-CD20 bispecific antigen-binding molecules of the invention include a first antigen-binding domain that specifically binds CD3 comprising HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, having the amino

acid sequences selected from the group consisting of: SEQ ID NOs: 1252-1254-1256-1260-1262-1264 (e.g. B53/20-001); 1268-1270-1272-1276-1278-1280 (e.g. B53/20-002); 1284-1286-1288-1292-1294-1296 (e.g. B53/20-003); 1300-1302-1304-1308-1310-1312 (e.g. B53/20-004); 1316-1318-1320-1324-1326-1328 (e.g. B53-20-005); and 1330-1331-1332-1334-1335-1336 (e.g. B53/20-007).

[0046] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the second antigen-binding domain that specifically binds CD20 comprises a heavy chain variable region (HCVR) having the amino acid sequence of SEQ ID NO:1242, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0047] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the second antigen-binding domain that specifically binds CD20 comprises a light chain variable region (LCVR) having the amino acid sequence selected from the group consisting of SEQ ID NOs:1258, 1274, 1290, 1306, 1322 and 1333, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0048] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the second antigen-binding domain that specifically binds CD20 comprises a HCVR and LCVR (HCVR/LCVR) amino acid sequence pair selected from the group consisting of SEQ ID NOs: 1242/1258, 1242/1274, 1242/1290, 1242/1306, 1242/1322 and 1242/1333.

[0049] The present invention also provides anti-CD3/anti-CD20 bispecific molecules, wherein the second antigen-binding domain that specifically binds CD20 comprises a heavy chain CDR3 (HCDR3) domain having the amino acid sequence of SEQ ID NO:1248, or a substantially similar sequence thereto having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR3 (LCDR3) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0050] In certain embodiments, the second antigen-binding domain that specifically binds CD20 comprises a HCDR3/LCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOs: 1248/1264, 1248/1280, 1248/1296, 1248/1312, 1248/1328 and 1248/1336.

[0051] The present invention also provides anti-CD3/anti-CD20 bispecific antigen-binding molecules, wherein the second antigen-binding domain that specifically binds CD20 comprises a heavy chain CDR1 (HCDR1) domain having the amino acid sequence of SEQ ID NO:1244, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a heavy chain CDR2 (HCDR2) domain having the amino acid sequence of SEQ ID NO:1246, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; a light chain CDR1 (LCDR1) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1260, 1276, 1292, 1308, 1324 and 1334, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity; and a light chain CDR2 (LCDR2) domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, or a substantially similar sequence thereof having at least 90%, at least 95%, at least 98% or at least 99% sequence identity.

[0052] Certain non-limiting, exemplary anti-CD3/anti-CD20 bispecific antigen-binding molecules of the invention include a second antigen-binding domain that specifically binds CD20 comprising HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, having the amino acid sequences selected from the group consisting of: SEQ ID NOs: 1244-1246-1248-1260-1262-1264 (e.g. B53/20-001); 1244-1246-1248-1276-1278-1280 (e.g. B53/20-002); 1244-1246-1248-1292-1294-1296 (e.g. B53/20-003); 1244-1246-1248-1308-1310-1312 (e.g. B53/20-004); 1244-1246-1248-1324-1326-1328 (e.g. B53-20-005); and 1244-1246-1248-1334-1335-1336 (e.g. B53/20-007).

[0053] In a related embodiment, the invention includes anti-CD3/anti-CD20 bispecific antigen-binding molecules wherein the second antigen-binding domain that specifically binds CD20 comprises the heavy and light chain CDR domains contained within heavy and light chain variable region (HCVR/LCVR) sequences selected from the group consisting of SEQ ID NOs: 1242/1258, 1242/1274, 1242/1290, 1242/1306, 1242/1322 and 1242/1333.

[0054] In another aspect, the present invention provides nucleic acid molecules encoding any of the HCVR, LCVR or CDR sequences of the anti-CD3/anti-CD20 bispecific antigen-binding molecules disclosed herein, including nucleic acid molecules comprising the polynucleotide sequences as set forth in Tables 20 and 21 herein, as well as nucleic acid molecules comprising two or more of the polynucleotide sequences as set forth in Tables 20 and 21 in any functional combination or arrangement thereof. Recombinant expression vectors carrying the nucleic acids of the invention, and host cells into which such vectors have been introduced, are also encompassed by the invention, as are methods of producing the antibodies by culturing the host cells under conditions permitting production of the antibodies, and recovering the antibodies produced.

[0055] The present invention includes anti-CD3/anti-CD20 bispecific antigen-binding molecules wherein any of the aforementioned antigen-binding domains that specifically bind CD3 is combined, connected or otherwise associated with any of the aforementioned antigen-binding domains that specifically bind CD20 to form a bispecific antigen-binding molecule that binds CD3 and CD20.

[0056] The present invention includes anti-CD3/anti-CD20 bispecific antigen-binding molecules having a modified glycosylation pattern. In some applications, modification to remove undesirable glycosylation sites may be useful, or an antibody lacking a fucose moiety present on the oligosaccharide chain, for example, to increase antibody dependent cellular cytotoxicity (ADCC) function (see Shield et al. (2002) JBC 277:26733). In other applications, modification of galactosylation can be made in order to modify complement dependent cytotoxicity (CDC).

[0057] In another aspect, the invention provides a pharmaceutical composition comprising an anti-CD3/anti-CD20 bispecific antigen-binding molecule as disclosed herein and a pharmaceutically acceptable carrier. In a related aspect, the invention features a composition which is a combination of an anti-CD3/anti-CD20 bispecific antigen-binding molecule and a second therapeutic agent. In one embodiment, the second therapeutic agent is any agent that is advantageously combined with an anti-CD3/anti-CD20 bispecific antigen-

binding molecule. Exemplary agents that may be advantageously combined with an anti-CD3/anti-CD20 bispecific antigen-binding molecule are discussed in detail elsewhere herein.

[0058] In yet another aspect, the invention provides therapeutic methods for targeting/killing tumor cells expressing CD20 using an anti-CD3/anti-CD20 bispecific antigen-binding molecule of the invention, wherein the therapeutic methods comprise administering a therapeutically effective amount of a pharmaceutical composition comprising an anti-CD3/anti-CD20 bispecific antigen-binding molecule of the invention to a subject in need thereof.

[0059] The present invention also includes the use of an anti-CD3/anti-CD20 bispecific antigen-binding molecule of the invention in the manufacture of a medicament for the treatment of a disease or disorder related to or caused by CD20 expression.

[0060] Other embodiments will become apparent from a review of the ensuing detailed description.

BRIEF DESCRIPTION OF THE FIGURES

[0061] FIG. **1** shows the tumor volume (in mm^3) over time in NOD/SCID mice implanted subcutaneously with a mixture of Raji tumor cells and PBMCs following tumor implantation and treatment, starting the day of tumor implantation, with either human Fc (hFc, solid line) or CD3×CD20 bispecific antibody (BS3/20-007, dashed line).

[0062] FIG. **2** shows the tumor volume (in mm^3) over time in NOD/SCID mice implanted subcutaneously with a mixture of Raji tumor cells and PBMCs following tumor implantation and treatment, starting 7 days after tumor implantation, with either human Fc (hFc, solid line) or CD3×CD20 bispecific antibody (BS3/20-007, dashed line).

[0063] FIG. **3** shows a plot of B-cell numbers (×1000/μL) over time in blood samples from cynomolgus monkeys treated with three different doses of bispecific antibody BS3/20-001 (0.01, 0.1 or 1.0 mg/kg); low-dose anti-CD20 control antibody (Control V, 0.01 mg/kg); or high-dose anti-CD20 control antibody (Control III (1.0 mg/kg).

[0064] FIG. **4** shows a plot of T-cell numbers (×1000/μL) over time in blood samples from cynomolgus monkeys treated with three different doses of bispecific antibody BS3/20-001 (0.01, 0.1 or 1.0 mg/kg); low-dose anti-CD20 control antibody (Control V, 0.01 mg/kg); or high-dose anti-CD20 control antibody (Control III (1.0 mg/kg).

[0065] FIGS. **5**A, **5**B, **5**C and **5**D show the pre-dose and post-dose levels (pg/mL) of IFN-gamma, IL-2, IL-6, and TNF-alpha, respectively, for cynomolgous monkeys treated with a single dose of BS3/20-001 (0.01, 0.1 or 1.0 mg/kg), low dose anti-CD20 control antibody (0.01 mg/kg Control V), or high-dose anti-CD20 control antibody (1.0 mg/kg Control III).

[0066] FIG. **6** shows the CD20 expression profile (expressed in terms of Log2 fold change in expression) determined from blood samples taken at various time points from cynomolgus monkeys treated with 0.01 mg/kg Control V (anti-CD20 antibody); 1.0 mg/kg Control III (anti-CD20 antibody); and 0.01 mg/kg, 0.1 mg/kg and 1.0 mg/kg BS3/20-001 (anti-CD3×CD20 bispecific antibody).

[0067] FIG. **7** shows the total serum concentration (pg/mL) of CD3×CD20 bispecific antibody (BS3/20-001) over time in blood samples from cynomolgus monkeys treated with 1.0 mg/kg (open triangles), 0.1 mg/kg (open squares) or 0.01 mg/kg (open diamonds) of CD3×CD20 bispecific antibody.

DETAILED DESCRIPTION

[0068] Before the present invention is described, it is to be understood that this invention is not limited to particular methods and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

[0069] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. As used herein, the term "about," when used in reference to a particular recited numerical value, means that the value may vary from the recited value by no more than 1%. For example, as used herein, the expression "about 100" includes 99 and 101 and all values in between (e.g., 99.1, 99.2, 99.3, 99.4, etc.).

[0070] Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All patents, applications and non-patent publications mentioned in this specification are incorporated herein by reference in their entireties.

Definitions

[0071] The expression "CD3," as used herein, refers to an antigen which is expressed on T cells as part of the multimolecular T cell receptor (TCR) and which consists of a homodimer or heterodimer formed from the association of two of four receptor chains: CD3-epsilon, CD3-delta, CD3-zeta, and CD3-gamma. Human CD3-epsilon comprises the amino acid sequence as set forth in SEQ ID NO:1370; human CD3-delta comprises the amino acid sequence as set forth in SEQ ID NO:1371. All references to proteins, polypeptides and protein fragments herein are intended to refer to the human version of the respective protein, polypeptide or protein fragment unless explicitly specified as being from a non-human species. Thus, the expression "CD3" means human CD3 unless specified as being from a non-human species, e.g., "mouse CD3," "monkey CD3," etc.

[0072] As used herein, "an antibody that binds CD3" or an "anti-CD3 antibody" includes antibodies and antigen-binding fragments thereof that specifically recognize a single CD3 subunit (e.g., epsilon, delta, gamma or zeta), as well as antibodies and antigen-binding fragments thereof that specifically recognize a dimeric complex of two CD3 subunits (e.g., gamma/epsilon, delta/epsilon, and zeta/zeta CD3 dimers). The antibodies and antigen-binding fragments of the present invention may bind soluble CD3 and/or cell surface expressed CD3. Soluble CD3 includes natural CD3 proteins as well as recombinant CD3 protein variants such as, e.g., monomeric and dimeric CD3 constructs, that lack a transmembrane domain or are otherwise unassociated with a cell membrane.

[0073] As used herein, the expression "cell surface-expressed CD3" means one or more CD3 protein(s) that is/are

expressed on the surface of a cell in vitro or in vivo, such that at least a portion of a CD3 protein is exposed to the extracellular side of the cell membrane and is accessible to an antigen-binding portion of an antibody. "Cell surface-expressed CD3" includes CD3 proteins contained within the context of a functional T cell receptor in the membrane of a cell. The expression "cell surface-expressed CD3" includes CD3 protein expressed as part of a homodimer or heterodimer on the surface of a cell (e.g., gamma/epsilon, delta/epsilon, and zeta/zeta CD3 dimers). The expression, "cell surface-expressed CD3" also includes a CD3 chain (e.g., CD3-epsilon, CD3-delta or CD3-gamma) that is expressed by itself, without other CD3 chain types, on the surface of a cell. A "cell surface-expressed CD3" can comprise or consist of a CD3 protein expressed on the surface of a cell which normally expresses CD3 protein. Alternatively, "cell surface-expressed CD3" can comprise or consist of CD3 protein expressed on the surface of a cell that normally does not express human CD3 on its surface but has been artificially engineered to express CD3 on its surface.

[0074] As used herein, the expression "anti-CD3 antibody" includes both monovalent antibodies with a single specificity, as well as bispecific antibodies comprising a first arm that binds CD3 and a second arm that binds a second (target) antigen, wherein the anti-CD3 arm comprises any of the HCVR/LCVR or CDR sequences as set forth in Table 1 or Tables 18/19 herein. Examples of anti-CD3 bispecific antibodies are described elsewhere herein. The term "antigen-binding molecule" includes antibodies and antigen-binding fragments of antibodies, including, e.g., bispecific antibodies.

[0075] The term "antibody", as used herein, means any antigen-binding molecule or molecular complex comprising at least one complementarity determining region (CDR) that specifically binds to or interacts with a particular antigen (e.g., CD3). The term "antibody" includes immunoglobulin molecules comprising four polypeptide chains, two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, as well as multimers thereof (e.g., IgM). Each heavy chain comprises a heavy chain variable region (abbreviated herein as HCVR or V_H) and a heavy chain constant region. The heavy chain constant region comprises three domains, C_H1, C_H2 and C_H3. Each light chain comprises a light chain variable region (abbreviated herein as LCVR or V_L) and a light chain constant region. The light chain constant region comprises one domain (C_L1). The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. In different embodiments of the invention, the FRs of the anti-CD3 antibody (or antigen-binding portion thereof) may be identical to the human germline sequences, or may be naturally or artificially modified. An amino acid consensus sequence may be defined based on a side-by-side analysis of two or more CDRs.

[0076] The term "antibody", as used herein, also includes antigen-binding fragments of full antibody molecules. The terms "antigen-binding portion" of an antibody, "antigen-binding fragment" of an antibody, and the like, as used herein, include any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Antigen-binding fragments of an antibody may be derived, e.g., from full antibody molecules using any suitable standard techniques such as proteolytic digestion or recombinant genetic engineering techniques involving the manipulation and expression of DNA encoding antibody variable and optionally constant domains. Such DNA is known and/or is readily available from, e.g., commercial sources, DNA libraries (including, e.g., phage-antibody libraries), or can be synthesized. The DNA may be sequenced and manipulated chemically or by using molecular biology techniques, for example, to arrange one or more variable and/or constant domains into a suitable configuration, or to introduce codons, create cysteine residues, modify, add or delete amino acids, etc.

[0077] Non-limiting examples of antigen-binding fragments include: (i) Fab fragments; (ii) F(ab')2 fragments; (iii) Fd fragments; (iv) Fv fragments; (v) single-chain Fv (scFv) molecules; (vi) dAb fragments; and (vii) minimal recognition units consisting of the amino acid residues that mimic the hypervariable region of an antibody (e.g., an isolated complementarity determining region (CDR) such as a CDR3 peptide), or a constrained FR3-CDR3-FR4 peptide. Other engineered molecules, such as domain-specific antibodies, single domain antibodies, domain-deleted antibodies, chimeric antibodies, CDR-grafted antibodies, diabodies, triabodies, tetrabodies, minibodies, nanobodies (e.g. monovalent nanobodies, bivalent nanobodies, etc.), small modular immunopharmaceuticals (SMIPs), and shark variable IgNAR domains, are also encompassed within the expression "antigen-binding fragment," as used herein.

[0078] An antigen-binding fragment of an antibody will typically comprise at least one variable domain. The variable domain may be of any size or amino acid composition and will generally comprise at least one CDR which is adjacent to or in frame with one or more framework sequences. In antigen-binding fragments having a V_H domain associated with a V_L domain, the V_H and V_L domains may be situated relative to one another in any suitable arrangement. For example, the variable region may be dimeric and contain V_H-V_H, V_H-V_L or V_L-V_L dimers. Alternatively, the antigen-binding fragment of an antibody may contain a monomeric V_H or V_L domain.

[0079] In certain embodiments, an antigen-binding fragment of an antibody may contain at least one variable domain covalently linked to at least one constant domain. Non-limiting, exemplary configurations of variable and constant domains that may be found within an antigen-binding fragment of an antibody of the present invention include: (i) V_H-C_H1; (ii) V_H-C_H2; (iii) V_H-C_H3; (iv) V_H-C_H1-C_H2; (v) V_H-C_H1-C_H2-C_H3; (vi) V_H-C_H2-C_H3; (ii) V_H-C_L; (viii) V_L-C_H1; (ix) V_L-C_H2; (x) V_L-C_H3; (xi) V_L-C_HI-C_H2; (xii) V_L-C_HI-C_H2-C_H3; (xiii) V_L-C_H2-C_H3; and (xiv) V_L-C_L. In any configuration of variable and constant domains, including any of the exemplary configurations listed above, the variable and constant domains may be either directly linked to one another or may be linked by a full or partial hinge or linker region. A hinge region may consist of at least 2 (e.g., 5, 10, 15, 20, 40, 60 or more) amino acids which result in a flexible or semi-flexible linkage between adjacent variable and/or constant domains in a single polypeptide molecule. Moreover, an antigen-binding fragment of an antibody of the present invention may comprise a homo-dimer or hetero-

dimer (or other multimer) of any of the variable and constant domain configurations listed above in non-covalent association with one another and/or with one or more monomeric V_H or V_L domain (e.g., by disulfide bond(s)).

[0080] As with full antibody molecules, antigen-binding fragments may be monospecific or multispecific (e.g., bispecific). A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format, including the exemplary bispecific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art.

[0081] The antibodies of the present invention may function through complement-dependent cytotoxicity (CDC) or antibody-dependent cell-mediated cytotoxicity (ADCC). "Complement-dependent cytotoxicity" (CDC) refers to lysis of antigen-expressing cells by an antibody of the invention in the presence of complement. "Antibody-dependent cell-mediated cytotoxicity" (ADCC) refers to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and thereby lead to lysis of the target cell. CDC and ADCC can be measured using assays that are well known and available in the art. (See, e.g., U.S. Pat. Nos. 5,500,362 and 5,821,337, and Clynes et al. (1998) Proc. Natl. Acad. Sci. (USA) 95:652-656). The constant region of an antibody is important in the ability of an antibody to fix complement and mediate cell-dependent cytotoxicity. Thus, the isotype of an antibody may be selected on the basis of whether it is desirable for the antibody to mediate cytotoxicity.

[0082] In certain embodiments of the invention, the anti-CD3 antibodies of the invention (monospecific or bispecific) are human antibodies. The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo), for example in the CDRs and in particular CDR3. However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences.

[0083] The antibodies of the invention may, in some embodiments, be recombinant human antibodies. The term "recombinant human antibody", as used herein, is intended to include all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as antibodies expressed using a recombinant expression vector transfected into a host cell (described further below), antibodies isolated from a recombinant, combinatorial human antibody library (described further below), antibodies isolated from an animal (e.g., a mouse) that is transgenic for human immunoglobulin genes (see e.g., Taylor et al. (1992) Nucl. Acids Res. 20:6287-6295) or antibodies prepared, expressed, created or isolated by any other means that involves splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable and constant regions derived from human germline immunoglobulin sequences. In certain embodiments, however, such recombinant human antibodies are subjected to in vitro mutagenesis (or, when an animal transgenic for human Ig sequences is used, in vivo somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire in vivo.

[0084] Human antibodies can exist in two forms that are associated with hinge heterogeneity. In one form, an immunoglobulin molecule comprises a stable four chain construct of approximately 150-160 kDa in which the dimers are held together by an interchain heavy chain disulfide bond. In a second form, the dimers are not linked via inter-chain disulfide bonds and a molecule of about 75-80 kDa is formed composed of a covalently coupled light and heavy chain (half-antibody). These forms have been extremely difficult to separate, even after affinity purification.

[0085] The frequency of appearance of the second form in various intact IgG isotypes is due to, but not limited to, structural differences associated with the hinge region isotype of the antibody. A single amino acid substitution in the hinge region of the human IgG4 hinge can significantly reduce the appearance of the second form (Angal et al. (1993) Molecular Immunology 30:105) to levels typically observed using a human IgG1 hinge. The instant invention encompasses antibodies having one or more mutations in the hinge, C_H2 or C_H3 region which may be desirable, for example, in production, to improve the yield of the desired antibody form.

[0086] The antibodies of the invention may be isolated antibodies. An "isolated antibody," as used herein, means an antibody that has been identified and separated and/or recovered from at least one component of its natural environment. For example, an antibody that has been separated or removed from at least one component of an organism, or from a tissue or cell in which the antibody naturally exists or is naturally produced, is an "isolated antibody" for purposes of the present invention. An isolated antibody also includes an antibody in situ within a recombinant cell. Isolated antibodies are antibodies that have been subjected to at least one purification or isolation step. According to certain embodiments, an isolated antibody may be substantially free of other cellular material and/or chemicals.

[0087] The present invention also includes one-arm antibodies that bind CD3. As used herein, a "one-arm antibody" means an antigen-binding molecule comprising a single antibody heavy chain and a single antibody light chain. The one-arm antibodies of the present invention may comprise any of the HCVR/LCVR or CDR amino acid sequences as set forth in Table 1 or Tables 18/19 herein.

[0088] The anti-CD3 antibodies disclosed herein may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences from which the antibodies were derived. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The present invention includes antibodies, and antigen-binding fragments thereof, which

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

[0089] The present invention also includes anti-CD3 antibodies comprising variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes anti-CD3 antibodies having HCVR, LCVR, and/or CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences set forth in Table 1 herein.

[0090] The term "epitope" refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

[0091] The term "substantial identity" or "substantially identical," when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95%, and more preferably at least about 96%, 97%, 98% or 99% of the nucleotide bases, as measured by any well-known algorithm of sequence identity, such as FASTA, BLAST or Gap, as discussed below. A nucleic acid molecule having substantial identity to a reference nucleic acid molecule may, in certain instances, encode a polypeptide having the same or substantially similar amino acid sequence as the polypeptide encoded by the reference nucleic acid molecule.

[0092] As applied to polypeptides, the term "substantial similarity" or "substantially similar" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) Methods Mol. Biol. 24: 307-331, herein incorporated by reference. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al. (1992) Science 256: 1443-1445, herein incorporated by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0093] Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypep-

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

Bispecific Antigen-Binding Molecules

[0094] The antibodies of the present invention may be monospecific, bi-specific, or multispecific. Multispecific antibodies may be specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, e.g., Tutt et al., 1991, J. Immunol. 147:60-69; Kufer et al., 2004, Trends Biotechnol. 22:238-244. The anti-CD3 antibodies of the present invention can be linked to or co-expressed with another functional molecule, e.g., another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment to produce a bi-specific or a multispecific antibody with a second binding specificity.

[0095] Use of the expression "anti-CD3 antibody" herein is intended to include both monospecific anti-CD3 antibodies as well as bispecific antibodies comprising a CD3-binding arm and a second arm that binds a target antigen. Thus, the present invention includes bispecific antibodies wherein one arm of an immunoglobulin binds human CD3, and the other arm of the immunoglobulin is specific for a target antigen. The target antigen that the other arm of the CD3 bispecific antibody binds can be any antigen expressed on or in the vicinity of a cell, tissue, organ, microorganism or virus, against which a targeted immune response is desired. The CD3-binding arm can comprise any of the HCVR/LCVR or CDR amino acid sequences as set forth in Table 1 or Tables 18/19 herein. In certain embodiments, the CD3-binding arm binds human CD3 and induces human T cell proliferation.

[0096] In the context of bispecific antibodies of the present invention wherein one arm of the antibody binds CD3 and the other arm binds a target antigen, the target antigen can be a tumor-associated antigen. Non-limiting examples of specific tumor-associated antigens include, e.g., AFP, ALK, BAGE proteins, β-catenin, brc-abl, BRCA1, BORIS, CA9, carbonic anhydrase IX, caspase-8, CCR5, CD19, CD20, CD30, CD40, CDK4, CEA, CTLA4, cyclin-B1, CYP1B1, EGFR, EGFRvIII, ErbB2/Her2, ErbB3, ErbB4, ETV6-AML, EpCAM, EphA2, Fra-1, FOLR1, GAGE proteins (e.g., GAGE-1, -2), GD2, GD3, GloboH, glypican-3, GM3, gp100, Her2, HLA/B-raf, HLA/k-ras, HLA/MAGE-A3, hTERT, LMP2, MAGE proteins (e.g., MAGE-1, -2, -3, -4, -6, and -12), MART-1, mesothelin, ML-IAP, Muc1, Muc2, Muc3, Muc4, Muc5, Muc16 (CA-125), MUM1, NA17, NY-BR1, NY-BR62, NY-BR85, NY-ESO1, OX40, p15, p53, PAP, PAX3, PAX5, PCTA-1, PLAC1, PRLR, PRAME, PSMA (FOLH1), RAGE proteins, Ras, RGS5, Rho, SART-1, SART-3, Steap-1, Steap-2, survivin, TAG-72, TGF-β, TMPRSS2, Tn, TRP-1, TRP-2, tyrosinase, and uroplakin-3.

[0097] In the context of bispecific antibodies of the present invention wherein one arm of the antibody binds CD3 and the other arm binds a target antigen, the target antigen can be an infectious disease-associated antigen. Non-limiting examples of infectious disease-associated antigens include, e.g., an antigen that is expressed on the surface of a virus particle, or preferentially expressed on a cell that is infected with a virus, wherein the virus is selected from the group consisting of HIV, hepatitis (A, B or C), herpes virus (e.g., HSV-1, HSV-2, CMV, HAV-6, VZV, Epstein Barr virus), adenovirus, influenza virus, flavivirus, echovirus, rhinovirus, coxsackie virus, coronavirus, respiratory syncytial virus, mumps virus, rotavirus, measles virus, rubella virus, parvovirus, vaccinia virus, HTLV, dengue virus, papillomavirus, molluscum virus, poliovirus, rabies virus, JC virus, and arboviral encephalitis virus. Alternatively, the target antigen can be an antigen that is expressed on the surface of a bacterium, or preferentially expressed on a cell that is infected with a bacterium, wherein the bacterium is selected from the group consisting of *chlamydia, rickettsia*, mycobacteria, staphylococci, streptococci, pneumonococci, meningococci, gonococci, *klebsiella, proteus, serratia, pseudomonas, legionella*, diphtheria, *salmonella*, bacilli, cholera, tetanus, botulism, anthrax, plague, leptospira, and Lyme disease bacteria. In certain embodiments, the target antigen is an antigen that is expressed on the surface of a fungus, or preferentially expressed on a cell that is infected with a fungus, wherein the fungus is selected from the group consisting of *Candida* (*albicans, krusei, glabrata, tropicalis*, etc.), *Crytococcus neoformans, Aspergillus* (*fumigatus, niger*, etc.), *Mucorales* (*mucor, absidia, rhizopus*, etc.), *Sporothrix schenkii, Blastomyces dermatitidis, Paracoccidioides brasiliensis, Coccidioides immitis*, and *Histoplasma capsulatum*. In certain embodiments, the target antigen is an antigen that is expressed on the surface of a parasite, or preferentially expressed on a cell that is infected with a parasite, wherein the parasite is selected from the group consisting of *Entamoeba histolytica, Balantidium coli*, Naegleriafowleri, *Acanthamoeba* sp., *Giardia lambia, Cryptosporidium* sp., *Pneumocystis carinii, Plasmodium vivax, Babesia microti, Trypanosoma brucei, Trypanosoma cruzi, Leishmania donovani, Toxoplasma gondii, Nippostrongylus brasiliensis, Taenia crassiceps*, and *Brugia malayi*. Non-limiting examples of specific pathogen-associated antigens include, e.g., HIV gp120, HIV CD4, hepatitis B glucoprotein L, hepatitis B glucoprotein M, hepatitis B glucoprotein S, hepatitis C E1, hepatitis C E2, hepatocyte-specific protein, herpes simplex virus gB, cytomegalovirus gB, and HTLV envelope protein.

[0098] According to certain exemplary embodiments, the present invention includes bispecific antigen-binding molecules that specifically bind CD3 and CD20. Such molecules may be referred to herein as, e.g., "anti-CD3/anti-CD20," or "anti-CD3×CD20" or "CD3×CD20" bispecific molecules, or other similar terminology.

[0099] The term "CD20," as used herein, refers to the human CD20 protein unless specified as being from a non-human species (e.g., "mouse CD20," "monkey CD20," etc.). The human CD20 protein has the amino acid sequence shown in SEQ ID NO:1369.

[0100] As used herein, the expression "antigen-binding molecule" means a protein, polypeptide or molecular complex comprising or consisting of at least one complementarity determining region (CDR) that alone, or in combination with one or more additional CDRs and/or framework regions (FRs), specifically binds to a particular antigen. In certain embodiments, an antigen-binding molecule is an antibody or a fragment of an antibody, as those terms are defined elsewhere herein.

[0101] As used herein, the expression "bispecific antigen-binding molecule" means a protein, polypeptide or molecular complex comprising at least a first antigen-binding domain and a second antigen-binding domain. Each antigen-binding domain within the bispecific antigen-binding molecule comprises at least one CDR that alone, or in combination with one or more additional CDRs and/or FRs, specifically binds to a particular antigen. In the context of the present invention, the first antigen-binding domain specifically binds a first antigen (e.g., CD3), and the second antigen-binding domain specifically binds a second, distinct antigen (e.g., CD20).

[0102] In certain exemplary embodiments of the present invention, the bispecific antigen-binding molecule is a bispecific antibody. Each antigen-binding domain of a bispecific antibody comprises a heavy chain variable domain (HCVR) and a light chain variable domain (LCVR). In the context of a bispecific antigen-binding molecule comprising a first and a second antigen-binding domain (e.g., a bispecific antibody), the CDRs of the first antigen-binding domain may be designated with the prefix "A1" and the CDRs of the second antigen-binding domain may be designated with the prefix "A2". Thus, the CDRs of the first antigen-binding domain may be referred to herein as A1-HCDR1, A1-HCDR2, and A1-HCDR3; and the CDRs of the second antigen-binding domain may be referred to herein as A2-HCDR1, A2-HCDR2, and A2-HCDR3.

[0103] The first antigen-binding domain and the second antigen-binding domain may be directly or indirectly connected to one another to form a bispecific antigen-binding molecule of the present invention. Alternatively, the first antigen-binding domain and the second antigen-binding domain may each be connected to a separate multimerizing domain. The association of one multimerizing domain with another multimerizing domain facilitates the association between the two antigen-binding domains, thereby forming a bispecific antigen-binding molecule. As used herein, a "multimerizing domain" is any macromolecule, protein, polypeptide, peptide, or amino acid that has the ability to associate with a second multimerizing domain of the same or similar structure or constitution. For example, a multimerizing domain may be a polypeptide comprising an immunoglobulin C_H3 domain. A non-limiting example of a multimerizing component is an Fc portion of an immunoglobulin (comprising a C_H2-C_H3 domain), e.g., an Fc domain of an IgG selected from the isotypes IgG1, IgG2, IgG3, and IgG4, as well as any allotype within each isotype group.

[0104] Bispecific antigen-binding molecules of the present invention will typically comprise two multimerizing domains, e.g., two Fc domains that are each individually part of a separate antibody heavy chain. The first and second multimerizing domains may be of the same IgG isotype such as, e.g., IgG1/IgG1, IgG2/IgG2, IgG4/IgG4. Alternatively, the first and second multimerizing domains may be of different IgG isotypes such as, e.g., IgG1/IgG2, IgG1/IgG4, IgG2/IgG4, etc.

[0105] In certain embodiments, the multimerizing domain is an Fc fragment or an amino acid sequence of 1 to about 200 amino acids in length containing at least one cysteine residues. In other embodiments, the multimerizing domain is a cysteine residue, or a short cysteine-containing peptide. Other multimerizing domains include peptides or polypeptides comprising or consisting of a leucine zipper, a helix-loop motif, or a coiled-coil motif.

[0106] Any bispecific antibody format or technology may be used to make the bispecific antigen-binding molecules of the present invention. For example, an antibody or fragment thereof having a first antigen binding specificity can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment having a second antigen-binding specificity to produce a bispecific antigen-binding molecule. Specific exemplary bispecific formats that can be used in the context of the present invention include, without limitation, e.g., scFv-based or diabody bispecific formats, IgG-scFv fusions, dual variable domain (DVD)-Ig, Quadroma, knobs-into-holes, common light chain (e.g., common light chain with knobs-into-holes, etc.), CrossMab, CrossFab, (SEED)body, leucine zipper, Duobody, IgG1/IgG2, dual acting Fab (DAF)-IgG, and Mabe bispecific formats (see, e.g., Klein et al. 2012, mAbs 4:6, 1-11, and references cited therein, for a review of the foregoing formats).

[0107] In the context of bispecific antigen-binding molecules of the present invention, the multimerizing domains, e.g., Fc domains, may comprise one or more amino acid changes (e.g., insertions, deletions or substitutions) as compared to the wild-type, naturally occurring version of the Fc domain. For example, the invention includes bispecific antigen-binding molecules comprising one or more modifications in the Fc domain that results in a modified Fc domain having a modified binding interaction (e.g., enhanced or diminished) between Fc and FcRn. In one embodiment, the bispecific antigen-binding molecule comprises a modification in a C_H2 or a C_H3 region, wherein the modification increases the affinity of the Fc domain to FcRn in an acidic environment (e.g., in an endosome where pH ranges from about 5.5 to about 6.0). Non-limiting examples of such Fc modifications include, e.g., a modification at position 250 (e.g., E or Q); 250 and 428 (e.g., L or F); 252 (e.g., L/Y/F/W or T), 254 (e.g., S or T), and 256 (e.g., S/R/Q/E/D or T); or a modification at position 428 and/or 433 (e.g., L/R/S/P/Q or K) and/or 434 (e.g., H/F or Y); or a modification at position 250 and/or 428; or a modification at position 307 or 308 (e.g., 308F, V308F), and 434. In one embodiment, the modification comprises a 428L (e.g., M428L) and 434S (e.g., N434S) modification; a 428L, 259I (e.g., V259I), and 308F (e.g., V308F) modification; a 433K (e.g., H433K) and a 434 (e.g., 434Y) modification; a 252, 254, and 256 (e.g., 252Y, 254T, and 256E) modification; a 250Q and 428L modification (e.g., T250Q and M428L); and a 307 and/or 308 modification (e.g., 308F or 308P).

[0108] The present invention also includes bispecific antigen-binding molecules comprising a first C_H3 domain and a second Ig C_H3 domain, wherein the first and second Ig C_H3 domains differ from one another by at least one amino acid, and wherein at least one amino acid difference reduces

binding of the bispecific antibody to Protein A as compared to a bi-specific antibody lacking the amino acid difference. In one embodiment, the first Ig C_H3 domain binds Protein A and the second Ig C_H3 domain contains a mutation that reduces or abolishes Protein A binding such as an H95R modification (by IMGT exon numbering; H435R by EU numbering). The second C_H3 may further comprise a Y96F modification (by IMGT; Y436F by EU). Further modifications that may be found within the second C_H3 include: D16E, L18M, N44S, K52N, V57M, and V82I (by IMGT; D356E, L358M, N384S, K392N, V397M, and V422I by EU) in the case of IgG1 antibodies; N44S, K52N, and V82I (IMGT; N384S, K392N, and V422I by EU) in the case of IgG2 antibodies; and Q15R, N44S, K52N, V57M, R69K, E79Q, and V82I (by IMGT; Q355R, N384S, K392N, V397M, R409K, E419Q, and V422I by EU) in the case of IgG4 antibodies.

[0109] In certain embodiments, the Fc domain may be chimeric, combining Fc sequences derived from more than one immunoglobulin isotype. For example, a chimeric Fc domain can comprise part or all of a C_H2 sequence derived from a human IgG1, human IgG2 or human IgG4 C_H2 region, and part or all of a C_H3 sequence derived from a human IgG1, human IgG2 or human IgG4. A chimeric Fc domain can also contain a chimeric hinge region. For example, a chimeric hinge may comprise an "upper hinge" sequence, derived from a human IgG1, a human IgG2 or a human IgG4 hinge region, combined with a "lower hinge" sequence, derived from a human IgG1, a human IgG2 or a human IgG4 hinge region. A particular example of a chimeric Fc domain that can be included in any of the antigen-binding molecules set forth herein comprises, from N- to C-terminus: [IgG4 C_H1]-[IgG4 upper hinge]-[IgG2 lower hinge]-[IgG4 CH2]-[IgG4 CH3]. Another example of a chimeric Fc domain that can be included in any of the antigen-binding molecules set forth herein comprises, from N- to C-terminus: [IgG1 C_H1]-[IgG1 upper hinge]-[IgG2 lower hinge]-[IgG4 CH2]-[IgG1 CH3]. These and other examples of chimeric Fc domains that can be included in any of the antigen-binding molecules of the present invention are described in U.S. Provisional Application No. 61/759,578, filed Feb. 1, 2013, which is herein incorporated in its entirety. Chimeric Fc domains having these general structural arrangements, and variants thereof, can have altered Fc receptor binding, which in turn affects Fc effector function.

Sequence Variants

[0110] The antibodies and bispecific antigen-binding molecules of the present invention may comprise one or more amino acid substitutions, insertions and/or deletions in the framework and/or CDR regions of the heavy and light chain variable domains as compared to the corresponding germline sequences from which the individual antigen-binding domains were derived. Such mutations can be readily ascertained by comparing the amino acid sequences disclosed herein to germline sequences available from, for example, public antibody sequence databases. The antigen-binding molecules of the present invention may comprise antigen-binding domains which are derived from any of the exemplary amino acid sequences disclosed herein, wherein one or more amino acids within one or more framework and/or CDR regions are mutated to the corresponding residue(s) of the germline sequence from which the antibody was derived, or to the corresponding residue(s) of another human germline sequence, or to a conservative amino acid substitution of the corresponding germline residue(s) (such sequence changes are referred to herein collectively as "germline mutations"). A person of ordinary skill in the art, starting with the heavy and light chain variable region sequences disclosed herein, can easily produce numerous antibodies and antigen-binding fragments which comprise one or more individual germline mutations or combinations thereof. In certain embodiments, all of the framework and/or CDR residues within the V_H and/or V_L domains are mutated back to the residues found in the original germline sequence from which the antigen-binding domain was originally derived. In other embodiments, only certain residues are mutated back to the original germline sequence, e.g., only the mutated residues found within the first 8 amino acids of FR1 or within the last 8 amino acids of FR4, or only the mutated residues found within CDR1, CDR2 or CDR3. In other embodiments, one or more of the framework and/or CDR residue(s) are mutated to the corresponding residue(s) of a different germline sequence (i.e., a germline sequence that is different from the germline sequence from which the antigen-binding domain was originally derived). Furthermore, the antigen-binding domains may contain any combination of two or more germline mutations within the framework and/or CDR regions, e.g., wherein certain individual residues are mutated to the corresponding residue of a particular germline sequence while certain other residues that differ from the original germline sequence are maintained or are mutated to the corresponding residue of a different germline sequence. Once obtained, antigen-binding domains that contain one or more germline mutations can be easily tested for one or more desired property such as, improved binding specificity, increased binding affinity, improved or enhanced antagonistic or agonistic biological properties (as the case may be), reduced immunogenicity, etc. Bispecific antigen-binding molecules comprising one or more antigen-binding domains obtained in this general manner are encompassed within the present invention.

[0111] The present invention also includes antigen-binding molecules wherein one or both antigen-binding domains comprise variants of any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein having one or more conservative substitutions. For example, the present invention includes antigen-binding molecules comprising an antigen-binding domain having HCVR, LCVR, and/or CDR amino acid sequences with, e.g., 10 or fewer, 8 or fewer, 6 or fewer, 4 or fewer, etc. conservative amino acid substitutions relative to any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. Examples of groups of amino acids that have side chains with similar chemical properties include (1) aliphatic side chains: glycine, alanine, valine, leucine and isoleucine; (2) aliphatic-hydroxyl side chains: serine and threonine; (3) amide-containing side chains: asparagine and glutamine; (4) aromatic side chains: phenylalanine, tyrosine, and tryptophan; (5) basic side chains: lysine, arginine, and histidine; (6) acidic side chains: aspartate and glutamate, and (7) sulfur-containing side chains are cysteine and methionine. Preferred conservative amino acids

substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, glutamate-aspartate, and asparagine-glutamine. Alternatively, a conservative replacement is any change having a positive value in the PAM250 log-likelihood matrix disclosed in Gonnet et al. (1992) Science 256: 1443-1445, herein incorporated by reference. A "moderately conservative" replacement is any change having a nonnegative value in the PAM250 log-likelihood matrix.

[0112] The present invention also includes antigen-binding molecules comprising an antigen-binding domain with an HCVR, LCVR, and/or CDR amino acid sequence that is substantially identical to any of the HCVR, LCVR, and/or CDR amino acid sequences disclosed herein. The term "substantial identity" or "substantially identical," when referring to an amino acid sequence means that two amino acid sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 95% sequence identity, even more preferably at least 98% or 99% sequence identity. Preferably, residue positions which are not identical differ by conservative amino acid substitutions. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of similarity may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well-known to those of skill in the art. See, e.g., Pearson (1994) Methods Mol. Biol. 24: 307-331, herein incorporated by reference.

