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(54) Title: MULTI-FUNCTIONAL CHIMERIC HEMATOPOIETIC RECEPTOR AGONISTS

(57) Abstract

Disclosed are novel multi-functional chimeric hematopoietic receptor agonist proteins, DNAs which encode the multi-functional chimeric hematopoietic receptor agonist proteins, methods of making the multi-functional chimeric hematopoietic receptor agonist proteins and methods of using the multi-functional chimeric hematopoietic receptor agonist proteins.

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SN	Senegal
SZ	Swaziland
TD	Chad
TG	Togo
TJ	Tajikistan
TM	Turkmenistan
TR	Turkey
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MULTI-FUNCTIONAL CHIMERIC HEMATOPOIETIC RECEPTOR AGONISTS

The present application claims priority under Title 35, United States Code, §119 of United States Provisional application Serial No. 60/029,629, filed October 25, 1996.

Field of the Invention

The present invention relates to multi-functional chimeric hematopoietic receptor agonists. These multi-functional chimeric hematopoietic receptor agonists retain one or more activities of individual components of the chimera molecule and may also show improved hematopoietic cell-stimulating activity and/or an improved activity profile which may include reduction of undesirable biological activities associated with individual hematopoietic growth factors and/or have improved physical properties which may include increased solubility, stability and refold efficiency.

Background of the Invention

Colony stimulating factors (CSFs) which stimulate the differentiation and/or proliferation of bone marrow cells have generated much interest because of their therapeutic potential for restoring depressed levels of hematopoietic stem cell-derived cells. CSFs in both human and murine systems have been identified and distinguished according to their activities. For example, granulocyte-CSF (G-CSF) and macrophage-CSF (M-CSF) stimulate the in vitro formation of neutrophilic granulocyte and macrophage colonies, respectively, while GM-CSF and interleukin-3 (IL-3) have broader activities and stimulate the formation of both macrophage, neutrophilic and eosinophilic granulocyte colonies. IL-3 also stimulates the formation of mast, megakaryocyte and pure and mixed erythroid colonies.

U.S. 4,877,729 and U.S. 4,959,455 disclose a gibbon IL-3 cDNA and a deduced human IL-3 DNA sequence and the protein sequences for which they code. The hIL-3 disclosed has serine rather than proline at position 8 in the protein sequence.

International Patent Application (PCT) WO 88/00598 discloses gibbon- and human-like IL-3. The hIL-3 contains a Ser^8 -> Pro^8 replacement. Suggestions are made to replace Cys by Ser, thereby breaking the disulfide bridge, and to replace one or more amino acids at the glycosylation sites.

U.S. 4,810,643 discloses a DNA sequence encoding human G-CSF.

WO 91/02754 discloses a fusion protein comprised of GM-CSF and IL-3 which has increased biological activity compared to GM-CSF or IL-3 alone. Also disclosed are nonglycosylated IL-3 and GM-CSF analog proteins as components of the multi-functional chimeric hematopoietic receptor agonist.

WO 92/04455 discloses fusion proteins composed of IL-3 fused to a lymphokine selected from the group consisting of IL-3, IL-6, IL-7, IL-9, IL-11, EPO and G-CSF.

WO 95/21197 and WO 95/21254 disclose fusion proteins capable of broad multi-functional hematopoietic properties.

GB 2,285,446 relates to the c-mpl ligand (thrombopoietin) and various forms of thrombopoietin which are shown to influence the replication, differentiation and maturation of megakaryocytes and megakaryocytes progenitors which may be used for the treatment of thrombocytopenia.

EP 675,201 A1 relates to the c-mpl ligand (Megakaryocyte growth and development factor (MGDF), allelic variations of c-mpl ligand and c-mpl ligand attached to water soluble polymers such as polyethylene glycol.

WO 95/21920 provides the murine and human c-mpl ligand and polypeptide fragments thereof. The proteins are useful for *in vivo* and *ex vivo* therapy for stimulating platelet production.

U.S. Patent No. 4,703,008 by Lin, F-K. discloses the a cDNA sequence encoding erythropoietin, methods of production and uses for erythropoietin.

WO 91/05867 discloses analogs of human erythropoietin having a greater number of sites for carbohydrate attachment than human erythropoietin, such as EPO (Asn^{69}), EPO (Asn^{125}, Ser^{127}), EPO (Thr^{125}), and EPO (Pro^{124}, Thr^{125}).

WO 94 /24160 discloses erythropoietin muteins which have enhanced activity, specifically amino acid substitutions at positions 20, 49, 73, 140, 143, 146, 147 and 154.

WO 94/28391 discloses the native flt3 ligand protein sequence and a cDNA sequence encoding the flt3 ligand, methods of expressing flt3 ligand in a host cell transfected with the cDNA and methods of treating patients with a hematopoietic disorder using flt3 ligand.

US Patent No. 5,554,512 is directed to human flt3 ligand as an isolated protein, DNA encoding the flt3 ligand, host cells transfected with cDNAs encoding flt3 ligand and methods for treating patients with flt3 ligand.

WO 94/26891 provides mammalianflt3 ligands, including an isolate that has an insertion of 29 amino acids, and fragments there of.

Rearrangement of Protein Sequences

In evolution, rearrangements of DNA sequences serve an important role in generating a diversity of protein structure and function. Gene duplication and exon shuffling provide an important mechanism to rapidly generate diversity and thereby provide organisms with a competitive advantage, especially since the basal mutation rate is low (Doolittle, *Protein Science* 1:191-200, 1992).

The development of recombinant DNA methods has made it possible to study the effects of sequence transposition on protein folding, structure and function. The approach used in creating new sequences resembles that of naturally occurring pairs of proteins that are related by linear reorganization of their amino acid sequences (Cunningham, et al., *Proc. Natl. Acad. Sci. U.S.A.* 76:3218-3222, 1979; Teather & Erfle, *J. Bacteriol.* 172: 3837-3841, 1990; Schimming et al., *Eur. J. Biochem.* 204: 13-19, 1992; Yamiuchi and Minamikawa, *FEBS Lett.* 260:127-130, 1991; MacGregor et al., *FEBS Lett.* 378:263-266). The first in vitro application of this type of rearrangement to proteins was described by Goldenberg and Creighton (*J. Mol. Biol.* 165:407-413, 1983). A new N-terminus is selected at an internal site (breakpoint) of the original sequence, the new sequence having the same order of amino acids as the original from the breakpoint until it reaches an amino acid that is at or near the original C-terminus. At this point the new sequence is joined, either directly or through an additional portion of sequence (linker), to an amino acid that is at or near the original N-terminus, and the new sequence continues with the same sequence as the original until it reaches a point that is at or near the amino acid that was N-terminal to the breakpoint site of the original sequence, this residue forming the new C-terminus of the chain.

This approach has been applied to proteins which range in size from 58 to 462 amino acids (Goldenberg & Creighton, *J. Mol. Biol.* 165:407-413, 1983; Li & Coffino, *Mol. Cell. Biol.* 13:2377-2383, 1993). The proteins examined have represented a broad range of structural classes, including proteins that contain predominantly a-helix (interleukin-4; Kreitman et al., *Cytokine* 7:311-318, 1995), b-sheet (interleukin-1; Horlick et al., *Protein Eng.* 5:427-431, 1992), or mixtures of the two (yeast phosphoribosyl anthranilate isomerase; Luger et al., *Science* 243:206-210, 1989). Broad categories of protein function are represented in these sequence reorganization studies:

Enzymes

T4 lysozyme	Zhang et al., *Biochemistry* 32:12311-12318, 1993; Zhang et al., *Nature Struct. Biol.* 1:434-438 (1995)
dihydrofolate reductase	Buchwalder et al., *Biochemistry* 31:1621-1630, 1994; Protasova et al., *Prot. Eng.* 7:1373-1377, 1995)
ribonuclease T1	Mullins et al., *J. Am. Chem. Soc.* 116:5529-5533, 1994; Garrett et al., *Protein Science* 5:204-211, 1996)
Bacillus b-glucanse	Hahn et al., *Proc. Natl. Acad. Sci. U.S.A.* 91:10417-10421, 1994)
aspartate transcarbamoylase	Yang & Schachman, *Proc. Natl. Acad. Sci. U.S.A.* 90:11980-11984, 1993)
phosphoribosyl anthranilate isomerase	Luger et al., *Science* 243:206-210 (1989; Luger et al., *Prot. Eng.* 3:249-258, 1990)
pepsin/pepsinogen	Lin et al., *Protein Science* 4:159-166, 1995)

glyceraldehyde-3-phosphate dehydrogenase	Vignais et al., *Protein Science* 4:994-1000, 1995)
ornithine decarboxylase	Li & Coffino, *Mol. Cell. Biol.* 13:2377-2383, 1993)
yeast phosphoglycerate dehydrogenase	Ritco-Vonsovici et al., *Biochemistry* 34:16543-16551, 1995)
Enzyme Inhibitor	
basic pancreatic trypsin inhibitor	Goldenberg & Creighton, *J. Mol. Biol.* 165:407-413, 1983)
Cytokines	
interleukin-1b	Horlick et al., *Protein Eng.* 5:427-431, 1992)
interleukin-4	Kreitman et al., *Cytokine* 7:311-318, 1995)
Tyrosine Kinase Recognition Domain	
a-spectrin SH3 domain	Viguera, et al., *J. Mol. Biol.* 247:670-681, 1995)
Transmembrane Protein	
omp A	Koebnik & Krämer, *J. Mol. Biol.* 250:617-626, 1995)
Chimeric Protein	

interleukin-4— *Pseudomonas* exotoxin	Kreitman et al., *Proc. Natl. Acad. Sci. U.S.A.* 91:6889-6893, 1994).

The results of these studies have been highly variable. In many cases substantially lower activity, solubility or thermodynamic stability were observed (*E. coli* dihydrofolate reductase, aspartate transcarbamoylase, phosphoribosyl anthranilate isomerase, glyceraldehyde-3-phosphate dehydrogenase, ornithine decarboxylase, omp A, yeast phosphoglycerate dehydrogenase). In other cases, the sequence rearranged protein appeared to have many nearly identical properties as its natural counterpart (basic pancreatic trypsin inhibitor, T4 lysozyme, ribonuclease T1, Bacillus b-glucanase, interleukin-1b, a-spectrin SH3 domain, pepsinogen, interleukin-4). In exceptional cases, an unexpected improvement over some properties of the natural sequence was observed, e.g., the solubility and refolding rate for rearranged a-spectrin SH3 domain sequences, and the receptor affinity and anti-tumor activity of transposed interleukin-4—Pseudomonas exotoxin fusion molecule (Kreitman et al., *Proc. Natl. Acad. Sci. U.S.A.* 91:6889-6893, 1994; Kreitman et al., *Cancer Res.* 55:3357-3363, 1995).

The primary motivation for these types of studies has been to study the role of short-range and long-range interactions in protein folding and stability. Sequence rearrangements of this type convert a subset of interactions that are long-range in the original sequence into short-range interactions in the new sequence, and vice versa. The fact that many of these sequence rearrangements are able to attain a conformation with at least some activity is persuasive evidence that protein folding occurs by multiple folding pathways (Viguera, et al., *J. Mol. Biol.* 247:670-681, 1995). In the case of the SH3 domain of a-spectrin, choosing new termini at locations that corresponded to b-hairpin turns resulted in proteins with slightly less stability, but which were nevertheless able to fold.

The positions of the internal breakpoints used in the studies cited here are found exclusively on the surface of proteins, and are distributed throughout the linear sequence without any obvious bias towards the ends or the middle (the variation in the relative distance from the original N-terminus to the breakpoint is ca. 10 to 80% of the total sequence length). The linkers connecting the original N- and C-termini in these studies have ranged from 0 to 9 residues. In one case (Yang & Schachman, *Proc. Natl. Acad. Sci. U.S.A.* 90:11980-11984, 1993), a portion of sequence has been deleted from the original C-terminal segment, and the connection made from the truncated C-terminus to the original N-terminus. Flexible hydrophilic residues such as Gly and Ser are frequently used in the linkers. Viguera, et al.(*J. Mol. Biol.* 247:670-681, 1995) compared joining the original N- and C- termini with 3- or 4-residue linkers; the 3-residue linker was less thermodynamically stable. Protasova et al. (*Protein Eng.* 7:1373-1377, 1994) used 3- or 5-residue linkers in connecting the original N-termini of *E. coli* dihydrofolate reductase; only the 3-residue linker produced protein in good yield.

Summary of the Invention

A hematopoietic protein comprising; an amino acid sequence of the formula:

R_1-L_1-R_2, R_2-L_1-R_1, R_1-R_2, or R_2-R_1

wherein R_1 and R_2 are independently selected from the group consisting of;

(I) A human EPO receptor agonist polypeptide, comprising a modified EPO amino acid sequence of the Formula:

```
AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys
                              10                            20

GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr
                              30                            40

ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla
                              50                            60

ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu
                              70                            80

LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer
                              90                           100

GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer
                             110                           120

ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys
                             130                           140

LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla
                             150                           160

CysArgThrGlyAspArg SEQ ID NO:464
                166
```

wherein optionally 1-6 amino acids from the N-terminus and 1-5 from the C-terminus can be deleted from said EPO receptor agonist polypeptide;

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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124-125
125-126
126-127
127-128
128-129
129-130
130-131
131-132
respectively; and

(II) A human stem cell factor receptor agonist polypeptide, comprising a modified stem cell factor amino acid sequence of the Formula:

GluGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeuValAla
10 20

AsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyMetAspValLeuPro
30 40

SerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeu
50 60

AspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleIleAspLysLeuVal
70 80

AsnIleValAspAspLeuValGluCysValLysGluAsnSerSerLysAspLeuLysLys
90 100

SerPheLysSerProGluProArgLeuPheThrProGluGluPhePheArgIlePheAsn
110 120

ArgSerIleAspAlaPheLysAspPheValValAlaSerGluThrSerAspCysValVal
130 140

SerSerThrLeuSerProGluLysAspSerArgValSerValThrLysProPheMetLeu
150 160

ProProValAlaAla SEQ ID NO:465
165

wherein optionally 1-23 amino acids can be deleted from the C-terminus of said stem cell factor receptor agonist polypeptide;

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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102-103
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110-111
respectively; and

(III) A human flt-3 receptor agonist polypeptide, comprising a modified flt-3 ligand amino acid sequence of the Formula:

```
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
                          10                            20

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
                          30                            40

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
                          50                            60

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
                          70                            80

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
                          90                            100

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
                          110                           120

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
                          130              SEQ ID NO:466
```

wherein 1-7 amino acids are optionally deleted from the C-terminus of said flt-3 receptor agonist polypeptide;

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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respectively; and

(IV) A polypeptide comprising; a modified human G-CSF amino acid sequence of the formula:

```
1                                     10
Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa

                        20
Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly

    30                                      40
Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa

                        50
Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp

    60                                      70
Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly

                        80
Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu

    90                                      100
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu

                        110
Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp
```

    120   130
Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr

                        140
Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala

    150   160
Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa

                        170
Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro SEQ ID NO:858

wherein

Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
Xaa at position 2 is Pro or Leu;
Xaa at position 3 is Leu, Arg, Tyr or Ser;
Xaa at position 13 is Phe, Ser, His, Thr or Pro;
Xaa at position 16 is Lys, Pro, Ser, Thr or His;
Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;
Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
Xaa at position 24 is Ile, Pro, Tyr or Leu;
Xaa at position 27 is Asp, or Gly;
Xaa at position 30 is Ala, Ile, Leu or Gly;
Xaa at position 34 is Lys or Ser;
Xaa at position 36 is Cys or Ser;
Xaa at position 42 is Cys or Ser;
Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;
Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;
Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
Xaa at position 47 is Leu or Thr;
Xaa at position 49 is Leu, Phe, Arg or Ser;
Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
Xaa at position 54 is Leu or His;
Xaa at position 64 is Cys or Ser;
Xaa at position 67 is Gln, Lys, Leu or Cys;
Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
Xaa at position 74 is Cys or Ser;
Xaa at position 104 is Asp, Gly or Val;
Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or Gly;
Xaa at position 115 is Thr, His, Leu or Ala;

Xaa at position 120 is Gln, Gly, Arg, Lys or His
Xaa at position 123 is Glu, Arg, Phe or Thr
Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or Glu;
Xaa at position 146 is Arg or Gln;
Xaa at position 147 is Arg or Gln;
Xaa at position 156 is His, Gly or Ser;
Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
Xaa at position 162 is Glu, Leu, Gly or Trp;
Xaa at position 163 is Val, Gly, Arg or Ala;
Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
Xaa at position 170 is His, Arg or Ser;

wherein optionally 1-11 amino acids from the N-terminus and 1-5 from the C-terminus can optionally be deleted from said modified human G-CSF amino acid sequence; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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135-136
136-137
137-138
138-139
139-140

60-61
61-62
98-99
99-100
140-141
141-142
or 142-143
respectively;

(V) A polypeptide comprising; a modified human IL-3 amino acid sequence of the formula:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 85 90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
95 100 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
110 115 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe SEQ ID NO:859
125 130

wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;
Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;

Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;
Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;
Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;
Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;
Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;
Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
Xaa at position 36 is Asp, Leu, or Val;
Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
Xaa at position 38 is Asn, or Ala;
Xaa at position 40 is Leu, Trp, or Arg;
Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;
Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly or Ser;
Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;
Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;
Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;
Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;
Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;
Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;
Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;
Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,

Thr, Ala, Tyr, Phe, Leu, Val or Lys;
Xaa at position 57 is Asn or Gly;
Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;
Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;
Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;
Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;
Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;
Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;
Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;
Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;
Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;
Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;
Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;
Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;
Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;
Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
Xaa at position 85 is Leu, Asn, Val, or Gln;
Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
Xaa at position 87 is Leu, Ser, Trp, or Gly;
Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;
Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;
Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His;
Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;

Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;
Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;
Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;
Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;
Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
Xaa at position 103 is Asp, or Ser;
Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;
Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;
Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;
Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;
Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;
Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;
Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;
Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;
Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;
Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;
Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg;
Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;
Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;
Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein from 1 to 14 amino acids can optionally be deleted from the N-terminus and/or from 1 to 15 amino acids can optionally be deleted from the C-terminus of said modified human IL-3 amino acid sequence; wherein from 0 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2), capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

26-27
27-28
28-29
29-30
30-31
31-32
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36-37
37-38
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39-40
40-41
41-42
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51-52
52-53
53-54
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64-65
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67-68
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69-70
70-71
71-72
72-73
82-83
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84-85
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86-87
87-88
88-89
89-90
90-91
91-92
92-93
97-98
98-99
99-100
100-101
101-102
102-103
or 103-104 respectively;

(VI) A polypeptide comprising; a modified human c-mpl ligand amino acid sequence of the formula:

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
1 5 10 15

HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
20 25 30 35

ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
40 45 50 55

ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
60 65 70 75

AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
80 85 90 95

GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
100 105 110

XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
115 120 125 130

LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
135 140 145 150

Arg SEQ ID NO:860
153

wherein;

Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro, Phe, Trp, or Met;
Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;
Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;
Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or Asn; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

26-27 51-52 108-109

27-28
28-29
29-30
30-31
32-33
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110-111
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112-113
113-114
114-115
115-116
116-117
117-118
118-119
119-120
120-121
121-122
122-123
123-124
124-125
125-126
126-127
or 127-128
respectively;

(VII) A polypeptide comprising; a modified human IL-3 amino acid sequence of the formula:

```
Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1               5                   10                  15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
                35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                65                  70                  75
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                80                  85                  90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                95                  100                 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                110                 115                 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe SEQ ID NO:859
                125                 130
```

wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;
Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;
Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;
Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;
Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;
Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;
Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;
Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
Xaa at position 36 is Asp, Leu, or Val;
Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
Xaa at position 38 is Asn, or Ala;
Xaa at position 40 is Leu, Trp, or Arg;
Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;
Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,

Gln, Arg, Thr, Gly or Ser;

Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;

Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;

Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;

Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;

Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;

Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;

Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;

Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;

Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;

Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;

Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;

Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;

Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;

Xaa at position 57 is Asn or Gly;

Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;

Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;

Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;

Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;

Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;

Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;

Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;

Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;

Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;

Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;

Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;

Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;

Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;

Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;

Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;

Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;

Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;

Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;
Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;
Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;
Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;
Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
Xaa at position 85 is Leu, Asn, Val, or Gln;
Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
Xaa at position 87 is Leu, Ser, Trp, or Gly;
Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;
Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;
Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His;
Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;
Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;
Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;
Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;
Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;
Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
Xaa at position 103 is Asp, or Ser;
Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;
Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;
Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;
Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;

Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;
Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;
Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;
Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;
Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;
Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;
Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg;
Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;
Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;
Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein from 1 to 14 amino acids can optionally be deleted from the N-terminus and/or from 1 to 15 amino acids can optionally be deleted from the C-terminus of said modified human IL-3 amino acid sequence; and wherein from 1 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

(VIII) a factor selected from the group consisting of: a colony stimulating factor, a cytokine, a lymphokine, an interleukin;

and wherein L_1 is a linker capable of linking R_1 to R_2;

with the proviso that at least R_1 or R_2 is selected from the polypeptide of formula (I) , (II), or (III); and

said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1}).

The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (I) above are; 23-24, 24-25, 25-26, 27-28, 28-29, 29-30, 30-31, 31-32, 32-33, 33-34, 34-35, 35-36, 36-37, 37-38, 38-39, 40-41, 41-42, 42-43, 52-53, 53-54, 54-55, 55-56, 77-78, 78-79, 79-80, 80-81, 81-82, 82-83, 83-84, 84-85, 85-86, 86-87, 109-110, 110-111, 110-111, 111-112, 112-113, 113-114, 114-115, 115-116, 116-117, 117-118, 118-119, 119-120, 120-121, 121-122, 122-123, 123-124, 124-125, 125-126, 126-127, 127-128, 128-129, 129-130, 130-131, and 131-132.

The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (I) above are; 23-24, 24-25, 31-32, 32-33, 37-38, 38-39, 82-83, 83-84, 85-86, 86-87, 87-88, 125-126, 126-127 and 131-132.

The EPO receptor agonists of the present invention may contain amino acid substitutions, such as those disclosed in WO 94/24160 or one or more of the glycosylation sites at Asn^{24}, Asn^{83}, and Asn^{126} are changed to other amino acids such as but not limited to Asp or Glu, deletions and/or insertions. It is also intended that the EPO receptor agonists of the present invention may also have amino acid deletions at either/or both the N- and C- termini of the original protein and or deletions from the new N- and/or C-termini of the sequence rearranged proteins in the formulas shown above.

The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide

(II) above are; 23-24, 24-25, 25-26, 33-34, 34-35, 35-36, 36-37, 38-39, 39-40, 40-41, 64-65, 65-66, 66-67, 67-68, 68-69, 69-70, 70-71, 89-90, 90-91, 91-92, 9-93, 93-94, 94-95, 95-96, 96-97, 97-98, 98-99, 99-100, 100-101, 101-102, 102-103, 103-104, 104-105 and 105-106 respectively.

The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (II) above are; 64-65, 65-66, 92-93 and 93-94 respectively.

The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (III) above are; 36-37, 37-38, 39-40, 41-42, 42-43, 64-65, 65-66, 66-67, 86-87, 87-88, 88-89, 89-90, 90-91, 91-92, 92-93, 93-94, 94-95, 95,-96, 96-97, 97-98, 98-99, 99-100 and 100-101

The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (III) above are; 39-40, 65-66, 89-90, 99-100 and 100-101.

The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (IV) above are; 38-39, 39-40, 40-41, 41-42, 48-49, 53-54, 54-55, 55-56, 56-57, 57-58, 58-59, 59-60, 60-61, 61-62, 62-63, 64-65, 65-66, 66-67, 67-68, 68-69, 69-70, 96-97, 125-126, 126-127, 127-128, 128-129, 129-130, 130-131, 131-132, 132-133, 133-134, 134-135, 135-136, 136-137, 137-138, 138-139, 139-140, 140-141 and 141-142.

The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (IV) above are; 38-39, 48-49, 96-97, 125-126, 132-133 and 141-142.

The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (V) above are; 28-29, 29-30, 30-31, 31-32, 32-33, 33-34, 34-35, 35-36, 36-37, 37-38, 38-39, 39-40, 66-67, 67-68, 68-69, 69-70, 70-71, 84-85, 85-86, 86-87, 87-88, 88-89, 89-90, 90-91, 98-99, 99-100, 100-101 and 101-102.

The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (V) above are; 34-35, 69-70 and 90-91.

The more preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (VI) above are; 80-81, 81-82, 82-83, 83-84, 84-85, 85-86, 86-87, 108-109, 109-110, 110-111, 111-112, 112-113, 113-114, 114-115, 115-116, 116-117, 117-118, 118-119, 119-120, 120-121, 121-122, 122-123, 123-124, 124-125, 125-126 and 126-127.

The most preferred breakpoints at which new C-terminus and N-terminus can be made in the polypeptide (VI) above are; 81-82, 108-109, 115-116, 119-120, 122-123 and 125-126.

The multi-functional receptor agonist of the present invention can also be represented by the following formulas:

$$(T^1)_a-(L^1)_b-X^1-(L)_c-X^2-(L^2)_d-(T^2)_e$$

or

$$X^1-(L)_c-X^2-(L)-Y^1-(L)_c-Y^2$$

in which:

X^1 is a peptide comprising an amino acid sequence corresponding to the sequence of residues n+1 through J of the original protein having amino acids residues numbered sequentially 1 through J with an amino terminus at residue 1;

L is an optional linker;

X^2 is a peptide comprising an amino acid sequence of residues 1 through n of the original protein;

Y^1 is a peptide comprising an amino acid sequence corresponding to the sequence of residues n=1 through K of the original protein having amino acids residues numbered sequentially 1 through K with an amino terminus at residue 1;

Y^2 is a peptide comprising an amino acid sequence of residues 1 through n of the original protein;

L^1 and L^2 are optional peptide spacers:

n is an integer ranging from 1 to J-1;

b, c, and d are each independently 0 or 1;

a and e are either 0 or 1, provided that both a and e cannot both be 0; and

T^1 and T^2 are proteins.

The multi-functional chimeric hematopoietic receptor agonists of the present invention may contain amino acid substitutions, deletions and/or insertions in the individual protein components of the chimera molecule. It is also intended that the multi-functional chimeric hematopoietic receptor agonists of the present invention may also have amino acid deletions at either/or both the N- and C- termini of the original protein and or deletions from the new N- and/or C-termini of the sequence rearranged proteins in the formulas shown above.

A preferred embodiment of the present invention the linker (L), (L^1) or (L^2), of the above formulas, joining the N-terminus to the C-terminus is a polypeptide selected from the group consisting of:

Ser;

Asn;
Gly;
Thr;
GlySer;
AlaAla;
GlySerGly;
GlyGlyGly;
GlyAsnGly;
GlyAlaGly;
GlyThrGly;
AlaSerAla;
AlaAlaAla;
GlyGlyGlySer SEQ ID NO:778;
GlyGlyGlySerGlyGlyGlySer SEQ ID NO:779;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySer SEQ ID NO:780;
SerGlyGlySerGlyGlySer SEQ ID NO:781;
GluPheGlyAsnMet SEQ ID NO:782;
GluPheGlyGlyAsnMet SEQ ID NO:783;
GluPheGlyGlyAsnGlyGlyAsnMet SEQ ID NO:784;
GlyGlySerAspMetAlaGly SEQ ID NO:785;
SerGlyGlyAsnGly SEQ ID NO:786;
SerGlyGlyAsnGlySerGlyGlyAsnGly SEQ ID NO:787;
SerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGlyAsnGly SEQ ID NO:788;
SerGlyGlySerGlySerGlyGlySerGly SEQ ID NO:789;
SerGlyGlySerGlySerGlyGlySerGlySerGlyGlySerGly SEQ ID NO:790;
GlyGlyGlySerGlyGly SEQ ID NO:791;
GlyGlyGlySerGlyGlyGly SEQ ID NO:792;
GlyGlyGlySerGlyGlyGlySerGlyGly SEQ ID NO:793;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly SEQ ID NO:794;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly SEQ ID NO:795;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly GlyGlySerGly SEQ ID NO:796;

ProProProTrpSerProArgProLeuGlyAlaThrAlaProThrAlaGly GlnProProLeu SEQ ID NO:797;
ProProProTrpSerProArgProLeuGlyAlaThrAlaProThr SEQ ID NO:798; and
ValGluThrValPheHisArgValSerGlnAspGlyLeuLeuThrSer SEQ ID NO:799.

Additionally, the present invention relates to recombinant expression vectors comprising nucleotide sequences encoding the multi-functional chimeric hematopoietic receptor agonists, related microbial expression systems, and processes for making the multi-functional chimeric hematopoietic receptor agonists. The invention also relates to pharmaceutical compositions containing the multi-functional chimeric hematopoietic receptor agonists, and methods for using the multi-functional chimeric hematopoietic receptor agonists.

In addition to the use of the multi-functional chimeric hematopoietic receptor agonists of the present invention in vivo, it is envisioned that in vitro uses would include the ability to stimulate bone marrow and blood cell activation and growth before infusion into patients. Another intended use is for the production of dendritic cells both *in vivo* and *ex vivo*.

It is believed that the reduced affinity of fusion proteins is due, at least in part, to the inability of the individual moieties to achieve their native conformation when incorporated into a chimeric molecule or to steric hindrance between the active site of the individual moieties of the fusion protein. This invention overcomes these limitations providing novel multi-functional chimeric hematopoietic receptor agonists that have a binding affinity comparable to or greater than the individual components of the chimeric molecule.

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Brief Description of the Figures

Figure 1 schematically illustrates the sequence rearrangement of a protein. The N-terminus (N) and the C-terminus (C) of the native protein are joined through a linker, or joined directly. The protein is opened at a breakpoint creating a new N-terminus (new N) and a new C-terminus (new-C) resulting in a protein with a new linear amino acid sequence. A rearranged molecule may be synthesized *de novo* as linear molecule and not go through the steps of joining the original N-terminus and the C-terminus and opening of the protein at the breakpoint.

Figure 2 shows a schematic of Method I, for creating new proteins in which the original N-terminus and C-terminus of the native protein are joined with a linker and different N-terminus and C-terminus of the protein are created. In the example shown the sequence rearrangement results in a new gene encoding a protein with a new N-terminus created at amino acid 97 of the original protein, the original C-terminus (a.a. 174) joined to the amino acid 11 (a.a. 1- 10 are deleted) through a linker region and a new C-terminus created at amino acid 96 of the original sequence.

Figure 3 shows a schematic of Method II, for creating new proteins in which the original N-terminus and C-terminus of the native protein are joined without a linker and different N-terminus and C-terminus of the protein are created. In the example shown the sequence rearrangement results in a new gene encoding a protein with a new N-terminus created at amino acid 97 of the original protein, the original C-terminus (a.a. 174) joined to the original N-terminus and a new C-terminus created at amino acid 96 of the original sequence.

Figure 4 shows a schematic of Method III, for creating new proteins in which the original N-terminus and C-terminus of the native protein are joined with a linker and different N-terminus and C-terminus of the protein are created. In the example shown the sequence rearrangement results in a new gene encoding a protein with a new N-terminus created at amino acid 97 of the original protein, the original C-terminus (a.a. 174) joined to amino acid 1 through a linker region and a new C-terminus created at amino acid 96 of the original sequence.

Figure 5 shows the bioactivity of the multi-functional receptor agonists comprising flt3 receptor agonists pMON32332, pMON32333, pMON32334 and pMON32335 compared to recombinant native flt3 (Genzyme) in the MUTZ-2 cell proliferation assay. MT = mock transfection

Figure 6 shows a DNA sequence encoding human mature EPO based on the sequence of Lin et al. (*PNAS* 82:7580-7584, 1985).

Figure 7a and 7b shows a DNA sequence encoding native stem cell factor based on the sequence of Martin et al. (*Cell* 63:203-211, 1990).

Figure 8 shows a DNA sequence encoding soluble stem cell factor based on the sequence of Langley et al. (*Archives of Bichemistry and Biophysica* 311:55-61, 1994).

Figure 9a and 9b shows the DNA sequence encoding the 209 amino acid mature form of flt3 ligand from Lyman et al. (*Oncogene* 11:1165-1172, 1995).

Figure 10 shows the DNA sequence encoding the 134 amino acid soluble form of flt3 ligand from Lyman et al.(*Oncogene* 11:1165-1172, 1995).

Detailed Description of the Invention

The present invention encompasses multi-functional chimeric hematopoietic receptor agonists formed from covalently linked polypeptides, each of which may act through a different and specific cell receptor to initiate complementary biological activities. Hematopoiesis requires a complex series of cellular events in which stem cells generate continuously into large populations of maturing cells in all major lineages. There are currently at least 20 known regulators with hematopoietic proliferative activity. Most of these proliferative regulators can only stimulate one or another type of colony formation in vitro, the precise pattern of colony formation stimulated by each regulator is quite distinctive. No two regulators stimulate exactly the same pattern of colony formation, as evaluated by colony numbers or, more importantly, by the lineage and maturation pattern of the cells making up the developing colonies. Proliferative responses can most readily be analyzed in simplified in vitro culture systems. Three quite different parameters can be distinguished: alteration in colony size, alteration in colony numbers and cell lineage. Two or more factors may act on the progenitor cell, inducing the formation of larger number of progeny thereby increasing the colony size. Two or more factors may allow increased number of progenitor cells to proliferate either because distinct subsets of progenitors cells exist that respond exclusively to one factor or because some progenitors require stimulation by two or more factors before being able to respond. Activation of additional receptors on a cell by the use of two or more factors is likely to enhance the mitotic signal because of coalescence of initially differing signal pathways into a common final pathway reaching the nucleus (Metcalf, *Nature* 339:27, 1989). Other mechanisms could explain synergy. For example, if one signaling pathway is limited by an intermediate activation of an additional signaling pathway which is caused by a second factor, then this may result in a super additive response. In some cases, activation of one receptor type can induce an enhanced expression of other receptors (Metcalf, *Blood* 82:3515-3523, 1993). Two or more factors may result in a different pattern of cell lineages than from a single factor. The use of multi-functional chimeric hematopoietic receptor agonists may have a potential clinical advantage resulting from a proliferative response that is not possible by any single factor.

The receptors of hematopoietic and other growth factors can be grouped into two distinct families of related proteins: (1) tyrosine kinase receptors, including those for epidermal growth factor, M-CSF (Sherr, *Blood* 75:1, 1990) and SCF (Yarden et al., *EMBO J.* 6:3341, 1987): and (2) hematopoietic receptors, not containing a tyrosine kinase domain, but exhibiting obvious homology in their extracellular domain (Bazan, *PNAS USA* 87:6934-6938, 1990). Included in this latter group are erythropoietin (EPO) (D'Andrea et al., *Cell* 57:277, 1989), GM-CSF (Gearing et al., *EMBO J.* 8:3667, 1989), IL-3 (Kitamura et al., *Cell* 66:1165, 1991), G-CSF (Fukunaga et al., *J. Bio. Chem.* 265:14008-15, 1990), IL-4 (Harada et al., *PNAS USA* 87:857, 1990), IL-5 (Takaki et al., *EMBO J.* 9:4367, 1990), IL-6 (Yamasaki et al., *Science* 241:825, 1988), IL-7 (Goodwin et al., *Cell* 60:941-51, 1990), LIF (Gearing et al., *EMBO J.* 10:2839, 1991) and IL-2 (Cosman et al., *Mol*-Immunol. 23: 935-94, 1986). Most of the latter group of receptors exists in a high-affinity form as heterodimers. After ligand binding, the specific a-chains become associated with at least one other receptor chain (b-chain, g-chain). Many of these factors share a common receptor subunit. The a-chains for GM-CSF, IL-3 and IL-5 share the same b-chain (Kitamura et al., *Cell* 66:1165, 1991), Takaki et al., *EMBO J.* 10:2833-8, 1991) and receptor complexes for IL-

6, LIF and IL-11 share a common b-chain (gp130) (Taga et al., *Cell* 58:573-81, 1989; Gearing et al., *Science* 255:1434-7, 1992). The receptor complexes of IL-2, IL-4, IL-7, IL-9 and IL-15 share a common g-chain (Kondo et al., *Science* 262:1874, 1993; Russell et al., *Science* 266: 1042-1045, 1993; Noguchi et al., *Science* 262:1877, 1993; Giri et al., *EMBO J.* 13:2822-2830, 1994).

The use of a multiply acting hematopoietic factor may also have a potential advantage by reducing the demands placed on factor-producing cells and their induction systems. If there are limitations in the ability of a cell to produce a factor, then by lowering the required concentrations of each of the factors, and using them in combination may usefully reduce demands on the factor-producing cells. The use of a multiply acting hematopoietic factor may lower the amount of the factors that would be needed, probably reducing the likelihood of adverse side-effects.

Novel compounds of this invention are represented by a formula selected from the group consisting of:

R_1-L_1-R_2, R_2-L_1-R_1, R_1-R_2, and R_2-R_1

Where R_1 and R_2 are as defined above.

R_2 is preferably a colony stimulating factor with a different but complementary activity than R_1. By complementary activity is meant activity which enhances or changes the response to another cell modulator. The R_1 polypeptide is joined either directly or through a linker segment to the R_2 polypeptide. The term "directly" defines multi-functional chimeric hematopoietic receptor agonists in which the polypeptides are joined without a peptide linker. Thus L_1 represents a chemical bond or polypeptide segment to which both R_1 and R_2 are joined in frame, most commonly L_1 is a linear peptide to which R1 and R_2 are joined by amide bonds linking the carboxy terminus of R_1 to the amino terminus of L_1 and carboxy terminus of L_1 to the amino terminus of R_2. By "joined in frame" is meant that there is no translation termination or disruption between the reading frames of the DNA encoding R_1 and R_2.

A non-exclusive list of other growth factors, i.e. colony stimulating factors (CSFs), are cytokines, lymphokines, interleukins, hematopoietic growth factors which can be joined to (I), (II) or (III) include GM-CSF, G-CSF, c-mpl ligand (also known as TPO or MGDF), M-CSF, erythropoietin (EPO), IL-1, IL-4, IL-2, IL-3, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-15, LIF, flt3/flk2 ligand, human growth hormone, B-cell growth factor, B-cell differentiation factor, eosinophil differentiation factor and stem cell factor (SCF) also known as steel factor or c-kit ligand. Additionally, this invention encompasses the use of modified R_1 or R_2 molecules or mutated or modified DNA sequences encoding these R_1 or R_2 molecules. The present invention also includes multi-functional chimeric hematopoietic receptor agonists in which R_1 or R_2 is an hIL-3 variant, c-mpl ligand variant, or G-CSF variant. A "hIL-3 variant" is defined as a hIL-3 molecule which has amino acid substitutions and/or portions of hIL-3 deleted as disclosed in WO 94/12638, WO 94/12639 and WO 95/00646, as well as other variants known in the art. A "c-mpl ligand variant" is defined an c-mpl ligand molecule which has amino acid substitutions and/or portions of c-mpl ligand deleted, disclosed in United States Application Serial Number 08/383,035 as well as other variants known in the art. A "G-CSF variant" is defined an G-CSF molecule which has amino acid substitutions and/or portions of G-CSF deleted, as disclosed herein, as well as other variants known in the art. In addition to the list above, IL-3 variants taught in WO 94/12639 and WO 94/12638, G-CSF receptor agonists disclosed in WO 97/12977, c-mpl receptor agonists disclosed in WO 97/12978, IL-3 receptor agonists disclosed in WO 97/12979 can be R_1 or R_2 of the present invention. As used herein "IL-3 variants" refer to IL-3 variants taught in WO 94/12639 and WO 94/12638. As used herein "fusion proteins" refer to fusion protein taught in WO 95/21197, and WO 95/21254. As used herein "G-CSF receptor agonists" refer to G-CSF receptor agonists disclosed in WO 97/12978. As used herein "c-mpl receptor agonists" refer to c-mpl receptor agonists disclosed in WO 97/12978. As used herein "IL-3 receptor agonists" refer to IL-3 receptor agonists disclosed in WO 97/12979. As used herein "multi-functional receptor agonists" refer to multi-functional receptor agonists taught in WO 97/12985.

The linking group (L_1) is generally a polypeptide of between 1 and 500 amino acids in length. The linkers joining the two molecules are preferably designed to (1) allow the two molecules to fold and act independently of each other, (2) not have a propensity for developing an ordered secondary structure which could interfere with the functional domains of the two proteins, (3) have minimal hydrophobic characteristics which could interact with the functional protein domains and (4) provide steric separation of R_1 and R_2 such that R_1 and R_2 could interact simultaneously with their corresponding receptors on a single cell. Typically surface amino acids in flexible protein regions include Gly, Asn and Ser. Virtually any permutation of amino acid sequences containing Gly, Asn and Ser would be expected to satisfy the above criteria for a linker sequence. Other neutral amino acids, such as Thr and Ala, may also be used in the linker sequence. Additional amino acids may also be included in the linkers due to the addition of unique restriction sites in the linker sequence to facilitate construction of the multi-functional chimeric hematopoietic receptor agonists.

Preferred L_1 linkers of the present invention include sequences selected from the group of formulas:

$(Gly^3Ser)^n$ (SEQ ID NO:861), $(Gly^4Ser)^n$ (SEQ ID NO:862), $(Gly^5Ser)^n$ (SEQ ID NO:863), $(Gly^nSer)^n$ (SEQ ID NO:864) or $(AlaGlySer)^n$ (SEQ ID NO:865).

One example of a highly-flexible linker is the glycine and serine-rich spacer region present within the pIII protein of the filamentous bacteriophages, e.g. bacteriophages M13 or fd (Schaller et al., *PNAS USA* 72: 737-741, 1975). This region provides a long, flexible spacer region between two domains of the pIII surface protein. The spacer region consists of the amino acid sequence:
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGluGlyGlyGlySerGlu
GlyGlyGlySerGluGlyGlyGlySerGluGlyGlyGlySerGlyGlyGlySer
(SEQ ID NO:800).

The present invention also includes linkers in which an endopeptidase recognition sequence is included. Such a cleavage site may be valuable to separate the individual components of the multi-functional chimeric hematopoietic receptor agonist to determine if they are properly folded and active in vitro. Examples of various endopeptidases include, but are not limited to, plasmin, enterokinase, kallikrein, urokinase, tissue plasminogen activator, clostripain, chymosin, collagenase, Russell's viper venom protease, postproline cleavage enzyme, V8 protease, Thrombin and factor Xa.

Peptide linker segments from the hinge region of heavy chain immunoglobulins IgG, IgA, IgM, IgD or IgE provide an angular relationship between the attached polypeptides. Especially useful are those hinge regions where the cysteines are replaced with serines. Preferred linkers of the present invention include sequences derived from murine IgG gamma 2b hinge region in which the cysteines have been changed to serines. These linkers may also include an endopeptidase cleavage site. Examples of such linkers include the following sequences:

IleSerGluProSerGlyProIleSerThrIleAsnProSerProProSerLys GluSerHisLysSerPro (SEQ ID NO:801) and

IleGluGlyArgIleSerGluProSerGlyProIleSerThrIleAsnProSer ProProSerLysGluSerHisLysSerPro (SEQ ID NO:802).

The present invention is, however, not limited by the form, size or number of linker sequences employed and the only requirement of the linker is that functionally it does not interfere with the folding and function of the individual molecules of the multi-functional chimeric hematopoietic receptor agonist.

Determination of the Linker L_2.

The length of the amino acid sequence of the linker L_2 to be used in R_1 and/or R_2 can be selected empirically or with guidance from structural information, or by using a combination of the two approaches.

When no structural information is available, a small series of linkers can be prepared for testing using a design whose length is varied in order to span a range from 0 to 50 Å and whose sequence is chosen in order to be consistent with surface exposure (hydrophilicity, Hopp & Woods, *Mol. Immunol.* 20: 483-489, 1983), Kyte & Doolittle, *J. Mol. Biol.* 157:105-132; solvent exposed surface area, Lee & Richards, *J. Mol. Biol.* 55:379-400, 1971) and the ability to adopt the necessary conformation with out deranging the conformation of R^1 or R^2 (conformationally flexible; Karplus & Schulz, *Naturwissenschaften* 72:212-213, 1985). Assuming an average of translation of 2.0 to 3.8 Å per residue, this would mean the length to test would be between 0 to 30 residues, with 0 to 15 residues being the preferred range. Exemplary of such an empirical series would be to construct linkers using a cassette sequence such as "Gly-Gly-Gly-Ser" repeated n times, where n is 1, 2, 3 or 4. Those skilled in the art will recognize that there are many such sequences that vary in length or composition that can serve as linkers with the primary consideration being that they be neither excessively long nor short (cf., Sandhu, *Critical Rev. Biotech.* 12: 437-462, 1992); if they are too long, entropy effects will likely destabilize the three-dimensional fold, and may also make folding kinetically impractical, and if they are too short, they will likely destabilize the molecule because of torsional or steric strain.

Those skilled in the analysis of protein structural information will recognize that using the distance between the chain ends, defined as the distance between the c-alpha carbons, can be used to define the length of the sequence to be used, or at least to limit the number of possibilities that must be tested in an empirical selection of linkers. They will also recognize that it is sometimes the case that the positions of the ends of the polypeptide chain are ill-defined in structural models derived from x-ray diffraction or nuclear magnetic resonance spectroscopy data, and that when true, this situation will therefore need to be taken into account in order to properly estimate the length of the linker required. From those residues whose positions are well defined are selected two residues that are close in sequence to the chain ends, and the distance between their c-alpha carbons is used to calculate an approximate length for a linker between them. Using the calculated length as a guide, linkers with a range of number of residues (calculated using 2 to 3.8Å per residue) are then selected. These linkers may be composed of the original sequence, shortened or lengthened as necessary, and when lengthened the additional residues may be chosen to be flexible and hydrophilic as described above; or optionally the original sequence may be substituted for using a series of linkers, one example being the "Gly-Gly-Gly-Ser" cassette approach mentioned above; or optionally a combination of the original sequence and new sequence having the appropriate total length may be used.

Determination of the Amino and Carboxyl Termini of R_1 and R_2

Sequences of R_1 and R_2 capable of folding to biologically active states can be prepared by appropriate selection of the beginning (amino terminus) and ending (carboxyl terminus) positions from within the original polypeptide chain while using the linker sequence L_2 as described above. Amino and carboxyl termini are selected from within a common stretch of sequence, referred to as a breakpoint region, using the guidelines described below. A novel amino acid sequence is thus generated by selecting amino and carboxyl termini from within the same breakpoint region. In many cases the selection of the new termini will be such that the original position of the carboxyl terminus immediately preceded that of the amino terminus. However, those skilled in the art will recognize that selections of termini anywhere within the region may function, and that these will effectively lead to either deletions or additions to the amino or carboxyl portions of the new sequence.

It is a central tenet of molecular biology that the primary amino acid sequence of a protein dictates folding to the three-dimensional structure necessary for expression of its biological function. Methods are known to those skilled in the art to obtain and interpret three-dimensional structural information using x-ray diffraction of single protein crystals or nuclear magnetic resonance spectroscopy of protein solutions. Examples of structural information that are relevant to the identification of breakpoint regions include the location and type of protein secondary structure (alpha and 3-10 helices, parallel and anti-parallel beta sheets, chain reversals and turns, and loops; Kabsch & Sander, *Biopolymers* 22: 2577-2637, 1983), the degree of solvent exposure of amino acid residues, the extent and type of interactions of residues with one another (Chothia, *Ann. Rev. Biochem.* 53:537-572, 1984) and the static and dynamic distribution of conformations along the polypeptide chain (Alber & Mathews, *Methods Enzymol.* 154: 511-533, 1987). In some cases additional information is known about solvent exposure of residues; one example is a site of post-translational attachment of carbohydrate which is necessarily on the surface of the protein. When experimental structural information is not available, or is not feasible to obtain, methods are also available to analyze the primary amino acid sequence in order to make predictions of protein tertiary and secondary structure, solvent accessibility and the occurrence of turns and loops. Biochemical methods are also sometimes applicable for empirically determining surface exposure when direct structural methods are not feasible; for example, using the identification of sites of chain scission following limited proteolysis in order to infer surface exposure (Gentile & Salvatore, *Eur. J. Biochem.* 218:603-621, 1993)

Thus using either the experimentally derived structural information or predictive methods (e.g., Srinivisan & Rose *Proteins: Struct., Funct. & Genetics*, 22: 81-99, 1995) the parental amino acid sequence is inspected to classify regions according to whether or not they are integral to the maintenance of secondary and tertiary structure. The occurrence of sequences within regions that are known to be involved in periodic secondary structure (alpha and 3-10 helices, parallel and anti-parallel beta sheets) are regions that should be avoided. Similarly, regions of amino acid sequence that are observed or predicted to have a low degree of solvent exposure are more likely to be part of the so-called hydrophobic core of the protein and should also be avoided for selection of amino and carboxyl termini. In contrast, those regions that are known or predicted to be in surface turns or loops, and especially those regions that are known not to be required for biological activity, are the preferred sites for location of the extremes of the polypeptide chain. Continuous stretches of amino acid sequence that are preferred based on the above criteria are referred to as a breakpoint region.

Additional peptide sequences may also be added to facilitate purification or identification of multi-functional chimeric hematopoietic receptor agonist proteins (e.g., poly-His). A highly antigenic peptide may also be added that would enable rapid assay and facile purification of the multi-functional chimeric hematopoietic receptor agonist protein by a specific monoclonal antibody.

"Mutant amino acid sequence," "mutant protein", "variant protein", "mutein", or "mutant polypeptide" refers to a polypeptide having an amino acid sequence which varies from a native sequence due to amino acid deletions, substitutions, or both, or is encoded by a nucleotide sequence intentionally made variant from a native sequence.. "Native sequence" refers to an amino acid or nucleic acid sequence which is identical to a wild-type or native form of a gene or protein.

Hematopoietic growth factors can be characterized by their ability to stimulate colony formation by human hematopoietic progenitor cells. The colonies formed include erythroid, granulocyte, megakaryocyte, granulocytic macrophages and mixtures thereof. Many of the hematopoietic growth factors have demonstrated the ability to restore bone marrow function and peripheral blood cell populations to therapeutically beneficial levels in studies performed initially in primates and subsequently in humans. Many or all of these biological activities of hematopoietic growth factors involve signal transduction and high affinity receptor binding. Multi-functional chimeric hematopoietic receptor agonists of the present invention may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties.

Multi-functional chimeric hematopoietic receptor agonists which have little or no agonist activity maybe useful as antagonists, as antigens for the production of antibodies for use in immunology or immunotherapy, as genetic probes or as intermediates used to construct other useful hIL-3 muteins.

Biological activity of the multi-functional chimeric hematopoietic receptor agonist proteins of the present invention can be determined by DNA synthesis in factor-dependent cell lines or by counting the colony forming units in an in vitro bone marrow assay.

The multi-functional chimeric hematopoietic receptor agonists of the present invention may have an improved therapeutic profile as compared to single acting hematopoietic agonists. For example, some multi-functional chimeric hematopoietic receptor agonists of the present invention may have a similar or more potent growth factor activity relative to other hematopoietic agonists without having a similar or corresponding increase in side-effects.

The present invention also includes the DNA sequences which code for the multi-functional chimeric hematopoietic receptor agonist proteins, DNA sequences which are substantially similar and perform substantially the same function, and DNA sequences which differ from the DNAs encoding the multi-functional chimeric hematopoietic receptor agonists of the invention only due to the degeneracy of the genetic code. Also included in the present invention are the oligonucleotide intermediates used to construct the mutant DNAs and the polypeptides coded for by these oligonucleotides.

Genetic engineering techniques now standard in the art (United States Patent 4,935,233 and Sambrook et al., "Molecular Cloning A Laboratory Manual", Cold Spring Harbor Laboratory, 1989) may be used in the construction of the DNA sequences of the present invention. One such method is cassette mutagenesis (Wells et al., *Gene* 34:315-323, 1985) in which a portion of the coding sequence in a plasmid is replaced with synthetic oligonucleotides that encode the desired amino acid substitutions in a portion of the gene between two restriction sites.

Pairs of complementary synthetic oligonucleotides encoding the desired gene can be made and annealed to each other. The DNA sequence of the oligonucleotide would encode sequence for amino acids of desired gene with the exception of those substituted and/or deleted from the sequence.

Plasmid DNA can be treated with the chosen restriction endonucleases then ligated to the annealed oligonucleotides. The ligated mixtures can be used to transform competent JM101 cells to resistance to an appropriate antibiotic. Single colonies can be picked and the plasmid DNA examined by restriction analysis and/or DNA sequencing to identify plasmids with the desired genes.

Cloning of the DNA sequences of the novel multi-functional hematopoietic agonists wherein at least one of the with the DNA sequence of the other colony stimulating factor may be accomplished by the use of intermediate vectors. Alternatively one gene can be cloned directly into a vector containing the other gene. Linkers and adapters can be used for joining the DNA sequences, as well as replacing lost sequences, where a restriction site was internal to the region of interest. Thus genetic material (DNA) encoding one polypeptide, peptide linker, and the other polypeptide is inserted into a suitable expression vector which is used to transform bacteria, yeast, insect cells or mammalian cells. The transformed organism is grown and the protein isolated by standard techniques. The resulting product is therefore a new protein which has a colony stimulating factor joined by a linker region to a second colony stimulating factor.

Another aspect of the present invention provides plasmid DNA vectors for use in the expression of these novel multi-functional chimeric hematopoietic receptor agonists. These vectors contain the novel DNA sequences described above which code for the novel polypeptides of the invention. Appropriate vectors which can transform microorganisms capable of expressing the multi-functional chimeric hematopoietic receptor agonists include expression vectors comprising nucleotide sequences coding for the multi-functional chimeric hematopoietic receptor agonists joined to transcriptional and translational regulatory sequences which are selected according to the host cells used.

Vectors incorporating modified sequences as described above are included in the present invention and are useful in the production of the multi-functional chimeric hematopoietic receptor agonist polypeptides. The vector employed in the method also contains selected regulatory sequences in operative association with the DNA coding sequences of the invention and which are capable of directing the replication and expression thereof in selected host cells.

As another aspect of the present invention, there is provided a method for producing the novel multi-functional chimeric hematopoietic receptor agonists.

The method of the present invention involves culturing suitable cells or cell line, which has been transformed with a vector containing a DNA sequence coding for expression of a novel multi-functional chimeric hematopoietic receptor agonist. Suitable cells or cell lines may be bacterial cells. For example, the various strains of *E. coli* are well-known as host cells in the field of biotechnology. Examples of such strains include *E. coli* strains JM101 (Yanish-Perron et al. *Gene* 33: 103-119, 1985) and MON105 (Obukowicz et al., *Applied Environmental Microbiology* 58: 1511-1523, 1992). Also included in the present invention is the expression of the multi-functional chimeric hematopoietic receptor agonist protein utilizing a chromosomal expression vector for *E. coli* based on the bacteriophage Mu (Weinberg et al., *Gene* 126: 25-33, 1993). Various strains of *B. subtilis* may also be employed in this method. Many strains of yeast cells known to those skilled in the art are also available as host cells for expression of the polypeptides of the present invention. When expressed in the *E. coli* cytoplasm, the gene encoding the multi-functional chimeric hematopoietic receptor agonists of the present invention may also be constructed such that at the 5′ end of the gene codons are added to encode Met^{-2}-Ala^{-1}- or Met^{-1} at the N-terminus of the protein. The N termini of proteins made in the cytoplasm of *E. coli* are affected by post-translational processing by methionine aminopeptidase (Ben Bassat et al., *J. Bac.* 169:751-757, 1987) and possibly by other peptidases so that upon expression the methionine is cleaved off the N-terminus. The multi-functional chimeric hematopoietic receptor agonists of the present invention may include multi-functional chimeric hematopoietic receptor agonist polypeptides having Met^{-1}, Ala^{-1} or Met^{-2}-Ala^{-1} at the N-terminus. These mutant multi-functional chimeric hematopoietic receptor agonists may also be expressed in *E. coli* by fusing a secretion signal peptide to the N-terminus. This signal peptide is cleaved from the polypeptide as part of the secretion process. Additional strategies for achieving high-level expression of genes in E. coli can be found in Savvas, C.M. (*Microbiological Reviews* 60;512-538, 1996).

Also suitable for use in the present invention are mammalian cells, such as Chinese hamster ovary cells (CHO). General methods for expression of foreign genes in mammalian cells are reviewed in Kaufman, R. J., 1987) Genetic Engineering, Principles and Methods, Vol. 9, J. K. Setlow, editor, Plenum Press, New York. An expression vector is constructed in which a strong promoter capable of functioning in mammalian cells drives transcription of a eukaryotic secretion signal peptide coding region, which is translationally joined to the coding region for the multi-functional chimeric hematopoietic receptor agonist. For example, plasmids such as pcDNA I/Neo, pRc/RSV, and pRc/CMV (obtained from Invitrogen Corp., San Diego, California) can be used. The eukaryotic secretion signal peptide coding region can be from the gene itself or it can be from another secreted mammalian protein (Bayne, M. L. et al., *Proc. Natl. Acad. Sci. USA* 84: 2638-2642, 1987). After construction of the vector containing the gene, the vector DNA is transfected into mammalian cells. Such cells can be, for example, the COS7, HeLa, BHK, CHO, or mouse L lines. The cells can be cultured, for example, in DMEM media (JRH Scientific). The polypeptide secreted into the media can be recovered by standard biochemical approaches following transient expression for 24 - 72 hours after transfection of the cells or after establishment of stable cell lines following selection for antibiotic resistance. The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Gething and Sambrook, *Nature*, 293:620-

625, 1981), or alternatively, Kaufman et al, *Mol. Cell. Biol.*, 5(7):1750-1759, 1985) or Howley et al., U.S. Pat. No. 4,419,446. Another suitable mammalian cell line is the monkey COS-1 cell line. A similarly useful mammalian cell line is the CV-1 cell line.

Where desired, insect cells may be utilized as host cells in the method of the present invention. See, e.g., Miller et al., *Genetic Engineering*, 8:277-298 (Plenum Press 1986) and references cited therein. In addition, general methods for expression of foreign genes in insect cells using Baculovirus vectors are described in: Summers, M. D. and Smith, G. E., 1987) - A manual of methods for Baculovirus vectors and insect cell culture procedures, Texas Agricultural Experiment Station Bulletin No. 1555. An expression vector is constructed comprising a Baculovirus transfer vector, in which a strong Baculovirus promoter (such as the polyhedron promoter) drives transcription of a eukaryotic secretion signal peptide coding region, which is translationally joined to the coding region for the multi-functional chimeric hematopoietic receptor agonist polypeptide. For example, the plasmid pVL1392 (obtained from Invitrogen Corp., San Diego, California) can be used. After construction of the vector carrying the gene encoding the multi-functional chimeric hematopoietic receptor agonist polypeptide, two micrograms of this DNA is co-transfected with one microgram of Baculovirus DNA (see Summers & Smith, 1987) into insect cells, strain SF9. Pure recombinant Baculovirus carrying the multi-functional chimeric hematopoietic receptor agonist is used to infect cells cultured, for example, in Excell 401 serum-free medium (JRH Biosciences, Lenexa, Kansas). The multi-functional chimeric hematopoietic receptor agonist secreted into the medium can be recovered by standard biochemical approaches. Supernatants from mammalian or insect cells expressing the multi-functional chimeric hematopoietic receptor agonist protein can be first concentrated using any of a number of commercial concentration units.

The multi-functional chimeric hematopoietic receptor agonists of the present invention may be useful in the treatment of diseases characterized by decreased levels of either myeloid, erythroid, lymphoid, or megakaryocyte cells of the hematopoietic system or combinations thereof. In addition, they may be used to activate mature myeloid and/or lymphoid cells. Among conditions susceptible to treatment with the polypeptides of the present invention is leukopenia, a reduction in the number of circulating leukocytes (white cells) in the peripheral blood. Leukopenia may be induced by exposure to certain viruses or to radiation. It is often a side effect of various forms of cancer therapy, e.g., exposure to chemotherapeutic drugs, radiation and of infection or hemorrhage. Therapeutic treatment of leukopenia with these multi-functional chimeric hematopoietic receptor agonists of the present invention may avoid undesirable side effects caused by treatment with presently available drugs.

The multi-functional chimeric hematopoietic receptor agonists of the present invention may be useful in the treatment of neutropenia and, for example, in the treatment of such conditions as aplastic anemia, cyclic neutropenia, idiopathic neutropenia, Chediak-Higashi syndrome, systemic lupus erythematosus (SLE), leukemia, myelodysplastic syndrome and myelofibrosis.

The multi-functional chimeric hematopoietic receptor agonist of the present invention may be useful in the treatment or prevention of thrombocytopenia. Currently the only therapy for thrombocytopenia is platelet transfusion which are costly and carry the significant risks of infection (HIV, HBV) and alloimunization. The multi-functional chimeric hematopoietic receptor agonist may alleviate or diminish the need for platelet transfusion. Severe thrombocytopenia may result from genetic defects such as Fanconi's Anemia, Wiscott-Aldrich, or May Hegglin syndromes. Acquired thrombocytopenia may result from auto- or allo-antibodies as in Immune Thrombocytopenia Purpura, Systemic Lupus Erythromatosis, hemolytic anemia, or fetal maternal incompatibility. In addition, splenomegaly, disseminated intravascular coagulation, thrombotic thrombocytopenic purpura, infection or prosthetic heart valves may result in thrombocytopenia. Severe thrombocytopenia may also result from chemotherapy and/or radiation therapy or cancer. Thrombocytopenia may also result from marrow invasion by carcinoma, lymphoma, leukemia or fibrosis.

The multi-functional chimeric hematopoietic receptor agonists of the present invention may be useful in the mobilization of hematopoietic progenitors and stem cells in peripheral blood. Peripheral blood derived progenitors have been shown to be effective in reconstituting patients in the setting of autologous marrow transplantation. Hematopoietic growth factors including G-CSF and GM-CSF have been shown to enhance the number of circulating progenitors and stem cells in the peripheral blood. This has simplified the procedure for peripheral stem cell collection and dramatically decreased the cost of the procedure by decreasing the number of pheresis required. The multi-functional chimeric hematopoietic receptor agonist may be useful in mobilization of stem cells and further enhance the efficacy of peripheral stem cell transplantation.

The multi-functional chimeric hematopoietic receptor agonists of the present invention may also be useful in the ex vivo expansion of hematopoietic progenitors and stem cells. Colony stimulating factors (CSFs), such as hIL-3, have been administered alone, co-administered with other CSFs, or in combination with bone marrow transplants subsequent to high dose chemotherapy to treat the neutropenia and thrombocytopenia which are often the result of such treatment. However the period of severe neutropenia and thrombocytopenia may not be totally eliminated. The myeloid lineage, which is comprised of monocytes (macrophages), granulocytes (including neutrophils) and megakaryocytes, is critical in preventing infections and bleeding which can be life-threatening. Neutropenia and thrombocytopenia may also be the result of disease, genetic disorders, drugs, toxins, radiation and many therapeutic treatments such as conventional oncology therapy.

Bone marrow transplants have been used to treat this patient population. However, several problems are associated with the use of bone marrow to reconstitute a compromised hematopoietic system including: 1) the number of stem cells in bone marrow, spleen, or peripheral blood is limited, 2) Graft Versus Host Disease, 3) graft rejection and 4) possible contamination with tumor cells. Stem cells make up a very small percentage of the nucleated cells in the bone marrow, spleen and peripheral blood. It is clear that a dose response exists such that a greater number of stem cells will enhance hematopoietic recovery. Therefore, the in vitro expansion of stem cells should enhance hematopoietic recovery and patient survival. Bone marrow from an allogeneic donor has been used to provide bone marrow for transplant. However, Graft Versus Host Disease and graft rejection limit bone marrow transplantation even in recipients with HLA-matched sibling donors. An alternative to allogeneic bone marrow transplants is autologous bone marrow transplants. In autologous bone marrow transplants, some of the patient's own marrow is harvested prior to myeloablative therapy, e.g. high dose chemotherapy, and is transplanted back into the patient afterwards. Autologous transplants eliminate the risk of Graft Versus Host Disease and graft rejection. However, autologous bone marrow transplants still present problems in terms of the limited number of stems cells in the marrow and possible contamination with tumor cells. The limited number of stem cells may be overcome by ex-vivo expansion of the stem cells. In addition, stem cells can be specifically isolated, based on the presence of specific surface antigens such as CD34+ in order to decrease tumor cell contamination of the marrow graft.

The following patents contain further details on separating stem cells, CD34+ cells, culturing the cells with hematopoietic factors, the use of the cells for the treatment of patients with hematopoietic disorders and the use of hematopoietic factors for cell expansion and gene therapy.

5,061,620 relates to compositions comprising human hematopoietic stem cells provided by separating the stem cells from dedicated cells.

5,199,942 describes a method for autologous hematopoietic cell transplantation comprising: (1) obtaining hematopoietic progenitor cells from a patient; (2) ex-vivo expansion of cells with a growth factor selected from the group consisting of IL-3, flt3 ligand, c-kit ligand, GM-CSF, IL-1, GM-CSF/IL-3 fusion protein and combinations thereof; (3) administering cellular preparation to a patient.

5,240,856 relates to a cell separator that includes an apparatus for automatically controlling the cell separation process.

WO 91/16116 describes devices and methods for selectively isolating and separating target cells from a mixture of cells.

WO 91/18972 describes methods for in vitro culturing of bone marrow, by incubating suspension of bone marrow cells, using a hollow fiber bioreactor.

WO 92/18615 relates to a process for maintaining and expanding bone marrow cells, in a culture medium containing specific mixtures of cytokines, for use in transplants.

WO 93/08268 describes a method for selectively expanding stem cells, comprising the steps of (a) separating CD34+ stem cells from other cells and (b) incubating the separated cells in a selective medium, such that the stem cells are selectively expanded.

WO 93/18136 describes a process for in vitro support of mammalian cells derived from peripheral blood.

WO 93/18648 relates to a composition comprising human neutrophil precursor cells with a high content of myeloblasts and promyelocytes for treating genetic or acquired neutropenia.

WO 94/08039 describes a method of enrichment for human hematopoietic stem cells by selection for cells which express c-kit protein.

WO 94/11493 describes a stem cell population that are CD34+ and small in size, which are isolated using a counterflow elutriation method.

WO 94/27698 relates to a method combining immunoaffinity separation and continuous flow centrifugal separation for the selective separation of a nucleated heterogeneous cell population from a heterogeneous cell mixture.

WO 94/25848 describes a cell separation apparatus for collection and manipulation of target cells.

The long term culturing of highly enriched CD34+ precursors of hematopoietic progenitor cells from human bone marrow in cultures containing IL-1a, IL-3, IL-6 or GM-CSF is discussed in Brandt et al *J. Clin. Invest.* 86:932-941, 1990).

One aspect of the present invention provides a method for selective ex-vivo expansion of stem cells. The term "stem cell" refers to the totipotent hematopoietic stem cells as well as early precursors and progenitor cells which can be isolated from bone marrow, spleen or peripheral blood. The term "expansion" refers to the differentiation and proliferation of the cells. The present invention provides a method for selective ex-vivo expansion of stem cells, comprising the steps of: (a) separating stem cells from other cells, (b) culturing said separated stem cells with a selective media which contains multi-functional chimeric hematopoietic receptor agonist protein(s) and (c) harvesting said stems cells. Stem cells, as well as committed progenitor cells destined to become neutrophils, erythrocytes, platelets, etc. may be distinguished from most other cells by the presence or absence of particular progenitor marker antigens, such as CD34, that are present on the surface of these cells and/or by morphological characteristics. The phenotype for a highly enriched human stem cell fraction is reported as CD34+, Thy-1+ and lin-, but it is to be understood that the present invention is not limited to the expansion of this stem cell population. The CD34+ enriched human stem cell fraction can be separated by a number of reported methods, including affinity columns or beads, magnetic beads or flow cytometry using antibodies directed to surface antigens such as the

CD34+. Further, physical separation methods such as counterflow elutriation may be used to enrich hematopoietic progenitors. The CD34+ progenitors are heterogeneous, and may be divided into several sub-populations characterized by the presence or absence of co-expression of different lineage associated cell surface associated molecules. The most immature progenitor cells do not express any known lineage associated markers, such as HLA-DR or CD38, but they may express CD90(thy-1). Other surface antigens such as CD33, CD38, CD41, CD71, HLA-DR or c-kit can also be used to selectively isolate hematopoietic progenitors. The separated cells can be incubated in selected medium in a culture flask, sterile bag or in hollow fibers. Various colony stimulating factors may be utilized in order to selectively expand cells. Representative factors that have been utilized for ex-vivo expansion of bone marrow include, c-kit ligand, IL-3, G-CSF, GM-CSF, IL-1, IL-6, IL-11, flt-3 ligand or combinations thereof. The proliferation of the stem cells can be monitored by enumerating the number of stem cells and other cells, by standard techniques (e.g. hemacytometer, CFU, LTCIC) or by flow cytometry prior and subsequent to incubation.

Several methods for ex-vivo expansion of stem cells have been reported utilizing a number of selection methods and expansion using various colony stimulating factors including c-kit ligand (Brandt et al., *Blood* 83:1507-1514 [1994], McKenna et al., *Blood* 86:3413-3420 [1995]), IL-3 (Brandt et al., *Blood* 83:1507-1514 [1994], Sato et al., *Blood* 82:3600-3609 [1993]), G-CSF (Sato et al., *Blood* 82:3600-3609 [1993]), GM-CSF (Sato et al., *Blood* 82:3600-3609 [1993]), IL-1 (Muench et al., *Blood* 81:3463-3473 [1993]), IL-6 (Sato et al., *Blood* 82:3600-3609 [1993]), IL-11 (Lemoli et al., *Exp. Hem.* 21:1668-1672 [1993], Sato et al., *Blood* 82:3600-3609 [1993]), flt-3 ligand (McKenna et al., *Blood* 86:3413 3420 [1995]) and/or combinations thereof (Brandt et al., *Blood*

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83:1507 1514 [1994], Haylock et al., *Blood* 80:1405-1412 [1992], Koller et al., *Biotechnology* 11:358-363 [1993], (Lemoli et al., *Exp. Hem.* 21:1668-1672 [1993]), McKenna et al., *Blood* 86:3413-3420 [1995], Muench et al., *Blood* 81:3463-3473 [1993], Patchen et al., *Biotherapy* 7:13-26 [1994], Sato et al., *Blood* 82:3600-3609 [1993], Smith et al., *Exp. Hem.* 21:870-877 [1993], Steen et al., *Stem Cells* 12:214-224 [1994], Tsujino et al., *Exp. Hem.* 21:1379-1386 [1993]). Among the individual colony stimulating factors, hIL-3 has been shown to be one of the most potent in expanding peripheral blood CD34+ cells (Sato et al., *Blood* 82:3600-3609 [1993], Kobayashi et al., *Blood* 73:1836-1841 [1989]). However, no single factor has been shown to be as effective as the combination of multiple factors. The present invention provides methods for ex vivo expansion that utilize multi-functional chimeric hematopoietic receptor agonists that are more effective than a single factor alone.

Another aspect of the invention provides methods of sustaining and/or expanding hematopoietic precursor cells which includes inoculating the cells into a culture vessel which contains a culture medium that has been conditioned by exposure to a stromal cell line such as HS-5 (WO 96/02662, Roecklein and Torok-Strob, *Blood* 85:997-1105, 1995) that has been supplemented with a multi-functional hematopoietic chimeric receptor agonist of the present invention.

It is also envisioned that uses of multi-functional hematopoietic chimeric receptor agonists of the present invention would include blood banking applications, where the EPO receptor agonists are given to a patent to increase the number of blood cells and blood products are removed from the patient, prior to some medical procedure. The blood products stored and transfused back into the patient after the medical procedure.

Additionally, it is envisioned that uses of multi-functional hematopoietic chimeric receptor agonists would include giving the multi-functional hematopoietic chimeric receptor agonists to a blood donor prior to blood donation to increase the number of blood cells, thereby allowing the donor to safely give more blood.

Another projected clinical use of growth factors has been in the in vitro activation of hematopoietic progenitors and stem cells for gene therapy. Due to the long life-span of hematopoietic progenitor cells and the distribution of their daughter cells throughout the entire body, hematopoietic progenitor cells are good candidates for ex vivo gene transfection. In order to have the gene of interest incorporated into the genome of the hematopoietic progenitor or stem cell one needs to stimulate cell division and DNA replication. Hematopoietic stem cells cycle at a very low frequency which means that growth factors may be useful to promote gene transduction and thereby enhance the clinical prospects for gene therapy. Potential applications of gene therapy (review Crystal, *Science* 270:404-410 [1995]) include; 1) the treatment of many congenital metabolic disorders and immunodeficiencies (Kay and Woo, *Trends Genet*. 10:253-257 [1994]), 2) neurological disorders (Friedmann, *Trends Genet*. 10:210-214 [1994]), 3) cancer (Culver and Blaese, *Trends Genet*. 10:174-178 [1994]) and 4) infectious diseases (Gilboa and Smith, *Trends Genet*. 10:139-144 [1994]).

There are a variety of methods, known to those with skill in the art, for introducing genetic material into a host cell. A number of vectors, both viral and non-viral have been developed for transferring therapeutic genes into primary cells. Viral based vectors include; 1) replication deficient recombinant retrovirus (Boris-Lawrie and Temin, *Curr. Opin. Genet. Dev.* 3:102-109 [1993], Boris-Lawrie and *Temin, Annal. New York Acad.*

Sci. 716:59-71 [1994], Miller, *Current Top. Microbiol. Immunol.* 158:1-24 [1992]) and replication-deficient recombinant adenovirus (Berkner, *BioTechniques* 6:616-629 [1988], Berkner, *Current Top. Microbiol. Immunol.* 158:39-66 [1992], Brody and Crystal, *Annal. New York Acad. Sci.* 716:90-103 [1994]). Non-viral based vectors include protein/DNA complexes (Cristiano et al., *PNAS USA.* 90:2122-2126 [1993], Curiel et al., *PNAS USA* 88:8850-8854 [1991], Curiel, *Annal. New York Acad. Sci.* 716:36-58 [1994]), electroporation and liposome mediated delivery such as cationic liposomes (Farhood et al., *Annal. New York Acad. Sci.* 716:23-35 [1994]).

The present invention provides an improvement to the existing methods of expanding hematopoietic cells, which new genetic material has been introduced, in that it provides methods utilizing multi-functional chimeric hematopoietic receptor agonist proteins that have improved biological activity, including an activity not seen by any single colony stimulation factor.

Many drugs may cause bone marrow suppression or hematopoietic deficiencies. Examples of such drugs are AZT, DDI, alkylating agents and anti-metabolites used in chemotherapy, antibiotics such as chloramphenicol, penicillin, gancyclovir, daunomycin and sulfa drugs, phenothiazones, tranquilizers such as meprobamate, analgesics such as aminopyrine and dipyrone, anti-convulsants such as phenytoin or carbamazepine, antithyroids such as propylthiouracil and methimazole and diuretics. The multi-functional chimeric hematopoietic receptor agonists of the present invention may be useful in preventing or treating the bone marrow suppression or hematopoietic deficiencies which often occur in patients treated with these drugs.

Hematopoietic deficiencies may also occur as a result of viral, microbial or parasitic infections, burns and as a result of treatment for renal disease or renal failure, e.g., dialysis. The multi-functional chimeric hematopoietic receptor agonists of the present invention may be useful in treating such hematopoietic deficiencies.

The treatment of hematopoietic deficiency may include administration of a pharmaceutical composition containing the multi-functional chimeric hematopoietic receptor agonists to a patient. The multi-functional chimeric hematopoietic receptor agonists of the present invention may also be useful for the activation and amplification of hematopoietic precursor cells by treating these cells in vitro with the multi-functional chimeric hematopoietic receptor agonist proteins of the present invention prior to injecting the cells into a patient.