[0113] Sequence similarity for polypeptides, which is also referred to as sequence identity, is typically measured using sequence analysis software. Protein analysis software matches similar sequences using measures of similarity assigned to various substitutions, deletions and other modifications, including conservative amino acid substitutions. For instance, GCG software contains programs such as Gap and Bestfit which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1. Polypeptide sequences also can be compared using FASTA using default or recommended parameters, a program in GCG Version 6.1. FASTA (e.g., FASTA2 and FASTA3) provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson (2000) supra). Another preferred algorithm when comparing a sequence of the invention to a database containing a large number of sequences from different organisms is the computer program BLAST, especially BLASTP or TBLASTN, using default parameters. See, e.g., Altschul et al. (1990) J. Mol. Biol. 215:403-410 and Altschul et al. (1997) Nucleic Acids Res. 25:3389-402, each herein incorporated by reference.

pH-Dependent Binding

[0114] The present invention includes anti-CD3 antibodies, and anti-CD3/anti-CD20 bispecific antigen-binding molecules, with pH-dependent binding characteristics. For example, an anti-CD3 antibody of the present invention may exhibit reduced binding to CD3 at acidic pH as compared to neutral pH. Alternatively, anti-CD3 antibodies of the invention may exhibit enhanced binding to CD3 at acidic pH as compared to neutral pH. The expression "acidic pH" includes pH values less than about 6.2, e.g., about 6.0, 5.95, 5.9, 5.85, 5.8, 5.75, 5.7, 5.65, 5.6, 5.55, 5.5, 5.45, 5.4, 5.35, 5.3, 5.25, 5.2, 5.15, 5.1, 5.05, 5.0, or less. As used herein, the expression "neutral pH" means a pH of about 7.0 to about 7.4. The expression "neutral pH" includes pH values of about 7.0, 7.05, 7.1, 7.15, 7.2, 7.25, 7.3, 7.35, and 7.4.

[0115] In certain instances, "reduced binding . . . at acidic pH as compared to neutral pH" is expressed in terms of a ratio of the K_D value of the antibody binding to its antigen at acidic pH to the K_D value of the antibody binding to its antigen at neutral pH (or vice versa). For example, an antibody or antigen-binding fragment thereof may be regarded as exhibiting "reduced binding to CD3 at acidic pH as compared to neutral pH" for purposes of the present invention if the antibody or antigen-binding fragment thereof exhibits an acidic/neutral K_D ratio of about 3.0 or greater. In certain exemplary embodiments, the acidic/neutral K_D ratio for an antibody or antigen-binding fragment of the present invention can be about 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11.0, 11.5, 12.0, 12.5, 13.0, 13.5, 14.0, 14.5, 15.0, 20.0, 25.0, 30.0, 40.0, 50.0, 60.0, 70.0, 100.0 or greater.

[0116] Antibodies with pH-dependent binding characteristics may be obtained, e.g., by screening a population of antibodies for reduced (or enhanced) binding to a particular antigen at acidic pH as compared to neutral pH. Additionally, modifications of the antigen-binding domain at the amino acid level may yield antibodies with pH-dependent characteristics. For example, by substituting one or more amino acids of an antigen-binding domain (e.g., within a CDR) with a histidine residue, an antibody with reduced antigen-binding at acidic pH relative to neutral pH may be obtained.

Antibodies Comprising Fc Variants

[0117] According to certain embodiments of the present invention, anti-CD3 antibodies, and anti-CD3/anti-CD20 bispecific antigen-binding molecules, are provided comprising an Fc domain comprising one or more mutations which enhance or diminish antibody binding to the FcRn receptor, e.g., at acidic pH as compared to neutral pH. For example, the present invention includes antibodies comprising a mutation in the C_H2 or a C_H3 region of the Fc domain, wherein the mutation(s) increases the affinity of the Fc domain to FcRn in an acidic environment (e.g., in an endosome where pH ranges from about 5.5 to about 6.0). Such mutations may result in an increase in serum half-life of the antibody when administered to an animal. Non-limiting examples of such Fc modifications include, e.g., a modification at position 250 (e.g., E or Q); 250 and 428 (e.g., L or F); 252 (e.g., L/Y/F/W or T), 254 (e.g., S or T), and 256 (e.g., S/R/Q/E/D or T); or a modification at position 428 and/or 433 (e.g., H/L/R/S/P/Q or K) and/or 434 (e.g., H/F or Y); or a modification at position 250 and/or 428; or a modification at position 307 or 308 (e.g., 308F, V308F), and 434. In one embodiment, the modification comprises a 428L (e.g., M428L) and 434S (e.g., N434S) modification; a 428L, 2591 (e.g., V259I), and 308F (e.g., V308F) modification; a 433K (e.g., H433K) and a 434 (e.g., 434Y) modification; a 252, 254, and 256 (e.g., 252Y, 254T, and 256E) modification; a 250Q and 428L modification (e.g., T250Q and M428L); and a 307 and/or 308 modification (e.g., 308F or 308P).

[0118] For example, the present invention includes anti-CD3 antibodies, and anti-CD3/anti-CD20 bispecific antigen-binding molecules, comprising an Fc domain compris-

ing one or more pairs or groups of mutations selected from the group consisting of: 250Q and 248L (e.g., T250Q and M248L); 252Y, 254T and 256E (e.g., M252Y, S254T and T256E); 428L and 434S (e.g., M428L and N434S); and 433K and 434F (e.g., H433K and N434F). All possible combinations of the foregoing Fc domain mutations, and other mutations within the antibody variable domains disclosed herein, are contemplated within the scope of the present invention.

Biological Characteristics of the Antibodies and Bispecific Antigen-Binding Molecules

[0119] The present invention includes antibodies and antigen-binding fragments thereof that bind human CD3 and induce T cell proliferation. For example, the present invention includes anti-CD3 antibodies that induce human T cell proliferation with an EC_{50} value of less than about 0.33 pM, as measured by an in vitro T cell proliferation assay, e.g., using the assay format as defined in Example 4 herein (e.g., assessing the proliferation of Jurkat cells or human PBMCs in the presence of anti-CD3 antibodies), or a substantially similar assay. In certain embodiments, the antibodies or antigen-binding fragments of the present invention induce human T cell proliferation (e.g., Jurkat cell proliferation and/or PBMC proliferation) with an EC_{50} value of less than about 0.32 pM, less than about 0.31 pM, less than about 0.30 pM, less than about 0.28 pM, less than about 0.26 pM, less than about 0.24 pM, less than about 0.22 pM, or less than about 0.20 pM, as measured by an in vitro T cell proliferation assay, e.g., using the assay format as defined in Example 4 herein, or a substantially similar assay.

[0120] The present invention also includes antibodies and antigen-binding fragments thereof that bind human CD3 and induce T cell-mediated killing of tumor cells. For example, the present invention includes anti-CD3 antibodies that induce T cell-mediated killing of tumor cells with an EC_{50} of less than about 2.3 pM, as measured in an in vitro T cell-mediated tumor cell killing assay, e.g., using the assay format as defined in Example 6 herein (e.g., assessing the extent of U937 tumor cell killing by human PBMCs in the presence of anti-CD3 antibodies), or a substantially similar assay. In certain embodiments, the antibodies or antigen-binding fragments of the present invention induce T cell-mediated tumor cell killing (e.g., PBMC-mediated killing of U937 cells) with an EC_{50} value of less than about 2.3 pM, less than about 2.2 pM, less than about 2.1 pM, less than about 2.0 pM, less than about 1.8 pM, less than about 1.6 pM, less than about 1.4 pM, less than about 1.2 pM, less than about 1.0 pM, less than about 0.8 pM, less than about 0.6 pM, or less than about 0.5 pM, as measured by an in vitro T cell-mediated tumor cell killing assay, e.g., using the assay format as defined in Example 6 herein, or a substantially similar assay.

[0121] The present invention includes antibodies and antigen-binding fragments thereof that bind human CD3 with high affinity. The present invention also includes antibodies and antigen-binding fragments thereof that bind human CD3 with medium or low affinity, depending on the therapeutic context and particular targeting properties that are desired. For example, in the context of a bispecific antigen-binding molecule, wherein one arm binds CD3 and another arm binds a target antigen (e.g., CD20), it may be desirable for the target antigen-binding arm to bind the target antigen with high affinity while the anti-CD3 arm binds CD3 with only moderate or low affinity. In this manner, preferential targeting of the antigen-binding molecule to cells expressing the target antigen may be achieved while avoiding general/untargeted CD3 binding and the consequent adverse side effects associated therewith.

[0122] According to certain embodiments, the present invention includes antibodies and antigen-binding fragments of antibodies that bind human CD3 (e.g., at 25° C.) with a K_D of less than about 15 nM as measured by surface plasmon resonance, e.g., using an assay format as defined in Example 3 herein. In certain embodiments, the antibodies or antigen-binding fragments of the present invention bind CD3 with a K_D of less than about 5 nM, less than about 2 nM, less than about 1 nM, less than about 800 pM, less than about 600 pM, less than about 500 pM, less than about 400 pM, less than about 300 pM, less than about 200 pM, less than about 180 pM, less than about 160 pM, less than about 140 pM, less than about 120 pM, less than about 100 pM, less than about 80 pM, less than about 60 pM, less than about 40 pM, less than about 20 pM, or less than about 10 pM, as measured by surface plasmon resonance, e.g., using an assay format as defined in Example 3 herein (e.g., mAb-capture or antigen-capture format), or a substantially similar assay.

[0123] The present invention also includes antibodies and antigen-binding fragments thereof that bind CD3 with a dissociative half-life (t½) of greater than about 10 minutes as measured by surface plasmon resonance at 25° C. or 37° C., e.g., using an assay format as defined in Example 3 herein, or a substantially similar assay. In certain embodiments, the antibodies or antigen-binding fragments of the present invention bind CD3 with a t½ of greater than about 20 minutes, greater than about 30 minutes, greater than about 40 minutes, greater than about 50 minutes, greater than about 60 minutes, greater than about 70 minutes, greater than about 80 minutes, greater than about 90 minutes, greater than about 100 minutes, greater than about 200 minutes, greater than about 300 minutes, greater than about 400 minutes, greater than about 500 minutes, greater than about 600 minutes, greater than about 700 minutes, greater than about 800 minutes, greater than about 900 minutes, greater than about 1000 minutes, or greater than about 1200 minutes, as measured by surface plasmon resonance at 25° C. or 37° C., e.g., using an assay format as defined in Example 3 herein (e.g., mAb-capture or antigen-capture format), or a substantially similar assay.

[0124] The present invention includes bispecific antigen-binding molecules (e.g., bispecific antibodies) which are capable of simultaneously binding to human CD3 and human CD20. According to certain embodiments, the bispecific antigen-binding molecules of the invention specifically interact with cells that express CD3 and/or CD20. The extent to which a bispecific antigen-binding molecule binds cells that express CD3 and/or CD20 can be assessed by fluorescence activated cell sorting (FACS), as illustrated in Example 8 herein. For example, the present invention includes bispecific antigen-binding molecules which specifically bind human T-cell lines which express CD3 but not CD20 (e.g., Jurkat), human B-cell lines which express CD20 but not CD3 (e.g., Raji), and/or primate T-cells (e.g., cynomolgus peripheral blood mononuclear cells [PBMCs]). The present invention includes bispecific antigen-binding molecules which bind any of the aforementioned cells and cell lines with an EC_{50} value of from about 9.0×10^{-6} to about

2.0×10^{-9}, or less, as determined using a FACS assay as set forth in Example 8 or a substantially similar assay.

[0125] The present invention also includes anti-CD3/anti-CD20 bispecific antigen-binding molecules which bind to CD3-expressing human T-cells (e.g., Jurkat) with an EC_{50} value of between 1.0 pM and 1000 nM. In certain embodiments, the anti-CD3/anti-CD20 bispecific antigen-binding molecules bind to CD3-expressing human T-cells with an EC_{50} value of between 1 nM and 60 nM. For example, the present invention includes anti-CD3/anti-CD20 bispecific antigen-binding molecules which bind to CD3-expressing human T-cells (e.g., Jurkat) with an EC_{50} value of about 1 pM. about 10 pM, about 100 pM, about 500 pM, about 1 nM, about 2 nM, about 5 nM, about 10 nM, about 20 nM, about 30 nM, about 40 nM, about 50 nM about 60 nM, about 70 nM, about 80 nM, about 90 nM, about 100 nM, about 200 nM, about 300 nM, about 500 nM, about 800 nM, about 1000 nM, or more.

[0126] The present invention also includes anti-CD3/anti-CD20 bispecific antigen-binding molecules which exhibit one or more characteristics selected from the group consisting of: (a) inducing PBMC proliferation in vitro (see, e.g., Example 9 herein); (b) activating T-cells, inducing IFN-gamma release and CD25 up-regulation in human whole blood (see, e.g., Example 10 herein); (c) inducing T-cell mediated cytotoxicity on anti-CD20-resistant cell lines (see, e.g., Example 11 herein); (d) inducing cytotoxicity to human B-cells (e.g., Raji; see, e.g., Example 13 herein); (e) depleting B-cells (e.g., CD19+ B-cells) in mice reconstituted with human immune cells (see, e.g., Example 14 herein); and (f) decreasing B-cell tumor volume (e.g., Raji tumor volume) in mouse xenografts (see, e.g., Example 15).

[0127] The present invention includes anti-CD3/anti-CD20 bispecific antigen-binding molecules which are capable of depleting B cells in a subject (see, e.g., Example 16). For example, according to certain embodiments, anti-CD3/anti-CD20 bispecific antigen-binding molecules are provided, wherein a single administration of the bispecific antigen-binding molecule to a subject (e.g., at a dose of about 0.1 mg/kg, about 0.08 mg/kg, about 0.06 mg/kg about 0.04 mg/kg, about 0.04 mg/kg, about 0.02 mg/kg, about 0.01 mg/kg, or less) causes a reduction in the number of B cells in the subject (e.g., in a blood sample taken from the subject) below detectable levels. In certain embodiments, a single administration of the anti-CD3/anti-CD20 bispecific antigen-binding molecule at a dose of about 0.1 mg/kg causes a reduction in the number of B cells in the subject below detectable levels by about day 7, about day 6, about day 5, about day 4, about day 3, about day 2, or about day 1 after administration of the bispecific antigen-binding molecule to the subject. According to certain embodiments, a single administration of an anti-CD3/anti-CD20 bispecific antigen-binding molecule of the invention, at a dose of about 0.01 mg/kg, causes the number of B-cells to remain below detectable levels until at least about 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 15 days, 16 days, 17 days or more, following the administration. As used herein, the expression "below detectable levels" means that no B cells can be directly or indirectly detected in a blood sample drawn from a subject using standard B-cell detection assays, e.g., a FACS assay for B-cell markers, as set forth in Example 16, herein.

[0128] In related embodiments, an anti-CD3/anti-CD20 bispecific antigen-binding molecule is provided, wherein the number of B-cells per microliter of blood drawn from a subject at about day 1 through about day 28 after administration of a single dose of about 0.01 mg/kg of the antigen-binding molecule to the subject is less than 25% the number of B-cells per microliter of blood drawn from the subject prior to the administration. In certain other embodiments, an anti-CD3/anti-CD20 bispecific antigen-binding molecule is provided, wherein the number of B-cells per microliter of blood drawn from a subject at about day 1 through about day 56 after administration of a single dose of about 0.01 mg/kg of the antigen-binding molecule to the subject is less than 50% the number of B-cells per microliter of blood drawn from the subject prior to the administration.

[0129] The present invention also provides anti-CD3/anti-CD20 bispecific antigen-binding molecules that, when administered to a subject, cause no more than a transient decrease in T cells. For example, anti-CD3/anti-CD20 bispecific antigen-binding molecules are provided that, when administered to a subject at a dose of about 0.01 mg/kg cause the number of T cells to decline at day 1 following administration, but wherein the number of T cells per microliter of blood rebounds at timepoints thereafter (e.g., by about day 2, day 7, day 14, day 28, day 42, day 56 or later following the administration). For example the present invention provides an anti-CD3/anti-CD20 bispecific antigen-binding molecule, wherein the number of T cells per microliter of blood drawn from the subject at about day 14 through about day 56 after administration of the antigen binding molecule to the subject at a dose of about 0.01 mg/kg is equal to or greater than the number of T cells per microliter of blood drawn from the subject prior to administration of the bispecific antigen-binding molecule.

Epitope Mapping and Related Technologies

[0130] The epitope on CD3 to which the antigen-binding molecules of the present invention bind may consist of a single contiguous sequence of 3 or more (e.g., 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) amino acids of a CD3 protein. Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) of CD3. The antibodies of the invention may interact with amino acids contained within a single CD3 chain (e.g., CD3-epsilon, CD3-delta or CD3-gamma), or may interact with amino acids on two or more different CD3 chains. The term "epitope," as used herein, refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

[0131] Various techniques known to persons of ordinary skill in the art can be used to determine whether an antigen-binding domain of an antibody "interacts with one or more amino acids" within a polypeptide or protein. Exemplary techniques include, e.g., routine cross-blocking assay such as that described Antibodies, Harlow and Lane (Cold Spring

Harbor Press, Cold Spring Harb., N.Y.), alanine scanning mutational analysis, peptide blots analysis (Reineke, 2004, Methods Mol Biol 248:443-463), and peptide cleavage analysis. In addition, methods such as epitope excision, epitope extraction and chemical modification of antigens can be employed (Tomer, 2000, Protein Science 9:487-496). Another method that can be used to identify the amino acids within a polypeptide with which an antigen-binding domain of an antibody interacts is hydrogen/deuterium exchange detected by mass spectrometry. In general terms, the hydrogen/deuterium exchange method involves deuterium-labeling the protein of interest, followed by binding the antibody to the deuterium-labeled protein. Next, the protein/antibody complex is transferred to water to allow hydrogen-deuterium exchange to occur at all residues except for the residues protected by the antibody (which remain deuterium-labeled). After dissociation of the antibody, the target protein is subjected to protease cleavage and mass spectrometry analysis, thereby revealing the deuterium-labeled residues which correspond to the specific amino acids with which the antibody interacts. See, e.g., Ehring (1999) *Analytical Biochemistry* 267(2):252-259; Engen and Smith (2001) *Anal. Chem.* 73:256A-265A. X-ray crystallography of the antigen/antibody complex may also be used for epitope mapping purposes.

[0132] The present invention further includes anti-CD3 antibodies that bind to the same epitope as any of the specific exemplary antibodies described herein (e.g. antibodies comprising any of the amino acid sequences as set forth in Table 1 herein). Likewise, the present invention also includes anti-CD3 antibodies that compete for binding to CD3 with any of the specific exemplary antibodies described herein (e.g. antibodies comprising any of the amino acid sequences as set forth in Table 1 herein).

[0133] The present invention also includes bispecific antigen-binding molecules comprising a first antigen-binding domain that specifically binds human CD3, and a second antigen binding domain that specifically binds human CD20, wherein the first antigen-binding domain binds to the same epitope on CD3 as any of the specific exemplary CD3-specific antigen-binding domains described herein, and/or wherein the second antigen-binding domain binds to the same epitope on CD20 as any of the specific exemplary CD20-specific antigen-binding domains described herein.

[0134] Likewise, the present invention also includes bispecific antigen-binding molecules comprising a first antigen-binding domain that specifically binds human CD3, and a second antigen binding domain that specifically binds human CD20, wherein the first antigen-binding domain competes for binding to CD3 with any of the specific exemplary CD3-specific antigen-binding domains described herein, and/or wherein the second antigen-binding domain competes for binding to CD20 with any of the specific exemplary CD20-specific antigen-binding domains described herein.

[0135] One can easily determine whether a particular antigen-binding molecule (e.g., antibody) or antigen-binding domain thereof binds to the same epitope as, or competes for binding with, a reference antigen-binding molecule of the present invention by using routine methods known in the art. For example, to determine if a test antibody binds to the same epitope on CD3 (or CD20) as a reference bispecific antigen-binding molecule of the present invention, the reference bispecific molecule is first allowed to bind to a CD3 protein (or CD20 protein). Next, the ability of a test antibody to bind to the CD3 (or CD20) molecule is assessed. If the test antibody is able to bind to CD3 (or CD20) following saturation binding with the reference bispecific antigen-binding molecule, it can be concluded that the test antibody binds to a different epitope of CD3 (or CD20) than the reference bispecific antigen-binding molecule. On the other hand, if the test antibody is not able to bind to the CD3 (or CD20) molecule following saturation binding with the reference bispecific antigen-binding molecule, then the test antibody may bind to the same epitope of CD3 (or CD20) as the epitope bound by the reference bispecific antigen-binding molecule of the invention. Additional routine experimentation (e.g., peptide mutation and binding analyses) can then be carried out to confirm whether the observed lack of binding of the test antibody is in fact due to binding to the same epitope as the reference bispecific antigen-binding molecule or if steric blocking (or another phenomenon) is responsible for the lack of observed binding. Experiments of this sort can be performed using ELISA, RIA, Biacore, flow cytometry or any other quantitative or qualitative antibody-binding assay available in the art. In accordance with certain embodiments of the present invention, two antigen-binding proteins bind to the same (or overlapping) epitope if, e.g., a 1-, 5-, 10-, 20- or 100-fold excess of one antigen-binding protein inhibits binding of the other by at least 50% but preferably 75%, 90% or even 99% as measured in a competitive binding assay (see, e.g., Junghans et al., Cancer Res. 1990:50:1495-1502). Alternatively, two antigen-binding proteins are deemed to bind to the same epitope if essentially all amino acid mutations in the antigen that reduce or eliminate binding of one antigen-binding protein reduce or eliminate binding of the other. Two antigen-binding proteins are deemed to have "overlapping epitopes" if only a subset of the amino acid mutations that reduce or eliminate binding of one antigen-binding protein reduce or eliminate binding of the other.

[0136] To determine if an antibody or antigen-binding domain thereof competes for binding with a reference antigen-binding molecule, the above-described binding methodology is performed in two orientations: In a first orientation, the reference antigen-binding molecule is allowed to bind to a CD3 protein (or CD20 protein) under saturating conditions followed by assessment of binding of the test antibody to the CD3 (or CD20) molecule. In a second orientation, the test antibody is allowed to bind to a CD3 (or CD20) molecule under saturating conditions followed by assessment of binding of the reference antigen-binding molecule to the CD3 (or CD20) molecule. If, in both orientations, only the first (saturating) antigen-binding molecule is capable of binding to the CD3 (or CD20) molecule, then it is concluded that the test antibody and the reference antigen-binding molecule compete for binding to CD3 (or CD20). As will be appreciated by a person of ordinary skill in the art, an antibody that competes for binding with a reference antigen-binding molecule may not necessarily bind to the same epitope as the reference antibody, but may sterically block binding of the reference antibody by binding an overlapping or adjacent epitope.

Preparation of Antigen-Binding Domains and Construction of Bispecific Molecules

[0137] Antigen-binding domains specific for particular antigens can be prepared by any antibody generating tech-

nology known in the art. Once obtained, two different antigen-binding domains, specific for two different antigens (e.g., CD3 and CD20), can be appropriately arranged relative to one another to produce a bispecific antigen-binding molecule of the present invention using routine methods. (A discussion of exemplary bispecific antibody formats that can be used to construct the bispecific antigen-binding molecules of the present invention is provided elsewhere herein). In certain embodiments, one or more of the individual components (e.g., heavy and light chains) of the multispecific antigen-binding molecules of the invention are derived from chimeric, humanized or fully human antibodies. Methods for making such antibodies are well known in the art. For example, one or more of the heavy and/or light chains of the bispecific antigen-binding molecules of the present invention can be prepared using VELOCIMMUNE™ technology. Using VELOCIMMUNE™ technology (or any other human antibody generating technology), high affinity chimeric antibodies to a particular antigen (e.g., CD3 or CD20) are initially isolated having a human variable region and a mouse constant region. The antibodies are characterized and selected for desirable characteristics, including affinity, selectivity, epitope, etc. The mouse constant regions are replaced with a desired human constant region to generate fully human heavy and/or light chains that can be incorporated into the bispecific antigen-binding molecules of the present invention.

[0138] Genetically engineered animals may be used to make human bispecific antigen-binding molecules. For example, a genetically modified mouse can be used which is incapable of rearranging and expressing an endogenous mouse immunoglobulin light chain variable sequence, wherein the mouse expresses only one or two human light chain variable domains encoded by human immunoglobulin sequences operably linked to the mouse kappa constant gene at the endogenous mouse kappa locus. Such genetically modified mice can be used to produce fully human bispecific antigen-binding molecules comprising two different heavy chains that associate with an identical light chain that comprises a variable domain derived from one of two different human light chain variable region gene segments. (See, e.g., US 2011/0195454 for a detailed discussion of such engineered mice and the use thereof to produce bispecific antigen-binding molecules).

Bioequivalents

[0139] The present invention encompasses antigen-binding molecules having amino acid sequences that vary from those of the exemplary molecules disclosed herein but that retain the ability to bind CD3 and/or CD20. Such variant molecules may comprise one or more additions, deletions, or substitutions of amino acids when compared to parent sequence, but exhibit biological activity that is essentially equivalent to that of the described bispecific antigen-binding molecules.

[0140] The present invention includes antigen-binding molecules that are bioequivalent to any of the exemplary antigen-binding molecules set forth herein. Two antigen-binding proteins, or antibodies, are considered bioequivalent if, for example, they are pharmaceutical equivalents or pharmaceutical alternatives whose rate and extent of absorption do not show a significant difference when administered at the same molar dose under similar experimental conditions, either single does or multiple dose. Some antigen-binding proteins will be considered equivalents or pharmaceutical alternatives if they are equivalent in the extent of their absorption but not in their rate of absorption and yet may be considered bioequivalent because such differences in the rate of absorption are intentional and are reflected in the labeling, are not essential to the attainment of effective body drug concentrations on, e.g., chronic use, and are considered medically insignificant for the particular drug product studied.

[0141] In one embodiment, two antigen-binding proteins are bioequivalent if there are no clinically meaningful differences in their safety, purity, and potency.

[0142] In one embodiment, two antigen-binding proteins are bioequivalent if a patient can be switched one or more times between the reference product and the biological product without an expected increase in the risk of adverse effects, including a clinically significant change in immunogenicity, or diminished effectiveness, as compared to continued therapy without such switching.

[0143] In one embodiment, two antigen-binding proteins are bioequivalent if they both act by a common mechanism or mechanisms of action for the condition or conditions of use, to the extent that such mechanisms are known.

[0144] Bioequivalence may be demonstrated by in vivo and in vitro methods. Bioequivalence measures include, e.g., (a) an in vivo test in humans or other mammals, in which the concentration of the antibody or its metabolites is measured in blood, plasma, serum, or other biological fluid as a function of time; (b) an in vitro test that has been correlated with and is reasonably predictive of human in vivo bioavailability data; (c) an in vivo test in humans or other mammals in which the appropriate acute pharmacological effect of the antibody (or its target) is measured as a function of time; and (d) in a well-controlled clinical trial that establishes safety, efficacy, or bioavailability or bioequivalence of an antigen-binding protein.

[0145] Bioequivalent variants of the exemplary bispecific antigen-binding molecules set forth herein may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine residues not essential for biological activity can be deleted or replaced with other amino acids to prevent formation of unnecessary or incorrect intramolecular disulfide bridges upon renaturation. In other contexts, bioequivalent antigen-binding proteins may include variants of the exemplary bispecific antigen-binding molecules set forth herein comprising amino acid changes which modify the glycosylation characteristics of the molecules, e.g., mutations which eliminate or remove glycosylation.

Species Selectivity and Species Cross-Reactivity

[0146] According to certain embodiments of the invention, antigen-binding molecules are provided which bind to human CD3 but not to CD3 from other species. Also provided are antigen-binding molecules which bind to human CD20 but not to CD20 from other species. The present invention also includes antigen-binding molecules that bind to human CD3 and to CD3 from one or more non-human species; and/or antigen-binding molecules that bind to human CD20 and to CD20 from one or more non-human species.

[0147] According to certain exemplary embodiments of the invention, antigen-binding molecules are provided

which bind to human CD3 and/or human CD20 and may bind or not bind, as the case may be, to one or more of mouse, rat, guinea pig, hamster, gerbil, pig, cat, dog, rabbit, goat, sheep, cow, horse, camel, cynomolgus, marmoset, rhesus or chimpanzee CD3 and/or CD20. For example, in a particular exemplary embodiment of the present invention bispecific antigen-binding molecules are provided comprising a first antigen-binding domain that binds human CD3 and cynomologous CD3, and a second antigen-binding domain that specifically binds human CD20.

Immunoconjugates

[0148] The present invention encompasses antigen-binding molecules conjugated to a therapeutic moiety ("immunoconjugate"), such as a cytotoxin, a chemotherapeutic drug, an immunosuppressant or a radioisotope. Cytotoxic agents include any agent that is detrimental to cells. Examples of suitable cytotoxic agents and chemotherapeutic agents for forming immunoconjugates are known in the art, (see for example, WO 05/103081).

Therapeutic Formulation and Administration

[0149] The present invention provides pharmaceutical compositions comprising the antigen-binding molecules of the present invention. The pharmaceutical compositions of the invention are formulated with suitable carriers, excipients, and other agents that provide improved transfer, delivery, tolerance, and the like. A multitude of appropriate formulations can be found in the formulary known to all pharmaceutical chemists: Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, Pa. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as LIPOFECTIN™, Life Technologies, Carlsbad, Calif.), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. See also Powell et al. "Compendium of excipients for parenteral formulations" PDA (1998) J Pharm Sci Technol 52:238-311.

[0150] The dose of antigen-binding molecule administered to a patient may vary depending upon the age and the size of the patient, target disease, conditions, route of administration, and the like. The preferred dose is typically calculated according to body weight or body surface area. When a bispecific antigen-binding molecule of the present invention is used for therapeutic purposes in an adult patient, it may be advantageous to intravenously administer the bispecific antigen-binding molecule of the present invention normally at a single dose of about 0.01 to about 20 mg/kg body weight, more preferably about 0.02 to about 7, about 0.03 to about 5, or about 0.05 to about 3 mg/kg body weight. Depending on the severity of the condition, the frequency and the duration of the treatment can be adjusted. Effective dosages and schedules for administering a bispecific antigen-binding molecule may be determined empirically; for example, patient progress can be monitored by periodic assessment, and the dose adjusted accordingly. Moreover, interspecies scaling of dosages can be performed using well-known methods in the art (e.g., Mordenti et al., 1991, *Pharmaceut. Res.* 8:1351).

[0151] Various delivery systems are known and can be used to administer the pharmaceutical composition of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the mutant viruses, receptor mediated endocytosis (see, e.g., Wu et al., 1987, J. Biol. Chem. 262:4429-4432). Methods of introduction include, but are not limited to, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The composition may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local.

[0152] A pharmaceutical composition of the present invention can be delivered subcutaneously or intravenously with a standard needle and syringe. In addition, with respect to subcutaneous delivery, a pen delivery device readily has applications in delivering a pharmaceutical composition of the present invention. Such a pen delivery device can be reusable or disposable. A reusable pen delivery device generally utilizes a replaceable cartridge that contains a pharmaceutical composition. Once all of the pharmaceutical composition within the cartridge has been administered and the cartridge is empty, the empty cartridge can readily be discarded and replaced with a new cartridge that contains the pharmaceutical composition. The pen delivery device can then be reused. In a disposable pen delivery device, there is no replaceable cartridge. Rather, the disposable pen delivery device comes prefilled with the pharmaceutical composition held in a reservoir within the device. Once the reservoir is emptied of the pharmaceutical composition, the entire device is discarded.

[0153] Numerous reusable pen and autoinjector delivery devices have applications in the subcutaneous delivery of a pharmaceutical composition of the present invention. Examples include, but are not limited to AUTOPEN™ (Owen Mumford, Inc., Woodstock, UK), DISETRONIC™ pen (Disetronic Medical Systems, Bergdorf, Switzerland), HUMALOG MIX 75/25™ pen, HUMALOG™ pen, HUMALIN 70/30™ pen (Eli Lilly and Co., Indianapolis, Ind.), NOVOPEN™ I, II and III (Novo Nordisk, Copenhagen, Denmark), NOVOPEN JUNIOR™ (Novo Nordisk, Copenhagen, Denmark), BD™ pen (Becton Dickinson, Franklin Lakes, N.J.), OPTIPEN™, OPTIPEN PRO™, OPTIPEN STARLET™, and OPTICLIK™ (sanofi-aventis, Frankfurt, Germany), to name only a few. Examples of disposable pen delivery devices having applications in subcutaneous delivery of a pharmaceutical composition of the present invention include, but are not limited to the SOLOSTAR™ pen (sanofi-aventis), the FLEXPEN™ (Novo Nordisk), and the KWIKPEN™ (Eli Lilly), the SURECLICK™ Autoinjector (Amgen, Thousand Oaks, Calif.), the PENLET™ (Haselmeier, Stuttgart, Germany), the EPIPEN (Dey, L. P.), and the HUMIRA™ Pen (Abbott Labs, Abbott Park Ill.), to name only a few.

[0154] In certain situations, the pharmaceutical composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, supra; Sefton, 1987, CRC Crit. Ref. Biomed. Eng. 14:201). In another embodiment, polymeric materials can be used; see, Medical Applications of Controlled Release, Langer and Wise (eds.), 1974, CRC Pres., Boca Raton, Fla. In yet

another embodiment, a controlled release system can be placed in proximity of the composition's target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, 1984, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer, 1990, Science 249:1527-1533.

[0155] The injectable preparations may include dosage forms for intravenous, subcutaneous, intracutaneous and intramuscular injections, drip infusions, etc. These injectable preparations may be prepared by methods publicly known. For example, the injectable preparations may be prepared, e.g., by dissolving, suspending or emulsifying the antibody or its salt described above in a sterile aqueous medium or an oily medium conventionally used for injections. As the aqueous medium for injections, there are, for example, physiological saline, an isotonic solution containing glucose and other auxiliary agents, etc., which may be used in combination with an appropriate solubilizing agent such as an alcohol (e.g., ethanol), a polyalcohol (e.g., propylene glycol, polyethylene glycol), a nonionic surfactant [e.g., polysorbate 80, HCO-50 (polyoxyethylene (50 mol) adduct of hydrogenated castor oil)], etc. As the oily medium, there are employed, e.g., sesame oil, soybean oil, etc., which may be used in combination with a solubilizing agent such as benzyl benzoate, benzyl alcohol, etc. The injection thus prepared is preferably filled in an appropriate ampoule.

[0156] Advantageously, the pharmaceutical compositions for oral or parenteral use described above are prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc. The amount of the aforesaid antibody contained is generally about 5 to about 500 mg per dosage form in a unit dose; especially in the form of injection, it is preferred that the aforesaid antibody is contained in about 5 to about 100 mg and in about 10 to about 250 mg for the other dosage forms.

Therapeutic Uses of the Antigen-Binding Molecules

[0157] The present invention includes methods comprising administering to a subject in need thereof a therapeutic composition comprising an anti-CD3 antibody or a bispecific antigen-binding molecule that specifically binds CD3 and a target antigen (e.g., CD20). The therapeutic composition can comprise any of the antibodies or bispecific antigen-binding molecules as disclosed herein and a pharmaceutically acceptable carrier or diluent. As used herein, the expression "a subject in need thereof" means a human or non-human animal that exhibits one or more symptoms or indicia of cancer (e.g., a subject expressing a tumor or suffering from any of the cancers mentioned herein below), or who otherwise would benefit from an inhibition or reduction in CD20 activity or a depletion of CD20+ B cells.

[0158] The antibodies and bispecific antigen-binding molecules of the invention (and therapeutic compositions comprising the same) are useful, inter alia, for treating any disease or disorder in which stimulation, activation and/or targeting of an immune response would be beneficial. In particular, the anti-CD3/anti-CD20 bispecific antigen-binding molecules of the present invention may be used for the treatment, prevention and/or amelioration of any disease or disorder associated with or mediated by CD20 expression or activity or the proliferation of CD20+ B cells. The mechanism of action by which the therapeutic methods of the invention are achieved include killing of the cells expressing CD20 in the presence of effector cells, for example, by CDC, apoptosis, ADCC, phagocytosis, or by a combination of two or more of these mechanisms. Cells expressing CD20 which can be inhibited or killed using the bispecific antigen-binding molecules of the invention include, for example, tumorigenic B cells.

[0159] The antigen-binding molecules of the present invention may be used to treat, e.g., primary and/or metastatic tumors arising in the brain and meninges, oropharynx, lung and bronchial tree, gastrointestinal tract, male and female reproductive tract, muscle, bone, skin and appendages, connective tissue, spleen, immune system, blood forming cells and bone marrow, liver and urinary tract, and special sensory organs such as the eye. In certain embodiments, the bispecific antigen-binding molecules of the invention are used to treat one or more of the following cancers: renal cell carcinoma, pancreatic carcinoma, breast cancer, head and neck cancer, prostate cancer, malignant gliomas, osteosarcoma, colorectal cancer, gastric cancer (e.g., gastric cancer with MET amplification), malignant mesothelioma, multiple myeloma, ovarian cancer, small cell lung cancer, non-small cell lung cancer, synovial sarcoma, thyroid cancer, or melanoma. According to certain exemplary embodiments, the bispecific antigen-binding molecules of the present invention are used to treat a B cell cancer (e.g., Hodgkin's lymphoma, non-Hodgkin's lymphoma [NHL], precursor B cell lymphoblastic leukemia/lymphoma, mature B cell neoplasms, B cell chronic lymphocytic leukemia/small lymphocytic lymphoma, B cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, mantle cell lymphoma, follicular lymphoma, cutaneous follicle center lymphoma, marginal zone B cell lymphoma, hairy cell leukemia, diffuse large B cell lymphoma, Burkitt's lymphoma, plasmacytoma, plasma cell myeloma, post-transplant lymphoproliferative disorder, Waldenstrom's macroglobulinemia, and anaplastic large-cell lymphoma).

[0160] According to certain embodiments of the present invention, the antigen-binding molecules are useful for treating a patient afflicted with a B-cell lymphoma (e.g., NHL) that is resistant to, or incompletely responsive to anti-CD20 therapy alone (e.g., resistant to rituximab therapy). According to other related embodiments of the invention, methods are provided comprising administering an anti-CD3/anti-CD20 bispecific antigen-binding molecule as disclosed herein to a patient who is afflicted with a B-cell lymphoma (e.g., NHL) that is refractory to anti-CD20 therapy (e.g., a patient with a rituximab-refractory tumor or with relapsed or refractory B-cell lymphoma). Analytic/diagnostic methods known in the art, such as tumor scanning, etc., may be used to ascertain whether a patient harbors as tumor that is resistant to, incompletely responsive to, or refractory to anti-CD20 therapy alone.

[0161] The present invention also includes methods for treating residual cancer in a subject. As used herein, the term "residual cancer" means the existence or persistence of one or more cancerous cells in a subject following treatment with an anti-cancer therapy.

[0162] According to certain aspects, the present invention provides methods for treating a disease or disorder associated with CD20 expression (e.g., B cell lymphoma) comprising administering one or more of the bispecific antigen-

binding molecules described elsewhere herein to a subject after the subject has received anti-CD20 mono-therapy (e.g., after administration of a pharmaceutical composition comprising an anti-CD20 antibody such as rituximab). For example, the present invention includes methods for treating B cell lymphoma comprising administering an anti-CD3/anti-CD20 bispecific antigen-binding molecule to a patient 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks, 3 weeks or 4 weeks, 2 months, 4 months, 6 months, 8 months, 1 year, or more after the subject has received anti-CD20 mono-therapy (e.g., rituximab treatment or an equivalent treatment thereof). In other aspects, a bispecific antigen-binding molecule of the invention (an anti-CD3/anti-CD20 bispecific antigen-binding molecule) comprising an IgG4 Fc domain is initially administered to a subject at one or more time points (e.g., to provide robust initial depletion of B cells), followed by administration of an equivalent bispecific antigen-binding molecule comprising a different IgG domain, such as an IgG1 Fc domain, at subsequent time points.

Combination Therapies and Formulations

[0163] The present invention provides methods which comprise administering a pharmaceutical composition comprising any of the exemplary antibodies and bispecific antigen-binding molecules described herein in combination with one or more additional therapeutic agents. Exemplary additional therapeutic agents that may be combined with or administered in combination with an antigen-binding molecule of the present invention include, e.g., an EGFR antagonist (e.g., an anti-EGFR antibody [e.g., cetuximab or panitumumab] or small molecule inhibitor of EGFR [e.g., gefitinib or erlotinib]), an antagonist of another EGFR family member such as Her2/ErbB2, ErbB3 or ErbB4 (e.g., anti-ErbB2, anti-ErbB3 or anti-ErbB4 antibody or small molecule inhibitor of ErbB2, ErbB3 or ErbB4 activity), an antagonist of EGFRvIII (e.g., an antibody that specifically binds EGFRvIII), a cMET anagonist (e.g., an anti-cMET antibody), an IGF1R antagonist (e.g., an anti-IGF1R antibody), a B-raf inhibitor (e.g., vemurafenib, sorafenib, GDC-0879, PLX-4720), a PDGFR-α inhibitor (e.g., an anti-PDGFR-α antibody), a PDGFR-β inhibitor (e.g., an anti-PDGFR-β antibody), a VEGF antagonist (e.g., a VEGF-Trap, see, e.g., U.S. Pat. No. 7,087,411 (also referred to herein as a "VEGF-inhibiting fusion protein"), anti-VEGF antibody (e.g., bevacizumab), a small molecule kinase inhibitor of VEGF receptor (e.g., sunitinib, sorafenib or pazopanib)), a DLL4 antagonist (e.g., an anti-DLL4 antibody disclosed in US 2009/0142354 such as REGN421), an Ang2 antagonist (e.g., an anti-Ang2 antibody disclosed in US 2011/0027286 such as H1H685P), a FOLH1 antagonist (e.g., an anti-FOLH1 antibody), a PRLR antagonist (e.g., an anti-PRLR antibody), a STEAP1 or STEAP2 antagonist (e.g., an anti-STEAP1 antibody or an anti-STEAP2 antibody), a TMPRSS2 antagonist (e.g., an anti-TMPRSS2 antibody), a MSLN antagonist (e.g., an anti-MSLN antibody), a CA9 antagonist (e.g., an anti-CA9 antibody), a uroplakin antagonist (e.g., an anti-uroplakin antibody), a monovalent CD20 antagonist (e.g., a monovalent anti-CD20 antibody such as rituximab), etc. Other agents that may be beneficially administered in combination with the antigen-binding molecules of the invention include cytokine inhibitors, including small-molecule cytokine inhibitors and antibodies that bind to cytokines such as IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-11, IL-12, IL-13, IL-17, IL-18, or to their respective receptors. The pharmaceutical compositions of the present invention (e.g., pharmaceutical compositions comprising an anti-CD3/anti-CD20 bispecific antigen-binding molecule as disclosed herein) may also be administered as part of a therapeutic regimen comprising one or more therapeutic combinations selected from "ICE": ifosfamide (e.g., Ifex®), carboplatin (e.g., Paraplatin®), etoposide (e.g., Etopophos®, Toposar®, VePesid®, VP-16); "DHAP": dexamethasone (e.g., Decadron®), cytarabine (e.g., Cytosar-U®, cytosine arabinoside, ara-C), cisplatin (e.g., Platinol®-AQ); and "ESHAP": etoposide (e.g., Etopophos®, Toposar®, VePesid®, VP-16), methylprednisolone (e.g., Medrol®), high-dose cytarabine, cisplatin (e.g., Platinol®-AQ).

[0164] The present invention also includes therapeutic combinations comprising any of the antigen-binding molecules mentioned herein and an inhibitor of one or more of VEGF, Ang2, DLL4, EGFR, ErbB2, ErbB3, ErbB4, EGFRvIII, cMet, IGF1R, B-raf, PDGFR-α, PDGFR-β, FOLH1, PRLR, STEAP1, STEAP2, TMPRSS2, MSLN, CA9, uroplakin, or any of the aforementioned cytokines, wherein the inhibitor is an aptamer, an antisense molecule, a ribozyme, an siRNA, a peptibody, a nanobody or an antibody fragment (e.g., Fab fragment; $F(ab')_2$ fragment; Fd fragment; Fv fragment; scFv; dAb fragment; or other engineered molecules, such as diabodies, triabodies, tetrabodies, minibodies and minimal recognition units). The antigen-binding molecules of the invention may also be administered and/or co-formulated in combination with antivirals, antibiotics, analgesics, corticosteroids and/or NSAIDs. The antigen-binding molecules of the invention may also be administered as part of a treatment regimen that also includes radiation treatment and/or conventional chemotherapy.

[0165] The additional therapeutically active component(s) may be administered just prior to, concurrent with, or shortly after the administration of an antigen-binding molecule of the present invention; (for purposes of the present disclosure, such administration regimens are considered the administration of an antigen-binding molecule "in combination with" an additional therapeutically active component).

[0166] The present invention includes pharmaceutical compositions in which an antigen-binding molecule of the present invention is co-formulated with one or more of the additional therapeutically active component(s) as described elsewhere herein.

Administration Regimens

[0167] According to certain embodiments of the present invention, multiple doses of an antigen-binding molecule (e.g., an anti-CD3 antibody or a bispecific antigen-binding molecule that specifically binds CD20 and CD3) may be administered to a subject over a defined time course. The methods according to this aspect of the invention comprise sequentially administering to a subject multiple doses of an antigen-binding molecule of the invention. As used herein, "sequentially administering" means that each dose of an antigen-binding molecule is administered to the subject at a different point in time, e.g., on different days separated by a predetermined interval (e.g., hours, days, weeks or months). The present invention includes methods which comprise sequentially administering to the patient a single initial dose of an antigen-binding molecule, followed by one or more

secondary doses of the antigen-binding molecule, and optionally followed by one or more tertiary doses of the antigen-binding molecule.

[0168] The terms "initial dose," "secondary doses," and "tertiary doses," refer to the temporal sequence of administration of the antigen-binding molecule of the invention. Thus, the "initial dose" is the dose which is administered at the beginning of the treatment regimen (also referred to as the "baseline dose"); the "secondary doses" are the doses which are administered after the initial dose; and the "tertiary doses" are the doses which are administered after the secondary doses. The initial, secondary, and tertiary doses may all contain the same amount of the antigen-binding molecule, but generally may differ from one another in terms of frequency of administration. In certain embodiments, however, the amount of an antigen-binding molecule contained in the initial, secondary and/or tertiary doses varies from one another (e.g., adjusted up or down as appropriate) during the course of treatment. In certain embodiments, two or more (e.g., 2, 3, 4, or 5) doses are administered at the beginning of the treatment regimen as "loading doses" followed by subsequent doses that are administered on a less frequent basis (e.g., "maintenance doses").

[0169] In one exemplary embodiment of the present invention, each secondary and/or tertiary dose is administered 1 to 26 (e.g., 1, 1½, 2, 2½, 3, 3½, 4, 4½, 5, 5½, 6, 6½, 7, 7½, 8, 8½, 9, 9½, 10, 10½, 11, 11½, 12, 12½, 13, 13½, 14, 14½, 15, 15½, 16, 16½, 17, 17½, 18, 18½, 19, 19½, 20, 20½, 21, 21½, 22, 22½, 23, 23½, 24, 24½, 25, 25½, 26, 26½, or more) weeks after the immediately preceding dose. The phrase "the immediately preceding dose," as used herein, means, in a sequence of multiple administrations, the dose of antigen-binding molecule which is administered to a patient prior to the administration of the very next dose in the sequence with no intervening doses.

[0170] The methods according to this aspect of the invention may comprise administering to a patient any number of secondary and/or tertiary doses of an antigen-binding molecule (e.g., an anti-CD3 antibody or a bispecific antigen-binding molecule that specifically binds CD20 and CD3). For example, in certain embodiments, only a single secondary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) secondary doses are administered to the patient. Likewise, in certain embodiments, only a single tertiary dose is administered to the patient. In other embodiments, two or more (e.g., 2, 3, 4, 5, 6, 7, 8, or more) tertiary doses are administered to the patient.

[0171] In embodiments involving multiple secondary doses, each secondary dose may be administered at the same frequency as the other secondary doses. For example, each secondary dose may be administered to the patient 1 to 2 weeks after the immediately preceding dose. Similarly, in embodiments involving multiple tertiary doses, each tertiary dose may be administered at the same frequency as the other tertiary doses. For example, each tertiary dose may be administered to the patient 2 to 4 weeks after the immediately preceding dose. Alternatively, the frequency at which the secondary and/or tertiary doses are administered to a patient can vary over the course of the treatment regimen. The frequency of administration may also be adjusted during the course of treatment by a physician depending on the needs of the individual patient following clinical examination.

Diagnostic Uses of the Antibodies

[0172] The anti-CD3 antibodies of the present invention may also be used to detect and/or measure CD3, or CD3-expressing cells in a sample, e.g., for diagnostic purposes. For example, an anti-CD3 antibody, or fragment thereof, may be used to diagnose a condition or disease characterized by aberrant expression (e.g., over-expression, under-expression, lack of expression, etc.) of CD3. Exemplary diagnostic assays for CD3 may comprise, e.g., contacting a sample, obtained from a patient, with an anti-CD3 antibody of the invention, wherein the anti-CD3 antibody is labeled with a detectable label or reporter molecule. Alternatively, an unlabeled anti-CD3 antibody can be used in diagnostic applications in combination with a secondary antibody which is itself detectably labeled. The detectable label or reporter molecule can be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I; a fluorescent or chemiluminescent moiety such as fluorescein isothiocyanate, or rhodamine; or an enzyme such as alkaline phosphatase, beta-galactosidase, horseradish peroxidase, or luciferase. Specific exemplary assays that can be used to detect or measure CD3 in a sample include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence-activated cell sorting (FACS). Samples that can be used in CD3 diagnostic assays according to the present invention include any tissue or fluid sample obtainable from a patient which contains detectable quantities of CD3 protein, or fragments thereof, under normal or pathological conditions. Generally, levels of CD3 in a particular sample obtained from a healthy patient (e.g., a patient not afflicted with a disease or condition associated with abnormal CD3 levels or activity) will be measured to initially establish a baseline, or standard, level of CD3. This baseline level of CD3 can then be compared against the levels of CD3 measured in samples obtained from individuals suspected of having a CD3 related disease or condition.

EXAMPLES

[0173] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (e.g., amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1. Generation of Anti-CD3 Antibodies

[0174] Anti-CD3 antibodies were obtained by immunizing a VELOCIMMUNE® mouse (i.e., an engineered mouse comprising DNA encoding human Immunoglobulin heavy and kappa light chain variable regions) with cells expressing CD3 or with DNA encoding CD3. The antibody immune response was monitored by a CD3-specific immunoassay. When a desired immune response was achieved splenocytes were harvested and fused with mouse myeloma cells to preserve their viability and form hybridoma cell lines. The hybridoma cell lines were screened and selected to identify cell lines that produce CD3-specific antibodies. Using this technique several anti-CD3 chimeric antibodies (i.e., anti-

bodies possessing human variable domains and mouse constant domains) were obtained. In addition, several fully human anti-CD3 antibodies were isolated directly from antigen-positive B cells without fusion to myeloma cells, as described in US 2007/0280945A1.

[0175] Certain biological properties of the exemplary anti-CD3 antibodies generated in accordance with the methods of this Example are described in detail in the Examples set forth below.

Example 2. Heavy and Light Chain Variable Region Amino Acid and Nucleic Acid Sequences

[0176] Table 1 sets forth the amino acid sequence identifiers of the heavy and light chain variable regions and CDRs of selected anti-CD3 antibodies of the invention. The corresponding nucleic acid sequence identifiers are set forth in Table 2.

TABLE 1

Amino Acid Sequence Identifiers								
Antibody	SEQ ID NOs:							
Designation	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H2712N	2	4	6	8	10	12	14	16
H1M2692N	18	20	22	24	26	28	30	32
H1M3542N	34	36	38	40	42	44	46	48
H1M3544N	50	52	54	56	58	60	62	64
H1M3549N	66	68	70	72	74	76	78	80
H1M3613N	82	84	86	88	90	92	94	96
H2M2689N	98	100	102	104	106	108	110	112
H2M2690N	114	116	118	120	122	124	126	128
H2M2691N	130	132	134	136	138	140	142	144
H2M2704N	146	148	150	152	154	156	158	160
H2M2705N	162	164	166	168	170	172	174	176
H2M2706N	178	180	182	184	186	188	190	192
H2M2707N	194	196	198	200	202	204	206	208
H2M2708N	210	212	214	216	218	220	222	224
H2M2709N	226	228	230	232	234	236	238	240
H2M2710N	242	244	246	248	250	252	254	256
H2M2711N	258	260	262	264	266	268	270	272
H2M2774N	274	276	278	280	282	284	286	288
H2M2775N	290	292	294	296	298	300	302	304
H2M2776N	306	308	310	312	314	316	318	320
H2M2777N	322	324	326	328	330	332	334	336
H2M2778N	338	340	342	344	346	348	350	352
H2M2779N	354	356	358	360	362	364	366	368
H2M2789N	370	372	374	376	378	380	382	384
H2M2862N	386	388	390	392	394	396	398	400
H2M2885N	402	404	406	408	410	412	414	416
H2M2886N	418	420	422	424	426	428	430	432
H2M3540N	434	436	438	440	442	444	446	448
H2M3541N	450	452	454	456	458	460	462	464
H2M3543N	466	468	470	472	474	476	478	480
H2M3547N	482	484	486	488	490	492	494	496
H2M3548N	498	500	502	504	506	508	510	512
H2M3563N	514	516	518	520	522	524	526	528
H1H5751P	530	532	534	536	538	540	542	544
H1H5752P	546	548	550	552	554	556	558	560
H1H5753B	562	564	566	568	570	572	574	576
H1H5754B	578	580	582	584	586	588	590	592
H1H5755B	594	596	598	600	602	604	606	608
H1H5756B	610	612	614	616	618	620	622	624
H1H5757B	626	628	630	632	634	636	638	640
H1H5758B	642	644	646	648	650	652	654	656
H1H5761P	658	660	662	664	666	668	670	672
H1H5763P	674	676	678	680	682	684	686	688
H1H5764P	690	692	694	696	698	700	702	704
H1H5769P	706	708	710	712	714	716	718	720
H1H5771P	722	724	726	728	730	732	734	736
H1H5772P	738	740	742	744	746	748	750	752
H1H5777P	754	756	758	460	762	764	766	768
H1H5778P	770	772	774	776	778	780	782	784
H1H5780P	786	788	790	792	794	796	798	800
H1H5781P	802	804	806	808	810	812	814	816
H1H5782P	818	820	822	824	826	828	830	832
H1H5785B	834	836	838	840	842	844	846	848
H1H5786B	850	852	854	856	858	860	862	864
H1H5788P	866	868	870	872	874	876	878	880
H1H5790B	882	884	886	888	890	892	894	896
H1H5791B	898	900	902	904	906	908	910	912
H1H5792B	914	916	918	920	922	924	926	928
H1H5793B	930	932	934	936	938	940	942	944

TABLE 1-continued

Amino Acid Sequence Identifiers								
Antibody	SEQ ID NOs:							
Designation	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H5795B	946	948	950	952	954	956	958	960
H1H5796B	962	964	966	968	970	972	974	976
H1H5797B	978	980	982	984	986	988	990	992
H1H5798B	994	996	998	1000	1002	1004	1006	1008
H1H5799P	1010	1012	1014	1016	1018	1020	1022	1024
H1H5801B	1026	1028	1030	1032	1034	1036	1038	1040
H1H7194B	1042	1044	1046	1048	1234	1236	1238	1240
H1H7195B	1050	1052	1054	1056	1234	1236	1238	1240
H1H7196B	1058	1060	1062	1064	1234	1236	1238	1240
H1H7198B	1066	1068	1070	1072	1234	1236	1238	1240
H1H7203B	1074	1076	1078	1080	1234	1236	1238	1240
H1H7204B	1082	1084	1086	1088	1234	1236	1238	1240
H1H7208B	1090	1092	1094	1096	1234	1236	1238	1240
H1H7211B	1098	1100	1102	1104	1234	1236	1238	1240
H1H7221B	1106	1108	1110	1112	1234	1236	1238	1240
H1H7223B	1114	1116	1118	1120	1234	1236	1238	1240
H1H7226B	1122	1124	1126	1128	1234	1236	1238	1240
H1H7232B	1130	1132	1134	1136	1234	1236	1238	1240
H1H7233B	1138	1140	1142	1144	1234	1236	1238	1240
H1H7241B	1146	1148	1150	1152	1234	1236	1238	1240
H1H7242B	1154	1156	1158	1160	1234	1236	1238	1240
H1H7250B	1162	1164	1166	1168	1234	1236	1238	1240
H1H7251B	1170	1172	1174	1176	1234	1236	1238	1240
H1H7254B	1178	1180	1182	1184	1234	1236	1238	1240
H1H7258B	1186	1188	1190	1192	1234	1236	1238	1240
H1H7269B	1194	1196	1198	1200	1234	1236	1238	1240
H1H7279B	1202	1204	1206	1208	1234	1236	1238	1240
H1xH7221G	1210	1212	1214	1216	1234	1236	1238	1240
H1xH7221G3	1218	1220	1222	1224	1234	1236	1238	1240
H1xH7221G5	1226	1228	1230	1232	1234	1236	1238	1240

TABLE 2

Nucleic Acid Sequence Identifiers								
Antibody	SEQ ID NOs:							
Designation	HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H1H2712N	1	3	5	7	9	11	13	15
H1M2692N	17	19	21	23	25	27	29	31
H1M3542N	33	35	37	39	41	43	45	47
H1M3544N	49	51	53	55	57	59	61	63
H1M3549N	65	67	69	71	73	75	77	79
H1M3613N	81	83	85	87	89	91	93	95
H2M2689N	97	99	101	103	105	107	109	111
H2M2690N	113	115	117	119	121	123	125	127
H2M2691N	129	131	133	135	137	139	141	143
H2M2704N	145	147	149	151	153	155	157	159
H2M2705N	161	163	165	167	169	171	173	175
H2M2706N	177	179	181	183	185	187	189	191
H2M2707N	193	195	197	199	201	203	205	207
H2M2708N	209	211	213	215	217	219	221	223
H2M2709N	225	227	229	231	233	235	237	239
H2M2710N	241	243	245	247	249	251	253	255
H2M2711N	257	259	261	263	265	267	269	271
H2M2774N	273	275	277	279	281	283	285	287
H2M2775N	289	291	293	295	297	299	301	303
H2M2776N	305	307	309	311	313	315	317	319
H2M2777N	321	323	325	327	329	331	333	335
H2M2778N	337	339	341	343	345	347	349	351
H2M2779N	353	355	357	359	361	363	365	367
H2M2789N	369	371	373	375	377	379	381	383
H2M2862N	385	387	389	391	393	395	397	399
H2M2885N	401	403	405	407	409	411	413	415
H2M2886N	417	419	421	423	425	427	429	431
H2M3540N	433	435	437	439	441	443	445	447
H2M3541N	449	451	453	455	457	459	461	463

TABLE 2-continued

Antibody Designation	Nucleic Acid Sequence Identifiers SEQ ID NOs: HCVR	HCDR1	HCDR2	HCDR3	LCVR	LCDR1	LCDR2	LCDR3
H2M3543N	465	467	469	471	473	475	477	479
H2M3547N	481	483	485	487	489	491	493	495
H2M3548N	497	499	501	503	505	507	509	511
H2M3563N	513	515	517	519	521	523	525	527
H1H5751P	529	531	533	535	537	539	541	543
H1H5752P	545	547	549	551	553	555	557	559
H1H5753B	561	563	565	567	569	571	573	575
H1H5754B	577	579	581	583	585	587	589	591
H1H5755B	593	595	597	599	601	603	605	607
H1H5756B	609	611	613	615	617	619	621	623
H1H5757B	625	627	629	631	633	635	637	639
H1H5758B	641	643	645	647	649	651	653	655
H1H5761P	657	659	661	663	665	667	669	671
H1H5763P	673	675	677	679	681	683	685	687
H1H5764P	689	691	693	695	697	699	701	703
H1H5769P	705	707	709	711	713	715	717	719
H1H5771P	721	723	725	727	729	731	733	735
H1H5772P	737	739	741	743	745	747	749	751
H1H5777P	753	755	757	759	761	763	765	767
H1H5778P	769	771	773	775	777	779	781	783
H1H5780P	785	787	789	791	793	795	797	799
H1H5781P	801	803	805	807	809	811	813	815
H1H5782P	817	819	821	823	825	827	829	831
H1H5785B	833	835	837	839	841	843	845	847
H1H5786B	849	851	853	855	857	859	861	863
H1H5788P	865	867	869	871	873	875	877	879
H1H5790B	881	883	885	887	889	891	893	895
H1H5791B	897	899	901	903	905	907	909	911
H1H5792B	913	915	917	919	921	923	925	927
H1H5793B	929	931	933	935	937	939	941	943
H1H5795B	945	947	949	951	953	955	957	959
H1H5796B	961	963	965	967	969	971	973	975
H1H5797B	977	979	981	983	985	987	989	991
H1H5798B	993	995	997	999	1001	1003	1005	1007
H1H5799P	1009	1011	1013	1015	1017	1019	1021	1023
H1H5801B	1025	1027	1029	1031	1033	1035	1037	1039
H1H7194B	1041	1043	1045	1047	1233	1235	1237	1239
H1H7195B	1049	1051	1053	1055	1233	1235	1237	1239
H1H7196B	1057	1059	1061	1063	1233	1235	1237	1239
H1H7198B	1065	1067	1069	1071	1233	1235	1237	1239
H1H7203B	1073	1075	1077	1079	1233	1235	1237	1239
H1H7204B	1081	1083	1085	1087	1233	1235	1237	1239
H1H7208B	1089	1091	1093	1095	1233	1235	1237	1239
H1H7211B	1097	1099	1101	1103	1233	1235	1237	1239
H1H7221B	1105	1107	1109	1111	1233	1235	1237	1239
H1H7223B	1113	1115	1117	1119	1233	1235	1237	1239
H1H7226B	1121	1123	1125	1127	1233	1235	1237	1239
H1H7232B	1129	1131	1133	1135	1233	1235	1237	1239
H1H7233B	1137	1139	1141	1143	1233	1235	1237	1239
H1H7241B	1145	1147	1149	1151	1233	1235	1237	1239
H1H7242B	1153	1155	1157	1159	1233	1235	1237	1239
H1H7250B	1161	1163	1165	1167	1233	1235	1237	1239
H1H7251B	1169	1171	1173	1175	1233	1235	1237	1239
H1H7254B	1177	1179	1181	1183	1233	1235	1237	1239
H1H7258B	1185	1187	1189	1191	1233	1235	1237	1239
H1H7269B	1193	1195	1197	1199	1233	1235	1237	1239
H1H7279B	1201	1203	1205	1207	1233	1235	1237	1239
H1xH7221G	1209	1211	1213	1215	1233	1235	1237	1239
H1xH7221G3	1217	1219	1221	1223	1233	1235	1237	1239
H1xH7221G5	1225	1227	1229	1231	1233	1235	1237	1239

[0177] Antibodies are typically referred to herein according to the following nomenclature: Fc prefix (e.g. "H1H," "HIM," "H2M," etc.), followed by a numerical identifier (e.g. "2712," "2692," etc., as shown in Table 1), followed by a "P," "N," or "B" suffix. Thus, according to this nomenclature, an antibody may be referred to herein as, e.g., "H1H2712N," "H1M2692N," "H2M2689N," etc. The H1H, H1M and H2M prefixes on the antibody designations used herein indicate the particular Fc region isotype of the antibody. For example, an "H1H" antibody has a human IgG1 Fc, an "HIM" antibody has a mouse IgG1 Fc, and an "H2M" antibody has a mouse IgG2 Fc, (all variable regions are fully human as denoted by the first 'H' in the antibody designation). As will be appreciated by a person of ordinary

skill in the art, an antibody having a particular Fc isotype can be converted to an antibody with a different Fc isotype (e.g., an antibody with a mouse IgG1 Fc can be converted to an antibody with a human IgG4, etc.), but in any event, the variable domains (including the CDRs)—which are indicated by the numerical identifiers shown in Table 1—will remain the same, and the binding properties are expected to be identical or substantially similar regardless of the nature of the Fc domain.

Control Constructs Used in the Following Examples

[0178] Various control constructs (anti-CD3 antibodies) were included in the following experiments for comparative purposes: "OKT-3," a mouse monoclonal antibody against human T-cell surface antigens available from the American Type Culture Collection (ATCC) under catalog no. CRL-8001; and "SP34," a commercially available mouse monoclonal antibody obtained from Biolegend, San Diego, Calif. (Cat. No. 302914), reactive against the epsilon chain of the T3 complex on human T lymphocyte cells.

Example 3. Surface Plasmon Resonance Derived Binding Affinities and Kinetic Constants of Human Monoclonal Anti-CD3 Antibodies

[0179] Binding affinities and kinetic constants of human monoclonal anti-CD3 antibodies were determined by surface plasmon resonance at 25° C. using either an antibody-capture format (Tables 3, 5 and 7) or an antigen-capture format (Tables 4, 6 and 8). Measurements were conducted on a T200 Biacore instrument.

[0180] In the antibody-capture format, the Biacore sensor surface was derivatized with a rabbit anti-mouse Fc for hybridoma capture (antibody prefix H1M or H2M) or a mouse anti-human Fc surface for human IgG formatted antibodies (antibody prefix H1H). Soluble heterodimeric CD3 protein (hCD3-epsilon/hCD3-delta; SEQ ID NOs: 1370/1371) with either a human Fc tag (hFcΔAdp/hFc; SEQ ID NOs:1372/1373) or a mouse Fc tag (mFcΔAdp/mFc; SEQ ID NOs:1374/1375) was injected over the antibody captured surface and the binding response was recorded. Heterodimeric CD3 protein was purified using the method described in Davis et al. (US2010/0331527).

[0181] In the antigen-capture format, heterodimeric CD3 protein was captured using a rabbit anti-mouse Fc or mouse anti-human Fc and the respective antibodies were injected over the captured antigen.

[0182] Antibodies were analyzed in their conventional divalent format (Tables 3 to 6) or in a monovalent 1-arm configuration (Tables 7 and 8) in which the second Fab from the antibody was removed and only the Fc portion (CH2-CH3) was expressed.

[0183] Kinetic association (k_a) and dissociation (k_d) rate constants were determined by processing and fitting the data to a 1:1 binding model using Scrubber 2.0 curve fitting software. Binding dissociation equilibrium constants (K_D) and dissociative half-lives ($t_{1/2}$) were calculated from the kinetic rate constants as: K_D (M)=k_d/k_a; and $t_{1/2}$ (min)=(In2/(60*k_d). NT=not tested; NB=no binding observed.

TABLE 3

Biacore Binding Affinities of Hybridoma mAbs (H1M and H2M) Binding at 25° C./Antibody-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H2M2689N	7.73E+05	3.23E−03	4.18E−09	4
H2M2690N	9.70E+03	2.02E−04	2.09E−08	57
H2M2691N	1.03E+04	2.07E−04	2.01E−08	56
H1M2692N	8.05E+03	4.34E−04	5.39E−08	27
H2M2704N	3.46E+04	6.92E−04	2.00E−08	17
H2M2705N	6.62E+04	9.10E−04	1.37E−08	13
H2M2706N	3.29E+04	4.44E−03	1.35E−07	3
H2M2707N	2.95E+04	1.87E−03	6.35E−08	6
H2M2708N	6.94E+04	6.12E−04	8.82E−09	19
H2M2709N	NT	NT	NT	NT
H2M2710N	6.72E+04	7.53E−04	1.12E−08	15
H2M2711N	6.72E+04	7.67E−04	1.14E−08	15
H1M2712N	9.32E+03	2.19E−04	2.35E−08	53
H2M2774N	7.79E+04	9.18E−04	1.18E−08	13
H2M2775N	6.97E+04	6.26E−04	8.98E−09	18
H2M2776N	6.29E+04	6.39E−04	1.02E−08	18
H2M2777N	3.70E+04	1.63E−03	4.39E−08	7
H2M2778N	2.13E+04	1.89E−04	8.90E−09	61
H2M2779N	2.18E+04	2.28E−04	1.05E−08	51
H2M2789N	NT	NT	NT	NT
H2M2862N	3.72E+04	3.00E−03	8.07E−08	4
H2M2885N	6.82E+04	6.51E−04	9.54E−09	18
H2M2886N	7.29E+04	6.53E−04	8.96E−09	18
H2M3540N	3.77E+04	6.11E−04	1.62E−08	19
H2M3541N	7.10E+03	1.35E−03	1.89E−07	9
H1M3542N	2.37E+04	5.08E−04	2.14E−08	23
H2M3543N	7.53E+03	2.26E−04	3.00E−08	51
H1M3544N	9.69E+03	1.42E−04	1.46E−08	82
H2M3547N	2.18E+04	3.47E−04	1.59E−08	33
H2M3548N	3.87E+04	5.04E−03	1.30E−07	2
H1M3549N	1.18E+04	9.19E−04	7.76E−08	13
H2M3563N	3.24E+04	1.19E−04	3.66E−09	97
H1M3613N	1.93E+04	3.04E−04	1.57E−08	38

TABLE 4

Biacore Binding Affinities of Hybridoma mAbs (H1M and H2M) Binding at 25° C./Antigen-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H2M2689N	1.71E+06	9.97E−05	5.83E−11	116
H2M2690N	7.51E+04	6.35E−06	7.99E−11	1820
H2M2691N	3.94E+04	9.98E−06	2.54E−10	1158
H1M2692N	4.19E+04	9.90E−06	2.38E−10	1167
H2M2704N	1.32E+06	2.48E−04	1.87E−10	47
H2M2705N	2.43E+06	3.41E−04	1.40E−10	34
H2M2706N	5.63E+05	3.06E−04	5.44E−10	38
H2M2707N	3.99E+05	2.85E−04	7.15E−10	41
H2M2708N	1.73E+06	2.27E−04	1.31E−10	51
H2M2709N	NT	NT	NT	NT
H2M2710N	1.59E+06	2.43E−04	1.53E−10	48
H2M2711N	1.59E+06	2.40E−04	1.51E−10	48
H1M2712N	4.75E+04	1.37E−05	2.95E−10	846
H2M2774N	2.49E+06	3.36E−04	1.35E−10	34
H2M2775N	1.56E+06	2.16E−04	1.38E−10	53
H2M2776N	1.58E+06	2.22E−04	1.40E−10	52
H2M2777N	5.80E+05	3.21E−04	5.54E−10	36
H2M2778N	1.50E+05	6.57E−06	4.68E−11	1758
H2M2779N	1.28E+05	1.23E−05	9.38E−11	941
H2M2789N	NT	NT	NT	NT
H2M2862N	5.91E+05	3.21E−04	5.41E−10	36
H2M2885N	1.37E+06	1.52E−04	1.11E−10	76
H2M2886N	1.42E+06	1.36E−04	9.56E−11	85
H2M3540N	2.55E+06	5.87E−04	2.31E−10	20
H2M3541N	8.40E+04	1.16E−03	1.38E−08	10
H1M3542N	4.37E+05	2.00E−04	4.57E−10	58
H2M3543N	1.22E+05	7.96E−05	6.53E−10	145
H1M3544N	5.74E+04	5.98E−05	1.04E−09	193

TABLE 4-continued

Biacore Binding Affinities of Hybridoma mAbs (H1M and H2M) Binding at 25° C./Antigen-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H2M3547N	4.70E−05	1.00E−05	2.15E−11	1155
H2M3548N	NT	NT	NT	NT
H1M3549N	2.81E+05	2.89E−04	1.03E−09	40
H2M3563N	6.16E+05	4.77E−05	7.73E−11	242
H1M3613N	2.20E+05	9.60E−05	4.35E−10	120

TABLE 5

Biacore Binding Affinities of Human Fc mAbs (H1H) Binding at 25° C./Antibody-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H1H2690N	NT	NT	NT	NT
H1H2712N	3.06E+03	2.70E−04	8.82E−08	43
H1H5751P	4.01E+03	5.18E−04	1.29E−07	22
H1H5752P	NB	NB	NB	NB
H1H5753B	NT	NT	NT	NT
H1H5755B	8.21E+03	4.72E−04	5.75E−08	24
H1H5756B	8.15E+03	2.66E−04	3.26E−08	43
H1H5757B	6.63E+03	7.85E−04	1.18E−07	15
H1H5758B	5.02E+03	1.17E−03	2.33E−07	10
H1H5761P	4.72E+03	2.44E−02	5.16E−06	0
H1H5763P	1.85E+04	5.40E−02	2.92E−06	0
H1H5764P	4.16E+03	1.59E−02	3.82E−06	1
H1H5769P	7.80E+03	9.41E−04	1.21E−07	12
H1H5771P	3.00E+04	6.26E−04	2.09E−08	18
H1H5772S	1.56E+04	1.55E−03	9.96E−08	7
H1H5777P	1.35E+04	3.02E−03	2.24E−07	4
H1H5778P	5.52E+03	1.54E−04	2.78E−08	75
H1H5780P	1.31E+04	3.99E−04	3.04E−08	29
H1H5781P	8.61E+03	4.97E−04	5.77E−08	23
H1H5782P	NB	NB	NB	NB
H1H5785B	NT	NT	NT	NT
H1H5786B	1.26E+04	1.08E−03	8.54E−08	11
H1H5788P	2.88E+03	2.91E−04	1.01E−07	40
H1H5790B	1.82E+04	5.17E−04	2.83E−08	22
H1H5791B	1.09E+04	7.90E−04	7.25E−08	15
H1H5792B	NT	NT	NT	NT
H1H5793B	8.54E+03	3.82E−04	4.47E−08	30
H1H5795B	1.73E+04	5.76E−04	3.33E−08	20
H1H5796B	1.47E+04	8.91E−04	6.05E−08	13
H1H5797B	NT	NT	NT	NT
H1H5798B	NT	NT	NT	NT
H1H5799P	1.36E+04	7.88E−03	5.79E−07	1
H1H5801B	6.57E+03	1.62E−03	2.46E−07	7
OKT3	2.10E+06	2.00E+00	1.00E−06	0.35 sec

TABLE 6

Biacore Binding Affinities of Human Fc mAbs (H1H) Binding at 25° C./Antigen-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H1H2690N	NT	NT	NT	NT
H1H2712N	8.93E+04	8.68E−05	9.71E−10	133
H1H5751P	7.24E+04	2.47E−04	3.42E−09	47
H1H5752P	NB	NB	NB	NB
H1H5753B	NT	NT	NT	NT
H1H5755B	2.15E+05	2.01E−04	9.36E−10	57
H1H5756B	1.44E+05	1.11E−04	7.67E−10	105
H1H5757B	1.80E+05	2.95E−04	1.64E−09	39
H1H5758B	1.42E+05	5.62E−04	3.97E−09	21
H1H5761P	2.11E+05	1.13E−02	5.34E−08	1
H1H5763P	1.84E+05	1.70E−02	9.24E−08	1
H1H5764P	3.50E+05	7.36E−03	2.10E−08	2

TABLE 6-continued

Biacore Binding Affinities of Human Fc mAbs (H1H) Binding at 25° C./Antigen-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H1H5769P	1.19E+05	5.23E−04	4.41E−09	22
H1H5771P	9.23E+05	3.42E−04	3.71E−10	34
H1H5772S	5.19E+05	8.69E−04	1.67E−09	13
H1H5777P	4.83E+05	1.70E−03	3.52E−09	7
H1H5778P	3.99E+05	3.42E−05	8.56E−11	338
H1H5780P	4.78E+05	1.71E−04	3.58E−10	68
H1H5781P	1.40E+05	2.68E−04	1.92E−09	43
H1H5782P	NB	NB	NB	NB
H1H5785B	NT	NT	NT	NT
H1H5786B	3.00E+06	4.24E−04	1.41E−10	27
H1H5788P	7.06E+04	1.64E−04	2.33E−09	70
H1H5790B	9.25E+05	2.36E−04	2.54E−10	49
H1H5791B	7.86E+05	3.40E−04	4.33E−10	34
H1H5792B	NT	NT	NT	NT
H1H5793B	4.78E+05	1.59E−04	3.33E−10	73
H1H5795B	1.58E+06	2.29E−04	1.45E−10	50
H1H5796B	1.05E+05	2.44E−04	2.32E−09	47
H1H5797B	NT	NT	NT	NT
H1H5798B	NT	NT	NT	NT
H1H5799P	7.18E+05	5.64E−03	7.85E−09	2
H1H5801B	3.31E+05	1.12E−03	3.38E−09	10
OKT3	3.94E+06	2.18E−02	5.53E−09	0.5

TABLE 7

Biacore Binding Affinities of monovalent 1-arm mAbs Binding at 25° C./Antibody-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H1H7194P	1.16E+04	1.51E−04	1.30E−08	76
H1H7195P	3.13E+04	9.89E−05	3.16E−09	117
H1H7196P	1.07E+04	4.43E−04	4.13E−08	26
H1H7198P	2.63E+04	1.58E−04	6.02E−09	73
H1H7203P	1.46E+04	2.67E−04	1.83E−08	43
H1H7204P	1.43E+04	3.62E−04	2.53E−08	32
H1H7208P	NT	NT	NT	NT
H1H7211P	1.41E+04	1.59E−04	1.13E−08	73
H1H7221P	1.07E+04	2.92E−04	2.75E−08	40
H1H7223P	1.60E+04	3.07E−04	1.92E−08	38
H1H7226P	1.30E+04	3.55E−04	2.72E−08	33
H1H7232P	8.03E+03	1.77E−03	2.20E−07	7
H1H7233P	1.11E+04	2.69E−04	2.42E−08	43
H1H7241P	1.34E+04	2.95E−04	2.20E−08	39
H1H7242P	2.15E+04	6.64E−04	3.09E−08	17
H1H7250P	2.34E+04	2.47E−04	1.05E−08	47
H1H7251P	2.56E+04	1.07E−03	4.17E−08	11
H1H7254P	2.60E+04	3.88E−04	1.49E−08	30
H1H7258P	1.26E+04	3.02E−04	2.40E−08	38
H1H7269P	2.57E+04	6.24E−03	2.43E−07	2
H1H7279P	NB	NB	NB	NB
H1xH7221G	NT	NT	NT	NT
H1xH7221G3	NB	NB	NB	NB
H1xH7221G5	NB	NB	NB	NB

TABLE 8

Biacore Binding Affinities of monovalent 1-arm mAbs Binding at 25° C./Antigen-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H1H7194P	3.50E+05	8.43E−05	2.41E−10	137
H1H7195P	5.66E+05	7.14E−05	1.26E−10	162
H1H7196P	1.85E+05	4.61E−04	2.49E−09	25
H1H7198P	6.28E+05	7.07E−05	1.12E−10	163
H1H7203P	4.79E+05	2.38E−04	4.98E−10	48

TABLE 8-continued

Biacore Binding Affinities of monovalent 1-arm mAbs Binding at 25° C./Antigen-Capture Format

Antibody	ka (Ms^{-1})	kd (s^{-1})	K_D (Molar)	T½ (min)
H1H7204P	1.73E+05	3.65E−04	2.12E−09	32
H1H7208P	NT	NT	NT	NT
H1H7211P	3.45E+05	9.61E−05	2.79E−10	120
H1H7221P	1.36E+05	2.39E−04	1.75E−09	48
H1H7223P	1.87E+05	2.86E−04	1.53E−09	40
H1H7226P	4.18E+05	2.36E−04	5.65E−10	49
H1H7232P	1.49E+05	1.49E−03	1.00E−08	8
H1H7233P	1.61E+05	2.04E−04	1.27E−09	57
H1H7241P	1.87E+05	2.36E−04	1.26E−09	49
H1H7242P	3.83E+05	1.01E−03	2.63E−09	11
H1H7250P	2.31E+05	1.89E−04	8.20E−10	61
H1H7251P	4.47E+05	1.19E−03	2.67E−09	10
H1H7254P	4.33E+05	3.30E−04	7.62E−10	35
H1H7258P	1.33E+05	2.90E−04	2.18E−09	40
H1H7269P	2.77E+05	6.89E−03	2.49E−08	2
H1H7279P	NB	NB	NB	NB
H1xH7221G	NT	NT	NT	NT
H1xH7221G3	NB	NB	NB	NB
H1xH7221G5	NB	NB	NB	NB

[0184] As shown in Tables 3-8, Several anti-CD3 antibodies of the present invention bind CD3, in either antibody-capture or antigen-capture formats, with high affinity.

Example 4. Anti-CD3 Antibodies Bind and Proliferate Human T-Cells

[0185] Anti-CD3 antibodies of the present invention were tested for their ability to bind to human T-cells and induce their proliferation. Binding was assessed using Jurkat cells (a CD3+ human T-cell line), while proliferation of Peripheral Blood Mononuclear Cells (PBMC) was assessed using ATP catalyzed quantification (CellTiter Glo®). Anti-CD3 antibody OKT3 acted as a positive control and irrelevant isotype matched antibodies served as negative controls.

[0186] FACS data was acquired using the following protocol: Cells at 2×10^5 per well were incubated with serially diluted antibodies for 30 min on ice. Post incubation, cells were washed and secondary antibody was added and incubated for an additional 30 minutes. After incubation, cells were washed, re-suspended in cold PBS containing 1% BSA and analyzed by flow cytometry with viable Jurkat cells gated by side and forward scatters. The EC_{50}s for cell binding titration were determined using Prism software with values calculated using a 4-parameter non-linear regression analysis.

[0187] Proliferation data was acquired using the following protocol: Human PBMC (5×10^4/well) were incubated with a 3-fold serial dilution of anti-CD3 and a fixed concentration of a commercial anti-CD28 antibody (200 ng/ml) in 96 well plates for 72 h at 37° C. Following incubation, CellTiter Glo® was added and luminescence was measured using a VICTOR X5 multi-label plate reader (PerkinElmer). The EC_{50} of cell viability (ATP catalyzed quantification) was calculated using a 4-parameter non-linear regression analysis in GraphPad Prism.

[0188] Results of the binding and proliferation experiments are summarized in Tables 9-11.