Various immunodeficiencies, e.g., in T and/or B lymphocytes, or immune disorders, e.g., rheumatoid arthritis, may also be beneficially affected by treatment with the multi-functional chimeric hematopoietic receptor agonists of the present invention. Immunodeficiencies may be the result of viral infections, e.g., HTLVI, HTLVII, HTLVIII, severe exposure to radiation, cancer therapy or the result of other medical treatment. The multi-functional chimeric hematopoietic receptor agonists of the present invention may also be employed, alone or in combination with other colony stimulating factors, in the treatment of other blood cell deficiencies, including thrombocytopenia (platelet deficiency), or anemia. Other uses for these novel polypeptides are the in vivo and ex vivo treatment of patients recovering from bone marrow transplants, and in the development of monoclonal and polyclonal antibodies generated by standard methods for diagnostic or therapeutic use.

Other aspects of the present invention are methods and therapeutic compositions for treating the conditions referred to above. Such compositions comprise a therapeutically effective amount of one or more of the multi-functional chimeric hematopoietic receptor agonists of the present invention in a mixture with a pharmaceutically acceptable carrier. This composition can be administered either parenterally, intravenously or subcutaneously. When administered, the therapeutic composition for use in this invention is preferably in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such a parenterally acceptable protein solution, having due regard to pH, isotonicity, stability and the like, is within the skill of the art.

Another intended use of the multi-functional chimeric hematopoietic receptor agonists of the present invention is for the generation of larger numbers of dendritic cells, from precursors, to be used as adjuvants for immunization. Dendritic cells play a crucial role in the immune system. They are the professional antigen-presenting cells most efficient in the activation of resting T cells and are the major antigen-presenting cells for activation of naïve T cells *in vivo* and, thus, for initiation of primary immune responses. They efficiently internalize, process and present soluble tumor-specific antigens (Ag). Dendritic cells have the unique capacity to cluster naïve T cells and to respond to Ag encounter by rapid upregulation of the expression of major histocompatability complex (MHC) and co-stimulatory molecules, the production of cytokines and migration towards lymphatic organs. Since dendritic cells are of central importance for sensitizing the host against a neoantigen for CD4-dependent immune responses, they may also play a crucial role in the generation and regulation of tumor immunity.

Dendritic cells originate from a bone marrow CD34+ precursor common to granulocytes and macrophages, and the existence of a separate dendritic cell colony-forming unit (CFU-DC) that give rise to pure dendritic cell colonies has been established in humans. In addition, a post-CFU CD14+ intermediate has been described with the potential to differentiate along the dendritic cell or the macrophage pathway under distinct cytokine conditions. This bipotential precursor is present in the bone marrow, cord blood and peripheral blood. Dendritic cells can be isolated based on specific cell surface markers, such as CD1a+, CD3-, CD4-, CD20-, CD40+, CD80+, and CD83+, to delineate the maturation of cultured dendritic cells.

Dendritic cells based strategies provide a method for enhancing immune response against tumors and infectious agents. AIDS is another disease for which dendritic cell based therapies can be used, since dendritic cells can play a major role in promoting HIV-1 replication. An immunotherapy requires the generation of dendritic cells from cancer patients, their *in vitro* exposure to tumor Ag, derived from surgically removed tumor masses, and reinjection of these cells into the tumor patients. Relatively crude membrane preparations of tumor cells will suffice as sources of tumor antigen, avoiding the necessity for molecular identification of the tumor antigen. The tumor antigen may also be synthetic peptides, carbohydrates, or nucleic acid sequences. In addition, concomitant administration of cytokines such as the multi-functional chimeric hematopoietic receptor agonists of the present invention may further facilitate the induction of tumor immunity. It is foreseen that the immunotherapy can be in an *in vivo* setting, wherein the multi-functional chimeric hematopoietic receptor agonists of the present invention is administered to a patient, having a tumor, alone or with other hematopoietic growth factors to increase the number of dendritic cells and endogenous tumor antigen is presented on the dendritic cells. It is also envisioned that *in vivo* immunotherapy can be with exogenous antigen. It is also envisioned that the immunotherapy treatment may include the mobilization of dendritic cell precursors or mature dendritic, by administering the multi-functional chimeric hematopoietic receptor agonists of the present invention alone or with other hematopoietic growth factors to the patient, removing the dendritic cell precursors or mature dendritic cells from the patient, exposing the dendritic cells to antigen and returning the dendritic cells to the patient. Furthermore, the dendritic cells that have been removed can be cultured *ex vivo* with the multi-functional chimeric hematopoietic receptor agonists of the present invention alone or with other hematopoietic growth factors to increase the number of dendritic cells prior to exposure to antigen. Dendritic cells based strategies also provide a method for reducing the immune response in auto-immune diseases.

Studies on dendritic cells have been greatly hampered by difficulties in preparing the cells in sufficient numbers and in a reasonably pure form. In an ex-vivo cell expansion setting, granulocyte-macrophage colony-stimulating factor (GM-CSF) and tumor necrosis factor-α (TNF-α) cooperate in the ex vivo generation of dendritic cells from hematopoietic progenitors (CD34+ cells) retrieved from bone marrow, cord blood, or peripheral blood and flk-2/flt-3 ligand and c-kit ligand (stem cell factor [SCF]) synergize to enhance the GM-CSF plus TNF-α induced generation of dendritic cells (Siena, S. *et al.* *Experimental Hematology* **23**:1463-1471, 1995). Also provide is a method of *ex vivo* expansion of dendritic cell precursors or mature dendritic cells using the multi-functional chimeric hematopoietic receptor agonists of the present invention to provide sufficient quantities of dendritic cells for immunotherapy.

The dosage regimen involved in a method for treating the above-described conditions will be determined by the attending physician considering various factors which modify the action of drugs, e.g., the condition, body weight, sex and diet of the patient, the severity of any infection, time of administration and other clinical factors. Generally, a daily regimen may be in the range of 0.2 - 150 µg/kg of multi-functional chimeric hematopoietic receptor agonist protein per kilogram of body weight. Dosages would be adjusted relative to the activity of a given multi-functional chimeric hematopoietic receptor agonist protein and it would not be unreasonable to note that dosage regimens may include doses as low as 0.1 microgram and as high as 1 milligram per kilogram of body weight per day. In addition, there may exist specific circumstances where dosages of multi-functional chimeric hematopoietic receptor agonist would be adjusted higher or lower than the range of 0.2 - 150 micrograms per kilogram of body weight. These include co-administration with other colony stimulating factors or IL-3 variants or growth factors; co-administration with chemotherapeutic drugs and/or radiation; the use of glycosylated multi-functional chimeric hematopoietic receptor agonist protein; and various patient-related issues mentioned earlier in this section. As indicated above, the therapeutic method and compositions may also include co-administration with other human factors. A non-exclusive list of other appropriate colony stimulating factors (CSFs), cytokines, lymphokines, hematopoietic growth factors and interleukins for simultaneous or serial co-administration with the polypeptides of the present invention includes GM-CSF, G-CSF, c-mpl ligand (also known as TPO or MGDF), M-CSF, erythropoietin (EPO), IL-1, IL-4, IL-2, IL-3, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-15, IL-16, LIF, flt3/flk2 ligand, B-cell growth factor, B-cell differentiation factor and eosinophil differentiation factor, stem cell factor (SCF) also known as steel factor or c-kit ligand, or combinations thereof. The dosage recited above would be adjusted to compensate for such additional components in the therapeutic composition. Progress of the treated patient can be monitored by periodic assessment of the hematological profile, e.g., differential cell count and the like.

MATERIALS AND METHODS

Unless noted otherwise, all specialty chemicals were obtained from Sigma, Co. (St. Louis, MO). Restriction endonucleases and T4 DNA ligase were obtained from New England Biolabs (Beverly, MA) or Boehringer Mannheim (Indianapolis, IN).

Transformation of *E. coli* strains

E. coli strains, such as DH5a™ (Life Technologies, Gaithersburg, MD) and TG1 (Amersham Corp., Arlington Heights, IL) are used for transformation of ligation reactions and are the source of plasmid DNA for transfecting mammalian cells. *E. coli* strains, such as JM101 (Yanisch-Perron, et al., *Gene*, 33: 103-119, 1985) and MON105 (Obukowicz, et al., *Appl. and Envir. Micr.*, 58: 1511-1523, 1992) can be used for expressing the multi-functional chimeric hematopoietic receptor agonist of the present invention in the cytoplasm or periplasmic space.

MON105 ATCC#55204: F-, lambda-,IN(rrnD, rrE)1, rpoD+, rpoH358

DH5a™: F-, phi80dlacZdeltaM15, delta(lacZYA-argF)U169, deoR, recA1, endA1, hsdR17(rk-,mk+), phoA, supE44lamda-, thi-1, gyrA96, relA1

TG1: delta(lac-pro), supE, thi-1, hsdD5/F'(traD36, proA+B+, lacIq, lacZdeltaM15)

JM101 ATCC#33876: delta (pro lac), *sup*E, *thi*, F'(*tra*D36, proA+B+, *lac*Iq, *lac*ZdeltaM15)

DH5a™ Subcloning efficiency cells are purchased as competent cells and are ready for transformation using the manufacturer's protocol, while both *E. coli* strains TG1 and MON105 are rendered competent to take up DNA using a $CaCl_2$ method. Typically, 20 to 50 mL of cells are grown in LB medium (1% Bacto-tryptone, 0.5% Bacto-yeast extract, 150 mM NaCl) to a density of approximately 1.0 optical density unit at 600 nanometers (OD600) as measured by a Baush & Lomb Spectronic spectrophotometer (Rochester, NY). The cells are collected by centrifugation and resuspended in one-fifth culture volume of $CaCl_2$ solution (50 mM $CaCl_2$, 10 mM Tris-Cl, pH7.4) and are held at 4°C for 30 minutes. The cells are again collected by centrifugation and resuspended in one-tenth culture volume of $CaCl_2$ solution. Ligated DNA is added to 0.2 mL of these cells, and the samples are held at 4°C for 30-60 minutes. The samples are shifted to 42°C for two minutes and 1.0 mL of LB is added prior to shaking the samples at 37°C for one hour. Cells from these samples are spread on plates (LB medium plus 1.5% Bacto-agar) containing either ampicillin (100 micrograms/mL, ug/mL) when selecting for ampicillin-resistant transformants, or spectinomycin (75 ug/mL) when selecting for spectinomycin-resistant transformants. The plates are incubated overnight at 37°C. Colonies are picked and inoculated into LB plus appropriate antibiotic (100 ug/mL ampicillin or 75 ug/mL spectinomycin) and are grown at 37°C while shaking.

<u>Methods for creation of genes with new N-terminus/C-terminus</u>

Method I. Creation of genes with new N-terminus/C-terminus which contain a linker region (L_2).

Genes with new N-terminus/C-terminus which contain a linker region (L_2) separating the original C-terminus and N-terminus can be made essentially following the method described in L. S. Mullins, et al (*J. Am. Chem. Soc.* 116, 5529-5533, 1994). Multiple steps of polymerase chain reaction (PCR) amplifications are used to rearrange the DNA sequence encoding the primary amino acid sequence of the protein. The steps are illustrated in Figure 2.

In the first step, the first primer set ("new start" and "linker start") is used to create and amplify, from the original gene sequence, the DNA fragment ("Fragment Start") that contains the sequence encoding the new N-terminal portion of the new protein followed by the linker (L_2) that connects the C-terminal and N-terminal ends of the original protein. In the second step, the second primer set ("new stop" and "linker stop") is used to create and amplify, from the original gene sequence, the DNA fragment ("Fragment Stop") that encodes the same linker as used above, followed by the new C-terminal portion of the new protein. The "new start" and "new stop" primers are designed to include the appropriate restriction sites which allow cloning of the new gene into expression plasmids. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 50°C annealing for one minute and 72°C extension for one minute; plus one cycle 72°C extension for seven minutes. A Perkin Elmer GeneAmp PCR Core Reagents kit is used. A 100 ul reaction contains 100 pmole of each primer and one ug of template DNA; and 1x PCR buffer, 200 uM dGTP, 200 uM dATP, 200 uM dTTP, 200 uM dCTP, 2.5 units AmpliTaq DNA polymerase and 2 mM

MgCl2. PCR reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT).

"Fragment Start" and "Fragment Stop", which have complementary sequence in the linker region and the coding sequence for the two amino acids on both sides of the linker, are joined together in a third PCR step to make the full-length gene encoding the new protein. The DNA fragments "Fragment Start" and "Fragment Stop" are resolved on a 1% TAE gel, stained with ethidium bromide and isolated using a Qiaex Gel Extraction kit (Qiagen). These fragments are combined in equimolar quantities, heated at 70°C for ten minutes and slow cooled to allow annealing through their shared sequence in "linker start" and "linker stop". In the third PCR step, primers "new start" and "new stop" are added to the annealed fragments to create and amplify the full-length new N-terminus/C-terminus gene. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 60°C annealing for one minute and 72°C extension for one minute; plus one cycle 72°C extension for seven minutes. A Perkin Elmer GeneAmp PCR Core Reagents kit is used. A 100 ul reaction contains 100 pmole of each primer and approximately 0.5 ug of DNA; and 1x PCR buffer, 200 uM dGTP, 200 uM dATP, 200 uM dTTP, 200 uM dCTP, 2.5 units AmpliTaq DNA polymerase and 2 mM $MgCl_2$. PCR reactions are purified using a Wizard PCR Preps kit (Promega).

Method II. Creation of genes with new N-terminus/C-terminus without a linker region.

New N-terminus/C-terminus genes without a linker joining the original N-terminus and C-terminus can be made using two steps of PCR amplification and a blunt end ligation. The steps are illustrated in Figure 3. In the first step, the primer set ("new start" and "P-bl

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start") is used to create and amplify, from the original gene sequence, the DNA fragment ("Fragment Start") that contains the sequence encoding the new N-terminal portion of the new protein. In the second step, the primer set ("new stop" and "P-bl stop") is used to create and amplify, from gene sequence, the DNA fragment ("Fragment Stop") that contains the sequence encoding the new C-terminal portion of the new protein. The "new start" and "new stop" primers are designed to include appropriate restriction sites which allow cloning of the new gene into expression vectors. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 50°C annealing for 45 seconds and 72°C extension for 45 seconds. Deep Vent polymerase (New England Biolabs) is used to reduce the occurrence of overhangs in conditions recommended by the manufacturer. The "P-bl start" and "P-bl stop" primers are phosphorylated at the 5′ end to aid in the subsequent blunt end ligation of "Fragment Start" and "Fragment Stop" to each other. A 100 ul reaction contained 150 pmole of each primer and one ug of template DNA; and 1x Vent buffer (New England Biolabs), 300 uM dGTP, 300 uM dATP, 300 uM dTTP, 300 uM dCTP, and 1 unit Deep Vent polymerase. PCR reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT). PCR reaction products are purified using a Wizard PCR Preps kit (Promega).

The primers are designed to include appropriate restriction sites which allow for the cloning of the new gene into expression vectors. Typically "Fragment Start" is designed to create NcoI restriction site , and "Fragment Stop" is designed to create a HindIII restriction site. Restriction digest reactions are purified using a Magic DNA Clean-up System kit (Promega). Fragments Start and Stop are resolved on a 1% TAE gel, stained with ethidium bromide and isolated using a Qiaex Gel Extraction kit (Qiagen). These fragments are combined with and annealed to the ends of the ~ 3800 base pair NcoI/HindIII vector fragment of pMON3934 by heating at 50°C for ten minutes and allowed to slow cool. The three fragments are ligated together using T4 DNA ligase (Boehringer Mannheim). The result is a plasmid containing the full-length new N-terminus/C-terminus gene. A portion of the ligation reaction is used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Plasmid DNA is purified and sequence confirmed as below.

Method III. Creation of new N-terminus/C-terminus genes by tandem-duplication method

New N-terminus/C-terminus genes can be made based on the method described in R. A. Horlick, et al *Protein Eng.* 5:427-431, 1992). Polymerase chain reaction (PCR) amplification of the new N-terminus/C-terminus genes is performed using a tandemly duplicated template DNA. The steps are illustrated in Figure 3.

The tandemly-duplicated template DNA is created by cloning and contains two copies of the gene separated by DNA sequence encoding a linker connecting the original C- and N-terminal ends of the two copies of the gene. Specific primer sets are used to create and amplify a full-length new N terminus/C-terminus gene from the tandemly-duplicated template DNA. These primers are designed to include appropriate restriction sites which allow for the cloning of the new gene into expression vectors. Typical PCR conditions are one cycle 95°C melting for two minutes; 25 cycles 94°C denaturation for one minute, 50°C annealing for one minute and 72°C extension for one minute; plus one cycle 72°C extension for seven minutes. A Perkin Elmer GeneAmp PCR Core Reagents kit (Perkin Elmer Corporation, Norwalk, CT) is used. A 100 ul reaction contains 100 pmole of each primer and one ug of template DNA; and 1x PCR buffer, 200 uM dGTP, 200 uM dATP, 200 uM dTTP, 200 uM dCTP, 2.5 units AmpliTaq DNA polymerase and 2 mM $MgCl_2$. PCR reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT). PCR reactions are purified using a Wizard PCR Preps kit (Promega).

Cloning of new N-terminus/C-terminus genes into multi-functional receptor agonist expression vectors.

The new N-terminus/C-terminus gene is digested with restriction endonucleases to create ends that are compatible to insertion into an expression vector containing another colony stimulating factor gene. This expression vector is likewise digested with restriction endonucleases to form compatible ends. After purification, the gene and the vector DNAs are combined and ligated using T4 DNA ligase. A portion of the ligation reaction is used to transform E. coli. Plasmid DNA is purified and sequenced to confirm the correct insert. The correct clones are grown for protein expression.

DNA isolation and characterization

Plasmid DNA can be isolated by a number of different methods and using commercially available kits known to those skilled in the art. A few such methods are shown herein. Plasmid DNA is isolated using the Promega Wizard™ Miniprep kit (Madison, WI), the Qiagen QIAwell Plasmid isolation kits (Chatsworth, CA) or Qiagen Plasmid Midi kit. These kits follow the same general procedure for plasmid DNA isolation. Briefly, cells are pelleted by centrifugation (5000 x g), plasmid DNA released with sequential NaOH/acid treatment, and cellular debris is removed by centrifugation (10000 x g). The supernatant (containing the plasmid DNA) is loaded onto a column containing a DNA-binding resin, the column is washed, and plasmid DNA eluted with TE. After screening for the colonies with the plasmid of interest, the *E. coli* cells are inoculated into 50-100 mLs of LB plus appropriate antibiotic for overnight growth at 37°C in an air incubator while shaking. The purified plasmid DNA is used for DNA sequencing, further restriction enzyme digestion, additional subcloning of DNA fragments and transfection into mammalian, *E. coli* or other cells.

Sequence confirmation.

Purified plasmid DNA is resuspended in dH_2O and quantitated by measuring the absorbance at 260/280 nm in a Bausch and Lomb Spectronic 601 UV spectrometer. DNA samples are sequenced using ABI PRISM™ DyeDeoxy™ terminator sequencing chemistry (Applied Biosystems Division of Perkin Elmer Corporation, Lincoln City, CA) kits (Part Number 401388 or 402078) according to the manufacturers suggested protocol usually modified by the addition of 5% DMSO to the sequencing mixture. Sequencing reactions are performed in a Model 480 DNA thermal cycler (Perkin Elmer Corporation, Norwalk, CT) following the recommended amplification conditions. Samples are purified to remove excess dye terminators with Centri-Sep™ spin columns (Princeton Separations, Adelphia, NJ) and lyophilized. Fluorescent dye labeled sequencing reactions are resuspended in deionized formamide, and sequenced on denaturing 4.75% polyacrylamide-8M urea gels using an ABI Model 373A automated DNA sequencer. Overlapping DNA sequence fragments are analyzed and assembled into master DNA contigs using Sequencher DNA analysis software (Gene Codes Corporation, Ann Arbor, MI).

Expression of multi-functional receptor agonists in mammalian cells

Mammalian Cell Transfection/Production of Conditioned Media

The BHK-21 cell line can be obtained from the ATCC (Rockville, MD). The cells are cultured in Dulbecco's modified Eagle media (DMEM/high-glucose), supplemented to 2 mM (mM) L-glutamine and 10% fetal bovine serum (FBS). This formulation is designated BHK growth media. Selective media is BHK growth media supplemented with 453 units/mL hygromycin B (Calbiochem, San Diego, CA). The BHK-21 cell line was previously stably transfected with the HSV transactivating protein VP16, which transactivates the IE110 promoter found on the plasmid pMON3359 (See Hippenmeyer et al., *Bio/Technology*, pp.1037-1041, 1993). The VP16 protein drives expression of genes inserted behind the IE110 promoter. BHK-21 cells expressing the transactivating protein VP16 are designated BHK-VP16. The plasmid pMON1118 (See Highkin et al., *Poultry Sci.*, 70: 970-981, 1991) expresses the hygromycin resistance gene from the SV40 promoter. A similar plasmid is available from ATCC, pSV2-hph.

BHK-VP16 cells are seeded into a 60 millimeter (mm) tissue culture dish at 3×10^5 cells per dish 24 hours prior to transfection. Cells are transfected for 16 hours in 3 mL of "OPTIMEM"™ (Gibco-BRL, Gaithersburg, MD) containing 10 ug of plasmid DNA containing the gene of interest, 3 ug hygromycin resistance plasmid, pMON1118, and 80 ug of Gibco-BRL "LIPOFECTAMINE"™ per dish. The media is subsequently aspirated and replaced with 3 mL of growth media. At 48 hours post-transfection, media from each dish is collected and assayed for activity (transient conditioned media). The cells are removed from the dish by trypsin-EDTA, diluted 1:10 and transferred to 100 mm tissue culture dishes containing 10 mL of selective media. After approximately 7 days in selective media, resistant cells grow into colonies several millimeters in diameter. The colonies are removed from the dish with filter paper (cut to approximately the same size as the colonies and soaked in trypsin/EDTA) and transferred to individual wells of a 24 well plate containing 1 mL of selective media. After the clones are grown to confluence, the conditioned media is re-assayed, and positive clones are expanded into growth media.

Expression of multi-functional receptor agonists in *E. coli*

E. coli strain MON105 or JM101 harboring the plasmid of interest are grown at 37°C in M9 plus casamino acids medium with shaking in a air incubator Model G25 from New Brunswick Scientific (Edison, New Jersey). Growth is monitored at OD600 until it reaches a value of 1.0 at which time Nalidixic acid (10 milligrams/mL) in 0.1 N NaOH is added to a final concentration of 50 µg/mL. The cultures are then shaken at 37°C for three to four additional hours. A high degree of aeration is maintained throughout culture period in order to achieve maximal production of the desired gene product. The cells are examined under a light microscope for the presence of inclusion bodies (IB). One mL aliquots of the culture are removed for analysis of protein content by boiling the pelleted cells, treating them with reducing buffer and electrophoresis via SDS-PAGE (see Maniatis et al. Molecular Cloning: A Laboratory Manual, 1982). The culture is centrifuged (5000 x g) to pellet the cells.

Inclusion Body preparation, Extraction, Refolding, Dialysis, DEAE Chromatography, and Characterization of the multi-functional chimeric hematopoietic receptor

agonists which accumulate as inclusion bodies in *E. coli.*

Isolation of Inclusion Bodies:

The cell pellet from a 330 mL *E. coli* culture is resuspended in 15 mL of sonication buffer (10 mM 2-amino-2-(hydroxymethyl) 1,3-propanediol hydrochloride (Tris-HCl), pH 8.0 + 1 mM ethylenediaminetetraacetic acid (EDTA). These resuspended cells are sonicated using the microtip probe of a Sonicator Cell Disruptor (Model W-375, Heat Systems-Ultrasonics, Inc., Farmingdale, New York). Three rounds of sonication in sonication buffer followed by centrifugation are employed to disrupt the cells and wash the inclusion bodies (IB). The first round of sonication is a 3 minute burst followed by a 1 minute burst, and the final two rounds of sonication are for 1 minute each.

Extraction and refolding of proteins from inclusion body pellets:

Following the final centrifugation step, the IB pellet is resuspended in 10 mL of 50 mM Tris-HCl, pH 9.5, 8 M urea and 5 mM dithiothreitol (DTT) and stirred at room temperature for approximately 45 minutes to allow for denaturation of the expressed protein.

The extraction solution is transferred to a beaker containing 70 mL of 5 mM Tris-HCl, pH 9.5 and 2.3 M urea and gently stirred while exposed to air at 4°C for 18 to 48 hours to allow the proteins to refold. Refolding is monitored by analysis on a Vydac (Hesperia, Ca.) C18 reversed phase high pressure liquid chromatography (RP-HPLC) column (0.46x25 cm). A linear gradient of 40% to 65% acetonitrile, containing 0.1% trifluoroacetic acid (TFA), is employed to monitor the refold. This gradient is developed over 30 minutes at a flow rate of 1.5 mL per minute. Denatured proteins generally elute later in the gradient than the refolded proteins.

Purification:

Following the refold, contaminating *E. coli* proteins are removed by acid precipitation. The pH of the refold solution is titrated to between pH 5.0 and pH 5.2 using 15% (v/v) acetic acid (HOAc). This solution is stirred at 4°C for 2 hours and then centrifuged for 20 minutes at 12,000 x g to pellet any insoluble protein.

The supernatant from the acid precipitation step is dialyzed using a Spectra/Por 3 membrane with a molecular weight cut off (MWCO) of 3,500 daltons. The dialysis is against 2 changes of 4 liters (a 50-fold excess) of 10 mM Tris-HCl, pH 8.0 for a total of 18 hours. Dialysis lowers the sample conductivity and removes urea prior to DEAE chromatography. The sample is then centrifuged (20 minutes at 12,000 x g) to pellet any insoluble protein following dialysis.

A Bio-Rad Bio-Scale DEAE2 column (7 x 52 mm) is used for ion exchange chromatography. The column is equilibrated in a buffer containing 10 mM Tris-HCl, pH 8.0, and a 0-to-500 mM sodium chloride (NaCl) gradient, in equilibration buffer, over 45 column volumes is used to elute the protein. A flow rate of 1.0 mL per minute is used throughout the run. Column fractions (2.0 mL per fraction) are collected across the gradient and analyzed by RP HPLC on a Vydac (Hesperia, Ca.) C18 column (0.46 x 25 cm). A linear gradient of 40% to 65% acetonitrile, containing 0.1% trifluoroacetic acid (TFA), is employed. This gradient is developed over 30 minutes at a flow rate of 1.5 mL per minute. Pooled fractions are then dialyzed against 2 changes of 4 liters (50-to-500-fold excess) of 10 mM ammonium acetate (NH4Ac), pH 4.0 for a total of 18 hours. Dialysis is performed using a Spectra/Por 3 membrane with a MWCO of

3,500 daltons. Finally, the sample is sterile filtered using a 0.22μm syringe filter (μStar LB syringe filter, Costar, Cambridge, Ma.), and stored at 4°C.

In some cases the folded proteins can be affinity purified using affinity reagents such as mAbs or receptor subunits attached to a suitable matrix. Alternatively, (or in addition) purification can be accomplished using any of a variety of chromatographic methods such as: ion exchange, gel filtration or hydrophobic chromatography or reversed phase HPLC.

These and other protein purification methods are described in detail in Methods in Enzymology, Volume 182 'Guide to Protein Purification' edited by Murray Deutscher, Academic Press, San Diego, CA (1990).

Protein Characterization:

The purified protein is analyzed by RP-HPLC, electrospray mass spectrometry, and SDS-PAGE. The protein quantitation is done by amino acid composition, RP-HPLC, and Bradford protein determination. In some cases tryptic peptide mapping is performed in conjunction with electrospray mass spectrometry to confirm the identity of the protein.

AML Proliferation Assay for Bioactive Human Interleukin-3

The factor-dependent cell line AML 193 was obtained from the American Type Culture Collection (ATCC, Rockville, MD). This cell line, established from a patient with acute myelogenous leukemia, is a growth factor dependent cell line which displayed enhanced growth in GM-CSF supplemented medium (Lange, B., et al., *Blood* 70: 192, 1987; Valtieri, M., et al., *J. Immunol.* 138:4042, 1987). The ability of AML 193 cells to proliferate in the presence of human IL-3 has also been documented. (Santoli, D., et al., *J. Immunol.* 139: 348, 1987). A cell line variant was used, AML 193 1.3, which was adapted for long term growth in IL-3 by washing out the growth factors and starving the cytokine dependent AML 193 cells for growth factors for 24 hours. The cells are then replated at $1x10^5$ cells/well in a 24 well plate in media containing 100 U/mL IL-3. It took approximately 2 months for the cells to grow rapidly in IL-3. These cells are maintained as AML 193 1.3 thereafter by supplementing tissue culture medium (see below) with human IL-3.

AML 193 1.3 cells are washed 6 times in cold Hanks balanced salt solution (HBSS, Gibco, Grand Island, NY) by centrifuging cell suspensions at 250 x g for 10 minutes followed by decantation of the supernatant. Pelleted cells are resuspended in HBSS and the procedure is repeated until six wash cycles are completed. Cells washed six times by this procedure are resuspended in tissue culture medium at a density ranging from 2×10^5 to 5×10^5 viable cells/mL. This medium is prepared by supplementing Iscove's modified Dulbecco's Medium (IMDM, Hazelton, Lenexa, KS) with albumin, transferrin, lipids and 2-mercaptoethanol. Bovine albumin (Boehringer-Mannheim, Indianapolis, IN) is added at 500 µg/mL; human transferrin (Boehringer-Mannheim, Indianapolis, IN) is added at 100 µg/mL; soybean lipid (Boehringer-Mannheim, Indianapolis, IN) is added at 50 µg/mL; and 2-mercaptoethanol (Sigma, St. Louis, MO) is added at 5×10^{-5} M.

Serial dilutions of human interleukin-3 or multi-functional chimeric hematopoietic receptor agonist proteins are made in triplicate series in tissue culture medium supplemented as stated above in 96 well Costar 3596 tissue culture plates. Each well contained 50 µl of medium containing interleukin-3 or multi-functional chimeric hematopoietic receptor agonist proteins once serial dilutions are completed. Control wells contained tissue culture medium alone (negative control). AML 193 1.3 cell suspensions prepared as above are added to each well by pipetting 50 µl (2.5 x 10^4 cells) into each well. Tissue culture plates are incubated at 37°C with 5% CO_2 in humidified air for 3 days. On day 3, 0.5 µCi ^{3}H-thymidine (2 Ci/mM, New England Nuclear, Boston, MA) is added in 50 µl of tissue culture medium. Cultures are incubated at 37°C with 5% CO_2 in humidified air for 18-24 hours. Cellular DNA is harvested onto glass filter mats (Pharmacia LKB, Gaithersburg, MD) using a TOMTEC cell harvester (TOMTEC, Orange, CT) which utilized a water wash cycle followed by a 70% ethanol wash cycle. Filter mats are allowed to air dry and then placed into sample bags to which scintillation fluid (Scintiverse II, Fisher Scientific, St. Louis, MO or BetaPlate Scintillation Fluid, Pharmacia LKB, Gaithersburg, MD) is added. Beta emissions of samples from individual tissue culture wells are counted in a LKB BetaPlate model 1205 scintillation counter (Pharmacia LKB, Gaithersburg, MD) and data is expressed as counts per minute of ^{3}H-thymidine incorporated into cells from each tissue culture well. Activity of each human interleukin-3 preparation or multi-functional chimeric hematopoietic receptor agonist protein preparation is quantitated by measuring cell proliferation (^{3}H-thymidine incorporation) induced by graded concentrations of interleukin-3 or multi-functional chimeric hematopoietic receptor agonist. Typically, concentration ranges from 0.05 pM - 10^5 pM are quantitated in these assays. Activity is determined by measuring the dose of interleukin-3 or multi-functional chimeric hematopoietic receptor agonist protein which provides 50% of maximal proliferation (EC_{50} = 0.5 x (maximum average counts per minute of ^{3}H-thymidine incorporated per well among triplicate cultures of all concentrations of interleukin-3 tested -

background proliferation measured by ^{3}H-thymidine incorporation observed in triplicate cultures lacking interleukin-3). This EC_{50} value is also equivalent to 1 unit of bioactivity. Every assay is performed with native interleukin-3 as a reference standard so that relative activity levels could be assigned.

Typically, the multi-functional chimeric hematopoietic receptor agonist proteins were tested in a concentration range of 2000 pM to 0.06 pM titrated in serial 2 fold dilutions.

Activity for each sample was determined by the concentration which gave 50% of the maximal response by fitting a four-parameter logistic model to the data. It was observed that the upper plateau (maximal response) for the sample and the standard with which it was compared did not differ. Therefore relative potency calculation for each sample was determined from EC50 estimations for the sample and the standard as indicated above. AML 193.1.3 cells proliferate in response to hIL-3, hGM-CSF and hG-CSF. Therefore the following additional assays were performed for some samples to demonstrate that the G-CSF receptor agonist portion of the multi-functional chimeric hematopoietic receptor agonist proteins was active. The proliferation assay was performed with the multi-functional chimeric hematopoietic receptor agonist plus and minus neutralizing monoclonal antibodies to the hIL-3 receptor agonist portion. In addition, a fusion molecule with the factor Xa cleavage site was cleaved then purified and the halves of the molecule were assayed for proliferative activity. These experiments showed that both components of the multi-functional chimeric hematopoietic receptor agonist proteins were active.

TF1 c-mpl ligand dependent proliferation assay

The c-mpl ligand proliferative activity can be assayed using a subclone of the pluripotential human cell line TF1 (Kitamura et al., J. Cell Physiol 140:323-334. [1989]). TF1 cells are maintained in h-IL3 (100 U/mL). To establish a sub-clone responsive to c-mpl ligand, cells are maintained in passage media containing 10% supernatant from BHK cells transfected with the gene expressing the 1-153 form of c-mpl ligand (pMON26448). Most of the cells die, but a subset of cells survive. After dilution cloning, a c-mpl ligand responsive clone is selected, and these cells are split into passage media to a density of 0.3 x 10^6 cells/mL the day prior to assay set-up. Passage media for these cells is the following: RPMI 1640 (Gibco), 10% FBS (Harlan, Lot #91206), 10% c-mpl ligand supernatant from transfected BHK cells, 1 mM sodium pyruvate (Gibco), 2 mM glutamine (Gibco), and 100 ug/mL penicillin-streptomycin (Gibco). The next day, cells are harvested and washed twice in RPMI or IMDM media with a final wash in the ATL, or assay media. ATL medium consists of the following: IMDM (Gibco), 500 ug/mL of bovine serum albumin, 100 ug/mL of human transferrin, 50 ug/mL soybean lipids, 4 x 10-8M beta-mercaptoethanol and 2 mL of A9909 (Sigma, antibiotic solution) per 1000 mL of ATL. Cells are diluted in assay media to a final density of 0.25 x 10^6 cells/mL in a 96-well low evaporation plate (Costar) to a final volume of 50 ul. Transient supernatants (conditioned media) from transfected clones are added at a volume of 50 ul as duplicate samples at a final concentration of 50% and diluted three-fold to a final dilution of 1.8%. Triplicate samples of a dose curve of IL-3 variant pMON13288 starting at 1 ng/mL and diluted using three-fold dilutions to 0.0014ng/mL is included as a positive control. Plates are incubated at 5% CO_2 and 37° C. At day six of culture, the plate is pulsed with 0.5 Ci of 3H/well (NEN) in a volume of 20 ul/well and allowed to incubate at 5% CO_2 and 37° C for four hours.

The plate is harvested and counted on a Betaplate counter.

MUTZ-2 Cell Proliferation Assay

A cell line such as MUTZ-2, which is a human myeloid leukemia cell line (German Collection of Microorganisms and Cell Cultures, DSM ACC 271), can be used to determine the cell proliferative activity of flt3 receptor agonists. MUTZ-2 cultures are maintained with recombinant native flt3 ligand (20-100ng/mL) in the growth medium. Eighteen hours prior to assay set-up, MUTZ-2 cells are washed in IMDM medium (Gibco) three times and are resuspended in IMDM medium alone at a concentration of 0.5-0.7 x 10E6 cells/mL and incubated at 37°C and 5%CO_2 to starve the cells of flt3 ligand. The day of the assay, standards and flt3 receptor agonists are diluted to two fold above desired final concentration in assay media in sterile tissue culture treated 96 well plates. Flt3 receptor agonists and standards are tested in triplicate. 50µl of assay media is loaded into all wells except row A. 75µl of the flt3 receptor agonists or standards are added to row A and 25µl taken from that row and serial dilutions (1:3) performed on the rest of the plate (rows B through G). Row H remains as a media only control. The starved MUTZ-2 cells are washed two times in IMDM medium and resuspended in 50µl assay media. 50µl of cells are added to each well resulting in a final concentration of 0.25 x 10E6cells/mL. Assay plates containing cells are incubated at 37°C and 5%CO_2 for 44hrs. Each well is then pulsed with 1µCi/well of tritiated thymidine in a volume of 20µl for four hours. Plates are then harvested and counted.

Other in vitro cell based proliferation assays

Other in vitro cell based assays, known to those skilled in the art, may also be useful to determine the activity of the multi-functional chimeric hematopoietic receptor agonists depending on the factors that comprise the molecule in a similar manner as described in the AML 193.1.3 cell proliferation assay. The following are examples of other useful assays.

TF1 proliferation assay: TF1 is a pluripotential human cell line (Kitamura et al., J. Cell Physiol 140:323-334. [1989]) that responds to hIL-3.

32D proliferation assay: 32D is a murine IL-3 dependent cell line which does not respond to human IL-3 but does respond to human G-CSF which is not species restricted.