TABLE 9

Hybridoma Anti-CD3 mAbs Bind & Proliferate Human T-Cells

Antibody	EC50 [M] FACS JURKAT	EC50 [M] hPBMC Proliferation
H2M2689N	NB	0.00E+00
H2M2690N	4.37E−09	5.37E−12
H2M2691N	6.77E−09	3.43E−11
H1M2692N	5.99E−09	1.42E−10
H2M2704N	8.45E−10	2.93E−12
H2M2705N	2.96E−10	1.76E−11
H2M2706N	2.37E−09	3.86E−12
H2M2707N	1.24E−07	1.92E−12
H2M2708N	6.58E−10	2.69E−08
H2M2709N	7.11E−10	2.48E−11
H2M2710N	7.10E−10	2.11E−10
H2M2711N	1.16E−09	6.48E−10
H1M2712N	2.19E−08	1.28E−10
H2M2774N	3.52E−10	4.92E−10
H2M2775N	1.32E−09	1.09E−09
H2M2776N	4.91E−10	2.84E−11
H2M2777N	2.16E−09	2.51E−11
H2M2778N	3.62E−09	0.00E+00
H2M2779N	NT	0.00E+00
H2M2789N	NT	2.85E−08
H2M2862N	7.68E−09	6.72E−13
H2M2885N	2.09E−09	2.49E−12
H2M2886N	3.97E−09	2.69E−12
H2M3540N	3.99E−09	3.16E−12
H2M3541N	3.70E−09	6.40E−12
H1M3542N	2.01E−09	0.00E+00
H2M3543N	5.63E−09	6.12E−12
H1M3544N	2.32E−08	0.00E+00
H2M3547N	2.71E−09	5.02E−12
H2M3548N	1.10E−09	1.89E−12
H1M3549N	2.30E−09	0.00E+00
H2M3563N	1.07E−09	7.74E−12
H1M3613N	1.03E−08	0.00E+00
Isotype Ctrl	NB	0.00E+00

NB: No Binding;
NT: Not Tested

TABLE 10

Human Fc Anti-CD3 mAbs Bind & Proliferate Human T-Cells

Antibody	EC50 [M] FACS JURKAT	EC50 [M] hPBMC Proliferation
H1H5751P	2.12E−09	9.29E−12
H1H5752P	3.43E−10	1.09E−12
H1H5753B	NB	9.14E−11
H1H5755B	1.23E−09	4.24E−12
H1H5756B	NB	0.00E+00
H1H5757B	3.38E−09	4.86E−12
H1H5758B	1.90E−09	2.13E−12
H1H5761P	2.10E−09	3.62E−13
H1H5763P	2.76E−09	3.11E−13
H1H5764P	8.80E−10	3.27E−13
H1H5769P	4.10E−09	6.17E−12
H1H5771P	NT	6.35E−12
H1H5772S	6.64E−10	4.42E−12
H1H5777P	5.71E−10	3.04E−12
H1H5778P	6.85E−10	5.04E−12
H1H5780P	7.62E−10	3.44E−12
H1H5781P	1.23E−09	6.08E−12
H1H5782P	NB	5.17E−12
H1H5785B	NB	0.00E+00
H1H5786B	1.10E−09	1.79E−12
H1H5788P	3.53E−09	4.62E−12
H1H5790B	3.55E−09	2.71E−12
H1H5791B	3.77E−09	1.75E−12

TABLE 10-continued

Human Fc Anti-CD3 mAbs Bind & Proliferate Human T-Cells

Antibody	EC50 [M] FACS JURKAT	EC50 [M] hPBMC Proliferation
H1H5792B	5.87E−09	6.47E−12
H1H5793B	4.62E−09	3.28E−12
H1H5795B	2.04E−09	3.09E−12
H1H5796B	9.82E−09	4.37E−12
H1H5797B	3.96E−08	1.07E−11
H1H5798B	5.57E−09	2.59E−12
H1H5799P	NT	1.63E−13
H1H5801B	1.55E−08	1.09E−12
OKT3	1.96E−10	3.30E−13
Isotype Ctrl	NB	0.00E+00

NB: No Binding;
NT: Not Tested

TABLE 11

Monovalent 1-arm Anti-CD3 mAbs Bind & Proliferate Human T-Cells

Antibody	EC50 [M] FACS JURKAT	EC50 [M] hPBMC Proliferation
H1H7194P	1.50E−09	2.37E−12
H1H7195P	3.42E−10	2.42E−12
H1H7196P	3.44E−08	1.27E−12
H1H7198P	7.26E−10	2.55E−12
H1H7203P	3.24E−09	1.64E−12
H1H7204P	2.29E−09	1.51E−12
H1H7208P	5.19E−08	1.46E−12
H1H7211P	7.01E−10	2.75E−12
H1H7221P	1.40E−09	2.60E−12
H1H7223P	9.37E−10	1.07E−12
H1H7226P	7.95E−10	9.52E−13
H1H7232P	1.50E−09	1.03E−12
H1H7233P	7.15E−10	7.34E−13
H1H7241P	1.01E−09	1.05E−12
H1H7242P	1.83E−09	2.13E−12
H1H7250P	1.37E−09	2.43E−12
H1H7251P	1.45E−09	1.30E−12
H1H7254P	1.09E−09	2.80E−12
H1H7258P	1.07E−09	2.17E−12
H1H7269P	1.95E−09	1.15E−12
H1H7279P	NB	0.00E+00
Isotype Ctrl	NB	0.00E+00

NB: No Binding;
NT: Not Tested

[0189] As shown in Tables 7-9, the vast majority of anti-CD3 antibodies of the invention bound human T-cells and induced T-cell proliferation.

Example 5. Anti-CD3 Antibodies Bind and Proliferate Monkey T-Cells

[0190] A subset of anti-CD3 antibodies of the invention was tested for the ability to bind to and induce proliferation of monkey T-cells.

[0191] FACS data was acquired using the following protocol: Cells at 2×10^5 per well were incubated with serially diluted antibodies for 30 min on ice. Post incubation, cells were washed and secondary antibodies were added and incubated for an additional 30 minutes. After incubation, cells were washed, re-suspended in cold PBS containing 1% BSA and analyzed by flow cytometry. CD4+ monkey T cells were gated by side and forward scatters, and on the CD2+ CD4+CD20− population. The EC_{50}s for cell binding titration were calculated using a 4-parameter non-linear regression analysis in GraphPad Prism.

[0192] Proliferation data was acquired using the following protocol: Freshly isolated cynomolgus monkey derived PBMC (5×10^4/well) were incubated with a 3-fold serial dilution of anti-CD3 antibody and a fixed concentration of a commercial anti-CD28 antibody (500 ng/ml) antibody in 96 well plates for 72 h at 37° C. Following incubation, CellTiter Glo® was added and luminescence was measured using a VICTOR X5 multi-label plate reader (Perkin Elmer). The EC_{50} of cell viability (ATP catalyzed quantification) was calculated using a 4-parameter non-linear regression analysis in GraphPad Prism.

[0193] Results of the binding and proliferation experiments are summarized in Tables 12 and 13.

TABLE 12

Anti-CD3 mAbs Bind & Proliferate monkey PBMCs

Antibody	EC50 [M] FACS PBMCs	EC50 [M] mfPBMC Proliferation
H1H2690N	5.66E−09	2.71E−12
H1H2712N	2.29E−09	2.72E−12
H2M3547N	1.12E−10	NT
H2M3563N	1.65E−10	NT
H1H5761P	NT	2.81E−09
H1H5763P	NT	0.00E+00
H1H5764P	NT	4.06E−10
H1H5769P	NT	8.33E−13
H1H5771P	NT	2.74E−12
H1H5772S	NT	1.47E−12
H1H5778P	NT	5.93E−13
H1H5780P	NT	3.13E−13
H1H5781P	NT	7.92E−13
H1H5788P	NT	2.01E−12
OKT3	NB	NT
SP34	7.03E−11	1.71E−12

NB: No Binding;
NT: not tested

TABLE 13

Monovalent 1-arm Anti-CD3 mAbs Bind & Proliferate Monkey PBMCs

Antibody	EC50 [M] FACS PBMCs	EC50 [M] mfPBMC Proliferation
H1H7194P	NT	4.84E−12
H1H7195P	NT	1.36E−12
H1H7196P	NT	1.40E−08
H1H7198P	NT	2.29E−12
H1H7203P	NT	4.97E−13
H1H7204P	NT	1.26E−11
H1H7208P	NT	7.02E−12
H1H7211P	NT	2.81E−13
H1H7221P	NT	1.72E−12
H1H7223P	NT	6.75E−11
H1H7226P	NT	2.26E−11
H1H7232P	NT	4.90E−11
H1H7233P	NT	4.35E−12
H1H7241P	NT	2.05E−11
H1H7242P	NT	1.38E−11
H1H7250P	NT	7.27E−11
H1H7251P	NT	1.83E−11
H1H7254P	NT	8.88E−11
H1H7258P	NT	1.11E−11

NB: No Binding;
NT: not tested

[0194] As shown in Tables 12 and 13, several anti-CD3 antibodies of the invention bound CD2+CD4+ monkey T-cells and induced their proliferation. OKT3 did not drive monkey PBMC proliferation, while SP34 was active against monkey PBMCs.

Example 6. Anti-CD3 mAbs Support T-Cell-Mediated Killing of Tumor Cells

[0195] The ability of anti-CD3 antibodies to redirect T-cell mediated killing via Fc/FcR interactions was studied using a calcein based U937 killing assay. Briefly, human PBMC were isolated over Ficoll-Paque and activated over a course of several days with media containing human IL-2 (30 U/ml) and T-cell activation beads (anti-CD3/CD28). U937 cells were labeled with calcein, and then incubated with activated T-cells at a 10:1 effector: target ratio using 3-fold serial dilutions of antibodies over a course of 3 hours at 37° C. Following incubation, the plates were centrifuged and supernatants were transferred to a translucent black clear bottom plate for fluorescence analysis. EC_{50} values, defined as the molar concentration of CD3 antibody that induces 50% cytotoxicity, were calculated using a 4-parameter non-linear regression analysis in GraphPad Prism. Results using hybridoma antibodies, human Fc antibodies, and monovalent one-arm antibodies are shown in Tables 14, 15 and 16, respectively.

TABLE 14

Hybridoma Anti-CD3 mAbs Redirect T-Cell Killing to U937 Cells

Antibody	U937 Cytotoxicity Human T-cells [M]
H2M2689N	0.00E+00
H2M2690N	2.79E−11
H2M2691N	2.34E−11
H1M2692N	3.59E−10
H2M2704N	2.49E−12
H2M2705N	1.73E−12
H2M2706N	7.91E−12
H2M2707N	7.21E−12
H2M2708N	3.27E−12
H2M2709N	3.47E−12
H2M2710N	3.97E−12
H2M2711N	3.66E−12
H1M2712N	3.14E−10
H2M2774N	2.46E−12
H2M2775N	3.38E−12
H2M2776N	4.06E−12
H2M2777N	4.86E−12
H2M2778N	0.00E+00
H2M2779N	6.75E−10
H2M2789N	NT
H2M2862N	7.66E−12
H2M2885N	3.71E−12
H2M2886N	8.06E−12
H2M3540N	1.25E−11
H2M3541N	5.39E−11
H1M3542N	2.92E−11
H2M3543N	1.31E−11
H1M3544N	1.72E−10
H2M3547N	3.17E−11
H2M3548N	5.50E−12
H1M3549N	1.07E−10
H2M3563N	4.05E−11
H1M3613N	8.66E−10
Isotype Ctrl	0.00E+00

NT: Not Tested

TABLE 15

Human Fc formatted Anti-CD3 mAbs Redirect T-Cell Killing to U937 Cells

Antibody	U937 Cytotoxicity Human T-cells [M]
H1H5751P	1.30E−10
H1H5752P	1.85E−11
H1H5753B	3.79E−10
H1H5755B	5.16E−11
H1H5756B	7.69E−11
H1H5757B	9.65E−11
H1H5758B	8.86E−08
H1H5761P	2.00E−12
H1H5763P	NT
H1H5764P	NT
H1H5769P	5.65E−11
H1H5771P	NT
H1H5772S	6.89E−13
H1H5777P	4.87E−13
H1H5778P	3.41E−13
H1H5780P	4.03E−12
H1H5781P	1.83E−12
H1H5782P	5.18E−12
H1H5785B	4.43E−11
H1H5786B	6.10E−11
H1H5788P	1.54E−11
H1H5790B	8.71E−11
H1H5791B	8.01E−11
H1H5792B	1.40E−10
H1H5793B	8.85E−11
H1H5795B	6.74E−11
H1H5796B	5.03E−10
H1H5797B	5.76E−10
H1H5798B	1.81E−10
H1H5799P	NT
H1H5801B	9.23E−11
OKT3	2.35E−12
Isotype Ctrl	0.00E+00

NT: Not Tested

TABLE 16

Monovalent 1-arm Anti-CD3 mAbs Redirect T-Cell Killing to U937 Cells

Antibody	U937 Cytotoxicity Human T-cells [M]
H1H7194P	4.71E−12
H1H7195P	6.10E−12
H1H7196P	1.96E−11
H1H7198P	5.21E−12
H1H7203P	5.47E−12
H1H7204P	1.08E−11
H1H7208P	4.59E−11
H1H7211P	7.89E−12
H1H7221P	9.21E−12
H1H7223P	5.30E−12
H1H7226P	1.04E−11
H1H7232P	9.96E−12
H1H7233P	1.19E−11
H1H7241P	1.23E−11
H1H7242P	7.50E−12
H1H7250P	5.91E−12
H1H7251P	1.81E−12
H1H7254P	4.18E−12
H1H7258P	1.53E−11
H1H7269P	1.08E−11
H1H7279P	0.00E+00
Isotype Ctrl	0.00E+00

NT: Not Tested

As shown in Tables 14-16, most anti-CD3 antibodies, as well as OKT3, supported redirected T-cell mediated killing

in this assay system. The observed killing, believed to be dependent on the antibody's Fc engagement with the Fc Receptor on U937 cells leading to clustering of CD3 on adjacent T-cells, was squelched by addition of non-specific human IgG (data not shown).

Example 7. Generation of Bispecific Antibodies that Bind CD3 and CD20

[0196] Bispecific antibodies comprising an anti-CD3-specific binding domain and an anti-CD20-specific binding domain were constructed using standard methodologies wherein a heavy chain and a light chain from an anti-CD3 antibody were combined with a heavy chain from an anti-CD20 antibody. The anti-CD3 antibodies used to construct the bispecific antibodies of this example were obtained by immunizing a VelocImmune® mouse with cells expressing CD3 or with DNA encoding CD3, or in the case of BS3/20-007 and -009, from a known anti-CD3 antibody (i.e., the anti-CD3 antibody "L2K" as set forth in WO2004/106380). The anti-CD20 antibodies used to construct the bispecific antibodies of this example are as set forth in U.S. Pat. No. 7,879,984.

[0197] The bispecific antibodies created in accordance with the present Example comprise two separate antigen-binding domains (i.e., binding arms). The first antigen-binding domain comprises a heavy chain variable region derived from an anti-CD20 antibody ("CD20-VH"), paired with a light chain variable region derived from an anti-CD3 antibody ("CD3-VL"). The CD20-VH/CD3-VL pairing creates an antigen-binding domain that specifically recognizes CD20. The second antigen-binding domain comprises a heavy chain variable region derived from an anti-CD3 antibody ("CD3-VH"), paired with a light chain variable region derived from an anti-CD3 antibody ("CD3-VL"). The CD3-VH/CD3-VL pairing creates an antigen-binding domain that specifically recognizes CD3. The same CD20-VH was used in all bispecific antibodies created in this example and is designated "CD20-VH-A" (except for BS3/20-009, which used a different CD20-VH called "CD20-VH-B"). However, several different CD3-VH and CD3-VL components (designated "CD3-VH-A, CD3-VH-B, etc. and CD3-VL-A, CD3-VL-B, etc., derived from different anti-CD3 antibodies) were used in the different bispecific antibodies of the following Examples.

[0198] A summary of the component parts of the antigen-binding domains of the various bispecific antibodies made in accordance with this Example is set forth in Table 17.

TABLE 17

	Anti-CD20 Antigen-Binding Domain		Anti-CD3 Antigen-Binding Domain	
Bispecific Antibody Identifier	Heavy Chain Variable Region	Light Chain Variable Region	Heavy Chain Variable Region	Light Chain Variable Region
BS3/20-001	CD20-VH-A	CD3-VL-A	CD3-VH-A	CD3-VL-A
BS3/20-002	CD20-VH-A	CD3-VL-B	CD3-VH-B	CD3-VL-B
BS3/20-003	CD20-VH-A	CD3-VL-C	CD3-VH-C	CD3-VL-C
BS3/20-004	CD20-VH-A	CD3-VL-D	CD3-VH-D	CD3-VL-D
BS3/20-005	CD20-VH-A	CD3-VL-E	CD3-VH-E	CD3-VL-E

TABLE 17-continued

	Anti-CD20 Antigen-Binding Domain		Anti-CD3 Antigen-Binding Domain	
Bispecific Antibody Identifier	Heavy Chain Variable Region	Light Chain Variable Region	Heavy Chain Variable Region	Light Chain Variable Region
BS3/20-007	CD20-VH-A	CD3-VL-F#	CD3-VH-F#	CD3-VL-F#
BS3/20-009*	CD20-VH-B	CD3-VL-F#	CD3-VH-F#	CD3-VL-F#

#The heavy and light chain variable regions of CD3-VH-F and CD3-VL-F were derived from the anti-CD3 antibody designated "L2K" as set forth in WO2004/106380.
*The anti-CD20 arm of BS3/20-009, comprising the CD20-VH-B/CD3-VL-F pairing, is non-functional; i.e., it does not bind CD20. However, the anti-CD3 arm (comprising the CD3-VH-F/CD3-VL-F pairing) specifically binds CD3. Thus, BS3/20-009 retains the same general "bispecific" structure of the other bispecific molecules generated in this example, but it only binds CD3.

[0199] Tables 18 and 19 set out the amino acid sequence identifiers for the various heavy chain variable regions (Table 18) and light chain variable regions (Table 19), and their corresponding CDRs, of the bispecific antibodies of this Example.

TABLE 18

(Heavy Chain Variable Region Amino Acid Sequences)

	SEQ ID NOs			
Heavy Chain Identifier	HCVR	HCDR1	HCDR2	HCDR3
CD20-VH-A	1242	1244	1246	1248
CD20-VH-B	1338	1340	1342	1344
CD3-VH-A	1250	1252	1254	1256
CD3-VH-B	1266	1268	1270	1272
CD3-VH-C	1282	1284	1286	1288
CD3-VH-D	1298	1300	1302	1304
CD3-VH-E	1314	1316	1318	1320
CD3-VH-F	1329	1330	1331	1332

TABLE 19

(Light Chain Variable Region Amino Acid Sequences)

	SEQ ID NOs			
Light Chain Identifier	LCVR	LCDR1	LCDR2	LCDR3
CD3-VL-A	1258	1260	1262	1264
CD3-VL-B	1274	1276	1278	1280
CD3-VL-C	1290	1292	1294	1296
CD3-VL-D	1306	1308	1310	1312
CD3-VL-E	1322	1324	1326	1328
CD3-VL-F	1333	1334	1335	1336

[0200] In addition, Tables 20 and 21 set out the sequence identifiers for the nucleotide sequences encoding the heavy chain variable regions (Table 20) and light chain variable regions (Table 21), and their corresponding CDRs, of the bispecific antibodies of this Example.

TABLE 20

(Nucleotide Sequences Encoding Heavy Chain Variable Region Sequences)

Heavy Chain	SEQ ID NOs			
Identifier	HCVR	HCDR1	HCDR2	HCDR3
CD20-VH-A	1241	1243	1245	1247
CD20-VH-B	1337	1339	1341	1343

TABLE 20-continued

(Nucleotide Sequences Encoding Heavy Chain Variable Region Sequences)

Heavy Chain	SEQ ID NOs			
Identifier	HCVR	HCDR1	HCDR2	HCDR3
CD3-VH-A	1249	1251	1253	1255
CD3-VH-B	1265	1267	1269	1271
CD3-VH-C	1281	1283	1285	1287
CD3-VH-D	1297	1299	1301	1303
CD3-VH-E	1313	1315	1317	1319

TABLE 21

(Nucleotide Sequences Encoding Light Chain Variable Region Sequences)

Light Chain	SEQ ID NOs			
Identifier	LCVR	LCDR1	LCDR2	LCDR3
CD3-VL-A	1257	1259	1261	1263
CD3-VL-B	1273	1275	1277	1279
CD3-VL-C	1289	1291	1293	1295
CD3-VL-D	1305	1307	1309	1311
CD3-VL-E	1321	1323	1325	1327

[0201] In addition to the bispecific antibodies described above, the following control antibodies were also used in certain of the experiments set out in the Examples that follow:

[0202] Control I: Monoclonal antibody "OKT-3" against human T-cell surface antigens as set forth in U.S. Pat. No. 4,361,549 and available from hybridoma CRL-8001 (American Type Culture Collection, Manassas, Va.).

[0203] Control II: Antibody "SP34" reactive against the epsilon chain of the T3 complex on human T lymphocyte cells, available from BD Pharmagen, Cat #55052.

[0204] Control III: anti-CD20 therapeutic antibody, with heavy and light chain sequences of Rituxan (Rituximab) as disclosed in U.S. Pat. No. 5,736,137.

[0205] Control IV: Monoclonal anti-CD20 antibody designated "3B9-10" as disclosed in U.S. Pat. No. 7,879,984, and set forth herein as an antibody comprising the HCVR/LCVR amino acid sequence pair of SEQ ID NOs: 1242/1346 and HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences of SEQ ID NOs: 1244-1246-1248-1348-1350-1352.

[0206] Control V: Monoclonal anti-CD20 antibody designated "10F2-13" as disclosed in U.S. Pat. No. 7,879,984, and set forth herein as an antibody comprising the HCVR/LCVR amino acid sequence pair of SEQ ID NOs: 1354/1362 and HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 amino acid sequences of SEQ ID NOs: 1356-1358-1360-1364-1366-1368.

Example 8. CD20×CD3 Bispecific Antibodies Selectively Bind Jurkat, Raji and Monkey T-Cells

[0207] CD20×CD3 bispecific antibodies and Control constructs, as set forth in Example 1, were tested via FACS for their ability to bind to Jurkat (CD3+, CD20− human T-cell line), Raji (CD3−, CD20+ Human B-cell line), or cynomolgus PBMCs ("mkT cells").

[0208] FACS data was acquired using the following protocol: Cells at 2×10^5 per well were incubated with serially diluted antibodies for 30 min on ice. Post incubation, cells were washed and appropriate secondary (Jurkat, RAJI cells) or cocktail of secondary antibodies (for cyno PBMC) was added and incubated for an additional 30 minutes. After incubation, cells were washed, re-suspended in cold PBS containing 1% BSA and analyzed by flow cytometry on a BD FACS Canto II. Jurkat and Raji cells were gated by side and forward scatters, while cynomolgus T cells were also gated in a CD2+CD4+ population. The EC_{50}s for cell binding titration were determined using Prism software with values calculated using a 4-parameter non-linear regression analysis. Results are shown in Table 22.

TABLE 22

EC50 Binding Values (Molar) for CD3 × CD20 Bispecific Antibodies

Antibody	FACS—Jurkat	FACS—RAJI	FACS—mkT cells
Control I (anti-CD3)	1.96E−10	NB	NB
Control II (anti-CD3)	(+)	NB	7.03E−11
Control IV (anti-CD20)	No Binding	(+)	NB
BS3/20-001	3.85E−08	5.99E−08	8.74E−06
BS3/20-002	5.62E−08	1.15E−08	NT
BS3/20-003	5.67E−08	9.24E−08	2.48E−08
BS3/20-004	4.89E−08	1.02E−08	NT
BS3/20-005	1.95E−09	8.17E−08	NT

(+) EC_{50} values not determined, but binding observed;
NB no binding;
NT not tested

[0209] As shown in Table 22, the panel of tested antibodies showed a range of binding affinities on the various cell lines, depending on their specificities. Bispecific antibodies (BS3/20-001, -002, -003, -004 and -005) showed the ability to bind both human target lines. A subset of antibodies also showed the ability to bind to cynomolgus cells (Control II, BS3/20-001 and BS3/20-003). Anti-CD3 Control I (OKT3), anti-CD3 Control II (SP34), and anti-CD20 Control IV bound to Jurkat, cynomolgus T cells, and RAJI, respectively.

Example 9. CD20×CD3 Bispecific Antibodies Induce PBMC Proliferation In Vitro

[0210] The ability of selected CD20×CD3 bispecific antibodies and Control constructs to stimulate Peripheral Blood Mononuclear Cells (PBMC) and induce proliferation was assessed using ATP catalyzed quantification (CellTiter Glo®). The activation of PBMCs results in the release of cytokines, which drive cellular proliferation.

[0211] Proliferation data was acquired using the following protocol: Human or cynomolgus monkey derived PBMC (5×10^5/well) were incubated with a 3-fold serial dilution of anti-CD3×CD20 or Control antibody in 96 well plates for 72 h at 37° C. Following incubation, CellTiter Glo® was added and luminescence was measured using a VICTOR X5 multilabel plate reader (PerkinElmer). The EC_{50} of cell viability (ATP catalyzed quantification) was determined using Prism software. Values were calculated using a 4-parameter nonlinear regression analysis and are shown in Table 23.

TABLE 23

EC_{50}s for human and cynomolgus PBMC proliferation induced by anti-CD20 × CD3 bispecific antibodies

Antibody	Human PBMC Proliferation EC_{50} [M]	Cyno PBMC Proliferation EC_{50} [M]
Control I	3.30E−13	NA
Control II	8.93E−12	1.71E−12
BS3/20-001	1.08E−11*	4.02E−11*
BS3/20-002	8.59E−12*	2.60E−11*
BS3/20-003	9.55E−12*	2.78E−11*
BS3/20-004	1.45E−12*	NT
BS3/20-005	1.05E−12*	NT

*Data are median values of 3 or more independent assays.

Data without a (*) are representative/average values of 1 or 2 independent assays.

NA = no activity; NT = not tested.

[0212] As shown in Table 23, all CD20×CD3 bispecific antibodies of the invention were activators of human or cynomolgus PBMCs. In general, anti-CD3 mono specific bivalent parental antibodies (Contros I and II) were 2-10 fold more potent than the bispecific counterparts. Control I (OKT3) did not drive monkey PBMC proliferation, while Control II (SP34) was active against both human and monkey PBMCs.

Example 10. CD20×CD3 Bispecific Antibodies Activate T-Cells and Induce IFN-Gamma Release and CD25 Upregulation in Human Whole Blood

[0213] Selected CD20×CD3 bispecific antibodies were tested for their ability to activate T-cells in human whole blood. The extent of T-cell activation was determined by measuring interferon-gamma (IFNγ) secretion as well as the upregulation of CD25 on CD8+ T cells.

[0214] Interferon-gamma (IFNγ) secretion was quantified by combining heparinized whole blood with 5-fold serial dilutions of bispecific antibodies in 96-well plates. After 20 hours, the plates were centrifuged for 5 minutes and plasma was removed for ELISA analysis to determine IFNγ levels. Extrapolated IFNγ concentrations were plotted versus antibody concentration, and EC_{50} values were calculated using a 4-parameter non-linear regression analysis using Prism software.

[0215] For analysis of CD25 expression on CD8+ T-cells, following incubation with antibodies and removal of plasma, 150 μl of blood was transferred to a deep well plate and lysed for 15 minutes with 1.5 mL RBC lysis buffer. Cells were washed twice, blocked for 10 minutes at room temperature with hFcR blocking reagent, and then incubated for 30 min at 4° C. with antibodies conjugated directly to CD2, CD19, CD4, CD8, and CD25. Next, cells were washed twice before analysis with a FACSCanto cytometer and FlowJo software.

[0216] The percentage of CD2+CD8+ T cells expressing the activation marker CD25 was plotted versus antibody concentration, and EC_{50} values were calculated using a 4-parameter non-linear regression analysis using Prism software. Results are shown in Table 24.

TABLE 24

EC_{50} values of Bispecific antibody mediated upregulation of CD25 and IFNγ production in whole blood

Bispecific Antibody	EC_{50} of CD25 Upregulation [M]	EC_{50} of IFNγ Production [M]	Max IFNγ (pg/mL)
BS3/20-001	1.3E−10	3.9E−10	1815
BS3/20-003	1.7E−10	5.7E−10	1693
BS3/20-004	2.9E−10	2.3E−09	5810

Median values of at least 3 independent experiments (except IFN-gamma expression of BS3/20-003, which is n = 2)

[0217] As shown in Table 24, the CD20×CD3 bispecific antibodies mediated the upregulation of CD25 on CD8+ T cells in whole blood with EC_{50} values ranging from 130-290 pM with corresponding EC_{50} values for IFNγ that were slightly higher ranging from 390 pM to 2 nM. BS3/20-004 was less slightly less potent then BS3/20-001 and BS3/20-003 in mediating CD25 upregulation and IFNγ production as determined by EC_{50}, however BS3/20-004 could induce greater levels of IFNγ in whole blood cultures.

Example 11. CD20×CD3 Bispecific Antibodies Induce T-Cell Mediated Cytotoxicity on Rituximab Resistant Cell Lines

[0218] The ability of selected CD20×CD3 bispecific antibodies and Control constructs to mediate complement-dependent cytotoxicity (CDC) and T-cell mediated cytotoxicity was evaluated using parental Raji cells and Raji SCID lines. The later (Raji SCID lines) were derived from individual anti-CD20 resistant tumors isolated from immunodeficient mice injected subcutaneously with Raji cells following treatment with the anti-CD20 mAb Rituximab. Four lines (Raji SCID 1-4) were used in this Example.

[0219] The expression of CD20 and the complement inhibitory molecules CD55 and CD59 on Raji cell lines was determined by FACS. Briefly, 1×10^6 cells were incubated in individual tubes for 30 minutes with antibodies directly conjugated to CD20, CD55 and CD59. Cells were washed twice before FACS acquisition by a FACSCanto cytometer and analysis with FlowJo software.

[0220] To determine the ability of anti-CD20 and anti-CD3×CD20 antibodies to mediate T-cell directed killing of Raji cell lines, calcein labeled Raji cells were incubated for 2 hours at 37° C. with pre-activated T cells (ficoll-isolated human PBMC activated with rhIL-2 (30U/mL) and anti-CD3/CD28 activation beads) and 3-fold serial dilutions of antibodies starting at 2 nM. Following incubation, plates were centrifuged and supernatants were transferred to a translucent black clear bottom plate for 530 nm fluorescence detection at 485 nm emission. Percent cytotoxicity was determined based on spontaneous (target cells alone) and maximum release (target cells lysed with detergent) values. EC_{50} values were calculated using a 4-parameter non-linear regression analysis using Prism software.

[0221] To determine the activity of the antibodies to mediate CDC, Raji cell lines were incubated with 5% normal human serum complement and 3-fold serial dilutions of antibodies starting at 100 nM. After incubation for 4.5 hours at 37C, cell death was determined using CellTiter Glo®. Percent cytotoxicity was determined based on spontaneous (target cells alone) and maximum release (target

cells lysed with detergent) values. EC_{50} values were calculated using a 4-parameter non-linear regression analysis using Prism software.

[0222] Results are shown in Table 25.

TABLE 25

EC50 values for antibody mediated CDC and T-cell mediated cytotoxicity

			CDC			T-Cell Mediated Cytotoxicity	
Cell Line	CD20 MFI	% CD55/	BS3/ 20-007	Control IV (anti-CD20)	Control III (anti-CD20)	BS3/ 20-007	Control IV (anti-CD20)
Raji	1709	8.81	2.62E−09	2.47E−10	9.66E−11	1.66E−12	No Activity
Raji SCID1	570	80.7	1.01E−07	5.19E−08	8.56E−08	1.11E−12	No Activity
Raji SCID2	1373	9.1	8.83E−09	2.29E−10	5.87E−11	6.52E−13	No Activity
Raji SCID3	1151	97.3	3.77E−08	5.71E−09	2.55E−08	2.93E−13	No Activity
Raji SCID4	1717	64.6	1.40E−07	1.14E−09	5.29E−09	1.53E−12	No Activity

[0223] Compared to parental Raji cells, 2 of 4 Raji SCID lines showed reduced expression of CD20 (Table 25; lines Raji SCID 1 and 3), with significantly higher percentage of cells expressing the complement inhibitory molecules CD55 and CD59. The sensitivity of the Raji SCID cells to CDC mediated by either anti-CD20 or anti-CD20×CD3 antibodies was dependent on the percentage of CD55/CD59 expressing cells, but not on the levels of CD20, such that increased expression of CD55/CD59 on target cells inhibited CDC.

[0224] The anti-CD20 antibodies (Control IV & Control III [Rituximab]) were more potent than the anti-CD20×CD3 (BS3/20-007) in mediating CDC, as the bispecific is monovalent for CD20. However, in contrast to CDC, T-cell mediated cytotoxicity was not dependent on CD20 or CD55/CD59 levels, as all cell lines were equally susceptible to cell death by activated T-cells in the presence of anti-CD20×CD3 bispecific antibody. Additionally, the bispecific antibody was 100-1000 fold more potent in mediating T-cell dependent killing of Raji cells than the anti-CD20 antibody in the CDC assay.

Example 12. CD25 Upregulation on CD8+ T-Cells is Dependent on CD20 Concentration when in the Presence of CD20×CD3 Bispecific Antibodies

[0225] To evaluate if higher concentrations of target cell (CD20+ lymphomas) would lead to an increased potency of CD20×CD3 bispecific antibodies, human peripheral blood mononuclear cells (PBMCs) were co-cultured in the presence of a Burkitt's lymphoma-derived cell line, i.e., Raji.

[0226] CD25 upregulation on CD8+ T-cells was determined using the following protocol: Human PBMCs (5×10^5/mL), isolated via centrifugation of mononuclear-cell enriched leukapharesis-derived blood over Ficoll, were incubated in the presence (1×10^5/mL) or absence of Raji cells, at 37° C. in 96-well flat bottom plates with 5-fold serial dilutions of the bispecific antibodies. After 48 hours, cells were washed 2×, blocked for 10 minutes at room temperature with hFcR blocking reagent, and then incubated for 30 minutes at 4° C. with directly conjugated antibodies to CD2, CD19, CD4, CD8, and CD25. After staining, cells were washed twice before FACS acquisition by a FACSCanto cytometer and analysis with FlowJo software. The percentage of activated CD2+CD8+ T cells expressing CD25 was plotted versus antibody concentration, and EC_{50} values were calculated using a 4-parameter non-linear regression analysis using Prism software. Results are shown in Table 26.

TABLE 26

CD25 upregulation on CD8+ T-cells following incubation of human PBMC with CD20 × CD3 bispecific antibodies plus or minus Raji cells

	PBMC		PBMC + Raji	
Antibody	EC_{50} (M)	Max % CD25+	EC_50 (M)	Max % CD25+
BS3/20-001	1.12E−10	14.2	1.35E−12	92.2
BS3/20-003	3.65E−10	21.1	3.38E−13	94.4

[0227] As shown in Table 26, activated T-cells when cultured in the presence of Raji (target) cells showed an upregulation of CD25, and a subsequent 100-fold decrease in their EC_{50} values.

Example 13. CD20×CD3 Bispecific Antibodies Induce Cytotoxicity to Raji Cells in the Presence of Activated T-Cells

[0228] The ability of CD20×CD3 bispecific antibodies to redirect T-cell mediated killing to CD20-expressing Raji cells was tested in an in vitro cytotoxicity assay. In addition, the ability of both bispecific and parental anti-CD3 antibodies to kill U937 cells via Fc/FcR interactions was also studied.

[0229] Calcein killing assays were carried out using the following protocol: Human and cynomolgus PBMC were isolated over ficoll-Plaque or via Lympholyte Mammal cell separation media, respectively. The isolated PBMCs were activated over a course of several days with media containing recombinant human IL-2 (30U/ml) and T-cell activation beads (anti-CD3/CD28 for human PBMC, anti-CD2/CD3/CD28 for cynomolgus PBMC).

[0230] Target cells (Raji for CD20 mediated killing and U937 for FcR mediated killing) were labeled with calcein, and incubated with activated T-cells at a 10:1 effector: target ratio using 3-fold serial dilutions of antibodies over a course

of 3 hours at 37° C. Following incubation, the plates were centrifuged and supernatants were transferred to a translucent black clear bottom plate for fluorescence analysis. EC_{50}s defined as the molar concentration of bispecific antibody that induces 50% cytotoxicity was determined using Prism. Values were calculated using a 4-parameter non-linear regression analysis. Results are summarized in Table 27.

TABLE 27

EC_{50} values for CD20 × CD3-Induced Cytotoxicity to Raji and U937 cells

Antibody	Raji Cytotoxicity Human T-cells [M]	U937 Cytotoxicity Human T-cells [M]	Raji Cytotoxicity Monkey T-cells [M]
Control I (anti-CD3)	NA	3.04E-12	NA
BS3/20-001	5.63E−11*	8.86E−11*	1.27E−12*
BS3/20-002	7.71E−11*	8.24E−10	NT
BS3/20-003	7.38E−11*	8.10E−11*	4.36E−14
BS3/20-004	1.29E−11*	6.07E−11	NT
BS3/20-005	1.95E−11	1.48E−10	NT

*Data are median values of 3 or more independent assays.
Data without a (*) are representative/average values of 1 or 2 independent assays.
NA = No Activity; NT = Not Tested.

[0231] As shown in Table 27, bispecific CD20×CD3 antibodies containing human-specific or human/cynomolgus cross reactive anti-CD3 arms were able to specifically redirect cytotoxicity to Raji cells in the presence of human activated T cells. In the presence of cynomolgus activated T cells, Raji were killed when they were incubated with BS3/20-001 or BS3/20-003, bispecific antibodies that have anti-CD3 arms that activate monkey T-cells. All bispecific antibodies as well as Control I, an anti-CD3 mAb, showed activity in the U937 Fc/FcR dependent killing assay. This activity could be blocked by the addition of blocking non-specific human IgG to the reaction (Data not shown).

Example 14. CD3×CD20 Bispecific Antibodies can Deplete CD19+ B-Cells in Mice Reconstituted with Human Immune Cells

[0232] To determine the in vivo potency of CD3×CD20 bispecific antibody administration, changes in CD19+ B-cell and CD2+ T-cell levels were examined via FACS after administration of 10 μg or 0.1 μg of anti-CD3×CD20 bispecific antibody into mice, which were reconstituted with human immune cells.

[0233] Briefly, newborn BALB/Rag2^{null}/γ_c^{null} mice were irradiated with 2×150 Rads and reconstituted with 4×10^5 human CD34$^+$ hematopoietic progenitor cells via intrahepatic injection. After 12 weeks, the composition of reconstituted human immune system in peripheral blood was determined by flow cytometry. Typically by three months post reconstitution, between 10%-60% percent of peripheral white blood cells are human CD45+ of which 40%-70% are B cells, 15%-40% are T-cells and the remaining are small populations of natural killer and dendritic cells.

[0234] Five months post-reconstitution, mice were injected intraperitoneally with 10 pg or 0.1 pg of anti-CD3×CD20 bispecific antibody BS3/20-007, 10 pg of a monovalent 1-arm CD3 antibody (BS3/20-009, see Table 1) or 10 pg of an irrelevant hIgG isotype control. One, eight, and twenty-five days post injection, mice were bled retro-orbitally and immune cell populations in the peripheral blood were determined by flow cytometry (FACS).

[0235] For FACS analysis, 100 μl of blood was incubated with 1.5 ml RBC lysis buffer in Eppendorf tubes for three minutes. Cells were centrifuged for five minutes at 0.4×g, washed 2× with FACS wash (PBS+3% FBS), and blocked for 10 minutes at room temperature with mouse Fc blocking reagent. Cells were then incubated for 30 minutes at 4° C. with directly conjugated antibodies to CD2, CD3, CD19, CD4, CD8, hCD45, hHLA-DR, and mCD45. After staining, cells were washed two times before FACS acquisition by a FACSCanto cytometer and analysis with FlowJo software. Results are shown in Table 28.

TABLE 28

Percentage of circulating CD45, CD19 and CD2 positive cells in mice reconstituted with human immune cells

		Isotype Ctrl (10 μg)		BS3/20-007 (10 μg)		BS3/20-007 (0.1 μg)			BS3/20-009 [one-arm CD3] (10 μg)	
		Mouse ID								
	Day	1	2	3	4	5	6	7	8	9
% huCD45+	Pre	13.7	14.8	16.1	30.9	37.2	22.5	25.5	26.6	33.3
	1 d	7.7	10.8	0.01	0.13	1.7	1.2	0.8	2.7	8.9
	8 d	14.1	12.7	0.12	0.16	3.3	7.7	3.9	3.2	4.5
	25 d	13.0	7.3	0.15	0.12	9.0	1.2	1.0	2.8	5.1
% CD19+	1 d	58.7	66.8	0.00	7.69	20.2	7.0	5.2	75.3	87.1
(of	8 d	66.2	56.2	0.00	0.00	21.3	0.4	0.0	70.4	76.6
huCD45+)	25 d	37.3	62.8	9.7	2.6	58.3	0.7	0.6	38.9	51.3
% CD2+	1 d	58.7	66.8	0.00	7.69	20.2	7.0	5.2	75.3	87.1
(of	8 d	66.2	56.2	0.00	0.00	21.3	0.4	0.0	70.4	76.6
huCD45+)	25 d	37.3	62.8	9.7	2.6	58.3	0.7	0.6	38.9	51.3

[0236] As shown in Table 28, a single 10 pg dose of anti-CD3×CD20 bispecific antibody BS3/20-007 resulted in a disappearance of circulating hCD45+ cells in 2 of 2 treated mice which did not recover over the length of the experiment. A single 0.1 μg dose of BS3/20-007 reduced circulating hCD45+ cells, including CD19+ B-cells and CD2+ T-cells 24 hours post injection in 2 of 3 treated mice. Once depleted, the percentage of hCD45+ cells did not recover significantly in the responding mice treated with 0.1 μg BS3/20-007. However, what cells remained in these mice were predominantly hCD2+ T-cells, and CD19+ B cells were not present in the responding mice even at 25 days post treatment. A single 10 μg dose of a monovalent 1-arm CD3 antibody (BS3/20-009) also resulted in a persistent but modest reduction in CD45+ cells, notably CD2+ T-cells, in 2 of 2 treated mice. A single 10 μg dose of an irrelevant hIgG1 control had no significant effect on the percentage of circulating hCD45+, hCD19+, or hCD2+ cells.

Example 15. Treatment with CD20×CD3 Bispecific Antibody Decreases Raji Tumor Volume in NOD/SCID Mice

[0237] To assess the efficacy of selected anti-CD3×CD20 bispecific antibodies in reducing Raji tumor growth, NOD/SCID mice (Taconic) were implanted subcutaneously with a mixture of 2×10^6 Raji tumor cells and 8×10^6 human PBMC. Mice were treated three times per week, starting on the day of tumor implantation, with either human Fc (hFc) or CD3×CD20 bispecific antibody (BS3/20-007) at a dose of 1 μg per mouse (N=20 mice per treatment group). Reagents were delivered by intraperitoneal (i.p.) injection. Tumor size was measured three times per week using calipers, and tumor volume calculated as Volume=(length×width^2)/2. Results are shown in FIG. **1**.

[0238] In a second experiment, NOD/SCID mice were implanted subcutaneously with a mixture of 2×10^6 Raji tumor cells and 4×10^6 human PBMC. Treatment with CD3×CD20 bispecific antibody (BS3/20-007) or control reagent (hFc) began 7 days post tumor implantation to allow tumors to become palpable. Mice were treated two times per week at a dose of 1 pg per mouse (N=6 mice per treatment group). Reagents were injected subcutaneously, away from the site of tumor implantation. Tumor size was measured two times per week using calipers, and tumor volume calculated as Volume=(length×width^2)/2. Results are shown in FIG. **2**.

[0239] This Example demonstrates that treatment with CD3×CD20 bispecific antibody BS3/20-007 was effective in inhibiting tumor growth both at the time of tumor implantation and once tumors were established. Tumor volume in mice was decreased 25 days post implantation in both studies, relative to control.

Example 16. CD20×CD3 Bispecific Antibodies Deplete B-Cell Populations in Cynomolgus Monkeys and Have a Pharmacokinetic Profile Typical of Monoclonal Antibodies

[0240] A pilot non-GLP toxicology and pharmacology study was performed in cynomolgus monkeys (*Macaca fascicularis*) to determine the ability of the CD3×CD20 bispecific antibodies to deplete B-cell populations in these animals. Male animals were organized into three cohorts. Cohort 1 received bispecific antibody BS3/20-001 and included three different dosing groups (0.01, 0.10 and 1.00 mg/kg) with 3-4 animals per dosing group. Cohort 2 was a two-animal cohort that received a low dose of anti-CD20 control antibody (Control V; 0.01 mg/kg). Cohort 3 was a four-animal cohort that received a high dose of anti-CD20 control antibody (Control III; 1.0 mg/kg). Blood was drawn at day −7 and immediately prior to dosing in order to establish baseline levels for B and T cells in these animals. Doses of drug at 0.01, 0.10, or 1.00 mg/kg were administered by i.v. infusion and blood was drawn at 5 minutes, 5 hours, and 1, 4, 7, and 14 days post dosing. Following day 14 post-dose, blood was drawn every two weeks until the conclusion of the study. Blood samples were analyzed by FACS for B and T cell markers and the absolute number of these cell types was determined. Serum samples were also analyzed for cytokine levels (IFNγ, IL-2, IL-6 and TNFα) using standard analytic methods. Results are shown in FIG. **3** (B-cells), FIG. **4** (T-cells), and FIGS. **5**A-**5**D (cytokines).

[0241] As shown in this Example, administration of the CD3×CD20 bispecific antibody resulted in depletion of circulating B-cells to baseline levels by the first time point measured (day 1). This depletion was not seen in the control animal cohort. B-cell depletion in the bispecific cohort was maintained until two weeks after dosing and in the 0.01 and 0.10 mg/kg dose cohorts was followed by a gradual recovery of B-cell levels until the experiment was concluded at around 11 weeks post dosing. In the 1.0 mg/kg cohort, however, no recovery of B-cell levels was seen for the duration of the experiment (11 weeks). T-cell levels were also monitored in this experiment. A transient loss of circulating T-cells was observed at day 1 post-dose in the bispecific cohorts. T-cell levels returned to baseline levels in these cohorts by the day 4 time-point and maintained at those baseline levels until the end of the experiment. In addition, serum cytokine levels for BS3/20-001 at 5 hours exhibited a dose- and time-dependent response that is consistent with T-cell activation (see FIGS. **5**A-**5**D).

[0242] Gene expression levels in the peripheral blood were also analyzed during this experiment. Blood samples were obtained from animals at two pre-dose time points (Day 7 pre-dose and immediately pre-dose) and at 5, 24, 72, 96, and 168 hours post-dosing. RNA was isolated from these samples and analyzed by microarray. When compared to pre-dose levels and gene expression levels from the control

group, a notable decrease in the gene expression of B-cell markers in animals treated with the bispecific antibody was observed; this effect was similar to the effect observed in samples obtained from animals treated with 1.0 mg/kg Control III (anti-CD20 antibody corresponding to Rituximab). The observed change in B-cell marker expression corresponds to the loss of B-cells detected in the blood of treated animals. The expression of T-cell marker genes in samples from animals treated with the CD3×CD20 bispecific antibody showed an initial decrease followed by a return to normal levels by the 24 hour time point. In addition, genes associated with an inflammatory response showed an initial upregulation in animals in the bispecific cohort but returned to normal or below normal levels after 24 hours. Finally, examination of the raw intensity of the CD20 gene expression signal suggests that a greater depletion of B-cells arises from treatment of animals with the CD3×CD20 bispecific antibody than with the control anti-CD20 antibodies. (See FIG. **6** and Table 29).

TABLE 29

CD20 Gene Expression Levels at Day 7

Antibody	Dose mg/kg	CD20 Expression (Raw Intensity)
Control V	0.01	26485.44
(anti-CD20)	0.01	24335.17
Control III	1.0	1813.46
(anti-CD20)	1.0	47.09
	1.0	98.88
	1.0	70.52
BS3/20-001	0.01	24.93
	0.01	226.45
	0.01	4.78
	0.01	8.12
	0.1	8.26
	0.1	5.62
	0.1	4.82
	0.1	23.61
	1.0	9.38
	1.0	9.19
	1.0	8.22

[0243] As shown in Table 29, at seven days post-dosing the raw intensity of CD20 signal remained at background levels in all but one of the CD3×CD20 animals while 3 of 4 animals treated with 1 mg/kg of Control III showed either marginal or detectable CD20 signal levels.

[0244] In the same experiment the pharmacokinetic profile of the bispecific antibody (FIG. **7**) was evaluated by obtaining blood samples at pre-dose and at 0.083, 5, 24, 48, 72, 168, 336, 504 and 840 hours. The resultant serum samples were analyzed by a direct enzyme linked immunosorbent assay (ELISA) to determine the concentration of total bispecific antibody. Serum total bispecific (BS3/20-001) concentration data were analyzed by non-compartmental analysis (Phoenix WinNonLin) to determine pharmacokinetic parameters Results are shown in Table 30 (AUC=area under the curve vs. time; C_{max}=maximum concentration of compound observed in matrix of interest).

TABLE 30

Pharmacokinetic Parameters of BS3/20-001 in Cynomolgus Monkey

		0.01 mg/kg		0.10 mg/kg		1.0 mg/kg	
Parameter	Units	Mean	SD	Mean	SD	Mean	SD
C_{max}	µg/mL	0.261	0.0413	2.32	0.274	33.4	4.20
C_{max}/Dose	kg * µg/mL/mg	26.1	4.13	23.2	2.74	33.4	4.20
t_{max}	hr	0.083	0.00	0.083	0.00	0.083	0.00
AUC_{all}	µg * hr/mL	4.42	2.37	289	87.2	4940	1080
AUC_{all}/Dose	hr * kg * µg/mL/mg	442	237	2890	872	4940	1080

[0245] Following a single intravenous dose of 0.01, 0.10 or 1.0 mg/kg of BS3/20-001 in cynomolgus monkeys, mean peak concentrations (C_{max}) of 0.261, 2.32 and 33.4 µg/mL, respectively, were observed at the first sampling time point (0.083 hr). Mean AUC_{all} values of 4.42, 289 and 4940 µg*hr/mL were observed at doses of 0.01, 0.1 and 1.0 mg/kg. Dose-normalized AUC values (AUC_{all}/Dose) of 442, 2890 and 4940 µg*hr/mL per mg/kg indicate that plasma exposure (AUC_{all}) increases with increasing dose in a non-linear fashion. Greater than proportional increase in plasma drug exposure was observed with increased antibody dose, suggesting that BS3/20-001 may be undergoing some target-mediated clearance. The overall pharmacokinetic profile of BS3/20-001 is typical of monoclonal antibodies dosed in cynomolgus monkey.

[0246] The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
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20 25 30

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35 40 45

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

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
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Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
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Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn Trp Pro Leu
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Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
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Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe Tyr Tyr Cys
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 41

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc ggccaagtca gagcattagc agctatttaa attggtttca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

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<210> SEQ ID NO 42
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 42

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

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

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

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

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

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

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

<210> SEQ ID NO 43
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 43

cagagcatta gcagctat 18

<210> SEQ ID NO 44
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 44

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 45
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 45

gctgcatcc 9

<210> SEQ ID NO 46
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 46

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Ala Ala Ser
1

<210> SEQ ID NO 47
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 47

caacagagtt acagtacccc tccgatcacc 30

<210> SEQ ID NO 48
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 48

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

<210> SEQ ID NO 49
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 49

gaagtacaac tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctaagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagtt 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggcag cttggcctac 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ttccctgtat 240

ctgcaaatga acagtcttca ccctgaggac acggccctct attactgtgt aaaagatggt 300

agtggctacg gccactactc ctactacggt ttggacgtct ggggccaggg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 50
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 50

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

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65 70 75 80

Leu Gln Met Asn Ser Leu His Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly His Tyr Ser Tyr Tyr Gly Leu Asp
100 105 110

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

<210> SEQ ID NO 51
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 51

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 52
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 52

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 53
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 53

attagttgga atagtggcag cttg 24

<210> SEQ ID NO 54
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 54

Ile Ser Trp Asn Ser Gly Ser Leu
1 5

<210> SEQ ID NO 55
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 55

gtaaaagatg gtagtggcta cggccactac tcctactacg gtttggacgt c 51

<210> SEQ ID NO 56
<211> LENGTH: 17

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 56

Val Lys Asp Gly Ser Gly Tyr Gly His Tyr Ser Tyr Tyr Gly Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 57
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 57

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gttcaccttg gacgttcggc 300

caagggacca aggtggaaat caaa 324

<210> SEQ ID NO 58
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 58

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

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

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

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

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

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

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

<210> SEQ ID NO 59
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 59

cagagtgtta gcagcagcta c 21

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<210> SEQ ID NO 60
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 60

Gln Ser Val Ser Ser Ser Tyr
1 5

<210> SEQ ID NO 61
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 61

ggtgcatcc 9

<210> SEQ ID NO 62
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 62

Gly Ala Ser
1

<210> SEQ ID NO 63
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 63

cagcagtatg gtagttcacc ttggacg 27

<210> SEQ ID NO 64
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 64

Gln Gln Tyr Gly Ser Ser Pro Trp Thr
1 5

<210> SEQ ID NO 65
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 65

gaagtacagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

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tcctgtgtag cctctggatt ccccttgct gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatatg 300

agtggctacg cccactactt ctactacggt atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 66
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 66

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

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

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

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

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

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

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Phe Tyr Tyr Gly Met Asp
100 105 110

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

<210> SEQ ID NO 67
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 67

ggattcccct ttgctgatta tacc 24

<210> SEQ ID NO 68
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 68

Gly Phe Pro Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 69
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 69

attagttgga atagtggtag cata 24

<210> SEQ ID NO 70
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 70

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 71
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 71

gcaaaagata tgagtggcta cgcccactac ttctactacg gtatggacgt c 51

<210> SEQ ID NO 72
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 72

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Phe Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 73
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 73

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctttgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 74
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 74

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

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

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

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

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

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

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

<210> SEQ ID NO 75
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 75

cagagcatta gcagctat 18

<210> SEQ ID NO 76
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 76

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 77
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 77

gctgcatcc 9

<210> SEQ ID NO 78
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 78

Ala Ala Ser
1

<210> SEQ ID NO 79

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<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 79

caacagagtt acagtacccc tccgatcacc 30

<210> SEQ ID NO 80
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 80

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

<210> SEQ ID NO 81
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 81

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgaaactc 60

tcctgtacag cctctggatt cacctttgct gattatacca tgcactgggt ccgacaaggt 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag taaaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatatg 300

agtggctacg cccactacta ctactacgct ttggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 82
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 82

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

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

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

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

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

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

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Tyr Tyr Tyr Ala Leu Asp

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            100                 105                 110

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


<210> SEQ ID NO 83
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 83

ggattcacct ttgctgatta tacc                                          24


<210> SEQ ID NO 84
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 84

Gly Phe Thr Phe Ala Asp Tyr Thr
1               5


<210> SEQ ID NO 85
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 85

attagttgga atagtggtag taaa                                          24


<210> SEQ ID NO 86
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 86

Ile Ser Trp Asn Ser Gly Ser Lys
1               5


<210> SEQ ID NO 87
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 87

gcaaaagata tgagtggcta cgcccactac tactactacg ctttggacgt c             51


<210> SEQ ID NO 88
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 88
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Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Tyr Tyr Tyr Ala Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 89
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 89

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta acccccccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 90
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 90

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

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

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

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

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

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

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

<210> SEQ ID NO 91
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 91

cagagcatta gcaactat 18

<210> SEQ ID NO 92
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 92

Gln Ser Ile Ser Asn Tyr
1 5

<210> SEQ ID NO 93
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 93

gctgcatcc 9

<210> SEQ ID NO 94
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 94

Ala Ala Ser
1

<210> SEQ ID NO 95
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 95

caacagagtt acagtaaccc cccgatcacc 30

<210> SEQ ID NO 96
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 96

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

<210> SEQ ID NO 97
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 97

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agaaaaggca tgcactgggt ccgccaggct 120

ccagtcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

-continued

ctgcaaatga acagcctgac agctgaggac acggctgtgt attactgtgc gaaagaaggg 300

gggcatgact atggtggtac ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> SEQ ID NO 98
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 98

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

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

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

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

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 99
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 99

ggattcacct tcagtagaaa aggc 24

<210> SEQ ID NO 100
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 100

Gly Phe Thr Phe Ser Arg Lys Gly
1 5

<210> SEQ ID NO 101
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 101

atatcatatg atggaagtaa taaa 24

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<210> SEQ ID NO 102
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 102

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> SEQ ID NO 103
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 103

gcgaaagaag gggggcatga ctatggtggt acctttgact ac 42

<210> SEQ ID NO 104
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 104

Ala Lys Glu Gly Gly His Asp Tyr Gly Gly Thr Phe Asp Tyr
1 5 10

<210> SEQ ID NO 105
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 105

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggcgagtca ggacattaac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagttcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgatgatc tcccattcac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> SEQ ID NO 106
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 106

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 Gln Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

-continued

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

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> SEQ ID NO 107
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 107

caggacatta acaactat 18

<210> SEQ ID NO 108
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 108

Gln Asp Ile Asn Asn Tyr
1 5

<210> SEQ ID NO 109
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 109

gatgcatcc 9

<210> SEQ ID NO 110
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 110

Asp Ala Ser
1

<210> SEQ ID NO 111
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 111

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caacagtatg atgatctccc attcact 27

<210> SEQ ID NO 112
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 112

Gln Gln Tyr Asp Asp Leu Pro Phe Thr
1 5

<210> SEQ ID NO 113
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 113

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300

agtggctacg gtcactacta ctacggaatg gacgtctggg gccaagggac cacggtcacc 360

gtcgcctca 369

<210> SEQ ID NO 114
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 114

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

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

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

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

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

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

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 115
<211> LENGTH: 24

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 115

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 116
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 116

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 117
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 117

attagttgga atagtggtag tata 24

<210> SEQ ID NO 118
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 118

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 119
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 119

gcaaaagata atagtggcta cggtcactac tactacggaa tggacgtc 48

<210> SEQ ID NO 120
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 120

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 121
<211> LENGTH: 321
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 121

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcac tatattaact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 122
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 122

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

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

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

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

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

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

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

<210> SEQ ID NO 123
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 123

cagagtgtta gcagcaac 18

<210> SEQ ID NO 124
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 124

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 125

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<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 125

ggtgcatcc 9

<210> SEQ ID NO 126
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 126

Gly Ala Ser
1

<210> SEQ ID NO 127
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 127

cagcactata ttaactggcc tctcact 27

<210> SEQ ID NO 128
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 128

Gln His Tyr Ile Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 129
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 129

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300

agtggctacg gtcactacta ctacggaatg gacgtctggg gccaagggac cacggtcacc 360

gtcgcctca 369

<210> SEQ ID NO 130
<211> LENGTH: 123
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 130

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

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

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

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

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

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

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 131
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 131

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 132
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 132

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 133
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 133

attagttgga atagtggtag tata 24

<210> SEQ ID NO 134
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 134

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Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 135
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 135

gcaaaagata atagtggcta cggtcactac tactacggaa tggacgtc 48

<210> SEQ ID NO 136
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 136

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 137
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 137

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcac tatattaact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 138
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 138

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

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

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

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

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

-continued

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

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

<210> SEQ ID NO 139
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 139

cagagtgtta gcagcaac 18

<210> SEQ ID NO 140
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 140

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 141
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 141

ggtgcatcc 9

<210> SEQ ID NO 142
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 142

Gly Ala Ser
1

<210> SEQ ID NO 143
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 143

cagcactata ttaactggcc tctcact 27

<210> SEQ ID NO 144
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 144

Gln His Tyr Ile Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 145
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 145

caggtgcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtggtg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccagact 120

ccaggcaggg ggctggagtg ggtggcaatg atatattatg atggaaataa taaatactat 180

gcagactccg tgaggggccg attcaccgtt tccagagaca attccaagaa caccctgtat 240

ctgcaaatga gcagcctgag agccgaggac acggctctat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 146
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 146

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 147
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 147

ggattcacct tcagaagtta tggc 24

<210> SEQ ID NO 148
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 148

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 149
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 149

atatattatg atggaaataa taaa 24

<210> SEQ ID NO 150
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 150

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> SEQ ID NO 151
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 151

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 152
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 152

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 153
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 153

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtattagc aggaacttgg cctggtacca gcaraaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

-continued

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataacc ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 154
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 38
<223> OTHER INFORMATION: Xaa = any amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 38
<223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 154

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

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

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

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

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

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

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

<210> SEQ ID NO 155
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 155

cagagtatta gcaggaac 18

<210> SEQ ID NO 156
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 156

Gln Ser Ile Ser Arg Asn
1 5

<210> SEQ ID NO 157
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 157

ggtgcatcc 9

<210> SEQ ID NO 158
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 158

Gly Ala Ser
1

<210> SEQ ID NO 159
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 159

cagcagtata ataaccggcc tctcact 27

<210> SEQ ID NO 160
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 160

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 161
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 161

caggtgcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

gcctgtgttg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg gactgcagtg ggtggcaatg atttactatg atggtaagaa taaatattat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacactgtat 240

ctgcaaatga acaatctgag agtcgaggac acggctatgt atttctgtgc gcgagggcct 300

gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcactgtttc ctca 354

<210> SEQ ID NO 162
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 162

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 163
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 163

ggattcacct tcagaagtta tggc 24

<210> SEQ ID NO 164
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 164

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 165
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 165

atttactatg atggtaagaa taaa 24

<210> SEQ ID NO 166
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 166

Ile Tyr Tyr Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 167

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<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 167

gcgcgagggc ctgggtacaa ttggctcgac ccc 33

<210> SEQ ID NO 168
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 168

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 169
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 169

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagaattagc agcaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaggatgttg cagtttatta ctgtcagcaa catcataact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 170
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 170

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

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

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

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His His Asn Trp Pro Leu
85 90 95

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

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<210> SEQ ID NO 171
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 171

cagagaatta gcagcaac 18

<210> SEQ ID NO 172
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 172

Gln Arg Ile Ser Ser Asn
1 5

<210> SEQ ID NO 173
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 173

ggtgcatcc 9

<210> SEQ ID NO 174
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 174

Gly Ala Ser
1

<210> SEQ ID NO 175
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 175

cagcaacatc ataactggcc tctcact 27

<210> SEQ ID NO 176
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 176

Gln Gln His His Asn Trp Pro Leu Thr
1 5

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<210> SEQ ID NO 177
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 177

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgctg cgtctggatt taccttcaga agttatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatg gtatactatg atggaaataa tcaatactat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 178
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 178

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

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

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

Ala Met Val Tyr Tyr Asp Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 179
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 179

ggatttacct tcagaagtta tgcc 24

<210> SEQ ID NO 180
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 180

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Gly Phe Thr Phe Arg Ser Tyr Ala
1 5

<210> SEQ ID NO 181
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 181

gtatactatg atggaaataa tcaa 24

<210> SEQ ID NO 182
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 182

Val Tyr Tyr Asp Gly Asn Asn Gln
1 5

<210> SEQ ID NO 183
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 183

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 184
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 184

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 185
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 185

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccggcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact ggcctctcac tttcggcgga 300

gggaccaagg tggtgatcaa a 321

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<210> SEQ ID NO 186
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 186

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

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

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

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

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

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

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

<210> SEQ ID NO 187
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 187

cagagtgtta gcaggaac 18

<210> SEQ ID NO 188
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 188

Gln Ser Val Ser Arg Asn
1 5

<210> SEQ ID NO 189
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 189

ggtgcatcc 9

<210> SEQ ID NO 190
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 190

Gly Ala Ser
1

<210> SEQ ID NO 191
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 191

cagcagtata ataactggcc tctcact 27

<210> SEQ ID NO 192
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 192

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 193
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 193

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtattg cgtctggatt taccttcaga agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatg atatattatg atggaaacaa taaatactat 180

gcagactccg tgaggggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 194
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 194

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 195
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 195

ggatttacct tcagaagtta tggc 24

<210> SEQ ID NO 196
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 196

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 197
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 197

atatattatg atggaaacaa taaa 24

<210> SEQ ID NO 198
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 198

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> SEQ ID NO 199
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 199

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 200
<211> LENGTH: 11
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 200

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 201
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 201

gaaatagtga tgacgcagtc tccagccaca ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataaca ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 202
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 202

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

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

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

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

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

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

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

<210> SEQ ID NO 203
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 203

cagagtgtta gcagcaac 18

<210> SEQ ID NO 204

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<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 204

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 205
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 205

ggtgcatcc 9

<210> SEQ ID NO 206
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 206

Gly Ala Ser
1

<210> SEQ ID NO 207
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 207

cagcagtata ataacaggcc tctcact 27

<210> SEQ ID NO 208
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 208

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 209
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 209

caggtgcagc tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggatt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

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gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 210
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 210

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 211
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 211

ggattcacct tcagaagttt tggc 24

<210> SEQ ID NO 212
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 212

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 213
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 213

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atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 214
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 214

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 215
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 215

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 216
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 216

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 217
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 217

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagtcacc 60

ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 218
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 218

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

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn

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```
            20                  25                  30

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

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

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

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
                85                  90                  95

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


<210> SEQ ID NO 219
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 219

cagagtatta gcaggaac                                                  18


<210> SEQ ID NO 220
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 220

Gln Ser Ile Ser Arg Asn
1               5


<210> SEQ ID NO 221
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 221

ggtgcatcc                                                             9


<210> SEQ ID NO 222
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 222

Gly Ala Ser
1


<210> SEQ ID NO 223
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 223
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cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 224
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 224

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 225
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 225

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggatt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 226
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 226

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 227
<211> LENGTH: 24
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 227

ggattcacct tcagaagttt tggc 24

<210> SEQ ID NO 228
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 228

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 229
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 229

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 230
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 230

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 231
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 231

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 232
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 232

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 233
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 233

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagtcacc 60

ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcaraaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 234
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 38
<223> OTHER INFORMATION: Xaa = Any amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 38
<223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 234

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

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

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

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

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

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

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

<210> SEQ ID NO 235
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 235

cagagtatta gcaggaac 18

<210> SEQ ID NO 236
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 236

Gln Ser Ile Ser Arg Asn
1 5

<210> SEQ ID NO 237
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 237

ggtgcatcc 9

<210> SEQ ID NO 238
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 238

Gly Ala Ser
1

<210> SEQ ID NO 239
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 239

cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 240
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 240

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 241
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 241

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggatt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gcagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

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<210> SEQ ID NO 242
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 242

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 243
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 243

ggattcacct tcagaagttt tggc 24

<210> SEQ ID NO 244
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 244

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 245
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 245

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 246
<211> LENGTH: 8
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 246

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 247
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 247

gcgcgagggc ctgggtacaa ttggctcgac ccc 33

<210> SEQ ID NO 248
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 248

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 249
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 249

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgta gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 250
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 250

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

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

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

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Val Pro Ala Arg Phe Ser Gly

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```
    50                  55                  60

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

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
                85                  90                  95

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


<210> SEQ ID NO 251
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 251

cagagtgtta gcaggaac                                                  18


<210> SEQ ID NO 252
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 252

Gln Ser Val Ser Arg Asn
1               5


<210> SEQ ID NO 253
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 253

ggtgcatcc                                                             9


<210> SEQ ID NO 254
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 254

Gly Ala Ser
1


<210> SEQ ID NO 255
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 255

cagcagtata ataataggcc tctcact                                        27


<210> SEQ ID NO 256
<211> LENGTH: 9
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 256

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 257
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 257

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggatt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gcagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 258
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 258

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 259
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 259

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ggattcacct tcagaagttt tggc 24

<210> SEQ ID NO 260
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 260

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 261
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 261

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 262
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 262

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 263
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 263

gcgcgagggc ctgggtacaa ttggctcgac ccc 33

<210> SEQ ID NO 264
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 264

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 265
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 265

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

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ctctcctgta gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttca ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 266
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 266

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

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

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

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

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

Glu Asp Phe Ala Val Phe His Cys Gln Gln Tyr Asn Asn Arg Pro Leu
85 90 95

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

<210> SEQ ID NO 267
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 267

cagagtgtta gcaggaac 18

<210> SEQ ID NO 268
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 268

Gln Ser Val Ser Arg Asn
1 5

<210> SEQ ID NO 269
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 269

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ggtgcatcc 9

<210> SEQ ID NO 270
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 270

Gly Ala Ser
1

<210> SEQ ID NO 271
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 271

cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 272
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 272

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 273
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 273

caggtgcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgttg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg gactgcagtg ggtggcaatg atttactatg atggtaagaa taaatattat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagtctgag agccgaagac acggctatgt atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcactgtctc ctca 354

<210> SEQ ID NO 274
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 274

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 275
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 275

ggattcacct tcagaagtta tggc 24

<210> SEQ ID NO 276
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 276

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 277
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 277

atttactatg atggtaagaa taaa 24

<210> SEQ ID NO 278
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 278

Ile Tyr Tyr Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 279
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 279

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 280
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 280

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 281
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 281

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagaattagc agcaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagatgttg cagtttatta ctgtcagcaa cataataact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 282
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 282

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

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

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

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

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

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Asn Asn Trp Pro Leu
85 90 95

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

<210> SEQ ID NO 283
<211> LENGTH: 18

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 283

cagagaatta gcagcaac 18

<210> SEQ ID NO 284
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 284

Gln Arg Ile Ser Ser Asn
1 5

<210> SEQ ID NO 285
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 285

ggtgcatcc 9

<210> SEQ ID NO 286
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 286

Gly Ala Ser
1

<210> SEQ ID NO 287
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 287

cagcaacata ataactggcc tctcact 27

<210> SEQ ID NO 288
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 288

Gln Gln His Asn Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 289
<211> LENGTH: 354
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 289

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggttt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 290
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 290

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 291
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 291

ggtttcacct tcagaagttt tggc 24

<210> SEQ ID NO 292
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 292

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

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<210> SEQ ID NO 293
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 293

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 294
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 294

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 295
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 295

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 296
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 296

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 297
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 297

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagtcatc 60

ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttta ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 298
<211> LENGTH: 107

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 298

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

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

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

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

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

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

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

<210> SEQ ID NO 299
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 299

cagagtatta gcaggaac 18

<210> SEQ ID NO 300
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 300

Gln Ser Ile Ser Arg Asn
1 5

<210> SEQ ID NO 301
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 301

ggtgcaacc 9

<210> SEQ ID NO 302
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 302

Gly Ala Thr

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1

<210> SEQ ID NO 303
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 303

cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 304
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 304

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 305
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 305

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggttt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 306
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 306

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

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

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

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

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

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

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Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 307
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 307

ggtttcacct tcagaagttt tggc 24

<210> SEQ ID NO 308
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 308

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 309
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 309

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 310
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 310

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 311
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 311

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 312
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 312

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 313
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 313

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagtcatc 60

ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcaraaacct 120

ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttta ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 314
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 38
<223> OTHER INFORMATION: Xaa = Any amino acid
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: 38
<223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 314

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

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

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

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

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

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

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

<210> SEQ ID NO 315
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 315

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cagagtatta gcaggaac 18

<210> SEQ ID NO 316
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 316

Gln Ser Ile Ser Arg Asn
1 5

<210> SEQ ID NO 317
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 317

ggtgcaacc 9

<210> SEQ ID NO 318
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 318

Gly Ala Thr
1

<210> SEQ ID NO 319
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 319

cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 320
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 320

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 321
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 321

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caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtattg cgtctggatt taccttcaga agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatg atatattatg atggaaacaa taaatactat 180

gcagactccg tgaggggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 322
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 322

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 323
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 323

ggatttacct tcagaagtta tggc 24

<210> SEQ ID NO 324
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 324

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 325
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 325

atatattatg atggaaacaa taaa 24

<210> SEQ ID NO 326
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 326

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> SEQ ID NO 327
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 327

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 328
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 328

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 329
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 329

gaaatagtga tgacgcagtc tccagccaca ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataaca ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 330
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 330

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

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

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

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

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

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

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

<210> SEQ ID NO 331
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 331

cagagtgtta gcagcaac 18

<210> SEQ ID NO 332
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 332

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 333
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 333

ggtgcatcc 9

<210> SEQ ID NO 334
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 334

Gly Ala Ser
1

<210> SEQ ID NO 335
<211> LENGTH: 27
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 335

cagcagtata ataacaggcc tctcact 27

<210> SEQ ID NO 336
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 336

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 337
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 337

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattattcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtcgtag catagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagataat 300

agtggctatg gccgctatta ctactacggg atggacgtct ggggccaagg gaccacggtc 360

tccgtctcct ca 372

<210> SEQ ID NO 338
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 338

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

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

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

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

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

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

Val Lys Asp Asn Ser Gly Tyr Gly Arg Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

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

<210> SEQ ID NO 339
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 339

ggattcacct ttgatgatta ttcc 24

<210> SEQ ID NO 340
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 340

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> SEQ ID NO 341
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 341

attagttgga atagtcgtag cata 24

<210> SEQ ID NO 342
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 342

Ile Ser Trp Asn Ser Arg Ser Ile
1 5

<210> SEQ ID NO 343
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 343

gtaaaagata atagtggcta tggccgctat tactactacg ggatggacgt c 51

<210> SEQ ID NO 344
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 344

Val Lys Asp Asn Ser Gly Tyr Gly Arg Tyr Tyr Tyr Tyr Gly Met Asp

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1 5 10 15

Val

<210> SEQ ID NO 345
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 345

aaaatagtga tgacgcagtc tcccgccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc ggcaacttag cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactag tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttattt ctgtcagcac tattataact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcag a 321

<210> SEQ ID NO 346
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 346

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

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

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

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

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

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

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

<210> SEQ ID NO 347
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 347

cagagtgtta gcggcaac 18

<210> SEQ ID NO 348
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 348

Gln Ser Val Ser Gly Asn
1 5

<210> SEQ ID NO 349
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 349

ggtgcatcc 9

<210> SEQ ID NO 350
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 350

Gly Ala Ser
1

<210> SEQ ID NO 351
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 351

cagcactatt ataactggcc tctcact 27

<210> SEQ ID NO 352
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 352

Gln His Tyr Tyr Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 353
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 353

gaagtgcaac tggtggagtc tgggggaggc ttagtacagc ctggcgggtc cctgagactc 60

tcctgtgcag ccactggatt cacctttgat gattttacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtag cataggctat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt actactgtgc aaaagataat 300

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agtggctacg gctattatta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 354
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 354

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

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

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

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

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

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

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 355
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 355

ggattcacct ttgatgattt tacc 24

<210> SEQ ID NO 356
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 356

Gly Phe Thr Phe Asp Asp Phe Thr
1 5

<210> SEQ ID NO 357
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 357

atcagttgga atagtggtag cata 24

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<210> SEQ ID NO 358
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 358

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 359
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 359

gcaaaagata atagtggcta cggctattat tactacggta tggacgtc 48

<210> SEQ ID NO 360
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 360

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 361
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 361

gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact 300

ccgtacactt ttggccaggg gaccaagctg gagatcaaa 339

<210> SEQ ID NO 362
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 362

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

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

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

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```
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

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

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

Tyr Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys


<210> SEQ ID NO 363
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 363

cagagtgttt tatacagctc caacaataag aactac                              36


<210> SEQ ID NO 364
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 364

Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1               5                   10


<210> SEQ ID NO 365
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 365

tgggcatct                                                             9


<210> SEQ ID NO 366
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 366

Trp Ala Ser
1


<210> SEQ ID NO 367
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 367
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cagcaatatt atagtactcc gtacact 27

<210> SEQ ID NO 368
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 368

Gln Gln Tyr Tyr Ser Thr Pro Tyr Thr
1 5

<210> SEQ ID NO 369
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 369

caggtcacct tgaaggagtc tggtcctgcg ctggtgaaac ccacacagac cctcacactg 60

acctgcacct tctctgggtt ctcactcagc actagtggaa tgtgtgtgag ctggatccgt 120

cagcccccag ggaaggccct ggagtggctt gcacgcattg attgggatga tgataaatac 180

tacagcacat ctctgaagac caggctcacc atctccaagg acacctccaa aaaccaggtg 240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggatg 300

gatatagtgg gagctagagg ggggtggttc gacccctggg gccagggaac cctggtcacc 360

gtctcctca 369

<210> SEQ ID NO 370
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 370

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

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

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

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

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Asp Ile Val Gly Ala Arg Gly Gly Trp Phe Asp Pro
100 105 110

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

<210> SEQ ID NO 371
<211> LENGTH: 30

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 371

gggttctcac tcagcactag tggaatgtgt 30

<210> SEQ ID NO 372
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 372

Gly Phe Ser Leu Ser Thr Ser Gly Met Cys
1 5 10

<210> SEQ ID NO 373
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 373

attgattggg atgatgataa a 21

<210> SEQ ID NO 374
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 374

Ile Asp Trp Asp Asp Asp Lys
1 5

<210> SEQ ID NO 375
<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 375

gcacggatgg atatagtggg agctagaggg gggtggttcg acccc 45

<210> SEQ ID NO 376
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 376

Ala Arg Met Asp Ile Val Gly Ala Arg Gly Gly Trp Phe Asp Pro
1 5 10 15

<210> SEQ ID NO 377
<211> LENGTH: 321
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 377

gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggcattagc aattatttag cctggtttca gcagaaacca 120

gggaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aagttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgccaacag tataatagtt acccgctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 378
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 378

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

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

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

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

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

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

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

<210> SEQ ID NO 379
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 379

cagggcatta gcaattat 18

<210> SEQ ID NO 380
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 380

Gln Gly Ile Ser Asn Tyr
1 5

<210> SEQ ID NO 381

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<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 381

gctgcatcc 9

<210> SEQ ID NO 382
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 382

Ala Ala Ser
1

<210> SEQ ID NO 383
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 383

caacagtata atagttaccc gctcact 27

<210> SEQ ID NO 384
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 384

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 385
<211> LENGTH: 404
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 385

caggtgcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgctg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatg atatattatg atggaaataa taaaaagtat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agtcgaggac acggctgtgt atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctcagccaaa 360

acaacagccc cacccgttta tccactggcc cctggaagct tggg 404

<210> SEQ ID NO 386
<211> LENGTH: 134
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 386

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Gly Ser Leu
130

<210> SEQ ID NO 387
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 387

ggattcacct tcagaagtta tggc 24

<210> SEQ ID NO 388
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 388

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 389
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 389

atatattatg atggaaataa taaa 24

<210> SEQ ID NO 390
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 390

Ile Tyr Tyr Asp Gly Asn Asn Lys
1 5

<210> SEQ ID NO 391
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 391

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 392
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 392

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 393
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 393

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc aggaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactga tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcattctca acatcagcag cctgcagtct 240

gaagattttg cactttatta ctgtcaacaa tatagtaact ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 394
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 394

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

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

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

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

-continued

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

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

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

<210> SEQ ID NO 395
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 395

cagagtgtta gcaggaac 18

<210> SEQ ID NO 396
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 396

Gln Ser Val Ser Arg Asn
1 5

<210> SEQ ID NO 397
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 397

ggtgcatcc 9

<210> SEQ ID NO 398
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 398

Gly Ala Ser
1

<210> SEQ ID NO 399
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 399

caacaatata gtaactggcc tctcact 27

<210> SEQ ID NO 400
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 400

Gln Gln Tyr Ser Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 401
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 401

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggttt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 402
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 402

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

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

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 403
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 403

ggtttcacct tcagaagttt tggc 24

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<210> SEQ ID NO 404
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 404

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 405
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 405

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 406
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 406

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 407
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 407

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 408
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 408

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 409
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 409

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagtcatc 60

ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcagaaacct 120

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ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttta ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 410
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 410

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

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

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

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

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

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

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

<210> SEQ ID NO 411
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 411

cagagtatta gcaggaac 18

<210> SEQ ID NO 412
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 412

Gln Ser Ile Ser Arg Asn
1 5

<210> SEQ ID NO 413
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 413

ggtgcaacc 9

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<210> SEQ ID NO 414
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 414

Gly Ala Thr
1

<210> SEQ ID NO 415
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 415

cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 416
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 416

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 417
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 417

caggtgcaat tggtggagtc tgggggaggc gtggtccagc cggggaggtc cctgagactc 60

tcctgtgctg cgtctggttt caccttcaga agttttggca tgcactgggt ccgccaggct 120

ccaggcaggg gactggagtg ggtggcaatg atatattttg atggaaaaaa taaatactat 180

gcagactccg tgaggggccg attcaccatt tccagagaca attccaagaa caccctgtat 240

ctggaaatga gtagcctgag agccgaggac acggctgtat atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 418
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 418

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

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

-continued

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

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

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

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

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 419
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 419

ggtttcacct tcagaagttt tggc 24

<210> SEQ ID NO 420
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 420

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 421
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 421

atatattttg atggaaaaaa taaa 24

<210> SEQ ID NO 422
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 422

Ile Tyr Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 423
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 423

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 424
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 424

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 425
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 425

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagtcatc 60

ctctcctgta gggccagtca gagtattagc aggaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcaaccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctacagtct 240

gaagattttg cagtttttta ctgtcagcag tataataata ggcctctcac tttcggcgga 300

gggaccgagg tggagatcaa a 321

<210> SEQ ID NO 426
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 426

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

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

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

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

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

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

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

<210> SEQ ID NO 427
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 427

cagagtatta gcaggaac 18

<210> SEQ ID NO 428
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 428

Gln Ser Ile Ser Arg Asn
1 5

<210> SEQ ID NO 429
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 429

ggtgcaacc 9

<210> SEQ ID NO 430
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 430

Gly Ala Thr
1

<210> SEQ ID NO 431
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 431

cagcagtata ataataggcc tctcact 27

<210> SEQ ID NO 432
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 432

Gln Gln Tyr Asn Asn Arg Pro Leu Thr
1 5

<210> SEQ ID NO 433
<211> LENGTH: 351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 433

caggtgcacc tggaagagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgttcag cgtctggttt caccttcagt agttatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaactaa taaatattat 180

ttagattccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgag agccgaagac acggctgtgt attactgtgc gagagatcgg 300

ggaagtataa taacccactg gggccaggga accctggtca ccgtctcctc a 351

<210> SEQ ID NO 434
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 434

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

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

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

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

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

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

Ala Arg Asp Arg Gly Ser Ile Ile Thr His Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> SEQ ID NO 435
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 435

ggtttcacct tcagtagtta tgcc 24

<210> SEQ ID NO 436
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 436

Gly Phe Thr Phe Ser Ser Tyr Ala
1 5

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<210> SEQ ID NO 437
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 437

atatggtatg atggaactaa taaa 24

<210> SEQ ID NO 438
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 438

Ile Trp Tyr Asp Gly Thr Asn Lys
1 5

<210> SEQ ID NO 439
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 439

gcgagagatc ggggaagtat aataacccac 30

<210> SEQ ID NO 440
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 440

Ala Arg Asp Arg Gly Ser Ile Ile Thr His
1 5 10

<210> SEQ ID NO 441
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 441

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctataggaga cagagtcacc 60

atcacttgcc gggcaagtca gaacattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag acttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 442
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 442

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

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

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

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

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

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

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

<210> SEQ ID NO 443
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 443

cagaacatta gcagctat 18

<210> SEQ ID NO 444
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 444

Gln Asn Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 445
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 445

gctgcatcc 9

<210> SEQ ID NO 446
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 446

Ala Ala Ser
1

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<210> SEQ ID NO 447
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 447

caacagactt acagtacccc tccgatcacc 30

<210> SEQ ID NO 448
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 448

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

<210> SEQ ID NO 449
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 449

gaagtacagc tggtggagtc tgggggaggc ttggtacggc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccgccaagct 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtgggac cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag acctgaggac acggccttgt attactgtgc aaaagatatg 300

agtggctacg cccactacta ctactacggt atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 450
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 450