Baf/3 proliferation assay: Baf/3 is a murine IL-3 dependent cell line which does not respond to human IL-3 or human c-mpl ligand but does respond to human G-CSF which is not species restricted.

T1165 proliferation assay: T1165 cells are a IL-6 dependent murine cell line (Nordan et al., 1986) which respond to IL-6 and IL-11.

Human Plasma Clot meg-CSF Assay: Used to assay megakaryocyte colony formation activity (Mazur et al., 1981).

<u>Transfected cell lines</u>:

Cell lines such as the murine Baf/3 cell line can be transfected with a colony stimulating factor receptor, such as the human G-CSF receptor or human c-mpl receptor, which the cell line does not have. These transfected cell lines can be used to determine the activity of the ligand for which the receptor has been transfected into the cell line.

One such transfected Baf/3 cell line was made by cloning the cDNA encoding c-mpl from a library made from a c-mpl responsive cell line and cloned into the multiple cloning site of the plasmid pcDNA3 (Invitrogen, San Diego Ca.). Baf/3 cells were transfected with the plasmid via electroporation. The cells were grown under G418 selection in the presence of mouse IL-3 in Wehi conditioned media. Clones were established through limited dilution.

In a similar manner the human G-CSF receptor can be transfected into the Baf/3 cell line and used to determine the bioactivity of the multi-functional chimeric hematopoietic receptor agonists.

Analysis of c-mpl ligand proliferative activity

Methods

1. Bone marrow proliferation assay

a. CD34+ Cell Purification:

Bone marrow aspirates (15-20 mL) were obtained from normal allogeneic marrow donors after informed consent. Cells were diluted 1:3 in phosphate buffered saline (PBS, Gibco-BRL), 30 mL were layered over 15 mL Histopaque-1077 (Sigma) and centrifuged for 30 minutes at 300 RCF. The mononuclear interface layer was collected and washed in PBS. CD34+ cells were enriched from the mononuclear cell preparation using an affinity column per manufacturers instructions (CellPro, Inc., Bothell WA). After enrichment, the purity of CD34+ cells was 70% on average as determined by using flow cytometric analysis using anti-CD34 monoclonal antibody conjugated to fluorescein and anti-CD38 conjugated to phycoerythrin (Becton Dickinson, San Jose CA).

Cells were resuspended at 40,000 cells/mL in X-Vivo 10 media (Bio-Whittaker, Walkersville, MD) and 1 mL was plated in 12-well tissue culture plates (Costar). The growth factor rhIL-3 was added at 100 ng/mL (pMON5873) was added to some wells. hIL3 variants were used at 10 ng/mL to 100 ng/mL. Conditioned media from BHK cells transfected with plasmid encoding c-mpl ligand or multi-functional chimeric hematopoietic receptor agonists were tested by addition of 100 µl of supernatant added to 1 mL cultures (approximately a 10% dilution). Cells were incubated at 37°C for 8-14 days at 5% CO_2 in a 37°C humidified incubator.

b. Cell Harvest and Analysis:

At the end of the culture period a total cell count was obtained for each condition. For fluorescence analysis and ploidy determination cells were washed in megakaryocyte buffer (MK buffer, 13.6 mM sodium citrate, 1 mM theophylline, 2.2 µm PGE1, 11 mM glucose, 3% w/v BSA, in PBS, pH 7.4,) (Tomer et al., *Blood* 70: 1735-1742, 1987) resuspended in 500 µl of MK buffer containing anti-CD41a FITC antibody (1:200, AMAC, Westbrook, ME) and washed in MK buffer. For DNA analysis cells were permeablized in MK buffer containing 0.5% Tween 20 (Fisher, Fair Lawn NJ)for 20 min. on ice followed by fixation in 0.5% Tween-20 and 1% paraformaldehyde (Fisher Chemical) for 30 minutes followed by incubation in propidium iodide (Calbiochem , La Jolla Ca) (50 µg/mL) with RNA-ase (400 U/mL) in 55% v/v MK buffer (200mOsm) for 1-2 hours on ice. Cells were analyzed on a FACScan or Vantage flow cytometer (Becton Dickinson, San Jose, CA). Green fluorescence (CD41a-FITC) was collected along with linear and log signals for red fluorescence (PI) to determine DNA ploidy. All cells were collected to determine the percent of cells that were CD41+. Data analysis was performed using software by LYSIS (Becton Dickinson, San Jose, CA). Percent of cells expressing the CD41 antigen was obtained from flow cytometry analysis(Percent).

Absolute (Abs) number of CD41+ cells/mL was calculated by: (Abs)=(Cell Count)*(Percent)/100.

2. Megakaryocyte fibrin clot assay.

CD34+ enriched population were isolated as described above. Cells were suspended at 25,000 cells/mL with or without cytokine(s) in a media consisting of a base Iscoves IMDM media supplemented with 0.3% BSA, 0.4mg/mL apo-transferrin, 6.67μM $FeCl_2$, 25μg/mL $CaCl_2$, 25μg/mL L-asparagine, 500μg/mL e-amino-n-caproic acid and penicillin/streptomycin. Prior to plating into 35mm plates, thrombin was added (0.25 Units/mL) to initiate clot formation. Cells were incubated at 37°C for 13 days at 5% CO_2 in a 37°C humidified incubator.

At the end of the culture period plates were fixed with methanol:acetone (1:3), air dried and stored at -200C until staining. A peroxidase immunocytochemistry staining procedure was used (Zymed, Histostain-SP. San Francisco, CA) using a cocktail of primary monoclonal antibodies consisting of anti-CD41a, CD42 and CD61. Colonies were counted after staining and classified as negative, CFU-MK (small colonies, 1-2 foci and less that approx. 25 cells), BFU-MK (large, multi-foci colonies with > 25 cells) or mixed colonies (mixture of both positive and negative cells.

<u>Methylcellulose Assay</u>

This assay reflects the ability of colony stimulating factors to stimulate normal bone marrow cells to produce different types of hematopoietic colonies *in vitro* (Bradley et al., *Aust. Exp Biol. Sci.* 44:287-300, 1966), Pluznik et al., *J. Cell Comp. Physio* 66:319-324, 1965).

Methods

Approximately 30 mL of fresh, normal, healthy bone marrow aspirate are obtained from individuals following informed consent. Under sterile conditions samples are diluted 1:5 with a 1X PBS (#14040.059 Life Technologies, Gaithersburg, MD.) solution in a 50 mL conical tube (#25339-50 Corning, Corning MD). Ficoll (Histopaque 1077 Sigma H-8889) is layered under the diluted sample and centrifuged, 300 x g for 30 min. The mononuclear cell band is removed and washed two times in 1X PBS and once with 1% BSA PBS (CellPro Co., Bothel, WA). Mononuclear cells are counted and CD34+ cells are selected using the Ceprate LC (CD34) Kit (CellPro Co., Bothel, WA) column. This fractionation is performed since all stem and progenitor cells within the bone marrow display CD34 surface antigen.

Cultures are set up in triplicate with a final volume of 1.0 mL in a 35 X 10 mm petri dish (Nunc#174926). Culture medium is purchased from Terry Fox Labs. (HCC-4230 medium (Terry Fox Labs, Vancouver, B.C., Canada) and erythropoietin (Amgen, Thousand Oaks, CA.) is added to the culture media. 3,000-10,000 CD34+ cells are added per dish. Recombinant IL-3, purified from mammalian cells or *E. coli*, and multi-functional chimeric hematopoietic receptor agonist proteins, in conditioned media from transfected mammalian cells or purified from conditioned media from transfected mammalian cells or *E. coli*, are added to give final concentrations ranging from .001 nM to 10 nM. Recombinant hIL-3, GM-CSF, c-mpl ligand and multi-functional chimeric hematopoietic receptor agonist are supplied in house. G-CSF (Neupogen) is from Amgen (Thousand Oaks Calf.). Cultures are resuspended using a 3cc syringe and 1.0 mL is dispensed per dish. Control (baseline response) cultures received no colony stimulating factors. Positive control cultures received conditioned media (PHA stimulated human cells: Terry Fox

Lab. H2400). Cultures are incubated at 37°C, 5% CO_2 in humidified air.

Hematopoietic colonies which are defined as greater than 50 cells are counted on the day of peak response (days 10-11) using a Nikon inverted phase microscope with a 40x objective combination. Groups of cells containing fewer than 50 cells are referred to as clusters. Alternatively colonies can be identified by spreading the colonies on a slide and stained or they can be picked, resuspended and spun onto cytospin slides for staining.

Human Cord Blood Hemopoietic Growth Factor Assays

Bone marrow cells are traditionally used for in vitro assays of hematopoietic colony stimulating factor (CSF) activity. However, human bone marrow is not always available, and there is considerable variability between donors. Umbilical cord blood is comparable to bone marrow as a source of hematopoietic stem cells and progenitors (Broxmeyer et al., *PNAS USA* 89:4109-113, 1992; Mayani et al., *Blood* 81:3252-3258, *1993*). In contrast to bone marrow, cord blood is more readily available on a regular basis. There is also a potential to reduce assay variability by pooling cells obtained fresh from several donors, or to create a bank of cryopreserved cells for this purpose. By modifying the culture conditions, and/or analyzing for lineage specific markers, it is be possible to assay specifically for granulocyte / macrophage colonies (CFU-GM), for megakaryocyte CSF activity, or for high proliferative potential colony forming cell (HPP-CFC) activity.

Methods

Mononuclear cells (MNC) are isolated from cord blood within 24 hr. of collection, using a standard density gradient (1.077 g/mL Histopaque). Cord blood MNC have been further enriched for stem cells and progenitors by several procedures, including immunomagnetic selection for CD14-, CD34+ cells; panning for SBA-, CD34+ fraction using coated flasks from Applied Immune Science (Santa Clara, CA); and CD34+ selection using a CellPro (Bothell, WA) avidin column. Either freshly isolated or cryopreserved CD34+ cell enriched fractions are used for the assay. Duplicate cultures for each serial dilution of sample (concentration range from 1 pM to 1204 pM) are prepared with $1x10^4$ cells in 1ml of 0.9% methylcellulose containing medium without additional growth factors (Methocult H4230 from Stem Cell Technologies, Vancouver, BC.). In some experiments, Methocult H4330 containing erythropoietin (EPO) was used instead of Methocult H4230, or Stem Cell Factor (SCF), 50 ng/mL (Biosource International, Camarillo, CA) was added. After culturing for 7-9 days, colonies containing >30 cells are counted. In order to rule out subjective bias in scoring, assays are scored blind.

Additional details about recombinant DNA methods which may be used to create the variants, express them in bacteria, mammalian cells or insect cells, purification and refold of the desired proteins and assays for determining the bioactvity of the proteins may be found in co-filed Applications WO 95/00646, WO 94/12639, WO 94/12638, WO 95/20976, WO 95/21197, WO 95/20977, WO 95/21254 and US 08/383,035 which are hereby incorporated by reference in their entirety.

Further details known to those skilled in the art may be found in T. Maniatis, et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, 1982) and references cited therein, incorporated herein by reference; and in J. Sambrook, et al., Molecular Cloning, A Laboratory Manual, 2nd edition, Cold Spring Harbor Laboratory, 1989) and references cited therein, incorporated herein by reference.

TABLE 1
OLIGONUCLEOTIDES

c-mplNcoI N=A,C,G or T	ACGTCCATGGCNTCNCCNGCNCCNCCTGCTTGTGCACTCCGAGTC SEQ ID NO:317
Ecompl	ATGCACGAATTCCCTGACGCAGAGGGTGGA SEQ ID NO:318
c-mplHindIII	TGACAAGCTTACCTGACGCAGAGGGTGGACCCT SEQ ID NO:319
4L-5′	AATTCGGCAA SEQ ID NO:320
4L-3′	CATGTTGCCG SEQ ID NO:321
5L-5′	AATTCGGCGGCAA SEQ ID NO:322
5L-3′	CATGTTGCCGCCG SEQ ID NO:323
8L-5′	AATTCGGCGGCAACGGCGGCAA SEQ ID NO:324
8L-3′	CATGTTGCCGCCGTTGCCGCCG SEQ ID NO:325
31-5′	CGATCCATGGAGGTTCACCCTTTGCCT SEQ ID NO:326
31-3′	GATCAAGCTTATGGGCACTGGCTCAGTCT SEQ ID NO:327
35-5′	CGATACATGTTGCCTACACCTGTCCTG SEQ ID NO:328
35-3′	GATCAAGCTTAAGGGTGAACCTCTGGGCA SEQ ID NO:329
39-5′	CGATCCATGGTCCTGCTGCCTGCTGTG SEQ ID NO:330
39-3′	GATCAAGCTTAAGGTGTAGGCAAAGGGTG SEQ ID NO:331
43-5′	CGATCCATGGCTGTGGACTTTAGCTTGGGA SEQ ID NO:332
43-3′	GATCAAGCTTAAGGCAGCAGGACAGGTGT SEQ ID NO:333
45-5′	CGATCCATGGACTTTAGCTTGGGAGAA SEQ ID NO:334
45-3′	GATCAAGCTTACACAGCAGGCAGCAGGAC SEQ ID NO:335
49-5′	CGATCCATGGGAGAATGGAAAACCCAG SEQ ID NO:336
49-3′	GATCAAGCTTACAAGCTAAAGTCCACAGC SEQ ID NO:337
82-5′	CGATCCATGGGACCCACTTGCCTCTCA SEQ ID NO:338
82-3′	GATCAAGCTTACAGTTGTCCCCGTGCTGC SEQ ID NO:339
109-5′	CAGTCCATGGGAACCCAGCTTCCTCCA SEQ ID NO:340
109-3′	GATCAAGCTTAAAGGAGGCTCTGCAGGGC SEQ ID NO:341
116-5′	CGATCCATGGGCAGGACCACAGCTCAC SEQ ID NO:342
116-3′	GATCAAGCTTACTGTGGAGGAAGCTGGGTT SEQ ID NO:343
120-5′	CGATCCATGGCTCACAAGGATCCCAATGCC SEQ ID NO:344
120-3′	GATCAAGCTTATGTGGTCCTGCCCTGTGG SEQ ID NO:345
123-5′	CGATCCATGGATCCCAATGCCATCTTCCTG SEQ ID NO:346
123-3′	GATCAAGCTTACTTGTGAGCTGTGGTCCT SEQ ID NO:347
126-5′	CGATCCATGGCCATCTTCCTGAGCTTCCAA SEQ ID NO:348
126-3′	GATCAAGCTTAATTGGGATCCTTGTGAGCTGT SEQ ID NO:349
SYNNOXA1.REQ	AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC TCC SEQ ID NO:350

SYNNOXA2.REQ	CCGGGGAGCC TCCACCGCCC TCTACGTACT GTTGAGCCTG CGCGTTCTCC AAGGTTTTCA GATAGAAGGT CAGTTTACGA CGG SEQ ID NO:351
L1syn.for	GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAACTGCTC TATAATGAT SEQ ID NO:352
L1syn.rev	CGATCATTAT AGAGCAGTTA GAGCCACCAC CCTGTTGTTC CTGCGCTTGC TCAAGG SEQ ID NO:353
L3syn.for	GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG CAGCGGCGGC GGTTCTAACT GCTCTATAAT GAT SEQ ID NO:354
L3syn.rev	CGATCATTAT AGAGCAGTTA GAACCGCCGC CGCTGCCACC GCCAGAGCCA CCACCCTGTT GTTCCTGCGC TTGCTCAAGG SEQ ID NO:355
35start.seq	GATCGACCAT GGCTCTGGAC CCGAACAACC TC SEQ ID NO:356
34rev.seq	CTCGATTACG TACAAAGGTG CAGGTGGT SEQ ID NO:357
70start.seq	GATCGACCAT GGCTAATGCA TCAGGTATTG AG SEQ ID NO:358
69rev.seq	CTCGATTACG TATTCTAAGT TCTTGACA SEQ ID NO:359
91start.seq	GATCGACCAT GGCTGCACCC TCTCGACATC CA SEQ ID NO:360
90rev.seq	CTCGATTACG TAGGCCGTGG CAGAGGGC SEQ ID NO:361
101start.seq	GATCGACCAT GGCTGCAGGT GACTGGCAAG AA SEQ ID NO:362
100rev.seq	CTCGATTACG TACTTGATGA TGATTGGA SEQ ID NO:363
L-11start.seq	GCTCTGAGAG CCGCCAGAGC CGCCAGAGGG CTGCGCAAGG TGGCGTAGAA CGCG SEQ ID NO:364
L-11stop.seq	CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAG SEQ ID NO:365
P-b1start.seq	GGGCTGCGCA AGGTGGCG SEQ ID NO:366
P-b1stop.seq	ACACCATTGG GCCCTGCCAG C SEQ ID NO:367
39start.seq	GATCGACCAT GGCTTACAAG CTGTGCCACC CC SEQ ID NO:368
38stop.Seq	CGATCGAAGC TTATTAGGTG GCACACAGCT TCTCCT SEQ ID NO:369
97start.seq	GATCGACCAT GGCTCCCGAG TTGGGTCCCA CC SEQ ID NO:370
96stop.Seq	CGATCGAAGC TTATTAGGAT ATCCCTTCCA GGGCCT SEQ ID NO:371
126start.seq	GATCGACCAT GGCTATGGCC CCTGCCCTGC AG SEQ ID NO:372
125stop.Seq	CGATCGAAGC TTATTATCCC AGTTCTTCCA TCTGCT SEQ ID NO:373
133start.seq	GATCGACCAT GGCTACCCAG GGTGCCATGC CG SEQ ID NO:374
132stop.seq	CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA SEQ ID NO:375
142start.seq	GATCGACCAT GGCTTCTGCT TTCCAGCGCC GG SEQ ID NO:376
141stop.Seq	CGATCGAAGC TTATTAGGCG AAGGCCGGCA TGGCAC SEQ ID NO:377
GLYXA1	GTAGAGGGCG GTGGAGGCTC C SEQ ID NO:378
GLYXA2	CCGGGGAGCC TCCACCGCCC TCTAC SEQ ID NO:379
1GGGSfor	TTCTACGCCA CCTTGCGCAG CCCGGCGGCG GCTCTGACAT GTCTACACCA TTG SEQ ID NO:380
1GGGSrev	CAATGGTGTA GACATGTCAG AGCCGCCGCC GGGCTGCGCA AGGTGGCGTA GAA SEQ ID NO:381
NCOFLT	CTGACCATGGCNACCCAGGACTGCTCCTTCCAA SEQ ID NO:807

HIND160	ACTGAAGCTTAGGGCTGACACTGCAGCTCCAG SEQ ID NO:808
HIND165	ACTGAAGCTTACAGGGTTGAGGAGTCGGGCTG SEQ ID NO:809
FL23For	GACTGCCATGGCNACYCAGGAYTGYTCYTTYCAACACAGCCCCATC SEQ ID NO:810
FH3AFor	GACTGCCATGGCNACYCAGGAYTGYTCYTTYCAACACAGCCCCATC SEQ ID NO:811
SCF.REV	TGTCCAAACTCATCAATGTATC SEQ ID NO:812
39FOR	CATGGCCATGGCCGACGAGGAGCTCTGCGGGGGCCTCT SEQ ID NO:813
39REV	GCTAGAAGCTTACTGCAGGTTGGAGGCCACGGTGAC SEQ ID NO:814
65FOR	CATGGCCATGGCCTCCAAGATGCAAGGCTTGCTGGAGC SEQ ID NO:815
65REV	GCTAGAAGCTTACCCAGCGACAGTCTTGAGCCGCTC SEQ ID NO:816
89FOR	CATGGCCATGGCCCCCCCCAGCTGTCTTCGCTTCGT SEQ ID NO:817
89REV	GCTAGAAGCTTAGGGCTGAAAGGCACATTTGGTGACA SEQ ID NO:818
L5A	CCCTGTCTGGCGGCAACGGCACCCAGGACTGCTCCTTCCAAC SEQ ID NO:819
L10A	GCGGTAACGGCAGTGGAGGTAATGGCACCCAGGACTGCTCCTTCCAAC SEQ ID NO:820
L15A	ACGGCAGTGGTGGCAATGGGAGCGGCGGAAATGGAACCCAGGACT GCTCCTTCCAAC SEQ ID NO:821
L5B	GTGCCGTTGCCGCCAGACAGGGTTGAGGAGTCGGGCTG SEQ ID NO:822
L10B	ATTACCTCCACTGCCGTTACCGCCTGACAGGGTTGAGGAGTCGGG CTG SEQ ID NO:823
L15B	GCTCCCATTGCCACCACTGCCGTTACCTCCAGACAGGGTTGAGGA GTCGGGCTG SEQ ID NO:824
L15C	GATGAGGATCCGGTGGCAATGGGAGCGGCGGAAATGGAACCCAGG ACTGCTCCTTCCACC SEQ ID NO:825
L15D	GATGACGGATCCGTTACCTCCAGACAGGGTTGAGGAGTCGGGCTG SEQ ID NO:826
L15E	GATGACGGATCCGGAGGTAATGGCACCCAGGACTGCTCCTTCCAAC SEQ ID NO:827
339FOR2	GACTGCCATGGCCGACGAGGAGCTCTGCG SEQ ID NO:828
339REV2	GACTCAAGCTTACTGCAGGTTGGAGGCC SEQ ID NO:829
339-10FOR3	GACTCGGGATCCGGAGGTTCTGGCACCCAGGACTGCTCC SEQ ID NO:830
339-15FOR2	GACTGGGATCCGGTGGCAGTGGGAGCGGCGGATCTGGAACC SEQ ID NO:831
339REV3	GACTTGGGATCCACTACCTCCAGACAGGGTTGAGGA GTC SEQ ID NO:832
FLN3	ACTGACGGATCCACCGCCCAGGGTTGAGGAGTCGGGCTG SEQ ID NO:833
FLN7	ACTGACGGATCCACCTCCTGACCCACCGCCCAGGGTTGAGGAGTCGGGCTG SEQ ID NO:834
FLN11	ACTGACGGATCCACCTCCTGACCCACCTCCTGACCCACCGCCCAG GGTTGAGGAGTCGGGCTG SEQ ID NO:835
C-term	ACGTAAAGCTTACAGGGTTGAGGAGTCG SEQ ID NO:836
FLC3	GTCAGTGGATCCGGAGGTACCCAGGACTGCTCCTTCCAA C SEQ ID NO:837
FLC4	GTCAGTGGATCCGGAGGTGGCACCCAGGACTGCTCCTTCCAAC SEQ ID NO:838
FLC10	TCAGTGGATCCGGAGGTGGCTCAGGGGGAGGTAGTGGTACCCAG GACTGCTCCTTCCAAC SEQ ID NO:839
N-term	TAGTCCATGGCCACCCAGGACTGCTCC SEQ ID NO:840
134.rev	GCATTACGTAGGGCTGACACTGCAGCTCCAG SEQ ID NO:841

139.rev	GCATTACGTACAGGGTTGAGGAGTCGGGCTG SEQ ID NO:842
Fl29for	GTCAGACCATGGCCGATTACCCAGTCACCGTGGCCTC SEQ ID NO:843;
FL29rev	TCTGACAAGCTTATTGAAGCAGGTAGTCAGACAGCTCAC SEQ ID NO:844;
FL35for	GTCAGCCCATGGCCGCCTCCAACCTGCAGGACGAGGA SEQ ID NO:845;
FL35rev	TCTGACAAGCTTACACGGTGACTGGGTAACTTGAAGC SEQ ID NO:846;
FL63for	GTCAGACCATGGCCGTCGCTGGGTCCAAGATGCAAGGC SEQ ID NO:847;
FL63rev	TCTGACAAGCTTAAGTCTTGAGCCGCTCCATCCAGCG SEQ ID NO:848;
FL95for	GTCAGACCATGGCCCGCTTCGTCCAGACCAACATCTCC SEQ ID NO:849;
FL95rev	TCTGACAAGCTTAAAGACAGCTGGGGGGGGGCTGAA SEQ ID NO:850;
FL99for	GTCAGACCATGGCCACCAACATCTCCCGCCTCCTGCAG SEQ ID NO:851;
FL99rev	CTCGACAAGCTTACTGGACGAAGCGAAGACAGCTGGG SEQ ID NO:852;
FLTAFLS1	GATCACATGTCTACAAATCAAGATCTGCCTGTG SEQ ID NO:853
FLTR1N	GATCGAATTCGTTGTCTTGGATGAAAGGGA SEQ ID NO:854
HGCFOR	ACTTGAATTCATCATCCTGGGCCTGTTCGGGC SEQ ID NO:855
HGCREV	ACTCAAGCTTAGAAGCTCCCCAGCGCCTCC SEQ ID NO:856
FL29FOR	GTCAGACCATGGCCGATTACCCAGTCACCGTGGCCTC SEQ ID NO:382
FL35FOR	GTCAGCCCATGGCCGCCTCCAACCTGCAGGACGAGGA SEQ ID NO:383
FL63FOR	GTCAGACCATGGCCGTCGCTGGGTCCAAGATGCAAGGC SEQ ID NO:384
FL95FOR	GTCAGACCATGGCCCGCTTCGTCCAGACCAACATCTCC SEQ ID NO:385
FL99FOR	GTCAGACCATGGCCACCAACATCTCCCGCCTCCTGCAG SEQ ID NO:386
FL29REV	TCTGACAAGCTTATTGAAGCAGGTAGTCAGACAGCTCAC SEQ ID NO:387
FL35REV	TCTGACAAGCTTACACGGTGACTGGGTAATCTTGAAGC SEQ ID NO:388
FL63REV	TCTGACAAGCTTAAGTCTTGAGCCGCTCCATCCAGCG SEQ ID NO:389
89 REVSTOP	GTCAAGAAGCTTACGGCTGAAAGGCACATTTG SEQ ID NO:390
FL95REV	TCTGACAAGCTTAAAGACAGCTGGGGGGGGGCTGAA SEQ ID NO:391
FL99REV	CTCGACAAGCTTACTGGACGAAGCGAAGACAGCTGGG SEQ ID NO:392
Flt36	GTTGCCATGGCNTCNAAYCTGCARGAYGARGARCTGTGCGGGGGCCTCTGGCGGCTG SEQ ID NO:393
Flt37	GTTGCCATGGCNAAYCTGCARGAYGARGARCTGTGYGGGGGCCTCTGGCGGCTGGTC SEQ ID NO:394
Flt38	GTTGCCATGGCNCTGCARGAYGARGARCTGTGYGGYGGCCTCTGGCGGCTGGTCCTG SEQ ID NO:395
Flt39	GTTGCCATGGCNCARGAYGARGARCTGTGYGGYGGYC

	TCTGGCGGCTGGTCCTGGCA SEQ ID NO:396
Flt40	GTTGCCATGGCNGAYGARGARCTGTGYGGYGGYCTCTGGCGGCTGGTCCTGGCACAG SEQ ID NO:397
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Flt42	GTTGCCATGGCNGARCTGTGYGGYGGYCTGTGGCGYCTGGTCCTGGCACAGCGCTGG SEQ ID NO:399
Flt43	GTTGCCATGGCNCTGTGYGGYGGYCTGTGGCGYCTGGTCCTGGCACAGCGCTGGATG SEQ ID NO:400
40 COLI	GTTGCCATGGCWGATGAAGAACTGTGTGGNGGNCTGTGGCGG SEQ ID NO:401
36REV	TATGCAAGCTTAGGCCACGGTGACTGGGTA SEQ ID NO:402
37REV	TATGCAAGCTTAGGAGGCCACGGTGACTGG SEQ ID NO:403
38REV	TATGCAAGCTTAGTTGGAGGCCACGGTGAC SEQ ID NO:404
39REV	TATGCAAGCTTACAGGTTGGAGGCCACGGT SEQ ID NO:405
41REV	TATGCAAGCTTAGTCCAGGTTGGAGGCCAC SEQ ID NO:406
42REV	TATGCAAGCTTACTCGTCCAGGTTGGAGGC SEQ ID NO:407
43REV	TATGCAAGCTTACTCCTCGTCCAGGTTGGA SEQ ID NO:408
39N TERM-2	GACTAGCCATGGCNGAYGARGARCTGTGYGGTGGCCTCTGGCGG SEQ ID NO:409
SNA B1CTERM	GACTAGTACGTACTGCAGGTTGGAGGCCACGG SEQ ID NO:410
29SMB1	GCAGGTTACGTATTGAAGCAGGTAGTCAGACAGCTC SEQ ID NO:411
34SNAB1	GCAGGTTACGTACACGGTGACTGGGTAATCTTGAAG SEQ ID NO:412
63SNAB1	GCAGGTTACGTAAGTCTTGAGCCGCTCCATCCAGC SEQ ID NO:413
66SNAB1	GCAGGTTACGTAGCCAGCGACAGTCTTGAGCCGCTC SEQ ID NO:414

89N-TERMCSLI	GTCAAGCCATGGCNCCRCCRAGCTGTCTRCGCT TCGTTCAGACCAACTC SEQ ID NO:415
89SNAB1	GCAGGTTACGTACGGCTGAAAGGCACATTTGGTGACAA SEQ ID NO:416
945 SMB1	GCAGGTTACGTAAAGACAGCTGGGGGGGGG SEQ ID NO:417
98SUAB1	GCAGGTTACGTACTGGACGAAGCGAAGACAGCTG SEQ ID NO:418
BAM FOR 1	TCAGTTGGATCCGGCGGCGGAAGCGGAGGTGGCTCTGGGGGAGGTA SEQ ID NO:426
BAM REV 1	TCAGTTGGATCCTCCGCCAGAACCACCGCCTGACCCACCTCCTGACCC SEQ ID NO:427
NAVREV L	GTCTGAGGCGCCACCGCACCGACCGCTGGACAACCGCCTCTGACCC AGGACTGCTCCTTC SEQ ID NO:428
NAVREV S	GTCTGAGGCGCCACCGCACCGACCACCCAGGACTGCTCCTTCCAAC SEQ ID NO:429
NAVFOR	GTCTGAGGCGCCGAGTGGACGCGGGCTCCACGGTGGCGGCAGGGT TGAGGAGTCGGGCTG SEQ ID NO:430
XBAFOR1	GCTACGTCTAGATCTCCTGACCTCGACCCAGGACTGCTCCTTCCAAC SEQ ID NO:447
XBAREV1	GCTAGTTCTAGACCATCCTGGCTGACACGGTGAAACACCGTCTCTACG GGCTGACACTGCAGCTCCAG SEQ ID NO:448
LNK1FOR	GTCAGTACTAGTATGGGTGTCCGGGCTCTTCGGCTCCTGCAGG TTGGAGGCCACGG SEQ ID NO:449
LNK1REV	GTCAGTACTAGTCCGCCATCTCCGACACCATTAGGCCCTGCCAGC SEQ ID NO:450
LNK2FOR	GTCAGTTCCGGAGATTTCGGTTCTGCAGAGGGCTGCGCAAGG TGGCGTA SEQ ID NO:451
LNK2REV	GTCAGTTCCGGATACTCATACCAGCCCGCCATCCCCGGGTTCTA ATCTGCAAGATGAAGAGCTG SEQ ID NO:452
LNK7FOR	GTCAGTACTAGTATGGGTGTCCGGGCTCTTCGGAAAGGCACATTT GGTGACAAAGTGTATC SEQ ID NO:453
LNK7REV	GTCAGTACTAGTCCGCCATCTCCGGGTACACCATTAGGCCCTG CCAGC SEQ ID NO:454
LNK8REV	GTCAGTTCCGGATACTCATACCAGCCCGCCATCCCCGGGTAAGGCC TTTCAGCCCCCCCCCAG SEQ ID NO:455
C1FOR	GTCAGACCATGGCCACTCAGGACTCCTCTTTTC SEQ ID NO:456

C3FOR	CACTTTGTCACCAAATCTGCCTTTCAG SEQ ID NO:457
C3REV	CTGAAAGGCAGATTTGGTGACAAAGTG SEQ ID NO:458
C5FOR	GCCCCCCCCCAGCTCTCTTCG SEQ ID NO:459
C5REV	CGAAGAGAGCTGGGGGGGGGC SEQ ID NO:460
C6REV	GTCAGTTACGTACAGGGTTGAAGGAGTCGGGCTGAGACTGC SEQ ID NO:461
GPFOR1	GTCAGTCCATGGCTACTCAAGGTGCTATGC SEQ ID NO:462
GPREV2	GTAGCATACGTAGGGCTGCAGGGCAGGGGCC SEQ ID NO:463

TABLE 2
GENE SEQUENCES

pMON30304

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
AACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGACTTCCAAACCTGGAGAGCTTCGTAAGG
GCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCC
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TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGT SEQ ID
NO:1

pMON26458

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pMON28548

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GTAGGAGGGTCCACCCTCTGCGTCAGG SEQ ID NO:3

pMON28500

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GCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTC
CTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAAT
GCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTC
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pMON28501

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CTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAAT
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GCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTG
GGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAG
GGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGT
TTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGG SEQ ID NO:5

pMON28502

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GCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTC
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SEQ ID NO:6
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Syntan1

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 51  GACCACCTGC  ACCTTTGCTG  GACCCGAACA  ACCTCAATGA  CGAAGACGTC
101  TCTATCCTGA  TGGACCGAAA  CCTTCGACTT  CCAAACCTGG  AGAGCTTCGT
151  AAGGGCTGTC  AAGAACTTAG  AAAATGCATC  AGGTATTGAG  GCAATTCTTC
201  GTAATCTCCA  ACCATGTCTG  CCCTCTGCCA  CGGCCGCACC  CTCTCGACAT
251  CCAATCATCA  TCAAGGCAGG  TGACTGGCAA  GAATTCCGGG  AAAAACTGAC
301  GTTCTATCTG  GTTACCCTTG  AGCAAGCGCA  GGAACAACAG  GGTGGTGGCT
351  CTAACTGCTC  TATAATGATC  GATGAAATTA  TACATCACTT  AAAGAGACCA
401  CCTGCACCTT  TGCTGGACCC  GAACAACCTC  AATGACGAAG  ACGTCTCTAT
451  CCTGATGGAC  CGAAACCTTC  GACTTCCAAA  CCTGGAGAGC  TTCGTAAGGG
501  CTGTCAAGAA  CTTAGAAAAT  GCATCAGGTA  TTGAGGCAAT  TCTTCGTAAT
551  CTCCAACCAT  GTCTGCCCTC  TGCCACGGCC  GCACCCTCTC  GACATCCAAT
601  CATCATCAAG  GCAGGTGACT  GGCAAGAATT  CCGGGAAAAA  CTGACGTTCT
651  ATCTGGTTAC  CCTTGAGCAA  GCGCAGGAAC  AACAGTAC
      SEQ ID NO:7
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Syntan3

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101  TCTATCCTGA  TGGACCGAAA  CCTTCGACTT  CCAAACCTGG  AGAGCTTCGT
151  AAGGGCTGTC  AAGAACTTAG  AAAATGCATC  AGGTATTGAG  GCAATTCTTC
201  GTAATCTCCA  ACCATGTCTG  CCCTCTGCCA  CGGCCGCACC  CTCTCGACAT
251  CCAATCATCA  TCAAGGCAGG  TGACTGGCAA  GAATTCCGGG  AAAAACTGAC
301  GTTCTATCTG  GTTACCCTTG  AGCAAGCGCA  GGAACAACAG  GGTGGTGGCT
351  CTGGCGGTGG  CAGCGGCGGC  GGTTCTAACT  GCTCTATAAT  GATCGATGAA
401  ATTATACATC  ACTTAAAGAG  ACCACCTGCA  CCTTTGCTGG  ACCCGAACAA
451  CCTCAATGAC  GAAGACGTCT  CTATCCTGAT  GGACCGAAAC  CTTCGACTTC
501  CAAACCTGGA  GAGCTTCGTA  AGGGCTGTCA  AGAACTTAGA  AATGCATCA
551  GGTATTGAGG  CAATTCTTCG  TAATCTCCAA  CCATGTCTGC  CCTCTGCCAC
601  GGCCGCACCC  TCTCGACATC  CAATCATCAT  CAAGGCAGGT  GACTGGCAAG
651  AATTCCGGGA  AAAACTGACG  TTCTATCTGG  TTACCCTTGA  GCAAGCGCAG
701  GAACAACAGT  AC  SEQ  ID  NO:8
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pMON31104

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 51  GGACCGAAAC  CTTCGACTTC  CAAACCTGGA  GAGCTTCGTA  AGGGCTGTCA
101  AGAACTTAGA  AAATGCATCA  GGTATTGAGG  CAATTCTTCG  TAATCTCCAA
151  CCATGTCTGC  CCTCTGCCAC  GGCCGCACCC  TCTCGACATC  CAATCATCAT
201  CAAGGCAGGT  GACTGGCAAG  AATTCCGGGA  AAAACTGACG  TTCTATCTGG
251  TTACCCTTGA  GCAAGCGCAG  GAACAACAGG  GTGGTGGCTC  TAACTGCTCT
301  ATAATGATCG  ATGAAATTAT  ACATCACTTA  AAGAGACCAC  CTGCACCTTT
351  GTACGTAGAG  GGCGGTGGAG  GCTCCCCGGG  TGAACCGTCT  GGTCCAATCT
401  CTACTATCAA  CCCGTCTCCT  CCGTCTAAAG  AATCTCATAA  ATCTCCAAAC
451  ATGGCTACCC  AGGGTGCCAT  GCCGGCCTTC  GCCTCTGCTT  TCCAGCGCCG
501  GGCAGGAGGG  GTCCTGGTTG  CTAGCCATCT  GCAGAGCTTC  CTGGAGGTGT
551  CGTACCGCGT  TCTACGCCAC  CTTGCGCAGC  CCTCTGGCGG  CTCTGGCGGC
601  TCTCAGAGCT  TCCTGCTCAA  GTCTTTAGAG  CAAGTGAGAA  AGATCCAGGG
651  CGATGGCGCA  GCGCTCCAGG  AGAAGCTGTG  TGCCACCTAC  AAGCTGTGCC
701  ACCCCGAGGA  GCTGGTGCTG  CTCGGACACT  CTCTGGGCAT  CCCCTGGGCT
751  CCCCTGAGCT  CCTGCCCCAG  CCAGGCCCTG  CAGCTGGCAG  GCTGCTTGAG
801  CCAACTCCAT  AGCGGCCTTT  TCCTCTACCA  GGGGCTCCTG  CAGGCCCTGG
851  AAGGGATATC  CCCCGAGTTG  GGTCCCACCT  TGGACACACT  GCAGCTGGAC
901  GTCGCCGACT  TTGCCACCAC  CATCTGGCAG  CAGATGGAAG  AACTGGGAAT
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951  GGCCCCTGCC CTGCAGCCCT AATAA SEQ ID NO:9
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pMON31105

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101  CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC
151  CTTGAGCAAG CGCAGGAACA ACAGGGTGGT GGCTCTAACT GCTCTATAAT
201  GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA CCTTTGCTGG
251  ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC
301  CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA
351  ATACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
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501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
951  GGCCCCTGCC CTGCAGCCCT AATAA SEQ ID NO:10
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pMON31106

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101  AGGAACAACA GGGTGGTGGC TCTAACTGCT CTATAATGAT CGATGAAATT
151  ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT
201  CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT CGACTTCCAA
251  ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT
301  ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC
351  CTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
451  ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
951  GGCCCCTGCC CTGCAGCCCT AATAA SEQ ID NO:11
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pMON31107

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201  CCGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA
251  ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA
301  TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA
351  GTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
401  CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
451  ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
501  GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
551  CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
601  TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
651  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
701  ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
751  CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
801  CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
851  AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
901  GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
951  GGCCCCTGCC CTGCAGCCCT AATAA SEQ ID NO:12
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pMON31108

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 51 GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA
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151 CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC CAATCATCAT
201 CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG TTCTATCTGG
251 TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TGGCGGTGGC
301 AGCGGCGGCG GTTCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA
351 CTTAAAGAGA CCACCTGCAC CTTTGTACGT AGAGGGCGGT GGAGGCTCCC
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451 AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
501 CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
551 ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
601 CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
651 AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
701 TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
751 CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
801 CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
851 ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
901 ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
951 GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
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pMON31109

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151 CTTGAGCAAG CGCAGGAACA ACAGGGTGGT GGCTCTGGCG GTGGCAGCGG
201 CGGCGGTTCT AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA
251 AGAGACCACC TGCACCTTTG CTGGACCCGA ACAACCTCAA TGACGAAGAC
301 GTCTCTATCC TGATGGACCG AAACCTTCGA CTTCCAAACC TGGAGAGCTT
351 CGTAAGGGCT GTCAAGAACT TAGAATACGT AGAGGGCGGT GGAGGCTCCC
401 CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
451 AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
501 CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
551 ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
601 CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
651 AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
701 TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
751 CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
801 CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
851 ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
901 ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
951 GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
      SEQ ID NO:14
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pMON31110

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  1 ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA
 51 AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC
101 AGGAACAACA GGGTGGTGGC TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC
151 TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC
201 ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA
251 TGGACCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC
301 AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA
351 ACCATGTCTG CCCTCTGCCA CGGCCTACGT AGAGGGCGGT GGAGGCTCCC
401 CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
451 AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
501 CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
551 ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
601 CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
651 AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
701 TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
751 CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
801 CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
851 ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
901 ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
951 GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
      SEQ ID NO:15
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pMON31111

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  1 ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT
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51 GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTGGCGGTG
101 GCAGCGGCGG CGGTTCTAAC TGCTCTATAA TGATCGATGA AATTATACAT
151 CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA
201 CGAAGACGTC TCTATCCTGA TGGACCGAAA CCTTCGACTT CCAAACCTGG
251 AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC AGGTATTGAG
301 GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC
351 CTCTCGACAT CCAATCATCA TCAAGTACGT AGAGGGCGGT GGAGGCTCCC
401 CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
451 AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
501 CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
551 ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
601 CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
651 AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
701 TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
751 CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
801 CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT
851 ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
901 ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
951 GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
SEQ ID NO:16

pMON13182

1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351 CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
401 ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC
451 ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC
501 AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC
551 TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA
601 CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA
651 AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG
701 CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC
751 CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC
801 GCAGCCCTCT GGCGGCTCTG GCGGCTCTCA GAGCTTCCTG CTCAAGTCTT
851 TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
901 CTGTGTGCCA CCTAATAA SEQ ID NO:17

pMON13183

1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTACAAG
451 CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC
501 CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT
551 GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG
601 GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA
651 GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
701 TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
751 GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
801 GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
851 CCTCTGGCGG CTCTGGCGGC TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG
901 CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG
951 TGCCACCTAA TAA SEQ ID NO:18

pMON13184

1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC

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251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC
401  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
451  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
501  GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC
551  GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG
601  TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG GCTCTGGCGG
651  CTCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA AAGATCCAGG
701  GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC
751  CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC
801  TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA
851  GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG
901  GAAGGGATAT CCTAATAA SEQ ID NO:19
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pMON13185

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCGAG
451  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
501  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
551  CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
601  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
651  CCGCGTTCTA CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC
701  AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT
751  GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC
801  CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC
851  TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA
901  CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG
951  GATATCCTAA TAA SEQ ID NO:20
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pMON13186

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 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
401  TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT
451  GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG
501  CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCTCTG
551  GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG
601  AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC
651  CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG
701  GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG
751  GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT
801  CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGGACA
851  CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG
901  GAAGAACTGG GATAATAA SEQ ID NO:21
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pMON13187

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTATGGCC
451  CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
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501  CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC
551  TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CTCTGGCGGC
601  TCTGGCGGCT CTCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGAAA
651  GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA
701  AGCTGTGCCA CCCCGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC
751  CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG
801  CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC
851  AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCCACCTT GGACACACTG
901  CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA
951  ACTGGGATAA TAA SEQ ID NO:22
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pMON13188

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
401  CCCAGGGTGC CATGCCGGCC TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA
451  GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC TTCCTGGAGG TGTCGTACCG
501  CGTTCTACGC CACCTTGCGC AGCCCTCTGG CGGCTCTGGC GGCTCTCAGA
551  GCTTCCTGCT CAAGTCTTTA GAGCAAGTGA GAAAGATCCA GGGCGATGGC
601  GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA
651  GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA
701  GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC
751  CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT
801  ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG
851  ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT
901  GCCCTGCAGC CCTAATAA SEQ ID NO:23
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pMON13189

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
451  GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
501  CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
551  TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC
601  CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
651  GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC
701  TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC
751  TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
801  CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC
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901  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
951  GCAGCCCTAA TAA SEQ ID NO:24
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pMON13190

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
401  CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG
451  AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTC
501  TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG
551  TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC
601  ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT
651  GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC
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701  TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG
751  CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA
801  CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA
851  TGGAAGAACT GGGAATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG
901  CCGGCCTTCG CCTAATAA SEQ ID NO:25
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pMON13191

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTCTGCT
451  TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT
501  CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG
551  GCTCTGGCGG CTCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA
601  AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA
651  CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA
701  TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA
751  GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT
801  GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC
851  TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA
901  GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC
951  CTTCGCCTAA TAA SEQ ID NO:26
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pMON13192

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 51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
401  ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC
451  ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC
501  AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC
551  TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA
601  CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA
651  AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG
701  CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC
751  CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC
801  GCAGCCCACA CCATTGGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC
851  TCAAGTCTTT AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC
901  CAGGAGAAGC TGTGTGCCAC CTAATAA SEQ ID NO:27
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pMON13193

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101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTACAAG
451  CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC
501  CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT
551  GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG
601  GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA
651  GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
701  TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
751  GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
801  GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
851  CCACACCATT GGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG
901  TCTTTAGAGC AAGTGAGAAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA
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 951  GAAGCTGTGT GCCACCTAAT AA SEQ ID NO:28
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pMON25190

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 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC
 401  CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
 451  GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
 501  GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC
 551  GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG
 601  TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCACACCAT TGGGCCCTGC
 651  CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA
 701  AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC
 751  AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT
 801  CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG
 851  GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG
 901  CAGGCCCTGG AAGGGATATC CTAATAA SEQ ID NO:29
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pMON25191

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  51  ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 401  CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCGAG
 451  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
 501  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
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 601  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
 651  CCGCGTTCTA CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT
 701  CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT GAGAAAGATC
 751  CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT
 801  GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT
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 951  CCTGGAAGGG ATATCCTAAT AA SEQ ID NO:30
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pMON13194

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 101  CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 151  AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 201  TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 251  CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 301  TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 351  CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA
 401  TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT
 451  GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG
 501  CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCACAC
 551  CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA
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 651  GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC
 701  ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC
 751  CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA
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 851  CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG
 901  CAGCAGATGG AAGAACTGGG ATAATAA SEQ ID NO:31
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pMON13195

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 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
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401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTATGGCC
451 CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
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551 TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CACACCATTG
601 GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA
651 AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG
701 CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT
751 CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA
801 GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG
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951 GATGGAAGAA CTGGGATAAT AA SEQ ID NO:32
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pMON13196

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101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
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251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
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651 CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG
701 CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG
751 AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC TGCAGGCCCT
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pMON13197

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101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
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401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
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651 TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
701 CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
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801 ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
851 GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
901 GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC
951 CCCTGCCCTG CAGCCCTAAT AA SEQ ID NO:34
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pMON13198

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101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
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551 TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
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651 ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG
701 CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC
751 TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC
801 CACCTTGGAC ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT
851 GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCCAG
901 GGTGCCATGC CGGCCTTCGC CTAATAA SEQ ID NO:35
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pMON13199

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101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
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251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTCTGCT
451 TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT
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551 TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG
601 CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG
651 TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT
701 CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG
751 CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA
801 GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG GGTCCCACCT
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pMON31112

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101 ATATCCTAAT GGACAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
201 AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC ACGCGACATC
251 CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
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401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
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851 CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
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951 GCAGCCCTAA TAA SEQ ID NO:37
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pMON31113

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251 CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
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401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
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501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
551 TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC
601 CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA
651 TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
701 CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
751 CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA
801 ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
851 GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
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951 CCCTGCCCTG CAGCCCTAAT AA SEQ ID NO:38

pMON31114

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151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
201 AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC ACGCGACATC
251 CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
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401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
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601 CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
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751 TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
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851 CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
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951 GCAGCCCTAA TAA SEQ ID NO:39

pMON31115

1 ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
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151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
201 AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC ACGCGACATC
251 CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
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951 CCCTGCCCTG CAGCCCTAAT AA SEQ ID NO:40

pMON28505

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pMON28506

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pMON28507

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pMON28508

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GGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTC
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ACACCTGTCCTGCTGCCT SEQ ID NO:44

pMON28509

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
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GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGACTTTAGCTTG
GGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGA
GTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGT
CTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGAT
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ACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGT
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GTCCTGCTGCCTGCTGTG SEQ ID NO:45

pMON28510

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGGAACCGTCTGG
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GACAACTGGGACCCACTTGCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCT
GCAGGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCATCTTCCTGA

GCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGGGGTCCACCCTCTGCGTCAGGGAATT
CGGCGGCAACATGGCGTCTCCCGCTCCGCCTGCTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCAT
GTCCTTCACAGCAGACTGACCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACT
TTAGTTG SEQ ID NO:46

pMON28511

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGGACCCACTTGC
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CAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTC
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CTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAA
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GCAGCACGGGGACAACTG SEQ ID NO:47

pMON28512

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
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CAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAA
ACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCA
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GCCCTGCAGAGCCTCCTT SEQ ID NO:48

pMON28513

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGGCAGGACCACA
GCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTT
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CGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCT
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GCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACT
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ACCCAGCTTCCTCCACAG SEQ ID NO:49

pMON28514

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
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CCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCC
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AAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCT
GTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATT
CTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCC
CTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCT
CCACAGGGCAGGACCACA SEQ ID NO:50

pMON28515

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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GCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCC
ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC

TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGATCCCAATGCC
ATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGC
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CGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTG
CCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCA
GTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGG
CAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGC
AGGACCACAGCTCACAAG SEQ ID NO:51

pMON28516

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
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CTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCT
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GCTCACAAGGATCCCAAT SEQ ID NO:52

pMON28519

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
AACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGACTTCCAAACCTGGAGAGCTTCGTAAGG
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGAGGTTCACCCT
TTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAG
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ACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTG
CTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCG
TCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGA
CTGAGCCAGTGCCCA SEQ ID NO:53

pMON28520

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGTTGCCTACACCT
GTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATT
CTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCC
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CCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAG
GTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCG
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CCAGAGGTTCACCCT SEQ ID NO:54

pMON28521

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
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ATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGAC
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CCTTTGCCTACACCT SEQ ID NO:55

pMON28522

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AAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGA
GGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCGAGTCCTC
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CCTGTCCTGCTGCCT SEQ ID NO:56

pMON28523

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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CTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTC
CTGCTGCCTGCTGTG SEQ ID NO:57

pMON28524

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCT
GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGGAGAATGGAAA
ACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCA
CGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGG
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TCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCTGCCTGCT
GTGGACTTTAGCTTG SEQ ID NO:58

pMON28525

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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
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GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGGACCCACTTGC
CTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACC
CAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTC
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GCACGGGGACAACTG SEQ ID NO:59

pMON28526

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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CAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGG
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CTGCAGAGCCTCCTT SEQ ID NO:60

pMON28527

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GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGGCAGGACCACA
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GTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTG
CCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCA
CAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGC
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CAGCTTCCTCCACAG SEQ ID NO:61

pMON28528

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTTGCTGGACCCGAAC
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ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
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GGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGCTCACAAGGAT
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CAGGGCAGGACCACA SEQ ID NO:62

pMON28529

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ACCACAGCTCACAAG SEQ ID NO:63

pMON28530

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CACAAGGATCCCAAT SEQ ID NO:64

pMON28533

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pMON28534

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pMON28535

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CCAGAGGTTCACCCTTTGCCTACACCT SEQ ID NO:67

pMON28536

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CCTTTGCCTACACCTGTCCTGCTGCCT SEQ ID NO:68

pMON28537

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CCTACACCTGTCCTGCTGCCTGCTGTG SEQ ID NO:69

pMON28538

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CTGCTGCCTGCTGTGGACTTTAGCTTG SEQ ID NO:70

pMON28539

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pMON28540

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CTCCTTGGGGCCCTGCAGAGCCTCCTT SEQ ID NO:72

pMON28541

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CTCCTTGGAACCCAGCTTCCTCCACAG SEQ ID NO:73

pMON28542

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CAGCTTCCTCCACAGGGCAGGACCACA SEQ ID NO:74

pMON28543

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CCACAGGGCAGGACCACAGCTCACAAG SEQ ID NO:75

pMON28544

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AGGACCACAGCTCACAAGGATCCCAAT SEQ ID NO:76

pMON28545

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CACAAG SEQ ID NO:77

pMON15981

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501  CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT
551  GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG
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651  GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
701  TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
751  GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
801  GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
851  CCGGCGGCGG CTCTGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG
901  CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG
951  CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAA TAA; SEQ ID NO:78
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pMON15982

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851 GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG
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951 CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCTAA TAA; SEQ ID NO:79
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pMON15965

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101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
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251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
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501 CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCGGCGGCG
551 GCTCTGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC
601 TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC
651 AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG
701 AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC
751 TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA
801 TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT
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pMON15966

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101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
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251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
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451 CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
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601 TCTGACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT
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701 CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCGAGGAG
751 CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC
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851 GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC
901 CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT
951 TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGATAA TAA SEQ ID NO:81
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pMON15967

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151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
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351   CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
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451   GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
501   CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
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601   GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA
651   AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG
701   CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT
751   CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA
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pMON15960

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 151  CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC
 201  CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC
 251  TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG
 301  TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
 351  CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC
 401  CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
 451  GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
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 601  TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA
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PMON32132

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PMON32133

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pMON32134

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Pmon13181

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251  TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA
301  CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAgag
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451  CCGCATGCAA GCTT SEQ ID NO:87
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Pmon13180.Seg

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251  TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA
301  CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAgag
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pMON32329.seq

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SEQ ID NO:97

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SEQ ID NO:100

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FLT3N.seq

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FLT3C.seq

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FLT7N.seq

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SEQ ID NO:109

FLT4C.seq

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pMON32335.seq

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pMON32338.seq

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pMON32339.seq

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pMON32364.seq

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pMON32377.seq

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pMON32392.seq

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pMON32358.seq

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pMON32359.seq

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pMON32362.seq

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pMON32393.seq

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pMON32372.seq

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pMON32373.seq

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pMON32374.seq

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pMON32375.seq

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pMON32376.seq

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pMON32378.seq

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pMON32379.seq

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pMON32380.seq

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pMON32381.seq

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pMON32382.seq

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pMON32383.seq

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pMON32384.seq

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pMON32385.seq

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pMON32386.seq

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pMON32387.seq

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pMON32388.seq

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pMON32389.seq

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hflt3-2829link10.seq

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hflt3-2829link15.seq

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hflt3-3435link10.seq

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hflt3-3435link15.seq

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hflt3-6263link10.seq

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hflt3-6263link15.seq

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ACT SEQ ID NO:166

hflt3-9495link10.seq

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CGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAG
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CGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGG
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hflt3-9495link15.seq

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AGTGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCAGGAGGTGGGTCA
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CTT SEQ ID NO:168

hflt3-9899link10.seq

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CCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTG
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hflt3-9899link15.seq

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CAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTCTGCGGGGGCCTC
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CAG SEQ ID NO:170

hflt3-2829link6.seq

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hflt3-2829link7.seq

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hflt3-2829link13.seq

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hflt3-2829link21.seq

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GGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTT
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TGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCAGGAGGTGGGTCAGG
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hflt3-3435link6.seq

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CTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGCCGCCTCCAAC
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CCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTC
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hflt3-3435link7.seq

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hflt3-3435link13.seq

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hflt3-3435link21.seq

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GCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCT
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CCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTC
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ACCCTGGGCGGTGGGTCAGGAGGTGGGTCAGGAGGTGGATCCGGAGGTGG
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hflt3-6263link6.seq

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hflt3-6263link7.seq

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CGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTC
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hflt3-6263link13.seq

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hflt3-6263link21.seq

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hflt3-9495link6.seq

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hflt3-9495link7.seq

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pMON32397.seq

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pMON32398.seq

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pMON32399.seq

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pMON35700.seq

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pMON35701.seq

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pMON35702.seq

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pMON35703.seq

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pMON35704.seq

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pMON35705.seq

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pMON35706.seq

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pMON35733.seq

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SEQ ID NO:209

pMON35734.seq

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SEQ ID NO:210

pMON35735.seq

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SEQ ID NO:211

pMON35736.seq

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SEQ ID NO:212

pMON35738.seq

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SEQ ID NO:213

pMON35739.seq

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pMON35740.seq

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SEQ ID NO:215

pMON35741.seq

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pMON35721.seq

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pMON35744.seq

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GGCTCCAACATGGCTGATGAAGAACTGTGTGGTGGTCTGTGGCGGCTGGTCCTGGCACAGCGCTGG
ATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAG
ATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAAC

ATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAG
AACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCAGGA
GGTGGGTCAGGAGGTGGATCCGGAGGTGGCTCAGGGGGAGGTAGTGGTACCCAGGACTGCTCCTTC
CAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAA
GATTACCCAGTCACCGTGGCCTCCAACCTGCAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAA
CCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAAC
ATGGCTACACCATTAGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA
GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGC
CACCCCGAGGAGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCTCCTGC
CCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTCCTCTACCAG
GGGCTCCTGCAGGCCCTGGAAGGGATATCCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTG
GACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCTGCCCTG
CAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGAGGGGTCCTG
GTTGCTAGCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCGCAGCCC
TGATAAGGATCCGAATTCGGCAGC SEQ ID NO:313

pMON35728.seq

GCCGACGAGGAGCTGTGCGGTGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
AAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTC
ACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTC
CTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGG
TGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCAGGAGGTGGGTCAGGA
GGTGGATCCGGAGGTGGAACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCT
GTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTG
CAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCG
TCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGCTAACTGCTCTATAATGATCGATGAA
ATTATACATCACTTAAAGAGACCACCTAACCCTTTGCTGGACCCGAACAACCTCAATTCTGAAGAC
ATGGATATCCTGATGGAACGAAACCTTCGAACTCCAAACCTGCTCGCATTCGTAAGGGCTGTCAAG
CACTTAGAAAATGCATCAGGTATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCC
ACGGCCGCACCCTCTCGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAA
CTGACGTTCTATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGC
TCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCAT
AAATCTCCAAACATGGCCGACGAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGC
TGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACG
GAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACC
AACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGC
CAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCA
GGAGGTGGGTCAGGAGGTGGATCCGGAGGTGGCACCCAGGACTGCTCCTTCCAACACAGCCCCATC
TCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACC
GTGGCCTCCAACCTGCAG SEQ ID NO:314

pMON32183.seq

GCTGATGAAGAACTGTGTGGTGGTCTGTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
AAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTC
ACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTC
CTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGG
TGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCAGGAGGTGGGTCAGGA
GGTGGATCCGGAGGTGGCTCAGGGGGAGGTAGTGGTACCCAGGACTGCTCCTTCCAACACAGCCCC
ATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTC
ACCGTGGCCTCCAACCTGCAGGAATTCAAGCTTGAGCCCAGAGGGCCCACAATCAAGCCCTGTCCT
CCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATC
AAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAGGAT
GACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACC
CATAGAGAGGATTACAACAGTACTCTCCGGGCGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGG
ATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGAACC
ATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAG
ATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTG
GAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGAT
GGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGCTAC
TCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACTCCG
GGTAAA SEQ ID NO:315

pMON32184.seq

GCCACCCAGGACTGCTCCTTTCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAG
CTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGACGAGGAGCTC
TGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGG
TCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTT
CAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCC
GAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAG
TGTCAGCCCGACTCCTCAACCCTGGAATTCAAGCTTGAGCCCAGAGGGCCCACAATCAAGCCCTGT
CCTCCATGCAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAG

ATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGATGTGAGCGAG
GATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAA
ACCCATAGAGAGGATTACAACAGTACTCTCCGGGCGGTCAGTGCCCTCCCCATCCAGCACCAGGAC
TGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCAGCGCCCATCGAGAGA
ACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAA
GAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTAC
GTGGAGTGGACCAACAACGGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCT
GATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGAAATAGC
TACTCCTGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACT
CCGGGTAAA SEQ ID NO:316

TABLE 3
PROTEIN SEQUENCES

pMON26458pep

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe SEQ ID NO:467

pMON28548pep

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAla
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArg SEQ ID NO:468

pMON28500

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSer
ProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisVal
LeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGln
AspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeu
GlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeu
GlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHis
LysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
LeuMetLeuValGlyGlySerThrLeuCysValArg SEQ ID NO:469

pMON28501

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAla
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArg SEQ ID NO:470

pMON28502

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu

LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGly
AsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThr
ProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAla
ArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnVal
ArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArg
ThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGly
LysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg SEQ ID NO:471

13182.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr SEQ ID NO:472

13183.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr SEQ ID NO:473

13184.Pept

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

Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser SEQ ID NO:474

13185.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser SEQ ID NO:475

13186.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu Gly SEQ ID NO:476

13187.Pept

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

Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu Gly SEQ ID NO:477

13188.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro SEQ ID NO:478

13189.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro SEQ ID NO:479

13190.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
Phe Ala SEQ ID NO:480

13191.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
Phe Ala SEQ ID NO:481

13192.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr SEQ ID NO:482

13193.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu

Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr SEQ ID NO:483

25190.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser SEQ ID NO:484

pMON25191.Pep

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser SEQ ID NO:485

13194.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met Glu Glu Leu Gly SEQ ID NO:486

13195.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met Glu Glu Leu Gly SEQ ID NO:487

13196.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
Pro Ala Leu Gln Pro SEQ ID NO:488

13197.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
Pro Ala Leu Gln Pro SEQ ID NO:489

13198.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
Met Pro Ala Phe Ala SEQ ID NO:490

13199.Pept

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
Met Pro Ala Phe Ala SEQ ID NO:491

31104.Pep

Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
Gln Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile
His His Leu Lys Arg Pro Pro Ala Pro Leu Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro SEQ ID NO:492

31105.Pep

Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro SEQ ID NO:493

31106.Pep

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

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro SEQ ID NO:494

31107.Pep

Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu
Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Asn
Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val
Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro SEQ ID NO:495

31108.Pep

Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro
Ala Pro Leu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro SEQ ID NO:496

31109.Pep

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

Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
SEQ ID NO:497

31110.Pep

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln
Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
Ala Thr Ala Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
SEQ ID NO:498

31111.Pep

Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu
Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly
Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu
Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro
Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn
Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys Asn
Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln
Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile
Ile Ile Lys Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
SEQ ID NO:499

pMON15981

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGly
ValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHis
LeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeu

ProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThr SEQ ID NO:500

pMON15982

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaProGluLeuGlyProThrLeuAspThrLeuGlnLeu
AspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaPro
AlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAla
GlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeu
ArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSer
SerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAsp
GlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeu
ValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGln
AlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGly
LeuLeuGlnAlaLeuGluGlyIleSer SEQ ID NO:501

pMON15965

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuVal
AlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGln
ProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSer
PheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGln
GluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAla
GlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeu
GluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAsp
PheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
ThrGlnGlyAlaMetProAlaPheAla SEQ ID NO:502

pMON15966

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaMetAlaProAlaLeuGlnProThrGlnGlyAlaMet
ProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeu
GlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProGlyGlyGly
SerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLys
SerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCys
AlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIle
ProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSer
GlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThr
IleTrpGlnGlnMetGluGluLeuGly SEQ ID NO:503

pMON15967

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeu

GlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLys
IleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHis
ProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer
CysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeu
AspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGlu
LeuGlyMetAlaProAlaLeuGlnPro SEQ ID NO:504

pMON31112.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleHisIleLysAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGlnSerPhe
LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSer
LeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGlu
GlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe
AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
SEQ ID NO:505

pMON31113.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleIleIleArgAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnPro SEQ ID NO:506

pMON31114.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsn
LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleIleIleArgAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGlnSerPhe
LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSer
LeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGlu
GlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe
AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
SEQ ID NO:507

pMON31115.pep

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsn

LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
ThrArgHisProIleHisIleLysAspGlyAspTrpAsnGluPheArgArgLysLeuThr
PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnPro SEQ ID NO:508

pMON28505

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGluValHisProLeuProThrProValLeuLeuProAlaVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeu
GlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThr
CysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeu
GlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerProAlaPro
ProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSer
ArgLeuSerGlnCysPro SEQ ID NO:509

pMON28506

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetLeuProThrProValLeuLeuProAlaValAspPheSerLeu
GlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThr
LeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSer
LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePhe
LeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySer
ThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAsp
LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGln
CysProGluValHisPro SEQ ID NO:510

pMON28507

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGln
LeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu
ProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGln
HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
ArgGluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeu
SerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluVal
HisProLeuProThrPro SEQ ID NO:511

pMON28508

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuPro SEQ ID NO:512

pMON28509

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThr
LysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArg
GlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArg
LeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThr
ThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLys
ValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsn
MetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAsp
SerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
ValLeuLeuProAlaVal SEQ ID NO:513

pMON28510

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerPro
AlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeu
HisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuPro
AlaValAspPheSerLeu SEQ ID NO:514

pMON28511

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
GlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeu
LeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeu
ProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMet
GluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMet
AlaAlaArgGlyGlnLeu SEQ ID NO:515

pMON28512

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMetAlaSerPro
AlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeu
HisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuPro
AlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeu SEQ ID NO:516

pMON28513

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
LeuCysValArgGluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeu
ArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys
ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGly
GluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeu
LeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeu
LeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGly
ThrGlnLeuProProGln SEQ ID NO:517

pMON28514

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
GluPheGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu
SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
ProGlnGlyArgThrThr SEQ ID NO:518

pMON28515

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLys SEQ ID NO:519

pMON28516

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
LeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThr
AlaHisLysAspProAsn SEQ ID NO:520

pMON28519

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGluValHisProLeuProThrProValLeuLeuProAlaVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeu
GlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThr
CysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeu
GlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAlaProPro
AlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArg
LeuSerGlnCysPro SEQ ID NO:521

pMON28520

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetLeuProThrProValLeuLeuProAlaValAspPheSerLeu
GlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThr
LeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSer
LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePhe
LeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySer
ThrLeuCysValArgGluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeu
ArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys
ProGluValHisPro SEQ ID NO:522

pMON28521

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGln
LeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu
ProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGln
HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
ArgGluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis

ProLeuProThrPro SEQ ID NO:523

pMON28522

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
AsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThr
ProValLeuLeuPro SEQ ID NO:524

pMON28523

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThr
LysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArg
GlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArg
LeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThr
ThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLys
ValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaVal SEQ ID NO:525

pMON28524

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAla
ProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHis
SerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuProAla
ValAspPheSerLeu SEQ ID NO:526

pMON28525

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu

GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeu SEQ ID NO:527

pMON28526

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAla
ProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHis
SerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuProAla
ValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIle
LeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyPro
ThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAla
LeuGlnSerLeuLeu SEQ ID NO:528

pMON28527

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
LeuCysValArgGluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArg
ValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysPro
GluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu
TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeu
LeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeu
GlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThr
GlnLeuProProGln SEQ ID NO:529

pMON28528

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
GluPheGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLys
LeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisPro
LeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGln
MetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSer
GlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProPro
GlnGlyArgThrThr SEQ ID NO:530

pMON28529

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
AsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArg
AspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThr
ProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAla

ArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnVal
ArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArg
ThrThrAlaHisLys SEQ ID NO:531

pMON28530

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAla
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsn SEQ ID NO:532

pMON28533

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGluValHisProLeuProThrProValLeuLeuProAlaVal
AspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeu
GlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThr
CysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeu
GlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSer
ProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisVal
LeuHisSerArgLeuSerGlnCysPro SEQ ID NO:533

pMON28534

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetLeuProThrProValLeuLeuProAlaValAspPheSerLeu
GlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThr
LeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSer
LeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePhe
LeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySer
ThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProPro
AlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArg
LeuSerGlnCysProGluValHisPro SEQ ID NO:534

pMON28535

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGln
LeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu
ProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGln

HisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
ArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeu
ArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys
ProGluValHisProLeuProThrPro SEQ ID NO:535

pMON28536

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuPro SEQ ID NO:536

pMON28537

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThr
LysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArg
GlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArg
LeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThr
ThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLys
ValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsn
GlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeu
LeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeu
ProThrProValLeuLeuProAlaVal SEQ ID NO:537

pMON28538

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAsp
IleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGly
ProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly
AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeu SEQ ID NO:538

pMON28539

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe

GlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeu
SerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluVal
HisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
GlyValMetAlaAlaArgGlyGlnLeu SEQ ID NO:539

pMON28540

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMet
AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
LeuLeuGlyAlaLeuGlnSerLeuLeu SEQ ID NO:540

pMON28541

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
LeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAla
CysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeu
SerGlnCysProGluValHisProLeuProThrProValLeuLeuProAlaValAspPhe
SerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAla
ValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeu
SerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSer
LeuLeuGlyThrGlnLeuProProGln SEQ ID NO:541

pMON28542

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
GluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArg
ValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysPro
GluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu
TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeu
LeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeu
GlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThr
GlnLeuProProGlnGlyArgThrThr SEQ ID NO:542

pMON28543

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer

LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu
SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
ProGlnGlyArgThrThrAlaHisLys SEQ ID NO:543

pMON28544

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
ArgThrThrAlaHisLysAspProAsn SEQ ID NO:544

pMON28545

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAla
HisLys SEQ ID NO:545

pMON32132

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArg SEQ ID NO:546

PMON32133

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla
GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAlaHisLysAspPro
AsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeu
ValGlyGlySerThrLeuCysValArg SEQ ID NO:547

PMON32134

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHis
ValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeu
LeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAla

GlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGln
LeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThrAla
HisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArg
PheLeuMetLeuValGlyGlySerThrLeuCysValArg SEQ ID NO:548

pMON30237.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyAlaLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
SEQ ID NO:549

pMON30238.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
SEQ ID NO:550

pMON30239.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnGluThrSerGluGlnLeuValAlaLeuLysPro
TrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeu SEQ ID NO:551

pMON32329.pep

GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
SEQ ID NO:552

pMON32330.pep

GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
SEQ ID NO:553

pMON32341.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
SEQ ID NO:554

pMON32342.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
SEQ ID NO:555

pMON32320.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:556

pMON32321.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGln SEQ ID NO:557

pMON32322.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGln SEQ ID NO:558

pMON32323.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGlyAsnGly
SerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyr
ProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeu
ValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:559

pMON32324.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGlyAsnGly
SerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArg
TrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:560

pMON32325.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe

SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGlyAsnGly
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGly SEQ ID NO:561

pMON32326.pep

AlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThr
SerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeu
GluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsn
GlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:562

pMON32327.pep

AlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThr
SerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeu
GluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsn
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnPro SEQ ID NO:563

pMON32328.pep

AlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThr
SerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeu
GluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGlyAsnGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCys
GlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
GlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnPro SEQ ID NO:564

pMON32348.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlySerGlySerGlyGlySerGlySerGlyGlySerGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:565

pMON32350.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlySerGlySerGlyGlySerGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGln SEQ ID NO:566

FLT3N.pep

MetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp

IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr LeuGlyGlyGlySer SEQ ID NO:567

FLT3C.pep

GlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla ValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSer AsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrp MetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsn ThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPhe ValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSer SerThrLeu SEQ ID NO:568

FLT7N.pep

MetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr LeuGlyGlyGlySerGlyGlyGlySer SEQ ID NO:569

FLT4C.pep

GlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArg TrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp SerSerThrLeu SEQ ID NO:570

FLT11N.pep

MetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer SEQ ID NO:571

FLT10C.pep

GlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSer ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGln GlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSer GluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu LeuGlnCysGlnProAspSerSerThrLeu SEQ ID NO:572

pMON32365.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr LeuGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr ValAlaSerAsnLeuGln SEQ ID NO:573

pMON32366.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSer
SerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGln SEQ ID NO:574

pMON32367.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGln SEQ ID NO:575

pMON32368.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:576

pMON32369.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:577

pMON32370.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
Gln SEQ ID NO:578

pMON30247.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyAlaLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys

LeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
Pro SEQ ID NO:579

pMON30248.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyAlaLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
ProAspSerSerThrLeu SEQ ID NO:580

pMON32332.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:581

pMON32333.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:582

pMON32334.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln

ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:583

pMON32335.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID
NO:584

pMON32336.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGly
AsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
Gln SEQ ID NO:585

pMON32337.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:586

pMON32338.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer

ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID
NO:587

pMON32339.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlySerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrp
ArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
Pro SEQ ID NO:588

pMON32364.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
Pro SEQ ID NO:589

pMON32377.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
ProAspSerSerThrLeu SEQ ID NO:590

pMON32352.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly

IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:591

pMON32353.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGly
AsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
Gln SEQ ID NO:592

pMON32354.pep
AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:593

pMON32355.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID
NO:594

pMON32356.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCys
GlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
Gly SEQ ID NO:595

pMON32357.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:596

pMON32358.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID
NO:597

pMON32359.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlySerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrp
ArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
Pro SEQ ID NO:598

pMON32360.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlySerGlySerGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:599

pMON32362.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlySerGlySerGlyGlySerGlySerGlyGly
SerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
Gln SEQ ID NO:600

pMON32392.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProTyrValGluGlyGly
GlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAsp
MetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAla
ValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCys
LeuProSerAlaThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrp
GlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:601

pMON32393.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMet
IleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsn
LeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeu
AlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArg

AsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGlu
GlnAlaGlnGluGlnGln SEQ ID NO:602

pMON32396.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ProHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeu SEQ ID NO:603

pMON32371.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:604

pMON32372.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:605

pMON32373.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys

GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:606

pMON32374.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrSerIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
SEQ ID NO:607

pMON32375.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
GlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
Gln SEQ ID NO:608

pMON32376.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
GlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSer
SerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGln SEQ ID NO:609

pMON32378.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer

HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:610

pMON32379.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSer
SerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:611

pMON32380.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID
NO:612

pMON32381.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGly
LeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SEQ ID NO:613

pMON32382.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer

ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCys
GlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
Gly SEQ ID NO:614

pMON32383.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGly SEQ ID NO:615

pMON32384.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaVal
LysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsn
LeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMet
GluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThr
GluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:616

pMON32385.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla
ValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSer
AsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrp
MetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsn
ThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:617

pMON32386.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID
NO:618

pMON32387.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyr
ProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeu
ValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGly
LeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
SEQ ID NO:619

pMON32388.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrp
ArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
Pro SEQ ID NO:620

pMON32389.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGlu
LeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr

ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheVal
ThrLysCysAlaPheGlnPro SEQ ID NO:621

hflt3-2829link10.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArg
GlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSer
SerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln SEQ ID
NO:622

hflt3-2829link15.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArg
GlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
Gln SEQ ID NO:623

hflt3-3435link10.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal SEQ ID
NO:624

hflt3-3435link15.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys

MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
Val SEQ ID NO:625

hflt3-6263link10.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGly
LeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr SEQ ID
NO:626

hflt3-6263link15.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThr
GlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGlu
LeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
Thr SEQ ID NO:627

hflt3-9495link10.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeu SEQ ID
NO:628

hflt3-9495link15.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer

ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
Leu SEQ ID NO:629

hflt3-9899link10.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlySerSer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGlu
LeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheVal
ThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln SEQ ID
NO:630

hflt3-9899link15.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaVal
LysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsn
LeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMet
GluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThr
GluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheVal
Gln SEQ ID NO:631

hflt3-2829link6.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArg
GlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla
ValLysIleArgGluLeuSerAspTyrLeuLeuGln SEQ ID NO:632

hflt3-2829link7.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArg
GlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGln SEQ ID NO:633

hflt3-2829link13.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArg
GlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
SEQ ID NO:634

hflt3-2829link21.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArg
TrpMetGluArgLeuLysThr SEQ ID NO:635

hflt3-3435link6.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrVal SEQ ID NO:636

hflt3-3435link7.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlyThr
GlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGlu
LeuSerAspTyrLeuLeuGlnAspTyrProValThrVal SEQ ID NO:637

hflt3-3435link13.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
SEQ ID NO:638

hflt3-3435link21.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrVal SEQ ID NO:639

hflt3-6263link6.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyr

ProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeu
ValLeuAlaGlnArgTrpMetGluArgLeuLysThr SEQ ID NO:640

hflt3-6263link7.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr SEQ ID NO:641

hflt3-6263link13.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
SEQ ID NO:642

hflt3-6263link21.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArg
TrpMetGluArgLeuLysThr SEQ ID NO:643

hflt3-9495link6.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyThrGln

AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGlu
LeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheVal
ThrLysCysAlaPheGlnProProProSerCysLeu SEQ ID NO:644

hflt3-9495link7.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlyThr
GlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGlu
LeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeu SEQ ID NO:645

hflt3-9495link13.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
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ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArg
TrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeu
SEQ ID NO:646

hflt3-9495link21.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeu SEQ ID NO:647

hflt3-9899link6.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlySerSer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer

HisLysSerProAsnMetAlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGly
LeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAla
PheGlnProProProSerCysLeuArgPheValGln SEQ ID NO:648

hflt3-9899link7.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlySerSer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlyThrGlnAspCysSer
PheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyr
LeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGly
GlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCys
AlaPheGlnProProProSerCysLeuArgPheValGln SEQ ID NO:649

hflt3-9899link13.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlySerSer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
SEQ ID NO:650

hflt3-9899link21.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnPro
LeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeu
ArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIle
SerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuVal
LeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeu
LeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGln SEQ ID NO:651

GlySerThrMetSerArgLeuProValLeuLeuLeuLeuGlnLeuLeuValArgProAlaMetSerThrAsnGln
AspLeuProValIleLysCysValLeuIleAsnHisLysAsnAsnAspSerSerValGlyLysSerSerSerTyr
ProMetValSerGluSerProGluAspLeuGlyCysAlaLeuArgProGlnSerSerGlyThrValTyrGluAla
AlaAlaValGluValAspValSerAlaSerIleThrLeuGlnValLeuValAspAlaProGlyAsnIleSerCys
LeuTrpValPheLysHisSerSerLeuAsnCysGlnProHisPheAspLeuGlnAsnArgGlyValValSerMet

ValIleLeuLysMetThrGluThrGlnAlaGlyGluTyrLeuLeuPheIleGlnSerGluAlaThrAsnTyrThr
IleLeuPheThrValSerIleArgAsnThrLeuLeuTyrThrLeuArgArgProTyrPheArgLysMetGluAsn
GlnAspAlaLeuValCysIleSerGluSerValProGluProIleValGluTrpValLeuCysAspSerGlnGly
GluSerCysLysGluGluSerProAlaValValLysLysGluGluLysValLeuHisGluLeuPheGlyMetAsp
IleArgCysCysAlaArgAsnGluLeuGlyArgGluCysThrArgLeuPheThrIleAspLeuAsnGlnThrPro
GlnThrThrLeuProGlnLeuPheLeuLysValGlyGluProLeuTrpIleArgCysLysAlaValHisValAsn
HisGlyPheGlyLeuThrTrpGluLeuGluAsnLysAlaLeuGluGluGlyAsnTyrPheGluMetSerThrTyr
SerThrAsnArgThrMetIleArgIleLeuPheAlaPheValSerSerValAlaArgAsnAspThrGlyTyrTyr
ThrCysSerSerSerLysHisProSerGlnSerAlaLeuValThrIleValGluLysGlyPheIleAsnAlaThr
AsnSerSerGluAspTyrGluIleAspGlnTyrGluGluPheCysPheSerValArgPheLysAlaTyrProGln
IleArgCysThrTrpThrPheSerArgLysSerPheProCysGluGlnLysGlyLeuAspAsnGlyTyrSerIle
SerLysPheCysAsnHisLysHisGlnProGlyGluTyrIlePheHisAlaGluAsnAspAspAlaGlnPheThr
LysMetPheThrLeuAsnIleArgArgLysProGlnValLeuAlaGluAlaSerAlaSerGlnAlaSerCysPhe
SerAspGlyTyrProLeuProSerTrpThrTrpLysLysCysSerAspLysSerProAsnCysThrGluGluIle
ThrGluGlyValTrpAsnArgLysAlaAsnArgLysValPheGlyGlnTrpValSerSerSerThrLeuAsnMet
SerGluAlaIleLysGlyPheLeuValLysCysCysAlaTyrAsnSerLeuGlyThrSerCysGluThrIleLeu
LeuAsnSerProGlyProPheProPheIleGlnAspAsnGluPheIleIleLeuGlyLeuPheGlyLeuLeuLeu
LeuLeuThrCysLeuCysGlyThrAlaTrpLeuCysCysSerProAsnArgLysAsnProLeuTrpProSerVal
ProAspProAlaHisSerSerLeuGlySerTrpValProThrIleMetGluGluAspAlaPheGlnLeuProGly
LeuGlyThrProProIleThrLysLeuThrValLeuGluGluAspGluLysLysProValProTrpGluSerHis
AsnSerSerGluThrCysGlyLeuProThrLeuValGlnThrTyrValLeuGlnGlyAspProArgAlaValSer
ThrGlnProGlnSerGlnSerGlyThrSerAspGlnValLeuTyrGlyGlnLeuLeuGlySerProThrSerPro
GlyProGlyHisTyrLeuArgCysAspSerThrGlnProLeuLeuAlaGlyLeuThrProSerProLysSerTyr
GluAsnLeuTrpPheGlnAlaSerProLeuGlyThrLeuValThrProAlaProSerGlnGluAspAspCysVal
PheGlyProLeuLeuAsnPheProLeuLeuGlnGlyIleArgValHisGlyMetGluAlaLeuGlySerPhe
SEQ ID NO:652

pMON30329.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
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LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
SEQ ID NO:653

pMON32173.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAla
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyr
LeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeu
ValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgVal
AsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSer
ArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu SEQ ID NO:654

pMON32175.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAla
ThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGln
GlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeu
SerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGly
ProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGly

MetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGly
ValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
SEQ ID NO:655

pMON32204.pep

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GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPhe
AlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuTyr
ValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLys
GluSerHisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla
ValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu SEQ
ID NO:656

pMON32205.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaProLeuLeuAspProAsn
AsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeuArgLeuProAsnLeuGluSerPheValArg
AlaValLysAsnLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArg
LeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeu
GluLeuGlnCysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeu SEQ ID NO:657

pMON32208.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAla
ThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGln
GlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeu
SerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGly
ProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGly
MetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGly
ValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProTyr
ValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLys
GluSerHisLysSerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla
ValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu SEQ
ID NO:658

pMON35767.pep/pMON32191.pep

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LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GlyGlySerGlyGlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeu
LysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLys
LeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThr
ThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPhe
AlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyr
ArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:659

pMON32397.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrp
MetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGln
GluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln SEQ ID
NO:660

pMON32398.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrp
MetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGln
GluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
Gln SEQ ID NO:661

pMON32399.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAlaSerAsn
LeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal SEQ ID
NO:662

pMON35700.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAlaSerAsn

LeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
Val SEQ ID NO:663

pMON35701.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGly
GlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla
ValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr SEQ ID
NO:664

pMON35702.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGly
GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIle
SerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSer
AsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLys
Thr SEQ ID NO:665

pMON35703.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaArgPheVal
GlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrp
ArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeu SEQ ID
NO:666

pMON35704.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaArgPheVal
GlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
Leu SEQ ID NO:667

pMON35705.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlySerSerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArg
CysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThr
GluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln SEQ ID
NO:668

pMON35706.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArg
CysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheVal
Gln SEQ ID NO:669

pMON35733.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAla SEQ ID NO:670

pMON35734.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
GlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSer SEQ ID NO:671

pMON35735.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaLeuGlnAsp
GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGly
GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSer

PheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyr
ProValThrValAlaSerAsn SEQ ID NO:672

pMON35736.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeu SEQ ID NO:673

pMON35738.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAsp SEQ ID NO:674

pMON35739.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaGluLeuCys
GlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGln
GlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeu
ArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIle
ThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGly
GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGlu SEQ ID NO:675

pMON35740.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaLeuCysGly
GlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGly
LeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGlu SEQ ID NO:676

pMON35741.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaSerAsnLeu

GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspSerAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAla SEQ ID NO:677

pMON35742.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaGlnAspGlu
GluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuArgGluThrSerGluGlnProValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeu SEQ ID NO:678

pMON35743.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsn
AsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArg
AlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaLeuCysGly
GlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGly
LeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysArgProAspSerSerThrLeuGlyGlyGlySerGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGlu SEQ ID NO:679

pMON32179.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIle
AsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIle
IleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeu
MetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIle
IleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGlu
GlnGln SEQ ID NO:680

pMON35707.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuArgProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArg
ProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArg
ThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArg
AsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrp
GlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGln SEQ ID
NO:681

pMON35708.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:682

pMON35709.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:683

pMON35710.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgLeuValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:684

pMON35711.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlyArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:685

pMON35719.pep

MetAlaAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuVal
LeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsn
ThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArg
CysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIle
AsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIle
IleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeu
MetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIle

IleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGlu
GlnGln SEQ ID NO:686

pMON35720.pep

AlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThr
LysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThr
SerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
ProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:687

pMON35721.pep

AlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAla
PheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSer
SerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMet
GluArgLeuLysThrTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:688

pMON35722.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGlyTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:689

pMON35723.pep

AlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:690

pMON35725.pep

AlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys

LeuArgPheValGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:691

pMON35726.pep

AlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
GlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysPheTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:692

pMON35744.pep

AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSer
GluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
AspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:693

pMON35745.pep

AlaAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCys
AlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGlu
GlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyr
LeuLeuGlnAspTyrProValThrValAlaSerTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:694

pMON35746.pep

AlaLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgLeuMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAla
PheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSer
SerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThr
GlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:695

pMON35747.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:696

pMON35748.pep

AlaGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
GlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:697

pMON35749.pep

AlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:698

pMON35750.pep

AlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:699

pMON35769.pep

AlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysArgProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer

ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:700

pMON35771.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGlyTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:701

pMON35774.pep

AlaGlnAspAspGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGly
GlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSer
ProAsnMetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeu
AspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAla
PheValArgAlaValLysHisLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeu
ProSerAlaThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLys
LeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGln SEQ ID NO:702

pMON35775.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
Gln SEQ ID NO:703

pMON35776.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrAlaGlyGlnProProLeuThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIle
MetIleAspGluIleIleHisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGlu
AspMetAspIleLeuMetGluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeu
GluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeu
GluGlnAlaGlnGluGlnGln SEQ ID NO:704

pMON32169.pep/pMON40000.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly

GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:705

pMON32188.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuVal
LeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsn
ThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnIleAsnIle
SerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArg
CysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAla
ValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSer SEQ ID NO:706

pMON32273.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCys
GlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGln
GlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:707

pMON35795.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThr
GluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
GlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaVal
LysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsn SEQ ID NO:708

pMON35796.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer

LysGluSerHisLysSerProAsnMetAlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArg
LeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeu
GluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGly
GlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu SEQ ID NO:709

pMON35797.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArg
TrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeu
GlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeu
GlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp SEQ ID NO:710

pMON35798.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrp
MetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPhe
ValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGln
GluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
GlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGlu
LeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGlu SEQ ID NO:711

pMON35799.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMet
GluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheVal
ThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGly
GlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGlu SEQ ID NO:712

pMON39914.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu

LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThr
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyr
LeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:713

pMON39915.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIle
SerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSer
AsnLeuGln SEQ ID NO:714

pMON39916.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThr
AlaGlyGlnProProLeuThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:715

pMON35712.pep

AlaAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThr
GluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCys
LeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
GlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGln SEQ ID NO:716

pMON35713.pep

AlaAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThr
LysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThr
SerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
ProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrVal SEQ ID NO:717

pMON35714.pep

AlaValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAla
PheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSer
SerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMet
GluArgLeuLysThr SEQ ID NO:718

pMON35715.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGly SEQ ID NO:719

pMON35716.pep

AlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnPro SEQ ID NO:720

pMON35717.pep

AlaArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
AspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
GlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeu SEQ ID NO:721

pMON35718.pep

AlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGln SEQ ID NO:722

pMON32170.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:723

pMON32187.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:724

pMON32271.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrAlaGlyGlnProProLeuThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGlyGly
GlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGln
ValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGlu
GluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIle
SerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGln
MetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGln
ArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHis
LeuAlaGlnPro SEQ ID NO:725

pMON32272.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGly
GlySerProGlyGlyGlySerGlyGlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGln
SerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCys
AlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeu
SerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGln
GlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAla
AspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAla
MetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeu
GluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:726

pMON32274.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGlyGlyGlySerAsnMetAlaThr
ProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGly
AspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGly
HisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSer
GlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyPro
ThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMet
AlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyVal
LeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ
ID NO:727

pMON35751.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuArgProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeu
LysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLys
LeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThr
ThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPhe
AlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyr
ArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:728

pMON35752.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:729

pMON35753.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValValArgHisLeuAlaGlnPro SEQ ID NO:730

pMON35754.pep

AlaProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerValPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValIleArgHisLeuAlaGlnPro SEQ ID NO:731

pMON35755.pep

AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSer
GluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
AspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerHisProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:732

pMON35756.pep

AlaAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCys
AlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGlu

GlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsp
SerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyr
LeuLeuGlnAspTyrProValThrValAlaSerTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValIleArgHisLeuAlaGlnPro SEQ ID NO:733

pMON35757.pep

AlaLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgLeuMetGluArgLeuLys
ThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAla
PheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGln
LeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSer
SerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThr
GlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeu
LeuGlnAspTyrProValThrValAlaSerAsnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:734

pMON35758.pep

AlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:735

pMON35759.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGlyTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:736

pMON35760.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu

LysThrValAlaGlyTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:737

pMON35761.pep

AlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysArgProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPhe
GlnHisSerProIleSerSerAsnPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrPro
ValThrValAlaSerAsnLeuGlnAspGluGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIlePheThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:738

pMON35762.pep

AlaGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGly
GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSer
PheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyr
ProValThrValAlaSerAsnLeuGlnAspGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:739

pMON35763.pep

AlaGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAla
GlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:740

pMON35764.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla

AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:741

pMON35765.pep

AlaThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:742

pMON35766.pep/pMON32190.pep/pMON40001.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGlu
GlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisPro
GluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeu
GlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGly
IleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGln
GlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArg
HisLeuAlaGlnPro SEQ ID NO:743

pMON35768.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGln
AspCysSerPheGlnHisSerProIleSerSerAspSerAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:744

pMON35770.pep

AlaLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySer
LysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysTyrAlaPheGlnProProPro
SerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLys
ProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysArgProAspSerSerThrLeuGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThr
IleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSer
LeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrp
AlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeu

AspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThr
GlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGln
SerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:745

pMON35772.pep

AlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro
ProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAla
LeuLysProTrpIleThrArgGlnAsnPhePheArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAla
SerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
LysThrValAlaGlyTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:746

pMON35773.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGly
GlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSer
ProAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnVal
ArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGlu
LeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeu
AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMet
GluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArg
ArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeu
AlaGlnPro SEQ ID NO:747

pMON35777.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuPro
GlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGly
AlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:748

pMON35778.pep

AlaGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThr
ValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrAlaGlyGlnProProLeuThrGln
AspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeu
GlnAspTyrProValThrValAlaSerAsnLeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla

LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:749

pMON35779.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGly
GlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSer
ProAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnVal
ArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGlu
LeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeu
AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMet
GluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArg
ArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeu
AlaGlnPro SEQ ID NO:750

pMON35780.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgProLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGly
GlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSer
ProAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnVal
ArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGlu
LeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeu
AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMet
GluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArg
ArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeu
AlaGlnPro SEQ ID NO:751

pMON35782.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuProProProTrpSerProArgProLeuGlyAlaThrAlaProThrAlaGlyGlnProProLeuThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlyThrProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrProLeuGly
ProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeu
GlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHis
SerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAla
LeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAla
SerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:752

pMON39908.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProValGluThrVal
PheHisArgValSerGlnAspGlyLeuAspLeuLeuThrSerThrGlnAspCysSerPheGlnHisSerProIle
SerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSer
AsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGlyGlyGlySerAsnMetAlaThrPro
LeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAsp
GlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGln
LeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThr
LeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAla
ProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeu

ValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:753

pMON32275.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProPro
SerLysGluSerHisLysSerProAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeu
LeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyr
LysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCys
ProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeu
GlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAla
ThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAla
PheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyPro
IleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnAspCysSer
PheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyr
ProValThrValAlaSerAsnLeuGln SEQ ID NO:754

pMON35781.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnGluProLysSerProAspThrHisThrSer
ProProSerProThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnVal
ArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGlu
LeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeu
AlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMet
GluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArg
ArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeu
AlaGlnProSerAlaGluProLysSerProAspThrHisThrSerProProSerProGlySerAsnLeuGlnAsp
GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProPro
ProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
SEQ ID NO:755

pMON35783.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyTrpGlnGlyArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheProLysSerProAspThrHisThrSerProProSer
ProGlyThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLys
IleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
SerAlaGluProLysSerProAspThrHisThrSerProProSerProGlyLysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysPro
TrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu SEQ ID NO:756

pMON32276.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysSerAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
SerSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGlu
GlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLysLeuCysHisPro
GluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeu
GlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGly
IleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGln
GlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe

GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArg
HisLeuAlaGlnPro SEQ ID NO:757

pMON32277.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysSerAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspSerSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:758

pMON32278.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerSerLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnSerGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGlu
GlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLysLeuCysHisPro
GluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeu
GlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGly
IleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGln
GlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArg
HisLeuAlaGlnPro SEQ ID NO:759

pMON32279.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerSerLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnSerGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:760

pMON35790.pep

AlaThrGlnAspSerSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysSerAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GlyGlySerGlyGlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeu
LysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLys
LeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThr
ThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPhe
AlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyr
ArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:761

pMON35791.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerSerLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnSerGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GlyGlySerGlyGlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeu
LysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLys
LeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThr
ThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPhe
AlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyr
ArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:762

pMON35792.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGlyGlyGlySerAsn
MetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLys
IleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLysLeuCysHisProGluGluLeuVal
LeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGlu
LeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGlu
LeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAla
GlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGln
Pro SEQ ID NO:763

pMON39905.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnSerGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GlyGlySerGlyGlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeu
LysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLys
LeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThr
ThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPhe
AlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyr
ArgValLeuArgHisLeuAlaGlnPro SEQ ID NO:764

pMON39906.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgArgLeuGluLeuGlnSerGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGly
GlyGlySerGlyGlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeu
LysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrAsnLys
LeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThr
ThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPhe
AlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyr
ArgValLeuArgHisLeuAlaGlnPr SEQ ID NO:765

pMON39909.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp

CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyVal
LeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProSerGly
GlySerGlyGlySerGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGly
IleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSer
GlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThr
LeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnPro SEQ ID NO:766

pMON39910.pep

AlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHis
LeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySer
GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeu
CysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyr
GlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProTyrValGlu
GlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMet
GluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheVal
ThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGlu
ThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGly
GlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeu
SerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:767

pMON35727.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGly
GlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:768

pMON32168.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGly
ProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnAspCys
SerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsn
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeu SEQ ID NO:769

pMON32195.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGlu

GlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisPro
GluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeu
GlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGly
IleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGln
GlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArg
HisLeuAlaGlnProTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGly
GlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln
SEQ ID NO:770

pMON32196.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGly
GlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLys
SerProAsnMetAlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGly
GlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGly
LeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArg
PheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu SEQ ID NO:771

pMON32197.pep

AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
TyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSer
LysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIle
HisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGlu
LeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIle
ArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGly
GlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLys
SerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArg
LeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLys
CysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSer
GluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
AspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:772

pMON32206.pep

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaProLeuLeuAspProAsn
AsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeuArgLeuProAsnLeuGluSerPheValArg
AlaValLysAsnLeuGluAsnAlaSerGlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAla
ThrAlaAlaProSerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSer
GlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAspGluGlu

LeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLys
MetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysPro
TrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGly
SerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGln
HisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThr
IleAsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeu
TrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheVal
GlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySer
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerProIleSer
SerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsn
LeuGln SEQ ID NO:773

pMON32207.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThr
LysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThr
SerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGln
ProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly
SerGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerPro
GlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSerHisLysSerProAsnMet
AlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLeuGluGlnValArgLysIle
GlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeu
LeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeu
GlyMetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro
STPSTPGlySerGluPheGlySer SEQ ID NO:774

pMON35728.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsn
ProSerProProSerLysGluSerHisLysSerProAsnMetAlaAsnCysSerIleMetIleAspGluIleIle
HisHisLeuLysArgProProAsnProLeuLeuAspProAsnAsnLeuAsnSerGluAspMetAspIleLeuMet
GluArgAsnLeuArgThrProAsnLeuLeuAlaPheValArgAlaValLysHisLeuGluAsnAlaSerGlyIle
GluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSerArgHisProIleIleIle
LysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPheTyrLeuValThrLeuGluGlnAlaGlnGluGln
GlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerProPro
SerLysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArg
LeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeu
GluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGly
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID NO:775

pMON32183.pep

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrVal
AlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
ProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuVal
AlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnGluPheLysLeuGluProArgGlyProThrIleLysProCys

ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp
ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAspValGln
IleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThr
LeuArgAlaValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn
AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr
ValLeuProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetPro
GluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAsp
SerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer
CysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGlyLys SEQ
ID NO:776

pMON32184.pep

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAsp
TyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArg
ValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThr
AsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPhe
SerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGluPheLysLeuGluProArgGlyProThr
IleLysProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProPro
LysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAsp
ProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAsp
TyrAsnSerThrLeuArgAlaValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLys
CysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArgAla
ProGlnValTyrValLeuProProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThr
AspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGlu
ProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArg
AsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrPro
GlyLys SEQ ID NO:777

The following examples will illustrate the invention in greater detail although it will be understood that the invention is not limited to these specific examples.

EXAMPLE 1

Construction of parental BHK expression vector

A. Removal of AflIII site from mammalian expression plasmid.

A new mammalian expression vector was constructed to accept NcoI-HindIII or AflIII-HindIII gene fragments in-frame and 3′ to the hIL-3 receptor agonist pMON13146 (WO 94/12638) gene and a mouse IgG2b linker fragment. First, the single AflIII site was removed from pMON3934, which is a derivative of pMON3359. pMON3359 is a pUC18-based vector containing a mammalian expression cassette. The cassette includes a herpes simplex viral promoter IE110 (-800 to +120) followed by a modified human IL-3 signal peptide sequence and an SV40 late poly-adenylation (poly-A) signal which has been subcloned into the pUC18 polylinker (See Hippenmeyer et al., Bio/Technology, 1993, pp.1037-1041). The modified human IL-3 signal sequence, which facilitates secretion of gene products outside of the cell, is flanked by a BamHI site on the 5′ end and a unique NcoI site on the 3′ end. A unique HindIII site is 3′ to the NcoI site and 5′ to the poly-A sequence. The DNA sequence encoding the signal peptide is shown below (restriction enzyme sites are indicated above). The ATG (methionine) codon within the NcoI site is in-frame with the initiator ATG of the signal peptide (underlined);

BamHI NcoI
5'GGATCCACCATGAGCCGCCTGCCCGTCCTGCTCCTGCTCCAACTCCTGGTCCGCCCCGCCATGG
(SEQ ID NO:857)

The single AflIII site was removed from pMON3934 by digestion with AflIII followed by filling in the overhangs by addition of a DNA polymerase and nucleotides. The digested DNA fragment was purified via Magic PCR Clean up kit (Promega) and ligated with T4 DNA ligase. The ligation reaction was transformed into DH5α ™ and the cells were plated onto LB-agar plus ampicillin. Individual colonies were screened for the loss of the AflIII site by restriction analysis with AflIII and HindIII which results in a single fragment if the AflIII site was removed. The resulting plasmid was designated pMON30275.

B. Transfer of hIL-3 receptor agonist pMON13416/IgG2b cassette into pMON30275.

The NcoI-HindIII fragment (ca. 425 bp) from pMON30245 was ligated to the NcoI-HindIII fragment (ca. 3800 bp) of the pMON30275. pMON30245 (WO 94/12638) contains the gene coding for hIL-3 receptor agonist pMON13416 joined to a mouse IgG2b hinge fragment. Immediately 3' to the IgG2b hinge and 5' to the HindIII site is an AflIII site. Genes can be cloned into the AflIII-HindIII sites as NcoI-HindIII or AflIII-HindIII fragments in frame with the hIL-3 variant pMON13416/IgG2b hinge to create novel chimeras. The NcoI site and the AflIII site have compatible overhangs and will ligate but both recognition sites are lost. The plasmid, pMON30304 containing the DNA sequence of (SEQ ID NO:1), coding for hIL-3 variant pMON13416 joined with a mouse IgG2b hinge region, was a result of this cloning.

EXAMPLE 2

Construction of an intermediate plasmid containing one copy of the c-mpl ligand (1-153) gene of the dimer template

In order to generate a plasmid DNA with the coding sequence of c-mpl (1-153) ligand followed by a unique EcoRI restriction site, the gene is isolated via reverse transcriptase/polymerase chain reaction (RT/PCR). Human fetal (lot #38130) and adult liver (lot #46018) A+ RNA are obtained from Clontech (Palo Alto, CA) for source of c-mpl ligand messenger RNA (mRNA). The first strand cDNA reactions are carried out using a cDNA Cycle™ Kit obtained from Invitrogen (San Diego, CA). In the RT reaction, random primers and oligo dT primer are used to generate cDNA from a combination of human and fetal liver mRNA. For amplification of c-mpl ligand gene fragment encoding amino acids 1-153, the RT product serves as the template for PCR with a combination of the primers, Forward primer: c-mplNcoI (SEQ ID NO:317) and Reverse primer: Ecompl. The c-mplNcoI primer anneals to the c-mpl ligand gene (bases #279-311 based on c-mpl ligand sequence from Gene bank accession #L33410 or de Sauvage et al., *Nature* **369**: 533-538 (1994)) and encodes a NcoI restriction enzyme site immediately 5′ to the first codon (Ser+1) of c-mpl ligand. The NcoI restriction enzyme site codes for methionine and alanine codons prior to Ser+1 and includes codon degeneracy for the Ala codon and the first four codons (Ser, Pro, Ala, & Pro) of c-mpl ligand. The Ecompl primer anneals to bases #720-737 of c-mpl ligand and encodes an EcoRI site (GAATTC) in-frame with the c-mpl ligand gene immediately following Arg-153. The EcoRI site creates Glu and Phe codons following Arg-153. The ca. 480 bp PCR product was purified, digested with NcoI and EcoRI and ligated to the NcoI-EcoRI vector fragment of pMON3993 (ca. 4550 bp.). pMON3993 was a derivative of pMON3359 (described in Example 1). The human IL-3 signal peptide sequence, which had been subcloned as a BamHI fragment into the unique BamHI site between the IE110 promoter and poly-A signal, contains an NcoI site at its 3′ end and is followed by a unique EcoRI site. The plasmid, pMON26458 containing the DNA sequence of (SEQ ID NO:2), coding for c-mpl ligand amino acids 1-153 (SEQ ID NO:467), was the result of this cloning.

EXAMPLE 3

Construction of the parental plasmids containing the second genes of the dimer templates

For amplification of c-mpl ligand gene fragments starting at amino acid 1 (Ser) with a termination codon following amino acid 153 (Arg), the RT reaction from Example 2 serves as the template for PCR with a combination of the following primers; c-mplNcoI (SEQ ID NO:317) (forward primer) and c-mplHindIII (SEQ ID NO:319) (reverse primer). The c-mplNcoI (SEQ ID NO:317) primer is described in Example 2. The c-mplHindIII (SEQ ID NO:319) primer, which anneals to bases #716-737 of c-mpl ligand, adds both a termination codon and a HindIII restriction enzyme site immediately following the final codon, Arg^{153}.

Two types of PCR products are generated from the RT cDNA samples, one with a deletion of the codons for amino acids 112-115 and one without the deletion of these codons. The c-mpl ligand PCR products (ca. 480 bp) are digested with NcoI and HindIII restriction enzymes for transfer to a mammalian expression vector, pMON3934. pMON3934 is digested with NcoI and HindIII (ca. 3800 bp) and will accept the PCR products.

Plasmid, pMON32132 (SEQ ID NO:84), coding for c-mpl ligand amino acids 1-153 (SEQ ID NO:546) was a result of this cloning. Plasmid, pMON32134 (SEQ ID NO:86), coding for c-mpl ligand amino acids 1-153 (SEQ ID NO:548) was a result of this cloning. Plasmid, pMON32133 (SEQ ID NO:85), coding for c-mpl ligand amino acids 1-153 with a deletion of codons 112-115 (Δ112-115) (SEQ ID NO:547) was also a result of this cloning.

EXAMPLE 4

Generation of PCR dimer template 5L with a 112-115 deletion in the second c-mpl ligand gene

A PCR template for generating novel forms of c-mpl ligand is constructed by ligating the 3.7 Kbp BstXI/EcoRI fragment of pMON26458 to the 1 Kbp NcoI/BstXI fragment from pMON32133 (containing a deletion of amino acids 112-115) along with the EcoRI/AflIII 5L synthetic oligonucleotide linker 5L-5′ (SEQ ID NO:322) and 5L-3′ (SEQ ID NO:323).

The EcoRI end of the linker will ligate to the EcoRI end of pMON26458. The AflIII end of the linker will ligate to the NcoI site of pMON32133, and neither restriction site will be retained upon ligation. The BstXI sites of pMON26458 and pMON32133 will ligate as well. Plasmid, pMON28548, is a result of the cloning and contains the DNA sequence of (SEQ ID NO:3) which encodes amino acids 1-153 c-mpl ligand fused via a GluPheGlyGlyAsnMet (SEQ ID NO:783) linker to amino acids 1-153 c-mpl ligand that contains a deletion of amino acids 112-115 (SEQ ID NO:468).

EXAMPLE 5

Generation of PCR dimer template 4L

A PCR template for generating novel forms of c-mpl ligand is constructed by ligating the 3.7 Kbp BstXI/EcoRI fragment of pMON26458 to the 1 Kbp NcoI/BstXI fragment from pMON32132 along with the EcoRI/AflIII 4L synthetic oligonucleotide linker 4L-5′ (SEQ ID NO:320) and 4L-3′ (SEQ ID NO:321).

The EcoRI end of the linker will ligate to the EcoRI end of pMON26458. The AflIII end of the linker will ligate to the NcoI site of pMON32132, and neither restriction site will be retained upon ligation. The BstXI sites of pMON26458 and pMON32132 will ligate as well. The plasmid, pMON28500, is a result of the cloning and contains the DNA sequence of (SEQ ID NO:4) which encodes amino acids 1-153 c-mpl ligand fused via a GluPheGlyAsnMetAla (SEQ ID NO:223) linker (4L) to amino acids 1-153 c-mpl ligand (SEQ ID NO:469).

EXAMPLE 6

Generation of PCR dimer template 5L

A PCR template for generating novel forms of c-mpl ligand is constructed by ligating the 3.7 Kbp BstXI/EcoRI fragment of pMON26458 to the 1 Kbp NcoI/BstXI fragment from pMON32132 along with the EcoRI/AflIII 5L synthetic oligonucleotide linker 5L-5′ (SEQ ID NO:322) and 5L-3′ (SEQ ID NO:323).

The EcoRI end of the linker will ligate to the EcoRI end of pMON26458. The AflIII end of the linker will ligate to the NcoI site of pMON32132, and neither restriction site will be retained upon ligation. The BstXI sites of pMON26458 and pMON32132 will ligate as well. Plasmid, pMON28501 is a result of the cloning and contains the DNA sequence of (SEQ ID NO:4) which encodes amino acids 1-153 c-mpl ligand fused via a GluPheGlyGlyAsnMet (SEQ ID NO:783) linker (5L) to amino acids 1-153 c-mpl ligand (SEQ ID NO:470).

EXAMPLE 7

Generation of PCR dimer templates 8L

A PCR template for generating novel forms of c-mpl ligand is constructed by ligating the 3.7 Kbp BstXI/EcoRI fragment of pMON26458 to the 1 Kbp NcoI/BstXI fragment from pMON32134 along with the EcoRI/AflIII 8L synthetic oligonucleotide linker 8L-5′ (SEQ ID NO:324) and 8L-3′ (SEQ ID NO:325).

The EcoRI end of the linker will ligate to the EcoRI end of pMON26458. The AflIII end of the linker will ligate to the NcoI site of pMON32134, and neither restriction site will be retained upon ligation. The BstXI sites of pMON26458 and pMON32134 will ligate as well. Plasmid, pMON28502 is a result of the cloning which contains the DNA sequence of (SEQ ID NO:6) and encodes amino acids 1-153 c-mpl ligand fused via a GluPheGlyGlyAsnGlyGlyAsnMetAla (SEQ ID NO:224) linker (8L) to amino acids 1-153 c-mpl ligand (SEQ ID NO:471).

EXAMPLES 8-44

Generation of novel c-mpl ligand genes with new N-terminus and C-terminus

A. PCR generation of genes encoding novel c-mpl ligand receptor agonists.

Genes encoding novel c-mpl ligand receptor agonists were generated using Method III (Horlick et al., *Prot. Eng.* **5**:427-433, 1992). The PCR reactions were carried out using dimer templates, pMONs 28500, 28501, 28502 or 28548 and one of the sets of synthetic primer sets below (The first number refers to the position of the first amino acid in the original sequence. For example, the

31-5' and 31-3' refers to the 5' and 3' oligo primers, receptively, for the sequence beginning at the codon corresponding to residue 31 of the original sequence.).

31-5′ (SEQ ID NO:326) and 31-3′ (SEQ ID NO:327), 35-5′ (SEQ ID NO:328) and 35-3′ (SEQ ID NO:329), 39-5′ (SEQ ID NO:330) and 39-3′ (SEQ ID NO:331), 43-5′ (SEQ ID NO:332) and 43-3′ (SEQ ID NO:333), 45-5′ (SEQ ID NO:334) and 45-3′ (SEQ ID NO:335), 49-5′ (SEQ ID NO:336) and 49-3′ (SEQ ID NO:337), 82-5′ (SEQ ID NO:338) and 82-3′ (SEQ ID NO:339), 109-5′ (SEQ ID NO:340) and 109-3′ (SEQ ID NO:341), 115-5′ (SEQ ID NO:342) and 115-3′ (SEQ ID NO:343), 120-5′ (SEQ ID NO:344) and 120-3′ (SEQ ID NO:345), 123-5′ (SEQ ID NO:346) and 123-3′ (SEQ ID NO:347), 126-5′ (SEQ ID NO:348) and 126-3′ (SEQ ID NO:349).
The templates and oligonucleotide sets used in the PCR reactions are shown in Table 4. The products that were generated were about 480 bp and were purified via Magic PCR Clean up kits (Promega).

B. Subcloning of novel c-mpl receptor agonist gene products into mammalian expression vector for generation of chimeras.

The c-mpl receptor agonist gene PCR products were digested with NcoI and HindIII or AflIII and HindIII restriction enzymes (ca. 470 bp) for transfer to a mammalian expression vector. The expression vector, pMON30304, was digested with NcoI and HindIII (ca. 4200 bp) and accepts the PCR products as NcoI-HindIII or AflIII-HindIII fragments. The restriction digest of the PCR product and the resulting plasmids are shown in Table 4.