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

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

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

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

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

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

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Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

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

<210> SEQ ID NO 451
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 451

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 452
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 452

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 453
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 453

attagttgga atagtgggac cata 24

<210> SEQ ID NO 454
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 454

Ile Ser Trp Asn Ser Gly Thr Ile
1 5

<210> SEQ ID NO 455
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 455

gcaaaagata tgagtggcta cgcccactac tactactacg gtatggacgt c 51

<210> SEQ ID NO 456
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 456

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 457
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 457

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 458
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 458

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

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

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

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

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

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

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

<210> SEQ ID NO 459
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 459

cagagcatta gcagctat 18

<210> SEQ ID NO 460
<211> LENGTH: 6

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 460

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 461
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 461

gctgcatcc 9

<210> SEQ ID NO 462
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 462

Ala Ala Ser
1

<210> SEQ ID NO 463
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 463

caacagagtt acagtacccc tccgatcacc 30

<210> SEQ ID NO 464
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 464

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

<210> SEQ ID NO 465
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 465

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctccgat attagttgga atagtggtag cataggctat 180

-continued

gcggactctg tgaagggccg attcaccgtc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aggtgaggac acggccctgt attactgtgc aaaagatatg 300

agtggctacg cccactacgg ctactacggt atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 466
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 466

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

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

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

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

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

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

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Gly Tyr Tyr Gly Met Asp
100 105 110

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

<210> SEQ ID NO 467
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 467

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 468
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 468

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 469
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 469

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attagttgga atagtggtag cata 24

<210> SEQ ID NO 470
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 470

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 471
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 471

gcaaaagata tgagtggcta cgcccactac ggctactacg gtatggacgt c 51

<210> SEQ ID NO 472
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 472

Ala Lys Asp Met Ser Gly Tyr Ala His Tyr Gly Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 473
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 473

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagg aactatttaa attggtatca gcagaaacca 120

gggaaagtcc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta accctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 474
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 474

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 Arg Asn Tyr
            20                  25                  30

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

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

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

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

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


<210> SEQ ID NO 475
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 475

cagagcatta ggaactat                                                 18


<210> SEQ ID NO 476
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 476

Gln Ser Ile Arg Asn Tyr
1               5


<210> SEQ ID NO 477
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 477

gctgcatcc                                                            9


<210> SEQ ID NO 478
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 478

Ala Ala Ser
1


<210> SEQ ID NO 479
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 479

caacagagtt acagtaaccc tccgatcacc 30

<210> SEQ ID NO 480
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 480

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

<210> SEQ ID NO 481
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 481

gaagcgcagc tggtggaatc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtacaa cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg gatctctgat attagttgga atggtggaac caaaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaaaaa ctccctgtat 240

ctgcaaatgg acagtctgag aggtgaggac acggccttat attactgtgt aaaagataaa 300

agtggctacg ggcacttcta cttcggtttg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 482
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 482

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

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

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

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

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

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

Val Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Phe Gly Leu Asp Val
100 105 110

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

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<210> SEQ ID NO 483
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 483

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 484
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 484

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 485
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 485

attagttgga atggtggaac caaa 24

<210> SEQ ID NO 486
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 486

Ile Ser Trp Asn Gly Gly Thr Lys
1 5

<210> SEQ ID NO 487
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 487

gtaaaagata aaagtggcta cgggcacttc tacttcggtt tggacgtc 48

<210> SEQ ID NO 488
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 488

Val Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Phe Gly Leu Asp Val
1 5 10 15

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<210> SEQ ID NO 489
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 489

gacatccaga tgacccagtc tccatcctcc ctgactgcgt ctgtaggaga cagagtcacc 60

ttcacttgcc gggcaagtca gagcattagc aggcatttaa gttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tggaaagtgg ggtcccttca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaccct 240

gaagattttg caacttacta ctgtcaacag agctacagta accctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 490
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 490

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

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

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

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

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

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

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

<210> SEQ ID NO 491
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 491

cagagcatta gcaggcat 18

<210> SEQ ID NO 492
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 492

Gln Ser Ile Ser Arg His

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1 5

<210> SEQ ID NO 493
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 493

gctgcatcc 9

<210> SEQ ID NO 494
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 494

Ala Ala Ser
1

<210> SEQ ID NO 495
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 495

caacagagct acagtaaccc tccgatcacc 30

<210> SEQ ID NO 496
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 496

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

<210> SEQ ID NO 497
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 497

gaagtgcagt tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt caagtttgct gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcagag attagttgga atagtggtag cataggttat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagataaa 300

agtggctacg ggcactacta tatcggtatg gacgtctggg gccaagggac cacggtcatc 360

gtctcctcc 369

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<210> SEQ ID NO 498
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 498

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ala Asp Tyr
20 25 30

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

Ser Glu Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Val Asp Ser Val
50 55 60

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

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

Val Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Ile Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 499
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 499

ggattcaagt ttgctgatta tgcc 24

<210> SEQ ID NO 500
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 500

Gly Phe Lys Phe Ala Asp Tyr Ala
1 5

<210> SEQ ID NO 501
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 501

attagttgga atagtggtag cata 24

<210> SEQ ID NO 502
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 502

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 503
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 503

gtaaaagata aaagtggcta cgggcactac tatatcggta tggacgtc 48

<210> SEQ ID NO 504
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 504

Val Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Ile Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 505
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 505

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagtattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 506
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 506

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

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

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

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

-continued

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

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

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

<210> SEQ ID NO 507
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 507

cagagtatta gcagctat 18

<210> SEQ ID NO 508
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 508

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 509
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 509

gctgcatcc 9

<210> SEQ ID NO 510
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 510

Ala Ala Ser
1

<210> SEQ ID NO 511
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 511

caacagagtt acagtacccc tccgatcacc 30

<210> SEQ ID NO 512
<211> LENGTH: 10
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 512

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

<210> SEQ ID NO 513
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 513

gaagtgcacc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctccgat attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccgtc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aggtgaggac acggccttgt attactgtgc aaaagatatg 300

agtggctacg gccactacgg caagtacggt atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 514
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 514

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

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

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

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

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

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

Ala Lys Asp Met Ser Gly Tyr Gly His Tyr Gly Lys Tyr Gly Met Asp
100 105 110

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

<210> SEQ ID NO 515
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 515

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ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 516
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 516

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 517
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 517

attagttgga atagtggtag cata 24

<210> SEQ ID NO 518
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 518

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 519
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 519

gcaaaagata tgagtggcta cggccactac ggcaagtacg gtatggacgt c 51

<210> SEQ ID NO 520
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 520

Ala Lys Asp Met Ser Gly Tyr Gly His Tyr Gly Lys Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 521
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 521

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagg agctatttaa attggtatca gcagaaacca 120

gggaaagtcc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcaacag tctgcaacct 240

gacgattttg caacttacta ctgtcaacag acttacagta accctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 522
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 522

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

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

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

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

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

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

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

<210> SEQ ID NO 523
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 523

cagagcatta ggagctat 18

<210> SEQ ID NO 524
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 524

Gln Ser Ile Arg Ser Tyr
1 5

<210> SEQ ID NO 525
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 525

gctgcatcc 9

<210> SEQ ID NO 526
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 526

Ala Ala Ser
1

<210> SEQ ID NO 527
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 527

caacagactt acagtaaccc tccgatcacc 30

<210> SEQ ID NO 528
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 528

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

<210> SEQ ID NO 529
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 529

gaggtgcagc tggtggagtc tgggggagac ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaatt attagttgga atggtaatac cattgactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

cttcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataag 300

agtggctacg gacacttcta ctattacgtt ttggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 530
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 530

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

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

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

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

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

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

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Val Leu Asp
100 105 110

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

<210> SEQ ID NO 531
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 531

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 532
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 532

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 533
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 533

attagttgga atggtaatac catt 24

<210> SEQ ID NO 534
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 534

Ile Ser Trp Asn Gly Asn Thr Ile
1 5

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<210> SEQ ID NO 535
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 535

gcaaaagata agagtggcta cggacacttc tactattacg ttttggacgt c 51

<210> SEQ ID NO 536
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 536

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Val Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 537
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 537

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattaac aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgct gcttccagtt tgcaaagtgg ggtcccgtca 180

aggttcagtg gcagtggttc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctctcaacag agttacagtt tcccgtggac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> SEQ ID NO 538
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 538

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

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

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

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

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

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

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

<210> SEQ ID NO 539
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 539

cagagcatta acaactat 18

<210> SEQ ID NO 540
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 540

Gln Ser Ile Asn Asn Tyr
1 5

<210> SEQ ID NO 541
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 541

gctgcttcc 9

<210> SEQ ID NO 542
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 542

Ala Ala Ser
1

<210> SEQ ID NO 543
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 543

caacagagtt acagtttccc gtggacg 27

<210> SEQ ID NO 544
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 544

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Gln Gln Ser Tyr Ser Phe Pro Trp Thr
1 5

<210> SEQ ID NO 545
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 545

caggtgcagc tggtggagtc ggggggaggc gtggtccagc ctgggaggtc cctgagaccc 60

tcctgtgcag cgtctggatt tagtttcagg gactatggca tgcactgggt ccgccaggct 120

ccaggtaagg gactagagtg gatggcacac atatggtata atggaaagaa taaatattat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctatat 240

ctgcaaatga acagcctgag acccgaggac acggctgtat attattgtgc gagagatggt 300

gtatcagcac gtggtactcc atttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> SEQ ID NO 546
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 546

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

Ser Leu Arg Pro Ser Cys Ala Ala Ser Gly Phe Ser Phe Arg Asp Tyr
20 25 30

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

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

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

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

Ala Arg Asp Gly Val Ser Ala Arg Gly Thr Pro Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 547
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 547

ggatttagtt tcagggacta tggc 24

<210> SEQ ID NO 548
<211> LENGTH: 8

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 548

Gly Phe Ser Phe Arg Asp Tyr Gly
1 5

<210> SEQ ID NO 549
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 549

atatggtata atggaaagaa taaa 24

<210> SEQ ID NO 550
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 550

Ile Trp Tyr Asn Gly Lys Asn Lys
1 5

<210> SEQ ID NO 551
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 551

gcgagagatg gtgtatcagc acgtggtact ccatttgact ac 42

<210> SEQ ID NO 552
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 552

Ala Arg Asp Gly Val Ser Ala Arg Gly Thr Pro Phe Asp Tyr
1 5 10

<210> SEQ ID NO 553
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 553

gaaacgacac tcacgcagtc tccagcattc atgtcagcgg ctccaggaga caaagtcagc 60

atctcctgca ttgccagcca gtacattgat gatgatgtga actggtacca acagaaacca 120

ggagaaactg ctattttcat tattcaagaa gcttctactc tcgttcctgg aatctcacct 180

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cgattcagtg gcagcgggta tggaacacat tttaccctca caattaataa catagattct 240

gaggatgctg cattttactt ctgtctccaa catgataatt tcccgtacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 554
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 554

Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Ala Pro Gly
1 5 10 15

Asp Lys Val Ser Ile Ser Cys Ile Ala Ser Gln Tyr Ile Asp Asp Asp
20 25 30

Val Asn Trp Tyr Gln Gln Lys Pro Gly Glu Thr Ala Ile Phe Ile Ile
35 40 45

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

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

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

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

<210> SEQ ID NO 555
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 555

cagtacattg atgatgat 18

<210> SEQ ID NO 556
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 556

Gln Tyr Ile Asp Asp Asp
1 5

<210> SEQ ID NO 557
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 557

gaagcttct 9

<210> SEQ ID NO 558

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<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 558

Glu Ala Ser
1

<210> SEQ ID NO 559
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 559

ctccaacatg ataatttccc gtacact 27

<210> SEQ ID NO 560
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 560

Leu Gln His Asp Asn Phe Pro Tyr Thr
1 5

<210> SEQ ID NO 561
<211> LENGTH: 384
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 561

caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctcttattt cacctttagc agttttgcca tgaactgggt ccgccaggct 120

ccagggcagg gcctggagtg ggtctcagct attagtggta gggtctcagc tattagtggt 180

agtggtggta tcacatacta cgcagactcc gtgaagggcc ggttcatcat ctccagagac 240

aattccaaga acacgctgta tctgcaaatg agcggcctga gagccgagga cacggccgta 300

tattactgtg cgaaaggccc ctatttgact acagtcaccc cctttgacta ctggggccag 360

ggaaccctgg tcaccgtctc ctca 384

<210> SEQ ID NO 562
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 562

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

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

-continued

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

Ser Ala Ile Ser Gly Arg Val Ser Ala Ile Ser Gly Ser Gly Gly Ile
    50                  55                  60

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

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Ser Gly Leu Arg Ala Glu
                85                  90                  95

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Gly Pro Tyr Leu Thr Thr Val
            100                 105                 110

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


<210> SEQ ID NO 563
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 563

tatttcacct ttagcagttt tgcc                                          24


<210> SEQ ID NO 564
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 564

Tyr Phe Thr Phe Ser Ser Phe Ala
1               5


<210> SEQ ID NO 565
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 565

attagtggta gtggtggtat caca                                          24


<210> SEQ ID NO 566
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 566

Ile Ser Gly Ser Gly Gly Ile Thr
1               5


<210> SEQ ID NO 567
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 567

gcgaaaggcc cctatttgac tacagtcacc ccctttgact ac 42

<210> SEQ ID NO 568
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 568

Ala Lys Gly Pro Tyr Leu Thr Thr Val Thr Pro Phe Asp Tyr
1 5 10

<210> SEQ ID NO 569
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 569

gacatccagt tgacccagtc tccatcttcc gtgtctgcat ctgtcggaga cagagtcacc 60

atcacttgtc gggcgagtca ggggattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaaactcct gatctatgct gtatccagtt tgcaaaatgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcaccctca ccatcagcag cctgcagcct 240

gaagactttg caacttacta ttgtcaacag gctaacagtt tcccattcac tttcggccct 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 570
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 570

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

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

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

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

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

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

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

<210> SEQ ID NO 571
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 571

caggggatta gcagctgg 18

<210> SEQ ID NO 572
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 572

Gln Gly Ile Ser Ser Trp
1 5

<210> SEQ ID NO 573
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 573

gctgtatcc 9

<210> SEQ ID NO 574
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 574

Ala Val Ser
1

<210> SEQ ID NO 575
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 575

caacaggcta acagtttccc attcact 27

<210> SEQ ID NO 576
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 576

Gln Gln Ala Asn Ser Phe Pro Phe Thr
1 5

<210> SEQ ID NO 577
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 577

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgct gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggttat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttat attactgtgt aaaagataat 300

agtggctacg catcctacta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 578
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 578

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

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

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

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

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

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

Val Lys Asp Asn Ser Gly Tyr Ala Ser Tyr Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 579
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 579

ggattcacct ttgctgatta tgcc 24

<210> SEQ ID NO 580
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 580

Gly Phe Thr Phe Ala Asp Tyr Ala
1 5

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<210> SEQ ID NO 581
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 581

attagttgga atagtggtag tata 24

<210> SEQ ID NO 582
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 582

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 583
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 583

gtaaaagata atagtggcta cgcatcctac tactacggta tggacgtc 48

<210> SEQ ID NO 584
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 584

Val Lys Asp Asn Ser Gly Tyr Ala Ser Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 585
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 585

gacatccagt tgacccagtc cccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctgcagcct 240

gaagatattg caacatatta ctgtcaacag tatgataatc tcccattcac tttcggccct 300

gggaccaaag tggatatcaa acga 324

<210> SEQ ID NO 586
<211> LENGTH: 108
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 586

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

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

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

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> SEQ ID NO 587
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 587

cagagcatta gcagctat 18

<210> SEQ ID NO 588
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 588

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 589
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 589

gatgcatcc 9

<210> SEQ ID NO 590
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 590

Asp Ala Ser
1

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<210> SEQ ID NO 591
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 591

caacagtatg ataatctccc attcact 27

<210> SEQ ID NO 592
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 592

Gln Gln Tyr Asp Asn Leu Pro Phe Thr
1 5

<210> SEQ ID NO 593
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 593

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt aactatggca tgcactgggt ccgccaggct 120

ccaggcaaag ggctggagtg ggtgacagtt atattacatg atggaagtta taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctacat 240

ctgcaaatga acagcctgag aactgaggac acggctgtat attactgtgc gaaagggcct 300

atgtttcggg gagtccctta caaccactac tatggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 594
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 594

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

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

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

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

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

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

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               85                  90                  95

Ala Lys Gly Pro Met Phe Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
            100                 105                 110

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


<210> SEQ ID NO 595
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 595

ggattcacct tcagtaacta tggc                                          24


<210> SEQ ID NO 596
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 596

Gly Phe Thr Phe Ser Asn Tyr Gly
1               5


<210> SEQ ID NO 597
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 597

atattacatg atggaagtta taaa                                          24


<210> SEQ ID NO 598
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 598

Ile Leu His Asp Gly Ser Tyr Lys
1               5


<210> SEQ ID NO 599
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 599

gcgaaagggc ctatgtttcg gggagtccct tacaaccact actatggtat ggacgtc        57


<210> SEQ ID NO 600
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 600

Ala Lys Gly Pro Met Phe Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 601
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 601

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcatcaga aatgatttag gctggtatca gcagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtctcatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtacac ttttggccag 300

gggaccaagg tggaaatcaa acga 324

<210> SEQ ID NO 602
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 602

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

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

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

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

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

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

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

<210> SEQ ID NO 603
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 603

cagggcatca gaaatgat 18

<210> SEQ ID NO 604

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<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 604

Gln Gly Ile Arg Asn Asp
1 5

<210> SEQ ID NO 605
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 605

gctgcatcc 9

<210> SEQ ID NO 606
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 606

Ala Ala Ser
1

<210> SEQ ID NO 607
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 607

ctacagcata atagttaccc gtacact 27

<210> SEQ ID NO 608
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 608

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 609
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 609

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtacag cgtcaggttt ccccttcagt cgctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggaatg ggtgacattt atatggtatg atggaagtaa taaatactat 180

-continued

gcagactccg cgaagggccg attcaccatc accagagaca attccaagaa cacggtgtat 240

ctgcaaatgg acagcctgag agccgatgac acggctgttt attattgtgt gagagatcag 300

gcagctctct actattttga ctcttggggc cagggaaccc tggtcaccgt ctcctca 357

<210> SEQ ID NO 610
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 610

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

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

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

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

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 611
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 611

ggtttcccct tcagtcgcta tggc 24

<210> SEQ ID NO 612
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 612

Gly Phe Pro Phe Ser Arg Tyr Gly
1 5

<210> SEQ ID NO 613
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 613

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atatggtatg atggaagtaa taaa 24

<210> SEQ ID NO 614
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 614

Ile Trp Tyr Asp Gly Ser Asn Lys
1 5

<210> SEQ ID NO 615
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 615

gtgagagatc aggcagctct ctactatttt gactct 36

<210> SEQ ID NO 616
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 616

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

<210> SEQ ID NO 617
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 617

gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggtattagc aggtggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctctgct gcatccagtt tgcaaagtgg agtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcgg cctgcagcct 240

gaagattttg caacttacta ttgtcaaaag gctaacagtt tccctttcac tttcggccct 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 618
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 618

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Trp

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            20                  25                  30

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

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

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

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

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


<210> SEQ ID NO 619
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 619

cagggtatta gcaggtgg                                                  18


<210> SEQ ID NO 620
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 620

Gln Gly Ile Ser Arg Trp
1               5


<210> SEQ ID NO 621
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 621

gctgcatcc                                                             9


<210> SEQ ID NO 622
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 622

Ala Ala Ser
1


<210> SEQ ID NO 623
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 623
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caaaaggcta acagtttccc tttcact 27

<210> SEQ ID NO 624
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 624

Gln Lys Ala Asn Ser Phe Pro Phe Thr
1 5

<210> SEQ ID NO 625
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 625

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgacagtt atattacatg atggaagtaa tagatactct 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctttat 240

ctgcaaatga acatcctgag agttgaggac acggctgtgt attactgtac gaaaggggct 300

atggttcggg gagtccctta caatcactac tacggcatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 626
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 626

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

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

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

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

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

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

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
100 105 110

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

<210> SEQ ID NO 627

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<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 627

ggattcacct tcagtagtta tggc 24

<210> SEQ ID NO 628
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 628

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 629
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 629

atattacatg atggaagtaa taga 24

<210> SEQ ID NO 630
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 630

Ile Leu His Asp Gly Ser Asn Arg
1 5

<210> SEQ ID NO 631
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 631

acgaaagggg ctatggttcg gggagtccct tacaatcact actacggcat ggacgtc 57

<210> SEQ ID NO 632
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 632

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
1 5 10 15

Met Asp Val

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<210> SEQ ID NO 633
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 633

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120

gggaaagccc ctaagcgcct aatctatgct gcatccattt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 634
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 634

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

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

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

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

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

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

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

<210> SEQ ID NO 635
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 635

cagggcatta gaaatgat 18

<210> SEQ ID NO 636
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 636

Gln Gly Ile Arg Asn Asp
1 5

-continued

<210> SEQ ID NO 637
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 637

gctgcatcc 9

<210> SEQ ID NO 638
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 638

Ala Ala Ser
1

<210> SEQ ID NO 639
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 639

ctacagcata atagttaccc gtacact 27

<210> SEQ ID NO 640
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 640

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 641
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 641

gaggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgacagtt atattacatg atggaagtaa tagatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctttat 240

ctgcaaatga acatcctgag agctgaggac acggctgtgt attactgtac gaaaggggct 300

atggttcggg gagtccctta caatcactac tacggcatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

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<210> SEQ ID NO 642
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 642

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

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

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

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

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

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

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
100 105 110

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

<210> SEQ ID NO 643
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 643

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 644
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 644

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 645
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 645

atattacatg atggaagtaa taga 24

<210> SEQ ID NO 646
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 646

Ile Leu His Asp Gly Ser Asn Arg
1 5

<210> SEQ ID NO 647
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 647

acgaaagggg ctatggttcg gggagtccct tacaatcact actacggcat ggacgtc 57

<210> SEQ ID NO 648
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 648

Thr Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn His Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 649
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 649

gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcatccaatt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 650
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 650

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

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

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

Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

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```
    50                  55                  60

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

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

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


<210> SEQ ID NO 651
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 651

cagggcatta gaaatgat                                                  18


<210> SEQ ID NO 652
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 652

Gln Gly Ile Arg Asn Asp
1               5


<210> SEQ ID NO 653
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 653

gctgcatcc                                                             9


<210> SEQ ID NO 654
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 654

Ala Ala Ser
1


<210> SEQ ID NO 655
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 655

ctacagcata atagttaccc gtacact                                        27


<210> SEQ ID NO 656
<211> LENGTH: 9
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 656

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 657
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 657

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagact attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt tttactgtgc gaaaggggct 300

atggttcggg gagtccctta caactactac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 658
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 658

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

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

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

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

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

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

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
100 105 110

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

<210> SEQ ID NO 659
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 659

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 660
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 660

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 661
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 661

atatcatatg atggaagtaa taaa 24

<210> SEQ ID NO 662
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 662

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> SEQ ID NO 663
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 663

gcgaaagggg ctatggttcg gggagtccct tacaactact actacggtat ggacgtc 57

<210> SEQ ID NO 664
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 664

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 665
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 665

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtttca gcagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 666
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 666

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

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

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

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

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

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

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

<210> SEQ ID NO 667
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 667

cagggcatta gaaatgat 18

<210> SEQ ID NO 668
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 668

Gln Gly Ile Arg Asn Asp
1 5

<210> SEQ ID NO 669
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 669

gctgcatcc 9

<210> SEQ ID NO 670
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 670

Ala Ala Ser
1

<210> SEQ ID NO 671
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 671

ctacagcata atagttaccc gtacact 27

<210> SEQ ID NO 672
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 672

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 673
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 673

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggact caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180

acagactccg tgaagggccg attcaccatc tccagagaca attctaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gaaaggggcc 300

atggttcggg gagtcccctta caactactac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 674
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 674

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

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

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

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

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

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

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
100 105 110

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

<210> SEQ ID NO 675
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 675

ggactcacct tcagtagcta tggc 24

<210> SEQ ID NO 676
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 676

Gly Leu Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 677
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 677

atatcatatg atggaagtaa taaa 24

<210> SEQ ID NO 678
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 678

Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

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<210> SEQ ID NO 679
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 679

gcgaaagggg ccatggttcg gggagtccct tacaactact actacggtat ggacgtc 57

<210> SEQ ID NO 680
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 680

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Tyr Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 681
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 681

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gggcattaga aatgatttag gctggtatca gcagaaacca 120

gggaaagccc ctaagcgcct gatctatgct gcgtccagtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 682
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 682

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Tyr

-continued

85 90 95

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

<210> SEQ ID NO 683
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 683

cagggcatta gaaatgat 18

<210> SEQ ID NO 684
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 684

Gln Gly Ile Arg Asn Asp
1 5

<210> SEQ ID NO 685
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 685

gctgcgtcc 9

<210> SEQ ID NO 686
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 686

Ala Ala Ser
1

<210> SEQ ID NO 687
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 687

ctacagcata atagttaccc gtacact 27

<210> SEQ ID NO 688
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 688

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Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 689
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 689

caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagg agctttggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atttcatatg atggaaatta taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtac attactgtgc gaaaggggct 300

atggttcggg gagtccctta caacttctac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctca 378

<210> SEQ ID NO 690
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 690

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

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

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

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

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

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

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Phe Tyr Tyr Gly
100 105 110

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

<210> SEQ ID NO 691
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 691

ggattcacct tcaggagctt tggc 24

<210> SEQ ID NO 692

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<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 692

Gly Phe Thr Phe Arg Ser Phe Gly
1 5

<210> SEQ ID NO 693
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 693

atttcatatg atggaaatta taaa 24

<210> SEQ ID NO 694
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 694

Ile Ser Tyr Asp Gly Asn Tyr Lys
1 5

<210> SEQ ID NO 695
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 695

gcgaaagggg ctatggttcg gggagtccct tacaacttct actacggtat ggacgtc 57

<210> SEQ ID NO 696
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 696

Ala Lys Gly Ala Met Val Arg Gly Val Pro Tyr Asn Phe Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 697
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 697

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca ggtcattaga aatgatttag gctggtatca gcagaaacca 120

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gggaaagccc ctaagcgcct gatctatgct gcatccagtt tgcaaagtgg gatcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca caatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtctacag cataatagtt acccgtacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> SEQ ID NO 698
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 698

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 Arg Asn Asp
20 25 30

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

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

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

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

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

<210> SEQ ID NO 699
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 699

caggtcatta gaaatgat 18

<210> SEQ ID NO 700
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 700

Gln Val Ile Arg Asn Asp
1 5

<210> SEQ ID NO 701
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 701

gctgcatcc 9

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<210> SEQ ID NO 702
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 702

Ala Ala Ser
1

<210> SEQ ID NO 703
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 703

ctacagcata atagttaccc gtacact 27

<210> SEQ ID NO 704
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 704

Leu Gln His Asn Ser Tyr Pro Tyr Thr
1 5

<210> SEQ ID NO 705
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 705

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagtt 120

ccaggaaagg gcctggagtg gatctcaggt attagttgga atagtggtag catggactat 180

gcggactctg tgaagggccg attcaccatc tctagagaca acgccaggaa ctccctgttt 240

ctgcaaatga acagtgtgag aactgaggac acggccttgt attactgtgc aaaagataag 300

agtggctacg gctccttcta ctacggtatg gacgtctggg gccaggggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 706
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 706

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

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

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

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

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

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 707
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 707

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 708
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 708

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 709
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 709

attagttgga atagtggtag catg 24

<210> SEQ ID NO 710
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 710

Ile Ser Trp Asn Ser Gly Ser Met
1 5

<210> SEQ ID NO 711
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 711

gcaaaagata agagtggcta cggctccttc tactacggta tggacgtc 48

<210> SEQ ID NO 712
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 712

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 713
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 713

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtgtcagc agcatctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagcgtgctc actcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 714
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 714

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

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

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

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

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

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

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

<210> SEQ ID NO 715
<211> LENGTH: 21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 715

cagagtgtca gcagcatcta c 21

<210> SEQ ID NO 716
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 716

Gln Ser Val Ser Ser Ile Tyr
1 5

<210> SEQ ID NO 717
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 717

ggtgcgtcc 9

<210> SEQ ID NO 718
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 718

Gly Ala Ser
1

<210> SEQ ID NO 719
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 719

cagcagcgtg ctcactcacc gtacact 27

<210> SEQ ID NO 720
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 720

Gln Gln Arg Ala His Ser Pro Tyr Thr
1 5

<210> SEQ ID NO 721
<211> LENGTH: 369
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 721

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggctt cagctttgat aattatgcca tgcactgggt ccggcaagct 120

ccaggacagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca atgccaggaa ctccctgttt 240

ctgcaaatga acagtctgag taatgaggac acggccatgt attactgcgc aaaagataag 300

agtggctacg gctcctactt ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 722
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 722

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

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

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

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

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

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 723
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 723

ggcttcagct ttgataatta tgcc 24

<210> SEQ ID NO 724
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 724

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Gly Phe Ser Phe Asp Asn Tyr Ala
1 5

<210> SEQ ID NO 725
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 725

attagttgga atagtggtag caga 24

<210> SEQ ID NO 726
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 726

Ile Ser Trp Asn Ser Gly Ser Arg
1 5

<210> SEQ ID NO 727
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 727

gcaaaagata agagtggcta cggctcctac ttctacggta tggacgtc 48

<210> SEQ ID NO 728
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 728

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 729
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 729

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtattaga aacatctatt tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gtttaccgta cacttttggc 300

caggggacca agctggagat caaa 324

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<210> SEQ ID NO 730
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 730

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

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

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

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

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

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

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

<210> SEQ ID NO 731
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 731

cagagtatta gaaacatcta t 21

<210> SEQ ID NO 732
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 732

Gln Ser Ile Arg Asn Ile Tyr
1 5

<210> SEQ ID NO 733
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 733

ggtgcgtcc 9

<210> SEQ ID NO 734
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 734

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Gly Ala Ser
1

<210> SEQ ID NO 735
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 735

cagcagcgtg ttagtttacc gtacact 27

<210> SEQ ID NO 736
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 736

Gln Gln Arg Val Ser Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 737
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 737

caggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggctt cagctttgat gattatgcca tgcactgggt ccggcaagct 120

ccaggacagg gcctggagtg ggtctcaggt attagttgga atggtggtag cagagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctccctgttt 240

ctgcaaatga acagtctgtt tactgaggac acggccttgt attactgtgc aaaagataag 300

agtggctacg gctcctactt ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 738
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 738

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Phe

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65 70 75 80

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 739
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 739

ggcttcagct ttgatgatta tgcc 24

<210> SEQ ID NO 740
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 740

Gly Phe Ser Phe Asp Asp Tyr Ala
1 5

<210> SEQ ID NO 741
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 741

attagttgga atggtggtag caga 24

<210> SEQ ID NO 742
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 742

Ile Ser Trp Asn Gly Gly Ser Arg
1 5

<210> SEQ ID NO 743
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 743

gcaaaagata agagtggcta cggctcctac ttctacggta tggacgtc 48

<210> SEQ ID NO 744
<211> LENGTH: 16

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 744

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Phe Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 745
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 745

gaaattgtgt tgacgcagtc tccaggcatt ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtattaga aacatctatt tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gttcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 746
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 746

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

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

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

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

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

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

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

<210> SEQ ID NO 747
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 747

cagagtatta gaaacatcta t 21

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<210> SEQ ID NO 748
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 748

Gln Ser Ile Arg Asn Ile Tyr
1 5

<210> SEQ ID NO 749
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 749

ggtgcgtcc 9

<210> SEQ ID NO 750
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 750

Gly Ala Ser
1

<210> SEQ ID NO 751
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 751

cagcagcgtg ttagttcacc gtacact 27

<210> SEQ ID NO 752
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 752

Gln Gln Arg Val Ser Ser Pro Tyr Thr
1 5

<210> SEQ ID NO 753
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 753

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

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ccaggaaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cagagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctccctgttt 240

ctgcaaatga acagtctgag tactgaggac acggccttgt attactgtgc aaaagataag 300

agtggctacg gctcctacta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 754
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 754

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

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

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

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

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

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 755
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 755

ggattcacct ttgatgatta tgcc 24

<210> SEQ ID NO 756
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 756

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> SEQ ID NO 757
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 757

attagttgga atagtggtag caga 24

<210> SEQ ID NO 758
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 758

Ile Ser Trp Asn Ser Gly Ser Arg
1 5

<210> SEQ ID NO 759
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 759

gcaaaagata agagtggcta cggctcctac tactacggta tggacgtc 48

<210> SEQ ID NO 760
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 760

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 761
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 761

gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtattaga agcatctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gctcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 762
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 762

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

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1 5 10 15

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ile
20 25 30

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

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

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

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

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

<210> SEQ ID NO 763
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 763

cagagtatta gaagcatcta c 21

<210> SEQ ID NO 764
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 764

Gln Ser Ile Arg Ser Ile Tyr
1 5

<210> SEQ ID NO 765
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 765

ggtgcgtcc 9

<210> SEQ ID NO 766
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 766

Gly Ala Ser
1

<210> SEQ ID NO 767
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 767

cagcagcgtg ttagctcacc gtacact 27

<210> SEQ ID NO 768
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 768

Gln Gln Arg Val Ser Ser Pro Tyr Thr
1 5

<210> SEQ ID NO 769
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 769

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgtag cctctggatt cacctttgct gattttacca tgcactgggt ccggcaagcg 120

ccagggaagg gccttgagtg ggtctcaggt attagttgga atagtaatag tatagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa atccctgttt 240

ctgcaaatgt ccagtctgag agctgaggac acggccttat attactgtgt caaagacaga 300

agcggatata gcagattcta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 770
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 770

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

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

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

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

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

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

Val Lys Asp Arg Ser Gly Tyr Ser Arg Phe Tyr Tyr Gly Met Asp Val
100 105 110

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

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<210> SEQ ID NO 771
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 771

ggattcacct ttgctgattt tacc 24

<210> SEQ ID NO 772
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 772

Gly Phe Thr Phe Ala Asp Phe Thr
1 5

<210> SEQ ID NO 773
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 773

attagttgga atagtaatag tata 24

<210> SEQ ID NO 774
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 774

Ile Ser Trp Asn Ser Asn Ser Ile
1 5

<210> SEQ ID NO 775
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 775

gtcaaagaca gaagcggata tagcagattc tactacggta tggacgtc 48

<210> SEQ ID NO 776
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 776

Val Lys Asp Arg Ser Gly Tyr Ser Arg Phe Tyr Tyr Gly Met Asp Val
1 5 10 15

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<210> SEQ ID NO 777
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 777

gaaattgtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccatc 60

ctctcctgca gggccagtca gaatattaat agcaacttgg cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tgtcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatccgcag cctgcaatct 240

gaagattttg cagtttatta ctgtcaacaa tattataatt ggccgatcac tttcggccac 300

gggacacgac tggagattaa a 321

<210> SEQ ID NO 778
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 778

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

Glu Arg Ala Ile Leu Ser Cys Arg Ala Ser Gln Asn Ile Asn Ser Asn
20 25 30

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

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

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

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

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

<210> SEQ ID NO 779
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 779

cagaatatta atagcaac 18

<210> SEQ ID NO 780
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 780

Gln Asn Ile Asn Ser Asn

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1 5

<210> SEQ ID NO 781
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 781

ggtgcatcc 9

<210> SEQ ID NO 782
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 782

Gly Ala Ser
1

<210> SEQ ID NO 783
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 783

caacaatatt ataattggcc gatcact 27

<210> SEQ ID NO 784
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 784

Gln Gln Tyr Tyr Asn Trp Pro Ile Thr
1 5

<210> SEQ ID NO 785
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 785

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccaggaaagg gcctggagtg ggtctcaggt attagttgga atggtggtag taaagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acaccaggaa ctccctgtct 240

ctgcaaatga acagtctgag aattgaagac acggccttat attactgtgc aaaagataag 300

agtggctacg gctccttcta ctacggtttg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

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<210> SEQ ID NO 786
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 786

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

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

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

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

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

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Leu Asp Val
100 105 110

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

<210> SEQ ID NO 787
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 787

ggattcacct ttgatgatta tgcc 24

<210> SEQ ID NO 788
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 788

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> SEQ ID NO 789
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 789

attagttgga atggtggtag taaa 24

<210> SEQ ID NO 790
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 790

Ile Ser Trp Asn Gly Gly Ser Lys
1 5

<210> SEQ ID NO 791
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 791

gcaaaagata agagtggcta cggctccttc tactacggtt tggacgtc 48

<210> SEQ ID NO 792
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 792

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

<210> SEQ ID NO 793
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 793

gaaatagtgt tgacacagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtattaga agcatctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcagggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagttta ttactgtcag cagcgtgtta gctcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 794
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 794

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

Asp Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Ser Ile
20 25 30

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

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

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

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

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

<210> SEQ ID NO 795
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 795

cagagtatta gaagcatcta c 21

<210> SEQ ID NO 796
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 796

Gln Ser Ile Arg Ser Ile Tyr
1 5

<210> SEQ ID NO 797
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 797

ggtgcgtcc 9

<210> SEQ ID NO 798
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 798

Gly Ala Ser
1

<210> SEQ ID NO 799
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 799

cagcagcgtg ttagctcacc gtacact 27

<210> SEQ ID NO 800
<211> LENGTH: 9
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 800

Gln Gln Arg Val Ser Ser Pro Tyr Thr
1 5

<210> SEQ ID NO 801
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 801

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gatttcacca tgcactgggt ccggcaagct 120

ccaggaaagg gcctggagtg ggtctcagat attagttgga atagtggtag catagactat 180

gcggactctg tgaagggccg attcaccatt tccagagaca atgccaggaa ctccctgttt 240

ctacaaatga gcagtctgag aactgaggac acggcctcgt attactgtat aaaagataag 300

agtggctacg gctcctacaa ctacggtctg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 802
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 802

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

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

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

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

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

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

Ile Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Asn Tyr Gly Leu Asp Val
100 105 110

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

<210> SEQ ID NO 803
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 803

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ggattcacct ttgatgattt cacc 24

<210> SEQ ID NO 804
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 804

Gly Phe Thr Phe Asp Asp Phe Thr
1 5

<210> SEQ ID NO 805
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 805

attagttgga atagtggtag cata 24

<210> SEQ ID NO 806
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 806

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 807
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 807

ataaaagata agagtggcta cggctcctac aactacggtc tggacgtc 48

<210> SEQ ID NO 808
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 808

Ile Lys Asp Lys Ser Gly Tyr Gly Ser Tyr Asn Tyr Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 809
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 809

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gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga cagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcatctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatccat ggtgcgtcca ccagggccac tggcatccca 180

gacaggttca gtggcagtgg gtcggggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcacttta ttactgtcac cagcgtgtta gttcaccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> SEQ ID NO 810
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 810

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

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

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

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

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

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

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

<210> SEQ ID NO 811
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 811

cagagtgtta gcagcatcta c 21

<210> SEQ ID NO 812
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 812

Gln Ser Val Ser Ser Ile Tyr
1 5

<210> SEQ ID NO 813
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 813

ggtgcgtcc 9

<210> SEQ ID NO 814
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 814

Gly Ala Ser
1

<210> SEQ ID NO 815
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 815

caccagcgtg ttagttcacc gtacact 27

<210> SEQ ID NO 816
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 816

His Gln Arg Val Ser Ser Pro Tyr Thr
1 5

<210> SEQ ID NO 817
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 817

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tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120

ccaggaaagg gcctggagtg ggtctcaggt attagttgga atagtggtag taaagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acaccaggaa ctccctgttt 240

ctgcaaatga acagtctgag aactgaagac acggccttat attactgtgc aaaagataag 300

agtggctacg gctccttcta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 818
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 818

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

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

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

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

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

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

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 819
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 819

ggattcacct ttgatgatta tgcc 24

<210> SEQ ID NO 820
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 820

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> SEQ ID NO 821
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 821

attagttgga atagtggtag taaa 24

<210> SEQ ID NO 822
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 822

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 823

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<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 823

gcaaaagata agagtggcta cggctccttc tactacggta tggacgtc 48

<210> SEQ ID NO 824
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 824

Ala Lys Asp Lys Ser Gly Tyr Gly Ser Phe Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 825
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 825

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggccagtca gagtattagt agctggttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcgtctagtt tagaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag tataatagtt attctccgtt cggccaaggg 300

accaaggtgg aaatcaaa 318

<210> SEQ ID NO 826
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 826

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

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

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

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

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

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

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

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<210> SEQ ID NO 827
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 827

cagagtatta gtagctgg 18

<210> SEQ ID NO 828
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 828

Gln Ser Ile Ser Ser Trp
1 5

<210> SEQ ID NO 829
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 829

aaggcgtct 9

<210> SEQ ID NO 830
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 830

Lys Ala Ser
1

<210> SEQ ID NO 831
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 831

caacagtata atagttattc tccg 24

<210> SEQ ID NO 832
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 832

Gln Gln Tyr Asn Ser Tyr Ser Pro
1 5

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<210> SEQ ID NO 833
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 833

caggtgcaac tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggact caccttcagt acctatgtca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggcgtg ggtggcagtt atagcaaatg atggaagtaa taaatattat 180

gcagactccg tgaagggccg attcaccatc tccagagaca actccaagaa cacgctgtat 240

ctgcaaatga atagcctgag acctgaggac acggctgtgt atttttgtgc gaaagagggg 300

ggtaccagtg ggtcctacta ttactatgga atggacgtct ggggtcaagg gactacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 834
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 834