TABLE 4

Example #	PCR template	PCR Product Primer set	PCR Product Restriction Digest	Linker	Resulting Plasmid pMON	Breakpoint in c-mpl ligand
Example 8	pMON28501	31	NcoI/HindIII	5L	28505	30-31
Example 9	pMON28501	35	AflIII/HindIII	5L	28506	34-35
Example 10	pMON28501	39	NcoI/HindIII	5L	28507	38-39
Example 11	pMON28501	43	NcoI/HindIII	5L	28508	42-43
Example 12	pMON28501	45	NcoI/HindIII	5L	28509	44-45
Example 13	pMON28501	49	NcoI/HindIII	5L	28510	48-49
Example 14	pMON28501	82	NcoI/HindIII	5L	28511	81-82
Example 15	pMON28501	109	NcoI/HindIII	5L	28512	108-109
Example 16	pMON28501	116	NcoI/HindIII	5L	28513	115-116
Example 17	pMON28501	120	NcoI/HindIII	5L	28514	119-120
Example 18	pMON28501	123	NcoI/HindIII	5L	28515	122-123
Example 19	pMON28501	126	NcoI/HindIII	5L	28516	125-126
Example 20	pMON28500	31	NcoI/HindIII	4L	28519	30-31
Example 21	pMON28500	35	AflIII/HindIII	4L	28520	34-35
Example 22	pMON28500	39	NcoI/HindIII	4L	28521	38-39
Example 23	pMON28500	43	NcoI/HindIII	4L	28522	42-43
Example 24	pMON28500	45	NcoI/HindIII	4L	28523	44-45
Example 25	pMON28500	49	NcoI/HindIII	4L	28524	48-49
Example 26	pMON28500	82	NcoI/HindIII	4L	28525	81-82
Example 27	pMON28500	109	NcoI/HindIII	4L	28526	108-109
Example 28	pMON28500	116	NcoI/HindIII	4L	28527	115-116
Example 29	pMON28500	120	NcoI/HindIII	4L	28528	119-120
Example 30	pMON28500	123	NcoI/HindIII	4L	28529	122-123
Example 31	pMON28500	126	NcoI/HindIII	4L	28530	125-126
Example 32	pMON28502	31	NcoI/HindIII	8L	28533	30-31
Example 33	pMON28502	35	AflIII/HindIII	8L	28534	34-35
Example 34	pMON28502	39	NcoI/HindIII	8L	28535	38-39
Example 35	pMON28502	43	NcoI/HindIII	8L	28536	42-43

TABLE 4 cont.

Example #	PCR template	PCR Product Primer set	PCR Product Restriction Digest	Linker	Resulting Plasmid pMON	Breakpoint in c-mpl ligand
Example 36	pMON28502	45	NcoI/HindIII	8L	28537	44-45
Example 37	pMON28502	49	NcoI/HindIII	8L	28538	48-49
Example 38	pMON28502	82	NcoI/HindIII	8L	28539	81-82
Example 39	pMON28502	109	NcoI/HindIII	8L	28540	108-109
Example 40	pMON28502	116	NcoI/HindIII	8L	28541	115-116
EXAMPLE 41	pMON28502	120	NcoI/HindIII	8L	28542	119-120
Example 42	pMON28502	123	NcoI/HindIII	8L	28543	122-123
Example 43	pMON28502	126	NcoI/HindIII	8L	28544	125-126
Example 44	pMON28548	123	NcoI/HindIII	5L	28545	122-123

EXAMPLE 45

Construction of pMON15960

Construction of pMON15960, an intermediate plasmid used for constructing plasmids containing DNA sequences encoding G-CSF Ser^{17} with a new N-terminus and C-terminus. Plasmid pACYC177 (Chang, A.C.Y. and Cohen, S.N. *J. Bacteriol.* **134**:1141-1156, 1978) DNA was digested with restriction enzymes HindIII and BamHI, resulting in a 3092 base pair HindIII, BamHI fragment. Plasmid, pMON13037 (WO 95/21254), DNA was digested with BglII and FspI, resulting in a 616 base pair BglII, FspI fragment. A second sample of plasmid, pMON13037, DNA was digested with NcoI and HindIII, resulting in a 556 base pair NcoI, HindIII fragment. The synthetic DNA oligonucleotides 1GGGSfor (SEQ ID NO:380) and 1GGGSrev (SEQ ID NO:381) were annealed to each other, and then digested with AflIII and FspI, resulting in a 21 base pair AflIII, FspI fragment. The restriction fragments were ligated, and the ligation reaction mixture was used to transform *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and analyzed by restriction analysis to confirm the correct insert.

EXAMPLE 46

Construction of pMON15981

Construction of pMON15981, a plasmid containing DNA sequences encoding a multi-functional hematopoietic receptor agonist. Plasmid, pMON15960, DNA was digested with restriction enzyme SmaI and used as template in a PCR reaction using synthetic DNA oligonucleotides 38 stop (SEQ ID NO:369) and 39 start (SEQ ID NO:368) as primers, resulting in the amplification of a DNA fragment of 576 base pairs. The amplified fragment was digested with restriction enzymes HindIII and NcoI, resulting in a HindIII, NcoI fragment of 558 base pairs. Plasmid, pMON13181, DNA was digested with HindIII and AflIII, resulting in a HindIII, AflIII fragment of 4068 base pairs. The restriction fragments were ligated, and the ligation reaction mixture was used to transform *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis, and sequenced to confirm the correct insert. The plasmid, pMON15981, contains the DNA sequence of (SEQ ID NO:78) which encodes the following amino acid sequence:

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaTyrLysLeuCysHisProGluGluLeuValLeuLeu
GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal

AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGly
ValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHis
LeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeu
ProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAla
AlaLeuGlnGluLysLeuCysAlaThr (SEQ ID NO:500)

EXAMPLE 47

Construction of pMON15982

Construction of pMON15982, a plasmid containing DNA sequences encoding a multi-functional hematopoietic receptor agonist. Plasmid, pMON15960, DNA was digested with restriction enzyme SmaI and used as template in a PCR reaction using synthetic DNA oligonucleotides 96 stop (SEQ ID NO:371) and 97 start (SEQ ID NO:370) as primers, resulting in the amplification of a DNA fragment of 576 base pairs. The amplified fragment was digested with restriction enzymes HindIII and NcoI, resulting in a HindIII, NcoI fragment of 558 base pairs. Plasmid, pMON13181, DNA was digested with HindIII and AflIII, resulting in a HindIII, AflIII fragment of 4068 base pairs. The restriction fragments were ligated, and the ligation reaction mixture was used to transform *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis, and sequenced to confirm the correct insert. The plasmid, pMON15982, contains the DNA sequence of (SEQ ID NO:79) which encodes the following amino acid sequence:

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaProGluLeuGlyProThrLeuAspThrLeuGlnLeu
AspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaPro
AlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAla
GlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeu
ArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSer
SerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAsp

GlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeu
ValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGln
AlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGly
LeuLeuGlnAlaLeuGluGlyIleSer (SEQ ID NO:501)

EXAMPLE 48

Construction of pMON15965

Construction of pMON15965, a plasmid containing DNA sequences encoding a multi-functional hematopoietic receptor agonist. Plasmid, pMON15960, DNA was digested with restriction enzyme SmaI and used as template in a PCR reaction using synthetic DNA oligonucleotides 142 stop (SEQ ID NO:377) and 141 start (SEQ ID NO:376) as primers, resulting in the amplification of a DNA fragment of 576 base pairs. The amplified fragment was digested with restriction enzymes HindIII and NcoI, resulting in a HindIII, NcoI fragment of 558 base pairs. Plasmid, pMON13181, DNA was digested with HindIII and AflIII, resulting in a HindIII, AflIII fragment of 4068 base pairs. The restriction fragments were ligated, and the ligation reaction mixture was used to transform *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis, and sequenced to confirm the correct insert. The plasmid, pMON15965, contains the DNA sequence of (SEQ ID NO:80) which encodes the following amino acid sequence:

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuVal
AlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGln
ProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSer
PheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGln
GluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAla

GlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeu
GluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAsp
PheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
ThrGlnGlyAlaMetProAlaPheAla (SEQ ID NO:502)

EXAMPLE 49

Construction of pMON15966

Construction of pMON15966, a plasmid containing DNA sequences encoding a multi-functional hematopoietic receptor agonist. Plasmid, pMON15960, DNA was digested with restriction enzyme SmaI and used as template in a PCR reaction using synthetic DNA oligonucleotides 126 stop (SEQ ID NO:372) and 125 start (SEQ ID NO:373) as primers, resulting in the amplification of a DNA fragment of 576 base pairs. The amplified fragment was digested with restriction enzymes HindIII and NcoI, resulting in a HindIII, NcoI fragment of 558 base pairs. Plasmid, pMON13181, DNA was digested with HindIII and AflIII, resulting in a HindIII, AflIII fragment of 4068 base pairs. The restriction fragments were ligated, and the ligation reaction mixture was used to transform *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis, and sequenced to confirm the correct insert. The plasmid, pMON15966, contains the DNA sequence of (SEQ ID NO:81) which encodes the following amino acid sequence:

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaMetAlaProAlaLeuGlnProThrGlnGlyAlaMet
ProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeu
GlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProGlyGlyGly
SerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLys
SerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCys
AlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIle

ProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSer
GlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThr
IleTrpGlnGlnMetGluGluLeuGly (SEQ ID NO:503)

EXAMPLE 50

Construction of pMON15967

Construction of pMON15967, a plasmid containing DNA sequences encoding a multi-functional hematopoietic receptor agonist. Plasmid, pMON15960, DNA was digested with restriction enzyme SmaI and used as template in a PCR reaction using synthetic DNA oligonucleotides 132 stop (SEQ ID NO:375) and 133 start (SEQ ID NO:374) as primers, resulting in the amplification of a DNA fragment of 576 base pairs. The amplified fragment was digested with restriction enzymes HindIII and NcoI, resulting in a HindIII, NcoI fragment of 558 base pairs. Plasmid, pMON13181, DNA was digested with HindIII and AflIII, resulting in a HindIII, AflIII fragment of 4068 base pairs. The restriction fragments were ligated, and the ligation reaction mixture was used to transform *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis, and sequenced to confirm the correct insert. The plasmid, pMON15967, contains the DNA sequence of (SEQ ID NO: 82) which encodes the following amino acid sequence:

MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
TyrArgValLeuArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeu
GlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLys
IleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHis
ProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer

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CysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeu
AspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGlu
LeuGlyMetAlaProAlaLeuGlnPro SEQ ID NO:504

EXAMPLE 51

Construction of pMON13180, an intermediate plasmid used for constructing plasmids that contain DNA sequence encoding multi-functional hematopoietic receptor agonists.

Plasmid, pMON13046 (WO 95/21254), DNA was digested with restriction endonucleases XmaI and SnaBI, resulting in a 4018 base pair vector fragment. The 4018 base pair XmaI-SnaBI fragment was purified using a Magic DNA Clean-up System kit (Promega, Madison, WI) in which the 25 base pair XmaI-SnaBI insert fragment is not retained. The complimentary pair of synthetic oligonucleotides, glyxa1 (SEQ ID NO:378) and glyxa2 (SEQ ID NO:379), were designed to remove sequence encoding a factor Xa cleavage site. When properly assembled these oligonucleotides also result in XmaI and SnaBI ends. The primers, Glyxa1 and glyxa2, were annealed in annealing buffer (20mM Tris-HCl pH7.5, 10 mM $MgCl_2$, 50 mM NaCl) by heating at 70°C for ten minutes and allowed to slow cool. The 4018 base pair XmaI-SnaBI fragment from pMON13046 was ligated with the assembled oligonucleotides using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated from the transformants and analyzed using a PCR based assay. Plasmid DNA from selected transformants was sequenced to confirm the correct insertion of the oligonucleotides. The resulting plasmid was designated pMON13180 (SEQ ID NO:88).

EXAMPLE 52

Construction of pMON13181, an intermediate plasmid used for constructing plasmids that contain DNA sequences encoding multi-functional hematopoietic receptor agonists.

Plasmid, pMON13047 (WO 95/21254), DNA was digested with restriction endonucleases XmaI and SnaBI, resulting in a 4063 base pair vector fragment. The 4063 base pair XmaI-SnaBI fragment was purified using a Magic DNA Clean-up System kit (Promega, Madison, WI) in which the 25 base pair XmaI-SnaBI insert fragment is not retained. The complimentary pair of synthetic oligonucleotides, glyxa1 (SEQ ID NO:378) and glyxa2 (SEQ ID NO:379), were designed to remove sequence encoding the factor Xa cleavage site. When properly assembled these oligonucleotides also result in XmaI and SnaBI ends. Glyxa1 and glyxa2 were annealed in annealing buffer by heating at 70°C for ten minutes and allowed to slow cool. The 4063 base pair XmaI-SnaBI fragment from pMON13047 was ligated with the assembled oligonucleotides using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated from the transformants and analyzed using a PCR based assay. Plasmid DNA from selected transformants was sequenced to confirm the correct insertion of the oligonucleotides. The resulting plasmid was designated pMON13181 (SEQ ID NO:87).

EXAMPLE 53

Construction of pMON13182

The new N-terminus/C-terminus gene in pMON13182 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 39 start (SEQ ID NO:368) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 38 stop (SEQ ID NO:369) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using primers 39 start and 38 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13182.

E. coli strain JM101 was transformed with pMON13182 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13182, contains the DNA sequence of (SEQ ID NO:17) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr (SEQ ID NO:472)

EXAMPLE 54

Construction of pMON13183

The new N-terminus/C-terminus gene in pMON13183 was created using Method I as described in Materials and Methods. "Fragment Start" was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 39 start (SEQ ID NO:368) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 38 stop (SEQ ID NO:369) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 39 start and 38 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic

DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13183.

E. coli strain JM101 was transformed with pMON13183 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13183, contains the DNA sequence of (SEQ ID NO:18) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr (SEQ ID NO:473)

EXAMPLE 55

Construction of pMON13184

The new N-terminus/C-terminus gene in pMON13184 was created using Method I as described in Materials and

Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 97 start (SEQ ID NO:370) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 96 stop (SEQ ID NO:371) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 97 start and 96 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13184.

E. coli strain JM101 was transformed with pMON13184 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13184, contains the DNA sequence of (SEQ ID NO:19) which encodes the following amino acid sequence:

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

Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser (SEQ ID NO:474)

EXAMPLE 56

Construction of pMON13185

The new N-terminus/C-terminus gene in pMON13185 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 97 start (SEQ ID NO:370) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 96 stop (SEQ ID NO:371) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 97 start and 96 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13185.

E. coli strain JM101 was transformed with pMON13185 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13185, contains the DNA sequence of (SEQ ID NO:20) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser (SEQ ID NO:475)

EXAMPLE 57

Construction of pMON13186

The new N-terminus/C-terminus gene in pMON13186 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 126 start (SEQ ID NO:372) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from

G-CSF Ser^{17} sequence in pMON13037 using the primer set, 125 stop (SEQ ID NO:373) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 126 start and 125 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13186.

E. coli strain JM101 was transformed with pMON13186 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13186, contains the DNA sequence of (SEQ ID NO:21) which encodes the following amino acid sequence:

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

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu Gly (SEQ ID NO:476)

EXAMPLE 58

Construction of pMON13187

The new N-terminus/C-terminus gene in pMON13187 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 126 start (SEQ ID NO:372) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 125 stop (SEQ ID NO:373) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 126 start and 125 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13187.

E. coli strain JM101 was transformed with pMON13187 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13187, contains the DNA sequence of (SEQ ID NO:22) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
Leu Gly (SEQ ID NO:477)

EXAMPLE 59

Construction of pMON13188

The new N-terminus/C-terminus gene in pMON13188 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 133 start (SEQ ID NO:374) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 132 stop (SEQ ID NO:375) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 133 start and 132 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13188.

E. coli strain JM101 was transformed with pMON13188 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13188, contains the DNA sequence of (SEQ ID NO:23) which encodes the following amino acid sequence:

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

Gln Pro (SEQ ID NO:478)

EXAMPLE 60

Construction of pMON13189

The new N-terminus/C-terminus gene in pMON13189 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 133 start (SEQ ID NO:374) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 132 stop (SEQ ID NO:375) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 133 start and 132 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13189.

E. coli strain JM101 was transformed with pMON13189 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13189, contains the DNA sequence of (SEQ ID NO:24) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro (SEQ ID NO:479)

EXAMPLE 61

Construction of pMON13190

The new N-terminus/C-terminus gene in pMON13190 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 142 start (SEQ ID NO:376) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 141 stop (SEQ ID NO:377) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 142 start and 141 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13190.

E. coli strain JM101 was transformed with pMON13190 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13190, contains the DNA sequence of (SEQ ID NO:25) which encodes the following amino acid sequence:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
Phe Ala (SEQ ID NO:480)
```

EXAMPLE 62

Construction of pMON13191

The new N-terminus/C-terminus gene in pMON13191 was created using Method I as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 142 start (SEQ ID NO:376) and L-11 start (SEQ ID NO:364). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 141 stop (SEQ ID NO:377) and L-11 stop (SEQ ID NO:365). The full-length new N terminus/C-terminus G-CSF Ser^{17} gene was created and amplified from the annealed Fragments Start and Stop using 142 start and 141 stop.

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and HindIII and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON13191.

E. coli strain JM101 was transformed with pMON13191 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13191, contains the DNA sequence of (SEQ ID NO:26) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
Phe Ala (SEQ ID NO:481)

EXAMPLE 63

Construction of pMON13192

The new N-terminus/C-terminus gene in pMON13192 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF sequence in pMON13037 using the primer set, 39 start (SEQ ID NO:368) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 38 stop (SEQ ID NO:369) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1%

TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON13192.

E. coli strain JM101 was transformed with pMON13192 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13192, contains the DNA sequence of (SEQ ID NO:27) which encodes the following amino acid sequence:

13192.Pept

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

Lys Leu Cys Ala Thr (SEQ ID NO:482)

EXAMPLE 64

Construction of pMON13193

The new N-terminus/C-terminus gene in pMON13193 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 39 start (SEQ ID NO:368) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 38 stop (SEQ ID NO:369) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct

insertion of the new gene. The resulting plasmid was designated pMON13193.

E. coli strain JM101 was transformed with pMON13193 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13193, contains the DNA sequence of (SEQ ID NO:28) encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr (SEQ ID NO:483)

EXAMPLE 65

Construction of pMON25190

The new N-terminus/C-terminus gene in pMON25190 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF sequence in pMON13037 using the primer set, 97 start (SEQ ID NO:370) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 96 stop (SEQ ID NO:371) and P-bl stop (SEQ ID NO:367). Fragment

Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON25190.

E. coli strain JM101 was transformed with pMON25190 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON25190, contains the DNA sequence of (SEQ ID NO:29) which encodes the following amino acid sequence:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
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Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser (SEQ ID NO:484)

EXAMPLE 66

Construction of pMON25191

The new N-terminus/C-terminus gene in pMON25191 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 97 start (SEQ ID NO:370) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 96 stop (SEQ ID NO:371) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The

intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON25191.

E. coli strain JM101 was transformed with pMON25191 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON25191, contains the DNA sequence of (SEQ ID NO:30) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser (SEQ ID NO:485)

EXAMPLE 67

Construction of pMON13194

The new N-terminus/C-terminus gene in pMON13194 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 126 start (SEQ ID NO:372) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 125 stop (SEQ ID NO:371) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct

insertion of the new gene. The resulting plasmid was designated pMON13194.

E. coli strain JM101 was transformed with pMON13194 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13194, contains the DNA sequence of (SEQ ID NO:31) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met Glu Glu Leu Gly (SEQ ID NO:486)

EXAMPLE 68

Construction of pMON13195

The new N-terminus/C-terminus gene in pMON13195 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 126 start (SEQ ID NO:372 and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 125 stop (SEQ ID NO:373) and P-bl stop (SEQ ID NO:367). Fragment

Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON13195.

E. coli strain JM101 was transformed with pMON13195 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13195, contains the DNA sequence of (SEQ ID NO:32) which encodes the following amino acid sequence:

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

Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
Met Glu Glu Leu Gly (SEQ ID NO:487)

EXAMPLE 69

Construction of pMON13196

The new N-terminus/C-terminus gene in pMON13196 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF sequence in pMON13037 using the primer set, 133 start (SEQ ID NO:374) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 132 stop (SEQ ID NO:375) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The

intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON13196.

E. coli strain JM101 was transformed with pMON13196 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13196, contains the DNA sequence of (SEQ ID NO:33) which encodes the following amino acid sequence:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
Pro Ala Leu Gln Pro (SEQ ID NO:488)
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EXAMPLE 70

Construction of pMON13197

The new N-terminus/C-terminus gene in pMON13197 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 133 start (SEQ ID NO:374) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 132 stop (SEQ ID NO:375) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct

insertion of the new gene. The resulting plasmid was designated pMON13197.

E. coli strain JM101 was transformed with pMON13197 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13197, contains the DNA sequence of (SEQ ID NO:34) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
Lys Leu Cys Ala Thr (SEQ ID NO:489)

EXAMPLE 71

Construction of pMON13198

The new N-terminus/C-terminus gene in pMON13198 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF sequence in pMON13037 using the primer set, 142 start (SEQ ID NO:376) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 141 stop

(SEQ ID NO:377) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The intermediate plasmid, pMON13180, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4023 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON13198.

E. coli strain JM101 was transformed with pMON13198 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13198, contains the DNA sequence of (SEQ ID NO:35) which encodes the following amino acid sequence:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
```

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
Met Pro Ala Phe Ala (SEQ ID NO:490)

EXAMPLE 72

Construction of pMON13199

The new N-terminus/C-terminus gene in pMON13199 was created using Method II as described in Materials and Methods. Fragment Start was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 142 start (SEQ ID NO:376) and P-bl start (SEQ ID NO:366). Fragment Stop was created and amplified from G-CSF Ser^{17} sequence in pMON13037 using the primer set, 141 stop (SEQ ID NO:377) and P-bl stop (SEQ ID NO:367). Fragment Start was digested with restriction endonuclease NcoI, and Fragment Stop was digested with restriction endonuclease HindIII. After purification, the digested Fragments Start and Stop were combined with and ligated to the approximately 3800 base pair NcoI-HindIII vector fragment of pMON3934.

The intermediate plasmid described above contained the full length new N-terminus/C-terminus G-CSF Ser^{17} gene and was digested with restriction endonucleases NcoI and HindIII. The digested DNA was resolved on a 1% TAE gel, stained with ethidium bromide and the full-length new N-terminus/C-terminus G-CSF Ser^{17} gene was isolated using Geneclean (Bio101, Vista, CA). The

intermediate plasmid, pMON13181, was digested with restriction endonucleases HindIII and AflIII, resulting in a 4068 base pair vector fragment, and purified using a Magic DNA Clean-up System kit (Promega, Madison, WI). The purified restriction fragments were combined and ligated using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insertion of the new gene. The resulting plasmid was designated pMON13199.

E. coli strain JM101 was transformed with pMON13199 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON13199, contains the DNA sequence of (SEQ ID NO:36) which encodes the following amino acid sequence:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
Met Pro Ala Phe Ala (SEQ ID NO:491)

EXAMPLE 73

Construction of tandemly-duplicated plasmid template, Syntan1

To create the tandemly-duplicated hIL-3 receptor agonist pMON13416 template, Syntan1, three DNAs were joined by means of ligation using T4 DNA ligase (Boehringer Mannheim). The three DNAs are: 1) pMON13046, containing hIL-3 receptor agonist pMON13416, digested with BstEII and SnaBI; 2) the annealed complimentary pair of synthetic oligonucleotides, L1syn.for (SEQ ID NO:352) and L1syn.rev (SEQ ID NO:353), which contain sequence encoding the linker that connects the C-terminal and N-terminal ends of the original protein and a small amount of surrounding pMON13416 sequence and which when properly assembled result in BstEII and ClaI ends; and 3) a portion of hIL-3 receptor agonist pMON13416 digested from pMON13046 with ClaI (DNA had been grown in the dam- cells, DM1 (Life Technologies)) and SnaBI. The digested DNAs were resolved on a 0.9% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101).

A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Miniprep DNA was isolated from the transformants, and the transformants were screened using a PCR based assay. Plasmid DNA from selected transformants was sequenced to obtain the correct template. The resulting plasmid was designated syntan1 and contains the DNA sequence of (SEQ ID NO:7).

EXAMPLE 74

Construction of tandemly-duplicated template, syntan3.

To create the tandemly-duplicated hIL-3 receptor agonist pMON13416 template, syntan3, three DNAs were joined by means of ligation using T4 DNA ligase (Boehringer Mannheim). The three DNAs are: 1) pMON13046, containing hIL-3 receptor agonist pMON13416, digested with BstEII and SnaBI; 2) the annealed complimentary pair of synthetic oligonucleotides, L3syn.for (SEQ ID NO:354) and L3syn.rev (SEQ ID NO:355), which contain sequence encoding the linker that connects the C-terminal and N-terminal ends of the original protein and a small amount of surrounding pMON13416 sequence and which when properly assembled result in BstEII and SnaBI ends; and 3) a portion of hIL-3 receptor agonist pMON13416 digested from pMON13046 with ClaI (DNA had been grown in the dam- cells, DM1 (Life Technologies)) and SnaBI. The digested DNAs were resolved on a 0.9% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101).

A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Miniprep DNA was isolated from the transformants, and the transformants were screened using a PCR based assay. Plasmid DNA from selected transformants was sequenced to obtain the correct template. The resulting plasmid was designated syntan3 and contains the DNA sequence of (SEQ ID NO:8).

EXAMPLE 75

Construction of pMON31104

The new N-terminus/C-terminus gene in pMON31104 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan1, using the primer set 35 start (SEQ ID NO:356) and 34 rev (SEQ ID NO:357).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector,pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31104.

E. coli strain JM101 was transformed with pMON31104 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31104, contains the DNA sequence of (SEQ ID NO:9) which encodes the following amino acid sequence:

```
Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
Gln Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile
His His Leu Lys Arg Pro Pro Ala Pro Leu Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
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Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:492)

EXAMPLE 76

Construction of pMON31105

The new N-terminus/C-terminus gene in pMON31105 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan1, using the primer set 70 start (SEQ ID NO:358) and 69 rev (SEQ ID NO:359).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31105.

E. coli strain JM101 was transformed with pMON31105 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31105, contains the DNA sequence of (SEQ ID NO:10) which encodes the protein with the following amino acid sequence:

Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:493)

EXAMPLE 77

Construction of pMON31106

The new N-terminus/C-terminus gene in pMON31106 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan1, using the primer set 91 start (SEQ ID NO:360) and 90 rev (SEQ ID NO:361).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a

1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31106.

E. coli strain JM101 was transformed with pMON31106 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31106, contains the DNA sequence of (SEQ ID NO:11) which encodes the protein with the following amino acid sequence:

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

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO;494)

EXAMPLE 78

Construction of pMON31107

The new N-terminus/C-terminus gene in pMON31107 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan1, using the primer set 101 start (SEQ ID NO:362) and 100 rev (SEQ ID NO:363).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested The DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31107.

E. coli strain JM101 was transformed with pMON31107 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31107, contains the DNA sequence of (SEQ ID NO:12) which encodes the following amino acid sequence:

Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu
Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Asn
Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val
Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu
Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Tyr Val Glu Gly Gly
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
Ala Pro Ala Leu Gln Pro (SEQ ID NO:495)

EXAMPLE 79

Construction of pMON31108

The new N-terminus/C-terminus gene in pMON31108 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan3, using the primer set 35 start (SEQ ID NO:356) and 34 rev (SEQ ID NO:357).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31108.

E. coli strain JM101 was transformed with pMON31108 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31108, contains the DNA sequence of (SEQ ID NO:13) which encodes the following amino acid sequence:

```
Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro
Ala Pro Leu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro (SEQ ID
NO:496)
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EXAMPLE 80

Construction of pMON31109

The new N-terminus/C-terminus gene in pMON31109 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan3, using the primer set 70 start (SEQ ID NO:358) and 69 rev (SEQ ID NO:359).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31109.

E. coli strain JM101 was transformed with pMON31109 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31109, contains the DNA sequence of (SEQ ID NO:14) which encodes the following amino acid sequence:

Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp
Glu Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp
Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg
Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys
Asn Leu Glu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro (SEQ ID NO:497)

EXAMPLE 81

Construction of pMON31110

The new N-terminus/C-terminus gene in pMON31110 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan3, using the primer set 91 start (SEQ ID NO:360) and 90 rev (SEQ ID NO:361).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31110.

E. coli strain JM101 was transformed with pMON31110 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31110, contains the DNA sequence of (SEQ ID NO:15) which encodes the following amino acid sequence:

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln
Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu
Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn
Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser
Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser
Ala Thr Ala Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro (SEQ ID NO:498)

EXAMPLE 82

Construction of pMON31111

The new N-terminus/C-terminus gene in pMON31111 was created using Method III as described in Materials and Methods. The full length new N-terminus/C-terminus gene of hIL-3 receptor agonist pMON13416 was created and amplified from the intermediate plasmid, Syntan3, using the primer set 101 start (SEQ ID NO:362) and 100 rev (SEQ ID NO:363).

The resulting DNA fragment which contains the new gene was digested with restriction endonucleases NcoI and SnaBI. The digested DNA fragment was resolved on a 1% TAE gel, stained with ethidium bromide and isolated using Geneclean (Bio101, Vista, CA). The purified digested DNA fragment was ligated into the expression vector pMON13189, using T4 DNA ligase (Boehringer Mannheim, Indianapolis, IN). The pMON13189 DNA had been previously digested with NcoI and SnaBI to remove the hIL3 receptor agonist pMON13416 coding sequence and the 4254 base pair vector fragment was isolated using Geneclean (Bio101, Vista, CA) after resolution on a 0.8% TAE gel and staining with ethidium bromide. A portion of the ligation reaction was used to transform *E. coli* strain DH5α cells (Life Technologies, Gaithersburg, MD). Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated and sequenced to confirm the correct insert. The resulting plasmid was designated pMON31111.

E. coli strain JM101 was transformed with pMON31111 for protein expression and protein isolation from inclusion bodies.

The plasmid, pMON31111, contains the DNA sequence of (SEQ ID NO:16) which encodes the following amino acid sequence:

Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu
Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser Gly
Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu
Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro
Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn
Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys Asn
Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln
Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile
Ile Ile Lys Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro (SEQ ID NO:499)

EXAMPLE 83

Construction of pMON31112

Construction of pMON31112, a plasmid containing DNA sequence encoding a multi-functional hematopoietic receptor agonist which activates the hIL-3 receptor and G-CSF receptor. Plasmid, pMON13189 DNA was digested with restriction enzymes NcoI and XmaI resulting in an NcoI, XmaI vector fragment that was isolated and purified from a 0.8% agarose gel. The DNA from a second plasmid, pMON13222 (WO 94/12639, US serial # 08/411,796) was digested with NcoI and EcoRI resulting in a 281 base pair NcoI, EcoRI fragment. This fragment was isolated and purified from a 1.0% agarose gel. Two oligonucleotides SYNNOXA1.REQ (SEQ ID NO:350) and

SYNNOXA2.REQ (SEQ ID NO:351) were annealed and ligated with the 281 base pair DNA fragment from pMON13222 to the DNA vector fragment from pMON13189. A portion of the ligation mixture was then transformed into *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis to show the presence of an EcoRV fragment, and sequenced to confirm the correct inserts.

The plasmid, pMON31112, contains the DNA sequence of (SEQ ID NO:37) which encodes the following amino acid sequence:

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeuProLeu
LeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsnLeuArgArgPro
AsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSerAlaIleGluSerIleLeu
LysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaProThrArgHisProIleHisIleLys
AspGlyAspTrpAsnGluPheArgArgLysLeuThrPheTyrLeuLysThrLeuGluAsnAlaGln
AlaGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIle
AsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnGlyAlaMetPro
AlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGln
SerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGly
IleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGln
LeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMet
GluGluLeuGlyMetAlaProAlaLeuGlnPro (SEQ ID NO:505)

Construction of pMON31113

Construction of pMON31113, a plasmid containing DNA sequence encoding a multi-functional hematopoietic receptor agonist which activates the hIL-3 receptor and G-CSF receptor. Plasmid, pMON13197 DNA was digested with restriction enzymes NcoI and XmaI resulting in an NcoI, XmaI vector fragment that was isolated and purified from a 0.8% agarose gel. The DNA from a second plasmid, pMON13239 (WO 94/12639, US serial # 08/411,796) was digested with NcoI and EcoRI resulting in a 281 base pair NcoI, EcoRI fragment. This fragment was isolated and purified from a 1.0% agarose gel. Two oligonucleotides SYNNOXA1.REQ (SEQ ID NO:350) and SYNNOXA2.REQ (SEQ ID NO:351) were annealed and ligated with the 281 base pair DNA fragment from pMON13239 to the DNA vector fragment from pMON13197. A portion of the ligation mixture was then transformed into *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis to show the presence of an EcoRV fragment, and sequenced to confirm the correct inserts.

The plasmid, pMON31113, contains the DNA sequence of (SEQ ID NO:38) which encodes the following amino acid sequence:

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeuProLeu
LeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsnLeuArgArgPro
AsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSerAlaIleGluSerIleLeu
LysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaProThrArgHisProIleIleIleArg
AspGlyAspTrpAsnGluPheArgArgLysLeuThrPheTyrLeuLysThrLeuGluAsnAlaGln
AlaGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIle
AsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnGlyAlaMetPro
AlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSer
LeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrp
GlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro (SEQ ID NO:506)

EXAMPLE 85

Construction of pMON31114

Construction of pMON31114, a plasmid containing DNA sequence encoding a multi-functional hematopoietic receptor agonist which activates the hIL-3 receptor and G-CSF receptor. Plasmid, pMON13189 DNA was digested with restriction enzymes NcoI and XmaI resulting in an NcoI, XmaI vector fragment that was isolated and purified from a 0.8% agarose gel. The DNA from a second plasmid, pMON13239 (WO 94/12639, US serial # 08/411,796), was digested with NcoI and EcoRI resulting in a 281 base pair NcoI, EcoRI fragment. This fragment was isolated and purified from a 1.0% agarose gel. Two oligonucleotides SYNNOXA1.REQ (SEQ ID NO:350) and SYNNOXA2.REQ (SEQ ID NO:351) were annealed and ligated with the 281 base pair DNA fragment from pMON13239 to the DNA vector fragment from pMON13189. A portion of the ligation mixture was then transformed into *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis to show the presence of an EcoRV fragment, and sequenced to confirm the correct inserts.

The plasmid, pMON31114, contains the DNA sequence of (SEQ ID NO:39) which encodes the following amino acid sequence:

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeuProLeu
LeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsnLeuArgArgPro
AsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSerAlaIleGluSerIleLeu
LysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaProThrArgHisProIleIleIleArg
AspGlyAspTrpAsnGluPheArgArgLysLeuThrPheTyrLeuLysThrLeuGluAsnAlaGln
AlaGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIle
AsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnGlyAlaMetPro
AlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGln
SerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGly
IleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGln
LeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeu
GlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMet
GluGluLeuGlyMetAlaProAlaLeuGlnPro (SEQ ID NO:507)

EXAMPLE 86

Construction of pMON31115

Construction of pMON31115, a plasmid containing DNA sequence encoding a multi-functional hematopoietic receptor agonist which activates the hIL-3 receptor and G-CSF receptor. Plasmid, pMON13197 DNA was digested with restriction enzymes NcoI and XmaI resulting in an NcoI, XmaI vector fragment that was isolated and purified from a 0.8% agarose gel. The DNA from a second plasmid, pMON13222, was digested with NcoI and EcoRI resulting in a 281 base pair NcoI, EcoRI fragment. This fragment was isolated and purified from a 1.0% agarose gel. Two oligonucleotides SYNNOXA1.REQ (SEQ ID NO:350) and SYNNOXA2.REQ (SEQ ID NO:351) were annealed and ligated with the 281 base pair DNA fragment from pMON13222 to the DNA vector fragment from pMON13197. A portion of the ligation mixture was then transformed into *E. coli* K-12 strain JM101. Transformant bacteria were selected on ampicillin-containing plates. Plasmid DNA was isolated, analyzed by restriction analysis to show the presence of an EcoRV fragment, and sequenced to confirm the correct inserts.

The plasmid, pMON31115, contains the DNA sequence of (SEQ ID NO:40) which encodes the following amino acid sequence:

MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeuProLeu
LeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsnLeuArgArgPro
AsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSerAlaIleGluSerIleLeu
LysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaProThrArgHisProIleHisIleLys
AspGlyAspTrpAsnGluPheArgArgLysLeuThrPheTyrLeuLysThrLeuGluAsnAlaGln
AlaGlnGlnTyrValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIle
AsnProSerProProSerLysGluSerHisLysSerProAsnMetAlaThrGlnGlyAlaMetPro
AlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPhe
LeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSer
LeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCys
LeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrp
GlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro (SEQ ID NO:508)

EXAMPLE 87

Determination of the in vitro activity of multi-functional hematopoietic receptor agonist proteins

The protein concentration of the multi-functional hematopoietic receptor agonist protein can be determined using a sandwich ELISA based on an affinity purified polyclonal antibody. Alternatively the protein concentration can be determined by amino acid composition analysis. The bioactivity of the multi-functional hematopoietic receptor agonist can be determined in a number of in vitro assays. For example a multi-functional hematopoietic receptor agonist which binds the hIL-3 receptor and G-CSF receptor can be assayed in cell proliferation assays using cell lines expressing the hIL-3 and/or G-CSF receptors. One such assay is the AML-193 cell proliferation assay. AML-193 cells respond to IL-3 and G-CSF which allows for the combined bioactivity of the IL-3/G-CSF multi-functional hematopoietic receptor agonist to be determined. Another such assay is the TF1 cell proliferation assay.