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

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

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

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

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

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

Ala Lys Glu Gly Gly Thr Ser Gly Ser Tyr Tyr Tyr Tyr Gly Met Asp
100 105 110

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

<210> SEQ ID NO 835
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 835

ggactcacct tcagtaccta tgtc 24

<210> SEQ ID NO 836
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 836

Gly Leu Thr Phe Ser Thr Tyr Val
1 5

<210> SEQ ID NO 837
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 837

atagcaaatg atggaagtaa taaa 24

<210> SEQ ID NO 838
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 838

Ile Ala Asn Asp Gly Ser Asn Lys
1 5

<210> SEQ ID NO 839
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 839

gcgaaagagg ggggtaccag tgggtcctac tattactatg gaatggacgt c 51

<210> SEQ ID NO 840
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 840

Ala Lys Glu Gly Gly Thr Ser Gly Ser Tyr Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 841
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 841

gacatccaga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta ttcaactcca tcaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagcttctcc tttactgggc atctacccgg 180

gaatccggga tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

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atcaccagcc tgcaggctga agatgtggca ctttattact gtcagcaata ttatagtatt 300

ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaac ga 342

<210> SEQ ID NO 842
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 842

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Phe Asn
20 25 30

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

Pro Pro Lys Leu Leu Leu Tyr Trp Ala Ser Thr Arg Glu Ser Gly Ile
50 55 60

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

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

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

Lys Arg

<210> SEQ ID NO 843
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 843

cagagtcttt tattcaactc catcaataag aactac 36

<210> SEQ ID NO 844
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 844

Gln Ser Leu Leu Phe Asn Ser Ile Asn Lys Asn Tyr
1 5 10

<210> SEQ ID NO 845
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 845

tgggcatct 9

<210> SEQ ID NO 846

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<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 846

Trp Ala Ser
1

<210> SEQ ID NO 847
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 847

cagcaatatt atagtattcc gtggacg 27

<210> SEQ ID NO 848
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 848

Gln Gln Tyr Tyr Ser Ile Pro Trp Thr
1 5

<210> SEQ ID NO 849
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 849

caggtgcagc tggtggagtc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaaga cttctggata caccttcacc ggctactata tgcactggat acgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta aaagtggtgg cacaaattat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggaactga gcaggctgag atccgacgac atggccgtgt attattgtgc gagaatgggg 300

gacggtgcag tgtttgactt ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 850
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 850

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

-continued

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

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

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 851
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 851

ggatacacct tcaccggcta ctat 24

<210> SEQ ID NO 852
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 852

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> SEQ ID NO 853
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 853

atcaacccta aaagtggtgg caca 24

<210> SEQ ID NO 854
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 854

Ile Asn Pro Lys Ser Gly Gly Thr
1 5

<210> SEQ ID NO 855
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 855

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gcgagaatgg gggacggtgc agtgtttgac ttc 33

<210> SEQ ID NO 856
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 856

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
1 5 10

<210> SEQ ID NO 857
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 857

gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gaggattagc agctttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ctatcagcag tctgcaacct 240

gaagattttg ctacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300

gggaccaagg tggaaatcaa acga 324

<210> SEQ ID NO 858
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 858

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

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

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

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

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

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

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

<210> SEQ ID NO 859
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 859

cagaggatta gcagcttt 18

<210> SEQ ID NO 860
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 860

Gln Arg Ile Ser Ser Phe
1 5

<210> SEQ ID NO 861
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 861

actgcatcc 9

<210> SEQ ID NO 862
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 862

Thr Ala Ser
1

<210> SEQ ID NO 863
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 863

caacagagtt acaggacccc gctcact 27

<210> SEQ ID NO 864
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 864

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

<210> SEQ ID NO 865
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 865

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gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga acagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatt tccagagaca acgccaagaa ctccctgtat 240

ttgcaaatga acagtctgag agctgaggac acggccttgt tttactgtgc aaaagatcaa 300

agtggttacg gccactacta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 866
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 866

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

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

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

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

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

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

Ala Lys Asp Gln Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

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

<210> SEQ ID NO 867
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 867

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 868
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 868

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 869

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<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 869

attagttgga acagtggtag cata 24

<210> SEQ ID NO 870
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 870

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 871
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 871

gcaaaagatc aaagtggtta cggccactac tactacggta tggacgtc 48

<210> SEQ ID NO 872
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 872

Ala Lys Asp Gln Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 873
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 873

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgta gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactga tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatca ctgtcagcag tataataact ggccgctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 874
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 874

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

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

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

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

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

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

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

<210> SEQ ID NO 875
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 875

cagagtgtta gcagcaac 18

<210> SEQ ID NO 876
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 876

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 877
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 877

ggtgcatcc 9

<210> SEQ ID NO 878
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 878

Gly Ala Ser
1

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<210> SEQ ID NO 879
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 879

cagcagtata ataactggcc gctcact 27

<210> SEQ ID NO 880
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 880

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 881
<211> LENGTH: 387
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 881

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tcctgtgcag cctctggatt caccttcagt tactatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatcatttg atggaaagaa taaatattat 180

gcagactccg tgatgggccg attcaccatc tccagagaca attccaagaa tacactgtat 240

ctgcaaatga acagcctgag agctgaggac tcggctgtgt ttttctgtgc gaggtcttac 300

gacattttga ctggttatgg agccggttac agctaccact acggtatgga cgtctggggc 360

caagggacca cggtcaccgt ctcctca 387

<210> SEQ ID NO 882
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 882

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

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

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

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

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

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

-continued

Ala Arg Ser Tyr Asp Ile Leu Thr Gly Tyr Gly Ala Gly Tyr Ser Tyr
100 105 110

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

Ser

<210> SEQ ID NO 883
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 883

ggattcacct tcagttacta tggc 24

<210> SEQ ID NO 884
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 884

Gly Phe Thr Phe Ser Tyr Tyr Gly
1 5

<210> SEQ ID NO 885
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 885

atatcatttg atggaaagaa taaa 24

<210> SEQ ID NO 886
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 886

Ile Ser Phe Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 887
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 887

gcgaggtctt acgacatttt gactggttat ggagccggtt acagctacca ctacggtatg 60

gacgtc 66

<210> SEQ ID NO 888
<211> LENGTH: 22
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 888

Ala Arg Ser Tyr Asp Ile Leu Thr Gly Tyr Gly Ala Gly Tyr Ser Tyr
1 5 10 15

His Tyr Gly Met Asp Val
            20

<210> SEQ ID NO 889
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 889

gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gaggattagc agctttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct aatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 890
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 890

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

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

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

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

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

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

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

<210> SEQ ID NO 891
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 891

cagaggatta gcagcttt 18

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<210> SEQ ID NO 892
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 892

Gln Arg Ile Ser Ser Phe
1 5

<210> SEQ ID NO 893
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 893

actgcatcc 9

<210> SEQ ID NO 894
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 894

Thr Ala Ser
1

<210> SEQ ID NO 895
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 895

caacagagtt acaggacccc gctcact 27

<210> SEQ ID NO 896
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 896

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

<210> SEQ ID NO 897
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 897

caggtgcagc tggtggagtc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtc 60

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tcctgcaaga cttctggata caccctctcc ggctattata tgcactggat gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg attaacccta aaagtggtgt cacaaattat 180

gcacagaagt ttcaggacag agtcgccatg accagggaca cgtccatcag cacagcctac 240

atggaactga gcaggctgag atctgacgac acggccgtgt attactgtgc gagaatgggg 300

gacggtgcag tgtttgactt ctgggcccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 898
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 898

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

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

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

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

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

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Ala Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 899
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 899

ggatacaccc tctccggcta ttat 24

<210> SEQ ID NO 900
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 900

Gly Tyr Thr Leu Ser Gly Tyr Tyr
1 5

<210> SEQ ID NO 901
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 901

attaacccta aaagtggtgt caca 24

<210> SEQ ID NO 902
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 902

Ile Asn Pro Lys Ser Gly Val Thr
1 5

<210> SEQ ID NO 903
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 903

gcgagaatgg gggacggtgc agtgtttgac ttc 33

<210> SEQ ID NO 904
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 904

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
1 5 10

<210> SEQ ID NO 905
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 905

gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gaggattagc agctttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct aatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 906
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 906

Asp Ile Gln Leu 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 Arg Ile Ser Ser Phe
20 25 30

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

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

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

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

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

<210> SEQ ID NO 907
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 907

cagaggatta gcagcttt 18

<210> SEQ ID NO 908
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 908

Gln Arg Ile Ser Ser Phe
1 5

<210> SEQ ID NO 909
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 909

actgcatcc 9

<210> SEQ ID NO 910
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 910

Thr Ala Ser
1

<210> SEQ ID NO 911
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 911

caacagagtt acaggacccc gctcact 27

<210> SEQ ID NO 912
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 912

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

<210> SEQ ID NO 913
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 913

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tcctgtgcag cctctggatt caccttcagt agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgtcaact atatcatttg atggaagtaa caaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag acctgaggac acggctgtgt attactgtgc gaaaggggggg 300

ggtaccagtg ggtcctactt ttactacggt atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 914
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 914

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

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

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

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

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

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

Ala Lys Gly Gly Gly Thr Ser Gly Ser Tyr Phe Tyr Tyr Gly Met Asp
100 105 110

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

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<210> SEQ ID NO 915
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 915

ggattcacct tcagtagcta tggc 24

<210> SEQ ID NO 916
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 916

Gly Phe Thr Phe Ser Ser Tyr Gly
1 5

<210> SEQ ID NO 917
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 917

atatcatttg atggaagtaa caaa 24

<210> SEQ ID NO 918
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 918

Ile Ser Phe Asp Gly Ser Asn Lys
1 5

<210> SEQ ID NO 919
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 919

gcgaaagggg ggggtaccag tgggtcctac ttttactacg gtatggacgt c 51

<210> SEQ ID NO 920
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 920

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

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Val

<210> SEQ ID NO 921
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 921

gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gaggattagc agctttttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct aatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 922
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 922

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

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

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

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

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

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

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

<210> SEQ ID NO 923
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 923

cagaggatta gcagcttt 18

<210> SEQ ID NO 924
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 924

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Gln Arg Ile Ser Ser Phe
1 5

<210> SEQ ID NO 925
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 925

actgcatcc 9

<210> SEQ ID NO 926
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 926

Thr Ala Ser
1

<210> SEQ ID NO 927
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 927

caacagagtt acaggacccc gctcact 27

<210> SEQ ID NO 928
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 928

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

<210> SEQ ID NO 929
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 929

caggttcagc tggtgcagtc tgggactgag gtgaagaagc ctggggcctc aatgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata ttcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgatgt cacaaagtat 180

gcacagaagt ttcagggcag ggtcaccttg accagggaca cgtccatcag tgcagcctat 240

attgacctga gcaggctgag atctgacgac acggccattt attactgtgc gagaatgggg 300

gacggtgcag tgtttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

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<210> SEQ ID NO 930
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 930

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

Ser Met Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Asn Ser Asp Val Thr Lys Tyr Ala Gln Lys Phe
50 55 60

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

Ile Asp Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 931
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 931

ggatacacct tcaccggcta ctat 24

<210> SEQ ID NO 932
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 932

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

<210> SEQ ID NO 933
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 933

atcaacccta acagtgatgt caca 24

<210> SEQ ID NO 934
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 934

Ile Asn Pro Asn Ser Asp Val Thr
1 5

<210> SEQ ID NO 935
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 935

gcgagaatgg gggacggtgc agtgtttgac tac 33

<210> SEQ ID NO 936
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 936

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr
1 5 10

<210> SEQ ID NO 937
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 937

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atcacttgcc gggcaagtca acgcattagc agctatttaa attggtatca acagaaacca 120

gggaaagccc ctaaggtgct gatctctgtt gcatccagtt tacaaagtgg ggtcccatca 180

aggttcagtg gcagtggatt tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaggattctg catcttacta ctgtcaacag agttacaata ccccgctcac tttcggcggc 300

gggaccaagc tggagatcaa acga 324

<210> SEQ ID NO 938
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 938

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

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

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

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

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

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

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

<210> SEQ ID NO 939
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 939

caacgcatta gcagctat 18

<210> SEQ ID NO 940
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 940

Gln Arg Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 941
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 941

gttgcatcc 9

<210> SEQ ID NO 942
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 942

Val Ala Ser
1

<210> SEQ ID NO 943
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 943

caacagagtt acaatacccc gctcact 27

<210> SEQ ID NO 944
<211> LENGTH: 9
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 944

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

<210> SEQ ID NO 945
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 945

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tcctgcaaga cttctggata cagtttcatt ggctattata tacactggat gcgacaggcc 120

cctggacaag ggcttgaatg gatgggatgg atcaacccta agagtggtgt cacaaattat 180

gcacagaggt ttcagggcag ggtcaccatg accagggaca cgtccatcag tactgcctac 240

atggaactga gcaggctgaa atctgacgac acggccgtgt atttctgtgc gagaatgggg 300

gacggtgcag tgtttgactt ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 946
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 946

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Ser Phe Ile Gly Tyr
20 25 30

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

Gly Trp Ile Asn Pro Lys Ser Gly Val Thr Asn Tyr Ala Gln Arg Phe
50 55 60

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

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 947
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 947

ggatacagtt tcattggcta ttat 24

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<210> SEQ ID NO 948
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 948

Gly Tyr Ser Phe Ile Gly Tyr Tyr
1 5

<210> SEQ ID NO 949
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 949

atcaacccta agagtggtgt caca 24

<210> SEQ ID NO 950
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 950

Ile Asn Pro Lys Ser Gly Val Thr
1 5

<210> SEQ ID NO 951
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 951

gcgagaatgg gggacggtgc agtgtttgac ttc 33

<210> SEQ ID NO 952
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 952

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
1 5 10

<210> SEQ ID NO 953
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 953

gacatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

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atcacttgcc gggcaagtca gaggattagc agctttttaa attggtatca gcagaaacca 120

gggaaagtcc ctaagctcct gatctatact gcatccaatt tacaaaatgg ggtcccatca 180

aggttcagtg gcactggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagga ccccgctcac tttcggcgga 300

gggaccaaag tggatatcaa acga 324

<210> SEQ ID NO 954
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 954

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> SEQ ID NO 955
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 955

cagaggatta gcagcttt 18

<210> SEQ ID NO 956
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 956

Gln Arg Ile Ser Ser Phe
1 5

<210> SEQ ID NO 957
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 957

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actgcatcc 9

<210> SEQ ID NO 958
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 958

Thr Ala Ser
1

<210> SEQ ID NO 959
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 959

caacagagtt acaggacccc gctcact 27

<210> SEQ ID NO 960
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 960

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

<210> SEQ ID NO 961
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 961

gaggtgcagc tggtggagtc tggggctgaa gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaaga cttctggata caccttcacc ggctactata tgcactggat acgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta aaagtggtgg cacaaattat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggaactga gcaggctgag atccgacgac atggccgtgt attattgtgc gagaatgggg 300

gacggtgcag tgtttgactt ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 962
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 962

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

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr

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```
            20                  25                  30

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

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

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

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

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210> SEQ ID NO 963
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 963

ggatacacct tcaccggcta ctat                                          24


<210> SEQ ID NO 964
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 964

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1               5


<210> SEQ ID NO 965
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 965

atcaacccta aaagtggtgg caca                                          24


<210> SEQ ID NO 966
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 966

Ile Asn Pro Lys Ser Gly Gly Thr
1               5


<210> SEQ ID NO 967
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 967

gcgagaatgg gggacggtgc agtgtttgac ttc 33

<210> SEQ ID NO 968
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 968

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Phe
1 5 10

<210> SEQ ID NO 969
<211> LENGTH: 327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 969

gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgct cactttcggc 300

ggagggacca aagtggatat caaacga 327

<210> SEQ ID NO 970
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 970

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

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

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

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

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> SEQ ID NO 971
<211> LENGTH: 18
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 971

cagagcatta gcagctat 18

<210> SEQ ID NO 972
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 972

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 973
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 973

gctgcatcc 9

<210> SEQ ID NO 974
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 974

Ala Ala Ser
1

<210> SEQ ID NO 975
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 975

caacagagtt acagtacccc tccgctcact 30

<210> SEQ ID NO 976
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 976

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

<210> SEQ ID NO 977
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 977

caggttcagc tggtgcagtc tgggactgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgatgt cacaaactat 180

gcacagaagt ttcagggcag ggtcaccttg accagggaca cgtccatcag tacagcctac 240

attgacctga gcaggctgag atctgacgac acggccattt attactgtgc gagaatgggg 300

gacggtgcag tgtttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 978
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 978

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

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

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

Gly Trp Ile Asn Pro Asn Ser Asp Val Thr Asn Tyr Ala Gln Lys Phe
50 55 60

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

Ile Asp Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 979
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 979

ggatacacct tcaccggcta ctat 24

<210> SEQ ID NO 980
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 980

Gly Tyr Thr Phe Thr Gly Tyr Tyr
1 5

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<210> SEQ ID NO 981
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 981

atcaacccta acagtgatgt caca 24

<210> SEQ ID NO 982
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 982

Ile Asn Pro Asn Ser Asp Val Thr
1 5

<210> SEQ ID NO 983
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 983

gcgagaatgg gggacggtgc agtgtttgac tac 33

<210> SEQ ID NO 984
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 984

Ala Arg Met Gly Asp Gly Ala Val Phe Asp Tyr
1 5 10

<210> SEQ ID NO 985
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 985

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gcgcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaggtgct gatctctgtt gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccattagtag tctgcaacct 240

gaggattttg catcttacta ctgtcaacag agttacaata ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 986
<211> LENGTH: 108
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 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 Arg Ile Ser Ser Tyr
20 25 30

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

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

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

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

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

<210> SEQ ID NO 987
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 987

cagcgcatta gcagctat 18

<210> SEQ ID NO 988
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 988

Gln Arg Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 989
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 989

gttgcatcc 9

<210> SEQ ID NO 990
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 990

Val Ala Ser
1

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<210> SEQ ID NO 991
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 991

caacagagtt acaatacccc gctcact 27

<210> SEQ ID NO 992
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 992

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

<210> SEQ ID NO 993
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 993

caggtgcagc tggtgcagtc tgggggaggc ttggtcaagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatgaca tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcatac attagtagta gtggtaatac catacattac 180

gcagactctg tgaagggccg attcaccatc tccagagaca attccaagaa ctcactttat 240

ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc gaaagccggt 300

cccgctacgg tgacacggag gtactactac tactacggtt tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc a 381

<210> SEQ ID NO 994
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 994

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

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

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

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

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

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

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```
               85                  90                  95

Ala Lys Ala Gly Pro Ala Thr Val Thr Arg Arg Tyr Tyr Tyr Tyr Tyr
            100                 105                 110

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


<210> SEQ ID NO 995
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 995

ggattcacct tcagtagcta tgac                                          24


<210> SEQ ID NO 996
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 996

Gly Phe Thr Phe Ser Ser Tyr Asp
1               5


<210> SEQ ID NO 997
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 997

attagtagta gtggtaatac cata                                          24


<210> SEQ ID NO 998
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 998

Ile Ser Ser Ser Gly Asn Thr Ile
1               5


<210> SEQ ID NO 999
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 999

gcgaaagccg gtcccgctac ggtgacacgg aggtactact actactacgg tttggacgtc     60


<210> SEQ ID NO 1000
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1000

Ala Lys Ala Gly Pro Ala Thr Val Thr Arg Arg Tyr Tyr Tyr Tyr Tyr
1 5 10 15

Gly Leu Asp Val
20

<210> SEQ ID NO 1001
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1001

gacatcgtga tgacccagtc tccatcctcc ctgtctgcat ctgtacgaga cagagtcacc 60

atcacttgcc gggcaagtca gagaattagc agctatttaa attggtttca gcagaaacca 120

gggaaagccc ctaaggtcct gatctatact gcatccagtt tgcaaaatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagactttg caacttacta ctgtcagcag agttacagga ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 1002
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1002

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

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

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

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

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

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

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

<210> SEQ ID NO 1003
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1003

cagagaatta gcagctat 18

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<210> SEQ ID NO 1004
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1004

Gln Arg Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 1005
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1005

actgcatcc 9

<210> SEQ ID NO 1006
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1006

Thr Ala Ser
1

<210> SEQ ID NO 1007
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1007

cagcagagtt acaggacccc gctcact 27

<210> SEQ ID NO 1008
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1008

Gln Gln Ser Tyr Arg Thr Pro Leu Thr
1 5

<210> SEQ ID NO 1009
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1009

caggtgcagc tggtacagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata cacattcatc ggctactata tgcactgggt gcgacaggcc 120

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cctggacaag ggcttgagtg gatgggatgg atcaacccta aaagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accggggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt tttactgtgc gagaatgggg 300

gacggtgcaa tgtttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 1010
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1010

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Gly Tyr
20 25 30

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

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

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

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

Ala Arg Met Gly Asp Gly Ala Met Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 1011
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1011

ggatacacat tcatcggcta ctat 24

<210> SEQ ID NO 1012
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1012

Gly Tyr Thr Phe Ile Gly Tyr Tyr
1 5

<210> SEQ ID NO 1013
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1013

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atcaacccta aaagtggtgg caca 24

<210> SEQ ID NO 1014
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1014

Ile Asn Pro Lys Ser Gly Gly Thr
1 5

<210> SEQ ID NO 1015
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1015

gcgagaatgg gggacggtgc aatgtttgac tac 33

<210> SEQ ID NO 1016
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1016

Ala Arg Met Gly Asp Gly Ala Met Phe Asp Tyr
1 5 10

<210> SEQ ID NO 1017
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1017

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagaattagc agctatttaa attggtatca gcagaaagca 120

gggaaagccc ctaaggtcct gatctatact gcatccagtt tgcaaagtgg ggtcccatca 180

cgattcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 1018
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1018

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 Arg Ile Ser Ser Tyr
            20                  25                  30

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

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

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

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

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


<210> SEQ ID NO 1019
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1019

cagagaatta gcagctat                                                  18


<210> SEQ ID NO 1020
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1020

Gln Arg Ile Ser Ser Tyr
1               5


<210> SEQ ID NO 1021
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1021

actgcatcc                                                             9


<210> SEQ ID NO 1022
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1022

Thr Ala Ser
1


<210> SEQ ID NO 1023
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic
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<400> SEQUENCE: 1023

caacagagtt acagtacccc gctcact 27

<210> SEQ ID NO 1024
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1024

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> SEQ ID NO 1025
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1025

caggtgcagc tggtacagtc tgggggaggc gtggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccgtcaagct 120

ccagggaagg gtctggagtg ggtctctctt attagtgggg atggtggtag cacatactat 180

gcagactctg tgaagggccg attcaccatc tccagagaca acagcaaaaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac accgccttgt attactgtgc aaaagatgat 300

agcagctcgt cctggtacta ctactactac ggtatggacg tctggggccg agggaccacg 360

gtcaccgtct cctca 375

<210> SEQ ID NO 1026
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1026

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

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

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

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

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

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

Ala Lys Asp Asp Ser Ser Ser Ser Trp Tyr Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<210> SEQ ID NO 1027
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1027

ggattcacct ttgatgatta tgcc 24

<210> SEQ ID NO 1028
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1028

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> SEQ ID NO 1029
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1029

attagtgggg atggtggtag caca 24

<210> SEQ ID NO 1030
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1030

Ile Ser Gly Asp Gly Gly Ser Thr
1 5

<210> SEQ ID NO 1031
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1031

gcaaaagatg atagcagctc gtcctggtac tactactact acggtatgga cgtc 54

<210> SEQ ID NO 1032
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1032

Ala Lys Asp Asp Ser Ser Ser Ser Trp Tyr Tyr Tyr Tyr Tyr Gly Met
1 5 10 15

Asp Val

-continued

<210> SEQ ID NO 1033
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1033

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gcgcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaaggtgct gatctctgtt gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaggattttg catcttacta ctgtcaacag agttacaata ccccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acga 324

<210> SEQ ID NO 1034
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 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 Gln Arg Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Ser Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> SEQ ID NO 1035
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1035

cagcgcatta gcagctat 18

<210> SEQ ID NO 1036
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1036

Gln Arg Ile Ser Ser Tyr

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1 5

<210> SEQ ID NO 1037
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1037

gttgcatcc 9

<210> SEQ ID NO 1038
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1038

Val Ala Ser
1

<210> SEQ ID NO 1039
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1039

caacagagtt acaatacccc gctcact 27

<210> SEQ ID NO 1040
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1040

Gln Gln Ser Tyr Asn Thr Pro Leu Thr
1 5

<210> SEQ ID NO 1041
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1041

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttggt gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctccgat attagttgga atagtggtag caaagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctctat 240

cttcaaatga acagtctgag aactgaggat acggcctttt attactgtgc aaaagatagt 300

aggggctacg gtctctacta ccacctcggt ttggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

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<210> SEQ ID NO 1042
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1042

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe Tyr Tyr Cys
85 90 95

Ala Lys Asp Ser Arg Gly Tyr Gly Leu Tyr Tyr His Leu Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1043
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1043

ggattcacct ttggtgatta tacc 24

<210> SEQ ID NO 1044
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1044

Gly Phe Thr Phe Gly Asp Tyr Thr
1 5

<210> SEQ ID NO 1045
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1045

attagttgga atagtggtag caaa 24

<210> SEQ ID NO 1046
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1046

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1047
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1047

gcaaaagata gtaggggcta cggtctctac taccacctcg gtttggacgt c 51

<210> SEQ ID NO 1048
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1048

Ala Lys Asp Ser Arg Gly Tyr Gly Leu Tyr Tyr His Leu Gly Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 1049
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1049

gaggtgcagc tggtggagtc tgggggaggc ttggtgcagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgct gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag tatagcctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctctat 240

cttcaaatga acagtctgag aactgaggac acggcctttt attactgtgc aaaagatagt 300

aggggctacg gtcactataa gtacctcggt ttggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1050
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1050

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

-continued

```
        35                  40                  45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Ile Ala Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe Tyr Tyr Cys
                85                  90                  95

Ala Lys Asp Ser Arg Gly Tyr Gly His Tyr Lys Tyr Leu Gly Leu Asp
            100                 105                 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 1051
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1051

ggattcacct ttgctgatta tacc                                          24


<210> SEQ ID NO 1052
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1052

Gly Phe Thr Phe Ala Asp Tyr Thr
1               5


<210> SEQ ID NO 1053
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1053

attagttgga atagtggtag tata                                          24


<210> SEQ ID NO 1054
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1054

Ile Ser Trp Asn Ser Gly Ser Ile
1               5


<210> SEQ ID NO 1055
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1055
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gcaaaagata gtaggggcta cggtcactat aagtacctcg gtttggacgt c 51

<210> SEQ ID NO 1056
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1056

Ala Lys Asp Ser Arg Gly Tyr Gly His Tyr Lys Tyr Leu Gly Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 1057
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1057

gaggtgcagc tggtggagtc tgggggaggc atggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt ccccttcaat gattacacca tgcactgggt ccggcaagtc 120

ccagggaggg gcctggagtg ggtctcagat attagttgga atagcggcag taaaggctat 180

gcggactctg tgaagggtcg attcatcatc tccagagaca acgccaagaa ctccctgtac 240

ctgcaaatga acagtctgag agttgaagac acggccttgt attactgtgt aaaagatgga 300

agtggctacg ggaggttcca ttattacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1058
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1058

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Met Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Asn Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Val Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Tyr Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<210> SEQ ID NO 1059
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1059

ggattcccct tcaatgatta cacc 24

<210> SEQ ID NO 1060
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1060

Gly Phe Pro Phe Asn Asp Tyr Thr
1 5

<210> SEQ ID NO 1061
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1061

attagttgga atagcggcag taaa 24

<210> SEQ ID NO 1062
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1062

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1063
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1063

gtaaaagatg gaagtggcta cgggaggttc cattattacg ctatggacgt c 51

<210> SEQ ID NO 1064
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1064

Val Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Tyr Tyr Ala Met Asp
1 5 10 15

Val

-continued

<210> SEQ ID NO 1065
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1065

gaggtgcagc tggtggagtc tggtggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgct gattatacca tgcactgggt ccgccaagtt 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag caaagactat 180

gcggactctg tgaagggccg cttcaccatc tccagagaca acgccaagaa tttcctgtat 240

ctgcaaatga acagtctgag agctgaagac acggccttgt attactgtgt aaaatatgga 300

agtggctacg ggaaattcta cttctacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1066
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1066

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Phe Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1067
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1067

ggattcacct ttgctgatta tacc 24

<210> SEQ ID NO 1068
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1068

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1069
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1069

attagttgga atagtggtag caaa 24

<210> SEQ ID NO 1070
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1070

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1071
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1071

gtaaaatatg gaagtggcta cgggaaattc tacttctacg ctatggacgt c 51

<210> SEQ ID NO 1072
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1072

Val Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr Phe Tyr Ala Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1073
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1073

gaggtgcagc tggtgcagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgct gattatacca tgcactgggt ccggcaaact 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag caaagactat 180

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gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaatatgga 300

agtggctacg ggagatattt cttctacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1074
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1074

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Arg Tyr Phe Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1075
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1075

ggattcacct ttgctgatta tacc 24

<210> SEQ ID NO 1076
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1076

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1077
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1077

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attagttgga atagtggtag caaa 24

<210> SEQ ID NO 1078
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1078

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1079
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1079

gcaaaatatg gaagtggcta cgggagatat ttcttctacg ctatggacgt c 51

<210> SEQ ID NO 1080
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1080

Ala Lys Tyr Gly Ser Gly Tyr Gly Arg Tyr Phe Phe Tyr Ala Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1081
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1081

gaggtgcagc tggtggagtc aaggggagcc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cgcctttaat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtaatag taaagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctctat 240

ctacaaatga acagtctgag agctgaggac acggccttgt attactgtgt aaaagatgga 300

agtggctacg ggaaattttc cctctacgct ttggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1082
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1082

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Glu Val Gln Leu Val Glu Ser Arg Gly Ala Leu Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Asp Tyr
            20                  25                  30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Asp Ile Ser Trp Asn Ser Asn Ser Lys Asp Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Val Lys Asp Gly Ser Gly Tyr Gly Lys Phe Ser Leu Tyr Ala Leu Asp
            100                 105                 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 1083
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1083

ggattcgcct ttaatgatta tacc                                          24


<210> SEQ ID NO 1084
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1084

Gly Phe Ala Phe Asn Asp Tyr Thr
1               5


<210> SEQ ID NO 1085
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1085

attagttgga atagtaatag taaa                                          24


<210> SEQ ID NO 1086
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1086

Ile Ser Trp Asn Ser Asn Ser Lys
1               5
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<210> SEQ ID NO 1087
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1087

gtaaaagatg gaagtggcta cgggaaattt tccctctacg ctttggacgt c 51

<210> SEQ ID NO 1088
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1088

Val Lys Asp Gly Ser Gly Tyr Gly Lys Phe Ser Leu Tyr Ala Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 1089
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1089

caggtgcagc tggtggagtc tgggggaggc ttggttcacc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt caaatttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctagagtg ggtctcagat attagttgga atagtggtag taaaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagga ttccctatat 240

ctgcagatgg acagtctgag agctgcagac acggccttct attactgtgc aaaagataaa 300

agtggctacg gccacttcta ctactacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1090
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1090

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asp Ser Leu Tyr
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Ala Ala Asp Thr Ala Phe Tyr Tyr Cys

-continued

```
               85                  90                  95

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Ala Met Asp
            100                 105                 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> SEQ ID NO 1091
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1091

ggattcaaat ttgatgatta tacc                                          24


<210> SEQ ID NO 1092
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1092

Gly Phe Lys Phe Asp Asp Tyr Thr
1               5


<210> SEQ ID NO 1093
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1093

attagttgga atagtggtag taaa                                          24


<210> SEQ ID NO 1094
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1094

Ile Ser Trp Asn Ser Gly Ser Lys
1               5


<210> SEQ ID NO 1095
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1095

gcaaaagata aaagtggcta cggccacttc tactactacg ctatggacgt c             51


<210> SEQ ID NO 1096
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1096

Ala Lys Asp Lys Ser Gly Tyr Gly His Phe Tyr Tyr Tyr Ala Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1097
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1097

gaggtgcagc tggtggagtc tgggggaggc ttggtacacc ctggcaggtc cctaagactc 60

tcctgtacag cctctggatt caagtttgct gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag taaaggctat 180

gcggactctg taaagggccg attcaccatc tccagagaca atgacaagaa ctccctgtat 240

ctgcaaatga acagtctgag aggtgaggac acggccttgt attactgtgc aaaagatgga 300

agtggctacg ggaggttcca cttctacgct atcgacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1098
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1098

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Lys Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Asp Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Phe Tyr Ala Ile Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1099
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1099

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ggattcaagt ttgctgatta tacc 24

<210> SEQ ID NO 1100
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1100

Gly Phe Lys Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1101
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1101

attagttgga atagtggtag taaa 24

<210> SEQ ID NO 1102
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1102

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1103
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1103

gcaaaagatg gaagtggcta cgggaggttc cacttctacg ctatcgacgt c 51

<210> SEQ ID NO 1104
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1104

Ala Lys Asp Gly Ser Gly Tyr Gly Arg Phe His Phe Tyr Ala Ile Asp
1 5 10 15

Val

<210> SEQ ID NO 1105
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 1105

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgtag cctctggatt cacctttgat gattattcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag caaagactat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaagac acggccttgt attactgtgc aaaatatgga 300

agtggctacg ggaagttcta ccactacggt ttggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1106
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1106

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Asp Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1107
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1107

ggattcacct ttgatgatta ttcc 24

<210> SEQ ID NO 1108
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1108

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

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<210> SEQ ID NO 1109
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1109

attagttgga atagtggtag caaa 24

<210> SEQ ID NO 1110
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1110

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1111
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1111

gcaaaatatg gaagtggcta cgggaagttc taccactacg gtttggacgt c 51

<210> SEQ ID NO 1112
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1112

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 1113
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1113

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tcctgtgcag cctctggatt cacctttgct gattatacca tgcactgggt ccggcaggct 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag catgggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa atccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatgga 300

agtggctacg ggaaatactt cttctacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

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<210> SEQ ID NO 1114
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1114

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Met Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Tyr Phe Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1115
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1115

ggattcacct ttgctgatta tacc 24

<210> SEQ ID NO 1116
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1116

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1117
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1117

attagttgga atagtggtag catg 24

<210> SEQ ID NO 1118
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1118

Ile Ser Trp Asn Ser Gly Ser Met
1 5

<210> SEQ ID NO 1119
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1119

gcaaaagatg gaagtggcta cgggaaatac ttcttctacg ctatggacgt c 51

<210> SEQ ID NO 1120
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1120

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Tyr Phe Phe Tyr Ala Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1121
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1121

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tcctgtgcag cctctggatt caccttttct gattatacta tgcattgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagat attagttgga atagtggtag taaaggctat 180

acggactctg tgaagggccg attcaccatt tccagagaca acgccaagaa gtccctgtat 240

ctacaaatga acagtctgag agctgaggac acggccttgt actactgtgt aaaagatgga 300

agtggctacg ggaaatacca cttctacgct atggacgtct ggggccaagg gaccctggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1122
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1122

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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Ser Asp Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly Lys Tyr His Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1123
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1123

ggattcacct tttctgatta tact 24

<210> SEQ ID NO 1124
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1124

Gly Phe Thr Phe Ser Asp Tyr Thr
1 5

<210> SEQ ID NO 1125
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1125

attagttgga atagtggtag taaa 24

<210> SEQ ID NO 1126
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1126

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1127
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1127

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gtaaaagatg gaagtggcta cgggaaatac cacttctacg ctatggacgt c 51

<210> SEQ ID NO 1128
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1128

Val Lys Asp Gly Ser Gly Tyr Gly Lys Tyr His Phe Tyr Ala Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1129
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1129

gaggtgcagc tggtggagtc ggggggaggc ttggttcacc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggaatg ggtctcagat attagttgga atagtggtag cagaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagata atgccgagaa ctccctgtac 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataaa 300

agtggctacg gccactacta ctactacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1130
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1130

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val His Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Ser Arg Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Glu Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Tyr Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<210> SEQ ID NO 1131
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1131

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 1132
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1132

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 1133
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1133

attagttgga atagtggtag caga 24

<210> SEQ ID NO 1134
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1134

Ile Ser Trp Asn Ser Gly Ser Arg
1 5

<210> SEQ ID NO 1135
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1135

gcaaaagata aaagtggcta cggccactac tactactacg ctatggacgt c 51

<210> SEQ ID NO 1136
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1136

Ala Lys Asp Lys Ser Gly Tyr Gly His Tyr Tyr Tyr Tyr Ala Met Asp
1 5 10 15

Val

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<210> SEQ ID NO 1137
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1137

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcgggtc cctgagactc 60

tcctgtgaag cctctggatt cacctttgct gattatacct tgcactgggt ccggcaagct 120

ccagggaagg gcctggaatg ggtctcagat attagttgga atagtggcac cagaggctat 180

gcggactctg tgaggggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag atctgaggac acggccttgt attactgtgt gaaagatgga 300

agtggctacg ggagatataa tttctacgct atggacgtct ggggccaagg gaccacggtc 360

accgtctcct ca 372

<210> SEQ ID NO 1138
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1138

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Asn Ser Gly Thr Arg Gly Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Gly Ser Gly Tyr Gly Arg Tyr Asn Phe Tyr Ala Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1139
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1139

ggattcacct ttgctgatta tacc 24

<210> SEQ ID NO 1140
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1140

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1141
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1141

attagttgga atagtggcac caga 24

<210> SEQ ID NO 1142
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1142

Ile Ser Trp Asn Ser Gly Thr Arg
1 5

<210> SEQ ID NO 1143
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1143

gtgaaagatg gaagtggcta cgggagatat aatttctacg ctatggacgt c 51

<210> SEQ ID NO 1144
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1144

Val Lys Asp Gly Ser Gly Tyr Gly Arg Tyr Asn Phe Tyr Ala Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1145
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1145

gaggtgcagc tggtggagtc tgggggaggc ttggttcagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt tacctttgct gactatacca tgcactgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaatac tataggctat 180

gcggactctg tgaagggccg attcgccatc tccagagaca acgccaagaa ctccctgtat 240

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cttcaaatga acagtctgcg acctgaggac acggccttat attactgtgt aaaggataaa 300

agtggctacg ggaaattcca atacggtttg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 1146
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1146

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Asn Ser Asn Thr Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1147
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1147

ggatttacct ttgctgacta tacc 24

<210> SEQ ID NO 1148
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1148

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1149
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1149

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attggttgga atagtaatac tata 24

<210> SEQ ID NO 1150
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1150

Ile Gly Trp Asn Ser Asn Thr Ile
1 5

<210> SEQ ID NO 1151
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1151

gtaaaggata aaagtggcta cgggaaattc caatacggtt tggacgtc 48

<210> SEQ ID NO 1152
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1152

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 1153
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1153

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt tacatttgac gattatacca tgcactgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaacag tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctccaaatga acagtctgag acctgaggac acggccttgt atttctgtgt aaaggataaa 300

agtggctacg ggaaattttt catcggtttg gacgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> SEQ ID NO 1154
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1154

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Asn Ser Asn Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Phe Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1155
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1155

ggatttacat ttgacgatta tacc 24

<210> SEQ ID NO 1156
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1156

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 1157
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1157

attggttgga atagtaacag tata 24

<210> SEQ ID NO 1158
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1158

Ile Gly Trp Asn Ser Asn Ser Ile
1 5

<210> SEQ ID NO 1159
<211> LENGTH: 48
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1159

gtaaaggata aaagtggcta cgggaaattt ttcatcggtt tggacgtc 48

<210> SEQ ID NO 1160
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1160

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 1161
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1161

caggtgcagt tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt tacatttgac gattatacca tgcactgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaatac taaaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ttccctgtat 240

ctccaaatga acagtctgag acctgaggac acggccttgt atttctgtgt gaaggataaa 300

agtggctacg ggaaattttt catcggtttg gacgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> SEQ ID NO 1162
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1162

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Asn Ser Asn Thr Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Phe Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
100 105 110

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Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1163
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1163

ggatttacat ttgacgatta tacc 24

<210> SEQ ID NO 1164
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1164

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 1165
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1165

attggttgga atagtaatac taaa 24

<210> SEQ ID NO 1166
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1166

Ile Gly Trp Asn Ser Asn Thr Lys
1 5

<210> SEQ ID NO 1167
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1167

gtgaaggata aaagtggcta cgggaaattt ttcatcggtt tggacgtc 48

<210> SEQ ID NO 1168
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1168

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val

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1 5 10 15

<210> SEQ ID NO 1169
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1169

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tcctgtgcag cctccggatt cacctttgct gattatacca tgcactgggt ccggcaaggt 120

ccagggacgg gcctggagtg ggtctcagat attggttgga gtggtggtag tttaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ttggaaatga acaatctgcg acctgaagac acggccttgt attattgtgt aaaggataaa 300

agtggctacg ggaaattcca gtacggtttg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 1170
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1170

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Thr Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Ser Gly Gly Ser Leu Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Glu Met Asn Asn Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1171
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1171

ggattcacct ttgctgatta tacc 24

<210> SEQ ID NO 1172
<211> LENGTH: 8
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1172

Gly Phe Thr Phe Ala Asp Tyr Thr
1 5

<210> SEQ ID NO 1173
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1173

attggttgga gtggtggtag ttta 24

<210> SEQ ID NO 1174
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1174

Ile Gly Trp Ser Gly Gly Ser Leu
1 5

<210> SEQ ID NO 1175
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1175

gtaaaggata aaagtggcta cgggaaattc cagtacggtt tggacgtc 48

<210> SEQ ID NO 1176
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1176

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 1177
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1177

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tcctgtgcag cctctgggtt taaatttgat ggttatacca tgcactgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaacac tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

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ctccaaatga acagtctgag accagaggac acggccttgt atttctgtgt aaaggataaa 300

agtggctacg ggaaatttttt catcggtttg gacgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> SEQ ID NO 1178
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1178

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Asp Gly Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Asn Ser Asn Thr Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Phe Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1179
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1179

gggtttaaat ttgatggtta tacc 24

<210> SEQ ID NO 1180
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1180

Gly Phe Lys Phe Asp Gly Tyr Thr
1 5

<210> SEQ ID NO 1181
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1181

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attggttgga atagtaacac tata 24

<210> SEQ ID NO 1182
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1182

Ile Gly Trp Asn Ser Asn Thr Ile
1 5

<210> SEQ ID NO 1183
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1183

gtaaaggata aaagtggcta cgggaaattt ttcatcggtt tggacgtc 48

<210> SEQ ID NO 1184
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1184

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Phe Ile Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 1185
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1185

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tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagat attggttgga atagtaatac tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctccctgtat 240

ctgcaaatga acagtctgcg acctgaagac acggccttat attactgtgt aaaggataaa 300

agtggctacg ggaaattcca atacggtttg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 1186
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1186

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Gly Trp Asn Ser Asn Thr Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1187
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1187

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 1188
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1188

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 1189
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1189

attggttgga atagtaatac tata 24

<210> SEQ ID NO 1190
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1190

Ile Gly Trp Asn Ser Asn Thr Ile
1 5

<210> SEQ ID NO 1191
<211> LENGTH: 48
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1191

gtaaaggata aaagtggcta cgggaaattc caatacggtt tggacgtc 48

<210> SEQ ID NO 1192
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1192

Val Lys Asp Lys Ser Gly Tyr Gly Lys Phe Gln Tyr Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 1193
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1193

caggtgcaac tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt caagtttgat gattatacca tgcactgggt ccggcaaggt 120

ccagggaagg gcctggagtg ggtctcagac attagttgga gtggtggtag catagactat 180

acggactctg tgaagggccg attctccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agttgaagac acggccttgt attattgtgt aaaagataaa 300

agtggctacg ggaagtactc ttacggtttg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 1194
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1194

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asp Ile Ser Trp Ser Gly Gly Ser Ile Asp Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Asp Lys Ser Gly Tyr Gly Lys Tyr Ser Tyr Gly Leu Asp Val
100 105 110

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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1195
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1195

ggattcaagt ttgatgatta tacc 24

<210> SEQ ID NO 1196
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1196

Gly Phe Lys Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 1197
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1197

attagttgga gtggtggtag cata 24

<210> SEQ ID NO 1198
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1198

Ile Ser Trp Ser Gly Gly Ser Ile
1 5

<210> SEQ ID NO 1199
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1199

gtaaaagata aaagtggcta cgggaagtac tcttacggtt tggacgtc 48

<210> SEQ ID NO 1200
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1200

Val Lys Asp Lys Ser Gly Tyr Gly Lys Tyr Ser Tyr Gly Leu Asp Val

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1 5 10 15

<210> SEQ ID NO 1201
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1201

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tcctgtgcag cctctggatt ctctttcatt aacgcctgga tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttggccgt attaaaagca taagtgatgg tgggacaaca 180

gactacgctg catccgtgaa aggcagattc accatctcaa gagaagattc aaaaaatatg 240

ctgtttctgg aaatgaatag tctgaaaacc gaggacacag ccgtgtttta ctgtaccaca 300

gaggtcgcta gaactccgaa ctactggggc cggggaaccc tggtcaccgt ctcctca 357

<210> SEQ ID NO 1202
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1202

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Ile Ser Cys Ala Ala Ser Gly Phe Ser Phe Ile Asn Ala
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Arg Ile Lys Ser Ile Ser Asp Gly Gly Thr Thr Asp Tyr Ala Ala
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asp Ser Lys Asn Met
65 70 75 80

Leu Phe Leu Glu Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Phe
85 90 95

Tyr Cys Thr Thr Glu Val Ala Arg Thr Pro Asn Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 1203
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1203

ggattctctt tcattaacgc ctgg 24

<210> SEQ ID NO 1204
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1204

Gly Phe Ser Phe Ile Asn Ala Trp
1 5

<210> SEQ ID NO 1205
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1205

attaaaagca taagtgatgg tgggacaaca 30

<210> SEQ ID NO 1206
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1206

Ile Lys Ser Ile Ser Asp Gly Gly Thr Thr
1 5 10

<210> SEQ ID NO 1207
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1207

accacagagg tcgctagaac tccgaactac 30

<210> SEQ ID NO 1208
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1208

Thr Thr Glu Val Ala Arg Thr Pro Asn Tyr
1 5 10

<210> SEQ ID NO 1209
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1209

gaagtacagc ttgtagaatc cggcggagga ctggtacaac ctggaagaag tcttagactg 60

agttgcgcag ctagtgggtt tacattcgac gattacagca tgcattgggt gaggcaagct 120

cctggtaaag gattggaatg ggttagcggg atatcatgga actcaggaag caagggatac 180

gccgacagcg tgaaaggccg atttacaata tctagggaca acgcaaaaaa ctctctctac 240

cttcaaatga actctcttag ggcagaagac acagcattgt attattgcgc aaaatacggc 300

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agtggttatg gcaagtttta tcattatgga ctggacgtgt ggggacaagg gacaacagtg 360

acagtgagta gc 372

<210> SEQ ID NO 1210
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1210

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Lys Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1211
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1211

gggtttacat tcgacgatta cagc 24

<210> SEQ ID NO 1212
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1212

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> SEQ ID NO 1213
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1213

atatcatgga actcaggaag caag 24

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<210> SEQ ID NO 1214
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1214

Ile Ser Trp Asn Ser Gly Ser Lys
1 5

<210> SEQ ID NO 1215
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1215

gcaaaatacg gcagtggtta tggcaagttt tatcattatg gactggacgt g 51

<210> SEQ ID NO 1216
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1216

Ala Lys Tyr Gly Ser Gly Tyr Gly Lys Phe Tyr His Tyr Gly Leu Asp
1 5 10 15

Val

<210> SEQ ID NO 1217
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1217

gaagtacaac tggtcgaatc tggaggaggt cttgttcaac ctggtcgatc acttcgcctt 60

tcttgtgccg cttctggttt cactttcgac gattatagca tgcattgggt acgacaggct 120

cccggaaaag ggctggaatg ggtgtcagga attagttgga actcaggaag tattggatac 180

gctgattcag tcaaaggacg cttcacaatc tcaagggaca acgctaaaaa ctcactttat 240

ttgcaaatga actctctccg cgctgaagat accgctctct attattgcgc caaagatggg 300

tctggttacg gttatttttta ctactatgga atggacgttt ggggccaagg aacaactgtc 360

acagtatcat cc 372

<210> SEQ ID NO 1218
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1218

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met Asp
100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1219
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1219

ggtttcactt tcgacgatta tagc 24

<210> SEQ ID NO 1220
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1220

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> SEQ ID NO 1221
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1221

attagttgga actcaggaag tatt 24

<210> SEQ ID NO 1222
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1222

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 1223
<211> LENGTH: 51
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1223

gccaaagatg ggtctggtta cggttatttt tactactatg gaatggacgt t 51

<210> SEQ ID NO 1224
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1224

Ala Lys Asp Gly Ser Gly Tyr Gly Tyr Phe Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1225
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1225

gaagtgcaac tcgttgaaag cggaggagga ctggtccagc ccggcagatc tctcagattg 60

tcttgcgctg catccggatt tacatttgac gactattcaa tgcactgggt acggcaagcc 120

ccaggtaaag gactcgaatg ggtaagcggc atatcttgga actcaggcag tattggctac 180

gcagattcag taaaaggaag attcactatt tcaagggata atgctaagaa cagtctctac 240

ttgcaaatga atagcttgcg cgcagaagat acagcacttt attattgtgc aaaagatgga 300

agcggttatg ggaaatttta ttattatggt atggatgtat ggggtcaagg tacaacagtt 360

actgtgtcaa gt 372

<210> SEQ ID NO 1226
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1226

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp

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100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1227
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1227

ggatttacat ttgacgacta ttca 24

<210> SEQ ID NO 1228
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1228

Gly Phe Thr Phe Asp Asp Tyr Ser
1 5

<210> SEQ ID NO 1229
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1229

atatcttgga actcaggcag tatt 24

<210> SEQ ID NO 1230
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1230

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 1231
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1231

gcaaaagatg gaagcggtta tgggaaattt tattattatg gtatggatgt a 51

<210> SEQ ID NO 1232
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1232

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Ala Lys Asp Gly Ser Gly Tyr Gly Lys Phe Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> SEQ ID NO 1233
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1233

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> SEQ ID NO 1234
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1234

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> SEQ ID NO 1235
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1235

cagagcatta gcagctat 18

<210> SEQ ID NO 1236
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1236

Gln Ser Ile Ser Ser Tyr
1 5

<210> SEQ ID NO 1237
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1237

gctgcatcc 9

<210> SEQ ID NO 1238
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1238

Ala Ala Ser
1

<210> SEQ ID NO 1239
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1239

caacagagtt acagtacccc tccgatcacc 30

<210> SEQ ID NO 1240
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1240

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10

<210> SEQ ID NO 1241
<211> LENGTH: 382
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1241

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tcctgtgtag cctctggatt cacctttaat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggaatg ggtctcagtt attagttgga atagtgatag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

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ctgcaaatgc acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300

cactatggtt cggggagtta ttactactac caatacggta tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc ag 382

<210> SEQ ID NO 1242
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1242

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asn Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Ser Trp Asn Ser Asp Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met His Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn His Tyr Gly Ser Gly Ser Tyr Tyr Tyr Tyr Gln Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 1243
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1243

ggattcacct ttaatgatta tgcc 24

<210> SEQ ID NO 1244
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1244

Gly Phe Thr Phe Asn Asp Tyr Ala
1 5

<210> SEQ ID NO 1245
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1245

attagttgga atagtgatag cata 24

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<210> SEQ ID NO 1246
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1246

Ile Ser Trp Asn Ser Asp Ser Ile
1 5

<210> SEQ ID NO 1247
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1247

gcaaaagata atcactatgg ttcggggagt tattactact accaatacgg tatggacgtc 60

<210> SEQ ID NO 1248
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1248

Ala Lys Asp Asn His Tyr Gly Ser Gly Ser Tyr Tyr Tyr Tyr Gln Tyr
1 5 10 15

Gly Met Asp Val
20

<210> SEQ ID NO 1249
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1249

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300

agtggctacg gtcactacta ctacggaatg gacgtctggg gccaagggac cacggtcacc 360

gtcgcctca 369

<210> SEQ ID NO 1250
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1250

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
115 120

<210> SEQ ID NO 1251
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1251

ggattcacct ttgatgatta tacc 24

<210> SEQ ID NO 1252
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1252

Gly Phe Thr Phe Asp Asp Tyr Thr
1 5

<210> SEQ ID NO 1253
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1253

attagttgga atagtggtag tata 24

<210> SEQ ID NO 1254
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1254

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 1255

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<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1255

gcaaaagata atagtggcta cggtcactac tactacggaa tggacgtc 48

<210> SEQ ID NO 1256
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1256

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 1257
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1257

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcac tatattaact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa 320

<210> SEQ ID NO 1258
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1258

Ala Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro
1 5 10 15

Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
20 25 30

Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro
85 90 95

Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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<210> SEQ ID NO 1259
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1259

cagagtgtta gcagcaac 18

<210> SEQ ID NO 1260
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1260

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 1261
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1261

ggtgcatcc 9

<210> SEQ ID NO 1262
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1262

Gly Ala Ser
1

<210> SEQ ID NO 1263
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1263

cagcactata ttaactggcc tctcact 27

<210> SEQ ID NO 1264
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1264

Gln His Tyr Ile Asn Trp Pro Leu Thr
1 5

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<210> SEQ ID NO 1265
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1265

gaagtgcaac tggtggagtc tgggggaggc ttagtacagc ctggcgggtc cctgagactc 60

tcctgtgcag ccactggatt cacctttgat gattttacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt atcagttgga atagtggtag cataggctat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt actactgtgc aaaagataat 300

agtggctacg gctattatta ctacggtatg gacgtctggg gccaagggac cacggtcacc 360

gtctcctca 369

<210> SEQ ID NO 1266
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1266

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Asp Asp Phe
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1267
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1267

ggattcacct ttgatgattt tacc 24

<210> SEQ ID NO 1268
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 1268

Gly Phe Thr Phe Asp Asp Phe Thr
1 5

<210> SEQ ID NO 1269
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1269

atcagttgga atagtggtag cata 24

<210> SEQ ID NO 1270
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1270

Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> SEQ ID NO 1271
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1271

gcaaaagata atagtggcta cggctattat tactacggta tggacgtc 48

<210> SEQ ID NO 1272
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1272

Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 1273
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1273

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca cagtgttagc aggaactcag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagtct 240

gaagattttg caatttatta ctgtcagcag tataataatt ggcctctcac tttcggcgga 300

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gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 1274
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1274

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser His Ser Val Ser Arg Asn
20 25 30

Ser Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 1275
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1275

cacagtgtta gcaggaac 18

<210> SEQ ID NO 1276
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1276

His Ser Val Ser Arg Asn
1 5

<210> SEQ ID NO 1277
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1277

ggtgcatcc 9

<210> SEQ ID NO 1278
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1278

Gly Ala Ser
1

<210> SEQ ID NO 1279
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1279

cagcagtata ataattggcc tctcact 27

<210> SEQ ID NO 1280
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1280

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 1281
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1281

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag tataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagataat 300

agtggctacg gtcactacta ctacggaatg gacgtctggg gccaagggac cacggtcacc 360

gtcgcctca 369

<210> SEQ ID NO 1282
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1282

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val

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    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
        115                 120


<210> SEQ ID NO 1283
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1283

ggattcacct ttgatgatta tacc                                          24


<210> SEQ ID NO 1284
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1284

Gly Phe Thr Phe Asp Asp Tyr Thr
1               5


<210> SEQ ID NO 1285
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1285

attagttgga atagtggtag tata                                          24


<210> SEQ ID NO 1286
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1286

Ile Ser Trp Asn Ser Gly Ser Ile
1               5


<210> SEQ ID NO 1287
<211> LENGTH: 48
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1287

gcaaaagata atagtggcta cggtcactac tactacggaa tggacgtc                48
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<210> SEQ ID NO 1288
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1288

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> SEQ ID NO 1289
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1289

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcac tatattaact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 1290
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1290

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 1291
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1291

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cagagtgtta gcagcaac 18

<210> SEQ ID NO 1292
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1292

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 1293
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1293

ggtgcatcc 9

<210> SEQ ID NO 1294
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1294

Gly Ala Ser
1

<210> SEQ ID NO 1295
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1295

cagcactata ttaactggcc tctcact 27

<210> SEQ ID NO 1296
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1296

Gln His Tyr Ile Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 1297
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1297

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tcctgtgctg cgtctggatt taccttcaga agttatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatg gtatactatg atggaaataa tcaatactat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgatgac acggctgtgt atttctgtgc gcgagggcct 300

gggtacaact ggctcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> SEQ ID NO 1298
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1298

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Met Val Tyr Tyr Asp Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 1299
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1299

ggatttacct tcagaagtta tgcc 24

<210> SEQ ID NO 1300
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1300

Gly Phe Thr Phe Arg Ser Tyr Ala
1 5

<210> SEQ ID NO 1301
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1301

gtatactatg atggaaataa tcaa 24

<210> SEQ ID NO 1302
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1302

Val Tyr Tyr Asp Gly Asn Asn Gln
1 5

<210> SEQ ID NO 1303
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1303

gcgcgagggc ctgggtacaa ctggctcgac ccc 33

<210> SEQ ID NO 1304
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1304

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> SEQ ID NO 1305
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1305

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc aggaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccggcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tataataact ggcctctcac tttcggcgga 300

gggaccaagg tggtgatcaa a 321

<210> SEQ ID NO 1306
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1306

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Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Val Ile Lys
100 105

<210> SEQ ID NO 1307
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1307

cagagtgtta gcaggaac 18

<210> SEQ ID NO 1308
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1308

Gln Ser Val Ser Arg Asn
1 5

<210> SEQ ID NO 1309
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1309

ggtgcatcc 9

<210> SEQ ID NO 1310
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1310

Gly Ala Ser
1

<210> SEQ ID NO 1311
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1311

cagcagtata ataactggcc tctcact 27

<210> SEQ ID NO 1312
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1312

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 1313
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1313

caggtgcagt tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

gcctgtgttg cgtctggatt caccttcaga agttatggca tgcactgggt ccgccaggct 120

ccaggcaagg gactgcagtg ggtggcaatg atttactatg atggtaagaa taaatattat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacactgtat 240

ctgcaaatga acaatctgag agtcgaggac acggctatgt atttctgtgc gcgagggcct 300

gggtacaatt ggctcgaccc ctggggccag ggaaccctgg tcactgtttc ctca 354

<210> SEQ ID NO 1314
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1314

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gln Trp Val
35 40 45

Ala Met Ile Tyr Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Arg Val Glu Asp Thr Ala Met Tyr Phe Cys
85 90 95

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<210> SEQ ID NO 1315
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1315

ggattcacct tcagaagtta tggc 24

<210> SEQ ID NO 1316
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1316

Gly Phe Thr Phe Arg Ser Tyr Gly
1 5

<210> SEQ ID NO 1317
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1317

atttactatg atggtaagaa taaa 24

<210> SEQ ID NO 1318
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1318

Ile Tyr Tyr Asp Gly Lys Asn Lys
1 5

<210> SEQ ID NO 1319
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1319

gcgcgagggc ctgggtacaa ttggctcgac ccc 33

<210> SEQ ID NO 1320
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1320

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

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<210> SEQ ID NO 1321
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1321

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagaattagc agcaacttgg cctggtacca gcaaaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaggatgttg cagtttatta ctgtcagcaa catcataact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> SEQ ID NO 1322
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1322

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ser Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His His Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 1323
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1323

cagagaatta gcagcaac 18

<210> SEQ ID NO 1324
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1324

Gln Arg Ile Ser Ser Asn
1 5

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<210> SEQ ID NO 1325
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1325

ggtgcatcc 9

<210> SEQ ID NO 1326
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1326

Gly Ala Ser
1

<210> SEQ ID NO 1327
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1327

cagcaacatc ataactggcc tctcact 27

<210> SEQ ID NO 1328
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1328

Gln Gln His His Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 1329
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1329

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Thr Thr Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Val Thr Val Ser Ser
        115


<210> SEQ ID NO 1330
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1330

Gly Tyr Thr Phe Thr Arg Tyr Thr
1               5


<210> SEQ ID NO 1331
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1331

Ile Asn Pro Ser Arg Gly Tyr Thr
1               5


<210> SEQ ID NO 1332
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1332

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr
1               5                   10


<210> SEQ ID NO 1333
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1333

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr Met
            20                  25                  30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
        35                  40                  45

Asp Thr Ser Lys Val Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
    50                  55                  60

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Asn Ser Leu Glu Ala Glu
65                  70                  75                  80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
                85                  90                  95
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Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 1334
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1334

Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Tyr
1 5 10

<210> SEQ ID NO 1335
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1335

Asp Thr Ser
1

<210> SEQ ID NO 1336
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1336

Gln Gln Trp Ser Ser Asn Pro Leu Thr
1 5

<210> SEQ ID NO 1337
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1337

gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttttat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagctgga atagtgatac ataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttat attactgtac aaaagatggc 300

agctatggtc acttctactc cggtttggac gtctggggcc aagggaccac ggtcaccgtc 360

tcctcag 367

<210> SEQ ID NO 1338
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1338

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Asp Thr Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Thr Lys Asp Gly Ser Tyr Gly His Phe Tyr Ser Gly Leu Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 1339
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1339

ggattcacct tttatgatta tgcc 24

<210> SEQ ID NO 1340
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1340

Gly Phe Thr Phe Tyr Asp Tyr Ala
1 5

<210> SEQ ID NO 1341
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1341

attagctgga atagtgatac cata 24

<210> SEQ ID NO 1342
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1342

Ile Ser Trp Asn Ser Asp Thr Ile
1 5

<210> SEQ ID NO 1343

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<211> LENGTH: 45
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1343

acaaaagatg gcagctatgg tcacttctac tccggtttgg acgtc 45

<210> SEQ ID NO 1344
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1344

Thr Lys Asp Gly Ser Tyr Gly His Phe Tyr Ser Gly Leu Asp Val
1 5 10 15

<210> SEQ ID NO 1345
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1345

gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc cccgactcct catctatggt acatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcaacaa tataataact ggccgctcac tttcggcgga 300

gggaccaagg tggagatcaa ac 322

<210> SEQ ID NO 1346
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1346

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Thr Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

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<210> SEQ ID NO 1347
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1347

cagagtgtta gcagcaac 18

<210> SEQ ID NO 1348
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1348

Gln Ser Val Ser Ser Asn
1 5

<210> SEQ ID NO 1349
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1349

ggtacatcc 9

<210> SEQ ID NO 1350
<211> LENGTH: 3
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1350

Gly Thr Ser
1

<210> SEQ ID NO 1351
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1351

caacaatata ataactggcc gctcact 27

<210> SEQ ID NO 1352
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1352

Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

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<210> SEQ ID NO 1353
<211> LENGTH: 379
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1353

gaagagcaac tggtggagtc tgggggagac ttggtacagc ctggcaggtc cctgaggctc 60

tcctgtgcag cctctggatt cacctttcat gattacacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggaag tctaggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggccttat attactgtgc aaaagatccc 300

tcttatggtt cggggtcgta tcactcctac tacggaatgg acgtctgggg ccaagggacc 360

acggtcactg tctcctcag 379

<210> SEQ ID NO 1354
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1354

Glu Glu Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Leu Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Ser Tyr Gly Ser Gly Ser Tyr His Ser Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 1355
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1355

ggattcacct ttcatgatta cacc 24

<210> SEQ ID NO 1356
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

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<400> SEQUENCE: 1356

Gly Phe Thr Phe His Asp Tyr Thr
1 5

<210> SEQ ID NO 1357
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1357

attagttgga atagtggaag tcta 24

<210> SEQ ID NO 1358
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1358

Ile Ser Trp Asn Ser Gly Ser Leu
1 5

<210> SEQ ID NO 1359
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1359

gcaaaagatc cctcttatgg ttcggggtcg tatcactcct actacggaat ggacgtc 57

<210> SEQ ID NO 1360
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1360

Ala Lys Asp Pro Ser Tyr Gly Ser Gly Ser Tyr His Ser Tyr Tyr Gly
1 5 10 15

Met Asp Val

<210> SEQ ID NO 1361
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1361

gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgct gggccagtca gagtattagc aggtacttag tctggtacca acagaaatgt 120

ggccaggcac ccagactcct catctatgaa gcatctaaga gggccaccgg catcccagtc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagtct 240

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gaagattttg cagtttatta ttgtcagcag cgtttcaatt ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa ac 322

<210> SEQ ID NO 1362
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1362

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Trp Ala Ser Gln Ser Ile Ser Arg Tyr
20 25 30

Leu Val Trp Tyr Gln Gln Lys Cys Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Glu Ala Ser Lys Arg Ala Thr Gly Ile Pro Val Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Phe Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 1363
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1363

cagagtatta gcaggtac 18

<210> SEQ ID NO 1364
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1364

Gln Ser Ile Ser Arg Tyr
1 5

<210> SEQ ID NO 1365
<211> LENGTH: 9
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1365

gaagcatct 9

<210> SEQ ID NO 1366
<211> LENGTH: 3
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1366

Glu Ala Ser
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<210> SEQ ID NO 1367
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1367

cagcagcgtt tcaattggcc tctcact 27

<210> SEQ ID NO 1368
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic

<400> SEQUENCE: 1368

Gln Gln Arg Phe Asn Trp Pro Leu Thr
1 5

<210> SEQ ID NO 1369
<211> LENGTH: 297
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hCD20

<400> SEQUENCE: 1369

Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145 150 155 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175

-continued

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Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
        195                 200                 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
    210                 215                 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                 230                 235                 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
                245                 250                 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
            260                 265                 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
        275                 280                 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
    290                 295


<210> SEQ ID NO 1370
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hCD3 epsilon

<400> SEQUENCE: 1370

Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys Val
1               5                   10                  15

Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro Gly
            20                  25                  30

Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly Gly Asp Glu
        35                  40                  45

Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp His Leu Ser Leu Lys Glu
    50                  55                  60

Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr Val Cys Tyr Pro Arg Gly
65                  70                  75                  80

Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu Tyr Leu Arg Ala Arg Val
                85                  90                  95

Ser Glu Asn Ser Met Glu Met Asp
            100


<210> SEQ ID NO 1371
<211> LENGTH: 79
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys
1               5                   10                  15

Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val Gly Thr Leu Leu Ser
            20                  25                  30

Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly
        35                  40                  45

Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr
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    50                  55                  60

Val Gln Val His Tyr Arg Met Ser Gln Ser Ser Val Glu Leu Asp
65                  70                  75


<210> SEQ ID NO 1372
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: hFc-delta-Adp

<400> SEQUENCE: 1372

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225


<210> SEQ ID NO 1373
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 1373

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1               5                   10                  15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            20                  25                  30
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-continued

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Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        35                  40                  45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    50                  55                  60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
65                  70                  75                  80

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                85                  90                  95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            100                 105                 110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        115                 120                 125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
    130                 135                 140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
145                 150                 155                 160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                165                 170                 175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            180                 185                 190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        195                 200                 205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    210                 215                 220

Pro Gly Lys
225


<210> SEQ ID NO 1374
<211> LENGTH: 233
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: mFc-delta-Adp

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Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
1               5                   10                  15

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
            20                  25                  30

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
        35                  40                  45

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
    50                  55                  60

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
65                  70                  75                  80

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
                85                  90                  95

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
            100                 105                 110

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
        115                 120                 125

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
    130                 135                 140
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Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145                 150                 155                 160

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
                165                 170                 175

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
            180                 185                 190

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
        195                 200                 205

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn Arg Phe Thr Thr
    210                 215                 220

Lys Ser Phe Ser Arg Thr Pro Gly Lys
225                 230


<210> SEQ ID NO 1375
<211> LENGTH: 233
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: mFc

<400> SEQUENCE: 1375

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
1               5                   10                  15

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
            20                  25                  30

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
        35                  40                  45

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
    50                  55                  60

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
65                  70                  75                  80

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
                85                  90                  95

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
            100                 105                 110

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
        115                 120                 125

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
    130                 135                 140

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
145                 150                 155                 160

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
                165                 170                 175

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
            180                 185                 190

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
        195                 200                 205

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
    210                 215                 220

Lys Ser Phe Ser Arg Thr Pro Gly Lys
225                 230
```

What is claimed is:

1. An isolated antibody or antigen-binding fragment thereof that binds human CD3 and induces human T cell proliferation in vitro with an EC_{50} of less than about 0.33 pM.

2. An isolated antibody or antigen-binding fragment thereof that binds human CD3 and induces T cell-mediated killing of tumor cells in vitro with an EC_{50} of less than about 2.3 pM.

3. The isolated antibody or antigen-binding fragment of claim **2**, wherein the antibody or antigen-binding fragment thereof induces T cell-mediated killing of tumor cells in vitro with an EC_{50} of less than about 1 pM.

4. An isolated antibody or antigen-binding fragment thereof that binds human CD3 with a binding dissociation equilibrium constant (K_D) of less than about 1 nM as measured in a surface plasmon resonance assay at 25° C.

5. The isolated antibody or antigen-binding fragment of claim **4**, wherein the antibody or antigen-binding fragment thereof binds human CD3 with a K_D of less than about 500 pM as measured in a surface plasmon resonance assay at 25° C.

6. The isolated antibody or antigen-binding fragment of claim **5**, wherein the antibody or antigen-binding fragment thereof binds human CD3 with a K_D of less than about 100 pM as measured in a surface plasmon resonance assay at 25° C.

7. An isolated antibody or antigen-binding fragment thereof that binds human CD3 with a dissociative half-life (t½) of greater than about 10 minutes as measured in a surface plasmon resonance assay at 25° C.

8. The isolated antibody or antigen-binding fragment of claim **7**, wherein the antibody or antigen-binding fragment thereof binds human CD3 with a t½ of greater than about 100 minutes as measured in a surface plasmon resonance assay at 25° C.

9. The antibody or antigen-binding fragment of any one of claims **1** to **8**, wherein the antibody or antigen-binding fragment thereof competes for binding to CD3 with a reference antibody comprising an HCVR/LCVR amino acid sequence pair as set forth in Table 1.

10. The antibody or antigen-binding fragment of claim **9**, wherein the reference antibody comprises an HCVR/LCVR amino acid sequence pair selected from the group consisting of SEQ ID NOs: 2/10; 114/122; 514/522; 770/778; 1050/1234; and 1090/1234.

11. The antibody or antigen-binding fragment of any one of claims **1** to **8**, wherein the antibody or antigen-binding fragment thereof binds to the same epitope on CD3 as a reference antibody comprising an HCVR/LCVR amino acid sequence pair as set forth in Table 1.

12. The antibody or antigen-binding fragment of claim **11**, wherein the antibody or antigen-binding fragment thereof binds to the same epitope on CD3 as a reference antibody comprising an HCVR/LCVR amino acid sequence pair selected from the group consisting of SEQ ID NOs: 2/10; 114/122; 514/522; 770/778; 1050/1234; and 1090/1234.

13. An isolated antibody or antigen-binding fragment thereof that binds human CD3, wherein the antibody or antigen-binding fragment comprises: (a) the complementarity determining regions (CDRs) of a heavy chain variable region (HCVR) having an amino acid sequence as set forth in Table 1; and (b) the CDRs of a light chain variable region (LCVR) having an amino acid sequence as set forth in Table 1.

14. The isolated antibody or antigen-binding fragment of claim **13**, wherein the antibody or antigen-binding fragment comprises the heavy and light chain CDRs of a HCVR/LCVR amino acid sequence pair selected from the group consisting of: SEQ ID NOs: 2/10; 114/122; 514/522; 770/778; 1050/1234; and 1090/1234.

15. The isolated antibody or antigen-binding fragment of claim **14**, wherein the antibody or antigen-binding fragment comprises HCDR1-HCDR2-HCDR3-LCDR1-LCDR2-LCDR3 domains, respectively, selected from the group consisting of: SEQ ID NOs: 4-6-8-12-14-16; 116-118-120-124-126-128; 516-518-520-524-526-528; 772-774-776-780-782-784; 1052-1054-1056-1236-1238-1240; and 1092-1094-1096-1236-1238-1240.

16. An isolated antibody or antigen-binding fragment thereof that binds human CD3, wherein the antibody or antigen-binding fragment comprises: (a) a heavy chain variable region (HCVR) having an amino acid sequence selected from the group consisting of SEQ ID NOs: 2; 114; 514; 770; 1050; and 1090; and (b) a light chain variable region (LCVR) having an amino acid sequence selected from the group consisting of SEQ ID NOs: 10; 122; 522; 778; 1234; and 1234.

17. The isolated antibody or antigen-binding fragment of claim **16**, wherein the antibody or antigen-binding fragment comprises a HCVR/LCVR amino acid sequence pair selected from the group consisting of: SEQ ID NOs: 2/10; 114/122; 514/522; 770/778; 1050/1234; and 1090/1234.

18. A bispecific antibody comprising a first antigen-binding domain that binds human CD3 and a second antigen-binding domain that binds a target antigen, wherein the first antigen-binding domain is derived from the antibody or antigen-binding fragment of any one of claims **1** to **17**.

19. A pharmaceutical composition comprising the antibody or antigen-binding fragment of any one of claims **1** to **17**, or the bispecific antibody of claim **18**, and a pharmaceutically acceptable carrier or diluent.

20. A method for upmodulating an immune response in a subject, the method comprising administering to the subject the pharmaceutical composition of claim **19**.

21. A method for treating a tumor in a subject, the method comprising administering the pharmaceutical composition of claim **19** to a subject in need thereof.

22. A bispecific antigen-binding molecule comprising a first antigen-binding domain that specifically binds human CD3, and a second antigen-binding domain that specifically binds human CD20.

23. The bispecific antigen-binding molecule of claim **22**, wherein the antigen-binding molecule binds human cells expressing human CD3 and cynomolgus monkey cells expressing cynomolgus CD3.

24. The bispecific antigen-binding molecule of claim **22**, wherein the antigen-binding molecule induces proliferation of human and cynomolgus peripheral blood mononuclear cells (PBMCs) in vitro.

25. The bispecific antigen-binding molecule of claim **22**, wherein the antigen-binding molecule induces IFN-gamma release and CD25 up-regulation in human whole blood.

26. The bispecific antigen-binding molecule of claim **22**, wherein the antigen-binding molecule induces T-cell mediated cytotoxicity of human B-cells.

27. The bispecific antigen-binding molecule of claim **26**, wherein the antigen-binding molecule induces T-cell mediated cytotoxicity of human B-cells that are resistant to anti-CD20-mediated cytotoxicity.

28. The bispecific antigen-binding molecule of any one of claims **22** to **27**, wherein a single administration of the bispecific antigen-binding molecule to a subject at a dose of about 0.01 mg/kg causes a reduction in the number of B cells in the subject below detectable levels by about day 1 after administration of the bispecific antigen-binding molecule to the subject.

29. The bispecific antigen-binding molecule of claim **28**, wherein the number of B-cells remains below detectable levels until at least about 14 days after administration of a single dose of about 0.01 mg/kg of the bispecific antigen-binding molecule to the subject.

30. The bispecific antigen-binding molecule of claim **28** or **29**, wherein the number of B-cells per microliter of blood drawn from the subject at about day 1 through about day 28 after administration of a single dose of about 0.01 mg/kg of the antigen-binding molecule to the subject is less than 25% the number of B-cells per microliter of blood drawn from the subject prior to administration of the bispecific antigen-binding molecule.

31. The bispecific antigen-binding molecule of claim **28** or **29**, wherein the number of B-cells per microliter of blood drawn from the subject at about day 1 through about day 56 after administration of a single dose of about 0.01 mg/kg of the antigen-binding molecule to the subject is less than 50% the number of B-cells per microliter of blood drawn from the subject prior to administration of the bispecific antigen-binding molecule.

32. The bispecific antigen-binding molecule of any one of claims **28** to **31**, wherein the number of T cells per microliter of blood drawn from the subject at about day 14 through about day 56 after administration of the antigen-binding molecule to the subject is equal to or greater than the number of T cells per microliter of blood drawn from the subject prior to administration of the bispecific antigen-binding molecule.

33. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the first antigen-binding domain that specifically binds human CD3 comprises the heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) from a heavy chain variable region (HCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:1250, 1266, 1282, 1298, 1314 and 1329, and the light chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) from a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:1258, 1274, 1290, 1306, 1322 and 1333.

34. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the second antigen-binding domain that specifically binds human CD20 comprises the heavy chain complementarity determining regions (HCDR1, HCDR2 and HCDR3) from a heavy chain variable region (HCVR) comprising SEQ ID NO:1242, and the light chain complementarity determining regions (LCDR1, LCDR2 and LCDR3) from a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:1258, 1274, 1290, 1306, 1322 and 1333.

35. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the first antigen-binding domain that specifically binds human CD3 comprises three heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) and three light chain complementarity determining regions (A1-LCDR1, A1-LCDR2 and A1-LCDR3), wherein A1-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1252, 1268, 1284, 1300, 1316 and 1330; wherein A1-HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:1254, 1270, 1286, 1302, 1318 and 1331; wherein A1-HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1256, 1272, 1288, 1304, 1320 and 1332, wherein A1-LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1260, 1276, 1292, 1308, 1324 and 1334, wherein A1-LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, and wherein A1-LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336.

36. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the second antigen-binding domain that specifically binds human CD20 comprises three heavy chain complementarity determining regions (A2-HCDR1, A2-HCDR2 and A2-HCDR3) and three light chain complementarity determining regions (A2-LCDR1, A2-LCDR2 and A2-LCDR3), wherein A2-HCDR1 comprises the amino acid sequence of SEQ ID NO:1244, wherein A2-HCDR2 comprises the amino acid sequence of SEQ ID NO:1246, wherein A2-HCDR3 comprises SEQ ID NO:1248, wherein A2-LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:1260, 1276, 1292, 1308, 1324 and 1334, wherein A2-LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, and wherein A2-LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336.

37. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the first antigen-binding domain that specifically binds human CD3 comprises three heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) and three light chain complementarity determining regions (A1-LCDR1, A1-LCDR2 and A1-LCDR3), and wherein the second antigen-binding domain that specifically binds human CD20 comprises three heavy chain complementarity determining regions (A2-HCDR1, A2-HCDR2 and A2-HCDR3) and three light chain complementarity determining regions (A2-LCDR1, A2-LCDR2 and A2-LCDR3);

wherein A1-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1252, 1268, 1284, 1300, 1316 and 1330; wherein A1-HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1254, 1270, 1286, 1302, 1318 and 1331; wherein A1-HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1256, 1272, 1288, 1304, 1320 and 1332, wherein A1-LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1260, 1276, 1292, 1308, 1324 and 1334, wherein A1-LCDR2 com-

prises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, and wherein A1-LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336; and

wherein A2-HCDR1 comprises the amino acid sequence of SEQ ID NO:1244, wherein A2-HCDR2 comprises the amino acid sequence of SEQ ID NO:1246, wherein A2-HCDR3 comprises SEQ ID NO:1248, wherein A2-LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1260, 1276, 1292, 1308, 1324 and 1334, wherein A2-LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, and wherein A2-LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336.

38. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the first antigen-binding domain competes for binding to human CD3 with a reference antigen-binding protein comprising three heavy chain complementarity determining regions (A1-HCDR1, A1-HCDR2 and A1-HCDR3) and three light chain complementarity determining regions (A1-LCDR1, A1-LCDR2 and A1-LCDR3), wherein A1-HCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1252, 1268, 1284, 1300, 1316 and 1330; wherein A1-HCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1254, 1270, 1286, 1302, 1318 and 1331; wherein A1-HCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1256, 1272, 1288, 1304, 1320 and 1332, wherein A1-LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1260, 1276, 1292, 1308, 1324 and 1334, wherein A1-LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, and wherein A1-LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336.

39. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the first antigen-binding domain competes for binding to human CD3 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1250, 1266, 1282, 1298, 1314 and 1329, and a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1258, 1274, 1290, 1306, 1322 and 1333.

40. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the second antigen-binding domain competes for binding to human CD20 with a reference antigen-binding protein comprising three heavy chain complementarity determining regions (A2-HCDR1, A2-HCDR2 and A2-HCDR3) and three light chain complementarity determining regions (A2-LCDR1, A2-LCDR2 and A2-LCDR3), wherein A2-HCDR1 comprises the amino acid sequence of SEQ ID NO:1244, wherein A2-HCDR2 comprises the amino acid sequence of SEQ ID NO:1246, wherein A2-HCDR3 comprises SEQ ID NO:1248, wherein A2-LCDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1260, 1276, 1292, 1308, 1324 and 1334, wherein A2-LCDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1262, 1278, 1294, 1310, 1326 and 1335, and wherein A2-LCDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1264, 1280, 1296, 1312, 1328 and 1336.

41. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the second antigen-binding domain competes for binding to human CD20 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO:1242, and a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1258, 1274, 1290, 1306, 1322 and 1333.

42. The bispecific antigen-binding molecule of any one of claims **22** to **32**, wherein the first antigen-binding domain competes for binding to human CD3 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1250, 1266, 1282, 1298, 1314 and 1329, and a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1258, 1274, 1290, 1306, 1322 and 1333; and wherein the second antigen-binding domain competes for binding to human CD20 with a reference antigen-binding protein comprising a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO:1242, and a light chain variable region (LCVR) comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 1258, 1274, 1290, 1306, 1322 and 1333.

43. A pharmaceutical composition comprising a bispecific antigen-binding molecule of any one of claims **22** to **42** and a pharmaceutically acceptable carrier or diluent.

44. A method for treating a B-cell cancer in a subject, the method comprising administering to the subject the pharmaceutical composition of claim **43**.

45. The method of claim **44**, wherein the B-cell cancer is selected from the group consisting of: follicular lymphoma, B cell chronic lymphocytic leukemia, B cell lymphoblastic lymphoma, Hodgkin lymphoma, Non-Hodgkin lymphoma, diffuse large B cell lymphoma, marginal zone lymphoma, Mantle cell lymphoma, hairy cell leukemia and Burkitt lymphoma.

46. The method of claim **44** or **45**, wherein the subject is afflicted with a tumor that is resistant to, or incompletely responsive to anti-CD20 monospecific therapy alone.

47. The method of claim **46**, wherein the subject is afflicted with a tumor that is resistant to, or incompletely responsive to rituximab monotherapy.

48. The method of any one of claims **44** through **47**, wherein the subject has received an anti-CD20 monospecific antibody therapy at least 1 day to 1 year prior to the administration of the pharmaceutical composition.

49. The method of claim **48**, wherein the anti-CD20 monospecific therapy comprises or consists of an anti-CD20 mono-specific antibody.

50. The method of claim **49**, wherein the anti-CD20 mono-specific antibody is rituximab.

51. A method for treating a B-cell cancer in a subject, the method comprising: (a) selecting a subject who is afflicted with a tumor that is resistant to, or incompletely responsive

to anti-CD20 monospecific therapy alone; and (b) administering to the subject the pharmaceutical composition of claim **43**.

52. The method of claim **51**, wherein the subject is selected on the basis of having a tumor that is resistant to, or incompletely responsive to rituximab monotherapy.

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