In addition other factor dependent cell lines, such as M-NFS-60 (ATCC. CRL 1838) or 32D which are murine IL-3 dependent cell line, may be used. The activity of IL-3 is species specific whereas G-CSF is not, therefore the bioactivity of the G-CSF component of the IL-3/G-CSF multi-functional hematopoietic receptor agonist can be determined independently. Cell lines, such as BHK or murine Baf/3, which do not express the receptor for a given ligand can be transfected with a plasmid containing a gene encoding the desired receptor. An example of such a cell line is BaF3 transfected with the hG-CSF receptor (BaF3/hG-CSF). The activity of the multi-functional hematopoietic receptor agonist in these cell lines can be compared with hIL-3 or G-CSF alone or together. The bioactivity of examples of multi-functional hematopoietic receptor agonists of the present invention assayed in the BaF3/hG-CSF cell proliferation and TF1 cell proliferation assays is shown in Table 5 and Table 6. The bioactivity of the multi-functional hematopoietic receptor agonist is expressed as relative activity compared with a standard protein pMON13056 (WO 95/21254) which has IL-3 and G-CSF receptor binding activity. The bioactivity of examples of multi-functional hematopoietic receptor agonists of the present invention assayed in the BaF3/c-mpl cell proliferation and TF1 cell proliferation assays is shown in Table 7 and Table 8.

TABLE 5
CELL PROLIFERATIVE ACTIVITY OF DUAL IL-3/G-CSF RECEPTOR AGONISTS

pMON	**BaF3/hG-CSF receptor cell proliferation assay relative activity***	**TF1 cell proliferation assay relative activity***
13182	0.015	1.1
13183	0.02	nd
13184	0.01	0.3
13185	0.023	0.36
13186	0.36	0.45
13187	0.07	0.26
13188	0.64	1.3
13189	0.58	1.37
13190	0.045	1.2
13191	0.14	2.7
13192	0.09	2.2
13193	0.06	3.0
25190	nd	nd
25191	0.43	1.2
13194	nd	nd
13195	1.3	4.3
13196	0.66	0.5
13197	0.6	0.77
13198	0.6	0.5
13199	nd	nd
15982	0.7	1.9
15981	0.068	1.2
15965	0.7	0.82
15966	0.36	1.48
15967	0.62	1.37

nd = not determined

* The bioactivity of the multi-functional hematopoietic receptor agonist is expressed as relative activity compared with a standard protein pMON13056. n=3 or greater

TABLE 6

CELL PROLIFERATIVE ACTIVITY OF DUAL IL-3/G-CSF RECEPTOR AGONISTS

pMON	**BaF3/hG-CSF receptor cell proliferation assay relative activity**	**TF1 cell proliferation assay relative activity**
31104	+	+
31105	+	+
31106	+	+
31107	nd	nd
31108	+	+
31109	+	+
31110	nd	nd
31111	nd	nd
31112	+	+
31113	+	+
31114	+	+
31115	+	+
31116	nd	nd
31117	nd	nd

nd = not determined

† The bioactivity (n=1 or 2) of the multi-functional hematopoietic receptor agonist is expressed as relative activity compared with a standard protein pMON13056.

"+" indicates that the molecule was comparable to pMON13056.

TABLE 7

CELL PROLIFERATION ACTIVITY

pMON	**Baf3/c-mpl receptor cell proliferation assay activity***	**TF1 cell proliferation assay activity**
28505	-	+
28506	-	+
28507	-	+
28508	-	+
28509	-	+
28510	-	+
28511	+	+
28512	+	+
28513	+	+
28514	+	+
28519	-	+
28520	-	+
28521	-	+
28522	-	+
28523	-	+
28524	-	+
28525	+	+
28526	+	+
28533	-	+
28534	-	+
28535	-	+
28536	-	+
28537	-	+
28538	-	+
28539	+	+
28540	+	+
28541	+	+
28542	+	+
28543	+	+
28544	+	+
28545	+	+

* Activity measured in the Baf3 cell line transfected with the c-mpl receptor, relative to c-mpl ligand (1-153).

† Activity measured relative to pMON13056.

In a similar manner other factor dependent cell lines known to those skilled in the art can be used to measure the bioactivity of the desired multi-functional hematopoietic receptor agonist. The methylcellulose assay can be used to determine the effect of the multi-functional hematopoietic receptor agonists on the expansion of the hematopoietic progenitor cells and the pattern of the different types of hematopoietic colonies *in vitro*. The methylcellulose assay can provide an estimate of precursor frequency since one measures the frequency of progenitors per 100,000 input cells. Long term, stromal dependent cultures have been used to delineate primitive hematopoietic progenitors and stem cells. This assay can be used to determine whether the multi-functional hematopoietic receptor agonist stimulates the expansion of very primitive progenitors and/or stem cells. In addition, limiting dilution cultures can be performed which will indicate the frequency of primitive progenitors stimulated by the multi-functional hematopoietic receptor agonist.

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Table 8

pMON #	IL-3 agonist activity (AML cell proliferation assay)	c-mol reecptor agonist activity (Baf/3-c-mpl cell proliferation assay
28505	+	-
28506	+	-
28507	+	-
28508	+	-
28509	+	-
28510	+	-
28511	+	+
28512	+	+
28513	+	+
28514	+	+
28515	+	+
28519	+	-
28520	+	-
28521	+	-
28522	+	-
28523	+	-
28524	+	-
28525	+	+
28526	+	+
28527	+	+
28528	+	+
28529	+	+

Table 8 (cont)

28535	+	-
28539	+	+
28540	+	+
28541	+	+
28542	+	+
28545	+	+
28551	+	+
28571	+	+

EXAMPLE 88

G-CSF variants which contain single or multiple amino acid substitutions were made using PCR mutagenesis techniques as described in WO 94/12639 and WO 94/12638. These and other variants (i.e. amino acid substitutions, insertions or deletions and N-terminal or C-terminal extensions) could also be made, by one skilled in the art, using a variety of other methods including synthetic gene assembly or site-directed mutagenesis (see Taylor et al., *Nucl. Acids Res.*, 13: 7864-8785 [1985]; Kunkel et al., *Proc. Natl. Acad. Sci. USA*, 82: 488-492 [1985]; Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, [1989], (WO 94/12639) and (WO 94/12638)). These substitutions can be made one at a time or in combination with other amino acid substitutions, and/or deletions, and/or insertions and/or extensions. After sequence verification of the changes, the plasmid DNA can be transfected into an appropriate mammalian cell, insect cell or bacterial strain such as *E. coli* for production. Known variants of G-CSF, which are active, include substitutions at positions 1 (Thr to Ser, Arg or Gly, 2 (Pro to Leu), 3 (Leu to Arg or Ser) and 17 (Cys to Ser) and deletions of amino acids 1-11 (Kuga et al. *Biochemicla and*

Biophysical Research Comm. **159**:103-111 (1989)). These G-CSF amino acid substitution variants can be used as the template to create the G-CSF receptor agonists in which a new N-terminus and new C-terminys are created. Examples of G-CSF amino acid substitution variants are shown in Table 9.

EXAMPLE 89

Bioactivity determination of G-CSF amino acid substitution variants

The G-CSF amino acid substitution variants can be assayed for cell proliferation activity using the Baf/3 cell line transfected with the human G-CSF receptor. The bioactvity of examples of G-CSF amino acid substitution variants is shown in Table 9 relative to native human G-CSF. A "+" indicates a comparable activity to native and a "-" indicates significantly reduced or no measurable activity.

TABLE 9

CELL PROLIFERATION ACTIVITY OF G-CSF VARIANTS IN BAF3 CELL LINE TRANSFECTED WITH THE HUMAN G-CSF RECEPTOR

aa position	native aa	mutant aa	activity *
13	Phe	Ser	+
13	Phe	His	+
13	Phe	Thr	+
13	Phe	Pro	+
16	Lys	Pro	+
16	Lys	Ser	+
16	Lys	Thr	+
16	Lys	His	+
18	Leu	Pro	+
18	Leu	Thr	+
18	Leu	His	+
18	Leu	Cys	+
18	Leu	Ile	+
19	Glu	Ala	-
19	Glu	Thr	-
19	Glu	Arg	-
19	Glu	Pro	-
19	Glu	Leu	-
19	Glu	Ser	-
22	Arg	Tyr	+
22	Arg	Ser	+
22	Arg	Ala	+
22	Arg	Thr	+
24	Ile	Pro	+
24	Ile	Leu	+
24	Ile	Tyr	+

TABLE 9 cont.

aa position	native aa	mutant aa	activity
27	Asp	Gly	+
30	Ala	Ile	+
30	Ala	Leu	+
34	Lys	Ser	+
43	His	Gly	+
43	His	Thr	+
43	His	Val	+
43	His	Lys	+
43	His	Trp	+
43	His	Ala	+
43	His	Arg	+
43	His	Cys	+
43	His	Leu	+
44	Pro	Arg	+
44	Pro	Asp	+
44	Pro	Val	+
44	Pro	Ala	+
44	Pro	His	+
44	Pro	Gln	+
44	Pro	Trp	+
44	Pro	Gly	+
44	Pro	Thr	+
46	Glu	Ala	+
46	Glu	Arg	+
47	Leu	Thr	+
49	Leu	Phe	+
49	Leu	Arg	+
49	Leu	Ser	+
50	Leu	His	+
54	Leu	His	+

TABLE 8 cont.

aa position	native aa	mutant aa	activity
67	Gln	Lys	+
67	Gln	Leu	+
67	Gln	Cys	+
70	Gln	Pro	+
70	Gln	Leu	+
70	Gln	Arg	+
70	Gln	Ser	+
104	Asp	Gly	+
104	Asp	Val	+
108	Leu	Ala	+
108	Leu	Val	+
108	Leu	Arg	+
108	Leu	Gly	+
108	Leu	Trp	+
108	Leu	Gln	+
115	Thr	His	+
115	Thr	Leu	+
115	Thr	Ala	+
144	Phe	His	+
144	Phe	Arg	+
144	Phe	Pro	+
144	Phe	Leu	+
144	Phe	Glu	+
146	Arg	Gln	+
147	Arg	Gln	+
156	His	Asp	-
156	His	Ser	+
156	His	Gly	+

TABLE 8 cont.

aa position	native aa	mutant aa	activity
159	Ser	Arg	+
159	Ser	Thr	+
159	Ser	Tyr	+
159	Ser	Val	+
159	Ser	Gly	+
162	Glu	Gly	-
162	Glu	Trp	+
162	Glu	Leu	+
163	Val	Arg	+
163	Val	Ala	+
163	Val	Gly	+
165	Tyr	Cys	nd
169	Ser	Leu	+
169	Ser	Cys	+
169	Ser	Arg	+
170	His	Arg	+
170	His	Ser	+

* activity relative to native hG-CSF

nd = not determined

EXAMPLE 90

Isolation of cDNA encoding flt3 ligand

Three flt3 ligand clones were amplified from human bone morrow poly A+ RNA (Clontech) using NCOFLT, HIND160, and HIND165 PCR primers (according to the manufacturer's suggested conditions). These amplified PCR products were gel purified and cloned into the BHK expression vector pMON5723 generating pMON30237 (NCOFLT + HIND160), pMON30238 (NCOFLT + HIND165), and a deletion clone pMON30239 (NCOFLT + HIND165). The deletion in pMON30239 is of amino acid residues 89 through 106.

EXAMPLE 91

Sequence rearranged flt3 receptor agonists were constructed using several methods and linker types. The first set of constructs containing the linker peptide (SerGlyGlyAsnGly)X (where X = 1, 2, or 3) with the breakpoints 39/40, 65/66, and 89/90 were made using a two step PCR process described by Mullins et al. in which the front half and the back half of each final sequence rearranged molecule is made separately in the first PCR step, then the paired products of the first reaction step are combined in a second PCR step and extended in the absence of exogenous primers.
For example, to make the three 89/90 breakpoint precursor molecules with SerGlyGlyAsnGly SEQ ID NO:786, SerGlyGlyAsnGlySerGlyGlyAsnGly SEQ ID NO:787, and SerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGlyAsnGly SEQ ID NO:788 amino acid linkers (pMON32326, pMON32327 and pMON32328 respectively), six initial PCR products were generated. The following primer pairs were used in the first step PCR reaction: a) 89For/L5B; b) 89For/L10B; c) 89For/L15B; d) 89Rev/L5A; e) 89Rev/L10A; and f)

89Rev/L15A. The identical approach was used to make pMON32321 (39/40 breakpoint, primer pairs 39For/L10B and 39Rev/L10A) and pMON32325 (65/66 breakpoint, primer pairs 65For/L5B and 65Rev/L5A) precursors. Except as noted below, all subsequent PCR reactions utilized the components of the PCR Optimizer Kit (Invitrogen) and amplification conditions according to the manufacturers suggested protocol. Reactions were set up as follows: 50 pmol of each primer, 10 ul of 5X Buffer B [300 mM Tris-HCl (pH 8.5), 10 mM $MgCl_2$, 75 mM $(NH_4)2SO_4$], 5 U Taq polymerase, and 100 ng of heat denatured DNA (in this example pMON30238) template were combined, and brought to 45 ul final volume with dH_2O. Reactions were preincubated for 1-5 minute at 80°C, then 5 ul of 10 mM dNTP added to each reaction, and heat denatured for 2 minutes at 94°C prior to amplification in a Perkin Elmer model 480 DNA thermal cycler. Seven DNA amplification cycles were done under the following conditions: heat denature for one minute at 94°C, two minutes annealing at 65°C, followed by a three minute extension at 72°C. Twenty three additional cycles consisting of a one minute heat denaturation at 94°C followed by a four minute annealing/extension at 72°C were done, followed by a final 7 minute extension cycle at 72°C. With the exception of pMON32328, the PCR amplification products were run out on a 1.2% TAE agarose gel, and the appropriate size bands (the major amplification product) were excised and purified using Geneclean II (Bio 101). Samples were resuspended in 10 ul dH_2O. The amplication products for pMON32328 were purifed directly using a Wizard PCR Clean UP kit (Promega), and DNA eluted in 50 ul dH_2O.

The method to construct the precursors of pMON32322 (39/40 breakpoint, primer pairs 39For/L5B and 39Rev/L5A) was modified by increasing the amount of template to 1 ug, and by changing the PCR amplification conditions as follows: six cycles of 94°C, 1 minute, 65°C for 2 minute, and 72°C for 2 1/2 minutes, followed by 15 cycles of 94°C for 1 minute, 70°C for 2 minutes, and 72°C for 2 minutes, followed by a single 72°C extension cycle for seven minutes.

The second PCR step utilized the gel-purified precursors from the first PCR step as a combination of primer/template as follows: 5 ul each of each precursor molecule (i.e. for pMON32328 the PCR products from primer pairs 89For/L5B and 89Rev/L5A), 10 ul of 5X Buffer B, 5 U of Taq polymerase, and 24 ul dH_2O. The reactions were heated for five minutes at 80°C, 5 ul of 10 mM dNTP was added, and the reactions heat denatured for 94°C for two minutes. DNA amplification conditions were as follows: 15 cycles of 94°C for one minute, 69°C for two minutes, followed then by a three minute extension at 72°C. To allow for complete extension, the last cycle was followed by a single extension step at 72°C for seven minutes. The 80 deg incubation time was reduced to two minutes and the number of cycles was decreased to ten cycles for pMON32325 (PCR products 65For/L5B and 65Rev/L5A). PCR reaction products of the appropriate size were gel purified on a 1.2 % TAE agarose gel using Geneclean II. For pMON32322 (39For/L5B and 39Rev/L5A) the annealing temperature was reduced to 68°C, and the extension time reduced to two minutes. In addition, the PCR product was purified using a Wizard PCR Clean Up kit (Promega) according to the suppliers suggested protocol. The second PCR step was modified for pMON32326 (PCR products of 89For/L15B and 89Rev/L15A) as follows. Three sets of PCR reactions were set up identically as above, except for the sample buffer type (either 5X buffer B, D, or J - PCR Optimizer Kit). Composition of buffers D and J differ from buffer B only by pH or [$MgCl_2$]. The [$MgCl_2$] for buffer D is 3.5 mM, whereas the pH of buffer J is 9.5. The protocol was modified by increasing the number of PCR cycles 20, and 15 ul aliquots were withdrawn at the end of cycles 10, 15 and 20. Five uls of each aliquot timepoint were analyzed for the presence of amplfied material on a 1.2% TBE agarose gel. The remainder of the buffer B, D, and J PCR reaction mixtures were pooled and subsequently purified using the Wizard PCR Clean Up Kit protocol. The DNA was eluted in 50 ul dH_2O.

The purified samples from the second step PCR reaction were digested with NcoI/HindIII using one of two standardized digestion conditions. For Geneclean II purified samples, 10 ul of DNA were digested in a 20 ul reaction with 7.5 U each of NcoI/HindIII for two hours at 37°C, and gel purified on a 1.1% TAE agarose gel again with Geneclean II. Ligation-ready samples were resuspended in 10 ul dH_2O. For pMON32322, 20 ul of sample was digested in a 50 ul reaction volume with 20U each of NcoI and HindIII for 3 hour at 37°C. 0.1 volume 3M NaOAc (pH 5.5) and 2.5 volume of EtOH were added, mixed, and stored at -20°C overnight. The DNA was recovered by pelleting for 20 minutes at 13,000 rpm @ 4°C in a Sigma Mk 202 microfuge. The DNA pellet was rinsed with chilled 70% EtOH, lyophilized, and resuspended in 10 ul dH_2O.

EXAMPLE 92

An alternate approach was used to construct pMON32320 (39/40 breakpoint, fifteen amino acid linker), pMON32323 (65/66 breakpoint, fifteen AA linker), and pMON32324 (65/66 breakpoint, ten amino acid linker). New primers (L15C, L15D, L15E) were designed to incorporate BamHI restriction site in the primer that was inframe to allow cloninng into the BamHI site and maintain the proper reading frame. PCR reaction conditions for the first step were performed identically to that described for pMON32322, except that the following set of primer pairs were used: 65For/L15D and 65Rev/L15E (pMON32324);

39For/L15D and 39Rev/L15C (pMON32320); and 65For/L15D and 65Rev/L15C (pMON32323). The PCR reaction products were purified using a Wizard PCR Clean Up kit as described, and eluted in 50 ul dH_2O. Samples were digested with either NcoI/BamHI (39For/L15D and 65For/L15D) or BamHI/HindIII (39Rev/L15C, 65Rev/L15C, and 65Rev/L15E). Restriction digests were performed as follows: 10 ul of purified PCR reaction products, 3 ul of 10X universal restriction buffer, 15 U of either NcoI or HindIII, 15 U of BamHI, in a final reaction volume of 30 ul. Reactions were incubated for 90 minutes at 37°C, and the PCR products gel purified on a 1.1% TAE agarose gel using Geneclean II. Ligation-ready DNA was resuspended in 10 ul dH_2O.

Inserts were ligated to NcoI/ HindIII digested pMON3977 (BHK mammalian expression vector) that had been treated with shrimp alkaline phosphatase (SAP) either in a three way (pMON32320, pMON32323, or pMON32324) or a two way (pMON32321, pMON32322, pMON32325, pMON32326, pMON32327 and pMON32328) ligation reaction as follows: 2.5 ul of insert (2 ul of each primer pair amplicon for pMON32320, pMON32323, and pMON32324) was added to 50 ng of vector in a ten ul reaction using standard ligation conditions. Two ul of each reaction was transformed with 100 ul of chemically competent DH5α cells (Gibco/BRL) following the manufacturers suggested protocol. Twenty five ul and 200 ul aliquots were plated out on LB plates containing 50 ug/ml ampicillin and incubated overnight. Isolated colonies were picked and DNA prepared from 50 ml overnight cultures using Qiagen DNA midiprep kits. DNA was quantitated by absorbance at A260/A280, and verified for correct insert size by agarose gel electrophoresis following digestion of 1 ug template with NcoI/HindIII restriction endonucleases. Samples containing inserts of the predicted size were sequenced in both orientations using vector-specific primers using an automated fluorescent DNA sequencer model 373A (Perkin Elmer ABI). Sequencing reactions were done in 20 ul reaction volumes using a Perkin Elmer model 480 DNA thermal cycler as follows: one ug of template, 3.2 pmol primer, 1 ul DMSO, 9.5 ul Taq terminator dyedeoxy premix (Perkin Elmer ABI) were combined, and subjected to 25 cycles of sequencing amplification as follows: 30 seconds at 94°C, 15 second annealing at 50°C, followed by a four minute extension cycle at 60°C. Samples were purified using Centri-Sep spin columns (Princeton Separations) following the manufacturers suggested protocol, lyophized, and submitted for sequence analysis. Samples containing the predicted amino acid sequence were selected for analysis and assigned pMONnumbers.

EXAMPLE 93

A similar approach used to construct pMON32320, pMON32323, and pMON32324 was utilized to introduce the second linker type (SerGlyGlySerGly)X where x = 2 or 3, into two sequence rearranged sequences containing the 39/40 breakpoint (pMON32348 and 32350). The primer pairs were as follows: for pMON32348 the combinations of 339For2/339Rev3 and 339Rev2/339-10For3 and for pMON32350 the combinations of 339For2/339Rev3 and 339Rev2/339-15For3 were used to create three PCR amplification products. Each PCR amplification was set up as follows: to 100 ng of heat denatured pMON32320, 50 pmol of each primer pair, 10 ul of 5X Buffer B, 5 U of Taq polymerase and dH_2O was added to a final volume of 45 ul. Reactions were preincubated as described before. Fifteen amplification cycles were done under the following conditions: heat denature at 94°C, one minute, followed by a two minute annealing step at 70°C, and a three minute extension at 72°C. After the last cycle, a single 72 deg extension step of 7 minutes was done. The PCR amplification products of primer pairs

339For2/339Rev3, 339Rev2/339-10For3, and 339Rev2/339-15For2 were purified using a Wizard PCR Clean Up kit (Promega), and eluted in 50 ul dH_2O. NcoI/BamHI digests for the 339For2/339Rev3 primer pair as follows: 8 ul of DNA template was mixed with 2 ul universal restriction buffer and 10 U each of NcoI and BamHI in a 20 ul reaction volume, and incubated for 90 minutes at 37°C. The digestion products was purified using the Geneclean II direct purification protocol, and ligation ready DNA resuspended in 10 ul dH_2O. The restriction digests and subsequent purification for the 339Rev2/339-10For3 and 339Rev2/339-15For2 amplification products were done identically as described for the 339For2/339Rev3 amplicon, except that 10 U of HindIII was substituted for NcoI. Standard ligations were done by adding to 50 ng NcoI/HindIII/SAP-treated, gel purified pMON3977, 0.5 ul 339For2/Rev3 amplicon, 1 ul of either 339Rev2/339-10For3 (pMON32348) or 339Rev2/339-15For3 (pMON32350) amplicons, 5U T4 DNA ligase, and 1 ul 10 X ligase buffer in a 10 ul reaction volume for 60 minutes at ambient temperature. Subsequent steps leading to final DNA sequence confirmation were done as described above.

EXAMPLE 94

A third type of linker, with a variable (GlyGlyGlySer)X repeat motif, was incorporated into another set of sequence rearranged flt3 receptor agonists from modularly constructed templates. These linker lengths were; 6 AA linker (GlyGlyGlySerGlyGly SEQ ID NO:792), 7 AA linker (GlyGlyGlySerGlyGlyGly SEQ ID NO:793), 10 AA linker (GlyGlyGlySerGlyGlyGlySerGlyGly SEQ ID NO:794), 13 AA linker (GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly SEQ ID NO:795), 15 AA linker

(GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly SEQ ID NO:796); and
21 AA linker
(GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly SEQ ID NO:797) amino acid residues. These modular templates, each comprising a dimer of hflt3 ligand separated by a BamHI-containing linker of unique length, were constructed as follows. Six intermediate PLASMID templates, FL3N, FL7N, FL11N, FL3C, FL4C, and FL10C, were constructed by PCR using paired primers and pMON30238 as template using cycling conditions similar to those employed for pMON32322. Per reaction, 50 pmol of each primer was added to 100 ng of heat-denatured template and the reactions assembled as described for pMON32322. Cycle conditions were as follows: seven cycles of 94°C, one minute; two minutes at 65°C, and 2.5 minutes at 72°C; followed by ten cycles of one minute at 94°C, two minutes at 70°C, and 2.5 minutes at 72°C. A single seven minute extension at 72°C completed the cycling reactions. The primer pairs used to construct each intermediate were; N-term/FLN3 (FL3N); N-term/FLN7 (FL7N); N-term/FLN11 (FL11N); C term/FLC3 (FL3C); C-term/FLC4 (FL4C); and C-term/FLC10 (FL10C). The PCR amplification products were purified with Wizard PCR Clean Up kits (Promega) and eluted in 50 ul dH_2O. Purified DNA for the first subset, FL3N, FL7N, and FL11N, were digested with NcoI/BamHI, gel purified as described previously, and ligated to NcoI/BamHI/Sap-treated pSE420 vector DNA (Invitrogen). Intermediate templates of the second subset, FL3C, FL4C, and FL10C, were constructed in an identical manner except HindIII was utilized instead of NcoI. Subsequent steps leading to final DNA sequence confirmation were done as described above.

EXAMPLE 95

To make the final six templates, the two subsets of intermediates in pSE420 were digested with either NcoI/BamHI (FL3N, FL7N, FL11N-subset 1) or BamHI/HindIII (FL3C, FL4C, FL10C-subset 2) and gel purified using Geneclean II as described previously. One intermediate amplicon from each subset were ligated to NcoI/HindIII/SAP-treated pMON3977 per reaction and transformed in DH5α cells as described previously using the following combinations to generate specific linker lengths: six AA linker (FL3N and FL3C), seven AA linker (FL3N and FL4C), ten AA linker (FL7N and FL3C), thirteen AA linker (FL3N and FL10C), fifteen AA linker (FL11N and FL4C), and 21 AA linker (FL11N and FL10C). DNA was prepared 50 ml overnight cultures from single colonies from each of the six combination as described above, analyzed for correct insert size by NcoI/HindIII restriction analysis, and used as template.
Primer pairs 39For/39Rev (39/40 breakpoint); 65For/65Rev (65/66 breakpoint) and 89For/89Rev (89/90 breakpoint) were used to PCR amplify each templates as described for pMON32322, except 75 pmol of each primer was used. Amplification conditions were modified as follows: six cycles of 94°C for one minute, 2 minutes at 70°C, 2.5 minutes at 72°C; followed by nine cycles of 94°C for one minute, and three minutes at 72°C. After the last cycle, a final extension of six minutes at 72°C allowed ample time for full extension of products.
Samples were purified using a Wizard PCR Clean Up kit as described, and double digested with NcoI/HindIII. These amplification products were purified again using a Wizard PCR Clean Up kit. In addition, all six different linker length molecules for the 39/40 breakpoint were cloned into NcoI/HindIII/SAP-treated pMON3977 as single proteins (pMON32365, pMON32366, pMON32367, pMON32368, pMON32369 and 32370). Subsequent steps leading to final DNA sequence confirmation were done as described above.

EXAMPLE 96

Genes encoding multi-functional chimeric receptor agonist molecules consisting of an IL-3 receptor agonist, of pMON13416 (WO 94/12638) joined via an IgG2b linker to either native flt3 ligand or sequence rearranged flt3 receptor agonists, Examples 91-93, were constructed. Inserts containing the desired sequence rearranged flt3 receptor agonists molecule were isolated from the parental plasmid as a NcoI/HindIII restriction fragment and ligated to pMON30304 digested with AflIII/Hind III/SAP Subsequent steps leading to final DNA sequence confirmation were done as described above. The resulting plasmids, containing the DNA sequences encoding multi-functional chimeric molecules comprising an IL-3 receptor agonist (from pMON13416) and a sequence rearranged flt3 receptor agonist are indicated in Table 9.

Table 9

Resulting Plasmid	hflt3 ligand permutein precursors
pMON30247	pMON30237
pMON30248	pMON30238
pMON32332	pMON32321
pMON32333	pMON32320
pMON32334	pMON32325
pMON32335	pMON32324
pMON32336	pMON32323
pMON32337	pMON32328
pMON32338	pMON32327
pMON32339	pMON32326

EXAMPLE 97

Genes encoding multi-functional chimeric receptor agonist molecules consisting of an IL-3 receptor agonist, of pMON13288 (WO 94/12638) joined via an IgG2b linker to either native flt3 ligand or sequence rearranged flt3 receptor agonists, Examples 91-93, were constructed. Inserts containing the desired sequence rearranged flt3 receptor agonists molecule were isolated from the parental plasmid as a NcoI/HindIII restriction fragment and ligated to pMON30311 digested with AflIII/Hind III/SAP Subsequent steps leading to final DNA sequence confirmation were done as described above. The resulting plasmids, containing the DNA sequences encoding multi-functional chimeric molecules comprising an IL-3 receptor agonist (from pMON13288) and a sequence rearranged flt3 receptor agonist are indicated in Table 10.

Table 10

Resulting Plasmid	Flt3 ligand precursors
pMON32364	pMON30237
pMON32377	pMON30238
pMON32352	pMON32321
pMON32353	pMON32320
pMON32354	pMON32325
pMON32355	pMON32324
pMON32356	pMON32323
pMON32357	pMON32328
pMON32358	pMON32327
pMON32359	pMON32326
pMON32360	pMON32348
pMON32362	pMON32350
pMON32396	pMON30239

EXAMPLE 98

Two chimeric molecules with the sequence rearranged hflt3 receptor agonist component at the N-terminus of the chimeric molecule were constructed via PCR using pMON32360 and pMON32362 plasmid DNA as the template and primer pairs N-term/134rev and N-term/139 rev to replace the stop codon at the C terminus of the native flt3 ligand molecules with an inframe SnaBI restriction site. Reaction mixtures were set up as described previously for pMON32322. Cycle conditions and were as follows: seven cycles of 94°C, one minute, 65°C, two minutes, and 72°C 2 1/2 minutes and an additional 10 amplification cycles were performed in which the annealing temperature was elevated from 65°C to 70°C. Samples were purified using the Wizard PCR Purification kit and protocol, and eluted in 50 ul dH_2O, 20 ul of each sample was digested with NcoI and SnaBI. Plasmid, pMON26431, DNA was digested with NcoI and SnaBI and ligated with the NcoI/SnaBI digested PCR reactions. Transformation of competent DH5α cells and subsequent steps leading to final DNA sequence confirmation were done as described above.

EXAMPLE 99

Five additional hflt3 ligand breakpoints were made using the indicated primers 28/29(28For/28Rev), 34/35(34For/34Rev), 62/63 (62For/62Rev), 94/95 (94For/94Rev), and 98/99 (98For/98Rev) to amplify the ten and fifteen amino acid linker (GlyGlyGlySer)x as described above. The resulting PCR products were digested with NcoI/HindIII and ligated into pMON30311, digested with AflIII/HindIII/SAP as described previously. Transformation of competent DH5α cells and subsequent steps leading to final DNA sequence confirmation were done as described above.

EXAMPLE 100

For enhanced expression of sequence rearranged hflt3 receptor agonists in E. coli, N-terminal specific primers coding for degenerate codons were used to re-engineer both the 1-134 and 1-139 forms of native hflt3 ligand in the E. coli expression vector pMON5723. Primer pairs FH3AFor/SCF.rev (Ala2) and Flt23For/SCF (Gly2) were used to PCR amplify a N-terminal degenerate mixture of sequences encoding native flt3 ligand using reaction conditions as described for pMON23222, except that the number of amplification cycles was reduced to fifteen cycles of 1 minute at 95°C, 2 minutes at 55°C, and 2 1/2 minutes at 72°C. Amplicons were purified using Wizard PCR Clean up kit (Promega), and eluted in 50 ul dH_2O. Restriction digestion with NcoI/HindIII and subsequent gel purification using Geneclean II was performed as previously described. Inserts were ligated to NcoI/HindIII/SAP-treated, gel-purified pMON5723 plasmid DNA, and transformed into competent DH5α cells as previously described. Aliquots of transformed cells were plated out on LB agarose media plates containing 75 ug/mL spectinomycin, incubated for 14-16 hours at 37°C, and colonies counted. After confirmation of colonies, the remainder of each transformation mixture was incubated overnight (14-16hr) at 37°C in 2 x 5 mL of LB media containing 75 ug/mL spectinomycin. Miniprep DNA was prepared using a Wizard DNA 373A Miniprep kit (Promega) following the recommended protocol. Purified miniprep DNA was eluted in 50 ul dH_2O, and 1-2 ul used to transform chemically competent MON207 cells. 25 and 200 ul aliquots were plated out on LB media plates containing 75 ug/mL spectinomycin, and incubated for 12-15 hours at 37°C. 40-50 well-isolated colonies representing each original primer pair were selected and streaked out on

LB/spectinomycin master plates, and incubated an additional 4-6 hours at 37°C.

Individual sequence rearranged hflt3 receptor agonist clones were screened for E. coli expression in a 96 well microtiter format to select for improved expression levels. Per well, 100 ul of minimal M9 media (including 1% casamino acids) was inoculated by a single colony (40 - 50 isolates were analyzed for each hflt3 PCR primer pair), and incubated at 37°C at 200 rpm for 3-4 hr (I=0) and induced by addition of 5 ul/well of 1mg/mL freshly prepared Nalidixic acid (in 0.1 N NaOH). After an additional four hours incubation at 37°C (I=4), approximately 5-10 ul aliquots were withdrawn from each well, and analyzed by light microscopy for the presence of refractile bodies, and the results scored as a approximate percentage of cells containing refractile bodies to the total number of cells. The clones having the highest expression levels were selected for 10 mL benchtop scale expression studies as follows. Five mL overnight cultures were grown in LB media in the presence of 75ug/mL spectinomycin at 37°C. To 10 mL freshly prepared minimal M9 (with 1% casamino acids) in 125 mL shake flasks, inoculation with sufficient overnight cells to achieve an initial reading of 20 Klett units was done, and then incubated for ~ 3-4 hours at 37°C with shaking until a density of ~110-150 Klett units was reached (I=0) and induced with 50 ul of freshly prepared Nalidixic acid (10 mg/mL in 0.1 N NaOH). One mL aliquots were removed and the cells pelleted for one minute in a microfuge. The supernatants were removed by aspiration and the pellets stored at -20°C until ready for SDS-PAGE analysis. The remainder of the induced cells were incubated for an additional four hours at 37°C with shaking, after this time point (I=4) cell density (in Klett units) was measured. A one mL aliquot was removed from each sample, pelleted and stored as described above. Another 5-10 ul

aliquot was removed from each flask and analyzed by light microscopy for the presence of refractile bodies. Pelleted samples were resuspended in a volume (in ul) of 2X loading buffer (including 1% B-mercaptoethanol) equal to the I=4 Klett value, boiled for 5 minutes, and 6-7 ul loaded on a 12% or 14% Tris-Glycine SDS polyacrylamide gel (Novex) and electrophoresed for 90 minutes at 90 volts. Gels were fixed, stained and prepared for drying according the suggested protocol (Novex). Clones were selected at this point for scale up fermentation based upon enhanced expression levels of a single induced protein band (I=4) corresponding to the predicted size when compared to the I=0 samples.
Midiprep DNA was also prepared from selected clones expressing high level of induced protein as described previously and steps leading to final DNA sequence confirmation were done exactly as described above. These clones were designated pMON32329, pMON32330, pMON32341, and pMON32342

EXAMPLE 101

A set of multi-functional receptor agonist chimeric molecules comprising an IL-3 receptor agonist (from pMON13288) and native flt3 ligand were also constructed for expression in E. coli. The genes encoding the multi-functional receptor agonist chimeric molecules from pMON32364 and pMON32377 were released from the parental vector by digestion with NcoI/Hind III and ligated to pMON5677 vector, transformed into MON207 cells, and single isolates picked, as described above. These constructs were designated pMON32394 (insert from pMON32364) and pMON32395 (insert from pMON32377).

EXAMPLE 102

A truncated Flt3 receptor was isolated as a 1.4Kb PCR product using 50pmol of the primers FLTAFLS1 and FLTR1N with approximately 10ng of the plasmid pMON27184 as the template. The primers were designed to produce an AflIII restriction site just 5′ to the first Asn codon of the mature coding sequence, as well as an EcoRI restriction site just 5′ to the putative transmembrane region. The reaction was digested with AflIII and EcoRI using standard reaction conditions and ligated into the NcoI/EcoRI digested plasmid pMON26458. This plasmid contains the following DNA sequence: 5′ - GGATCCACCATGAGCCGCCTGCCCGTCCTGCTCCTGCTCCAACT CCTGGTCCGCCCCGCCATGGCTAAAGCTT - 3′ SEQ ID NO:857, encoding the IL-3 signal sequence. This sequence contains a BamHI restriction site on the 5′ end, and includes the ATG methionine as the first amino acid of the signal sequence 3′ to the BamHI site. This signal sequence is cleaved by the cell, leaving a 5′ Met/Ala generated by fusing the NcoI site from the signal sequence fused to the AflIII site of the receptor produced in the PCR reaction. The entire truncated form of the receptor along with the IL-3 signal sequence could be cut back out of the vector as a BamHI/EcoRI digest (hIL3L/hFflt3R).

The catalytic domain of pMON30298 (hG-CSFR) was reengineered to create an in frame EcoRI restriction site at the transmembrane/cytoplasmic bound via PCR as follows. To 0.5 ug of heat denatured pMON30298, 100 pmole each of primers HGCFfor and HGCFrev, 10 ul of 5X buffer J, 5U of Taq polymerase, and dH_2O were added to a final volume of 45 ul as described. PCR amplification was done as follows: six cycles (one minute at 94°C, two minutes at 64°C, and three minutes at 70°C), followed by nine cycles (one minute at 94°C, four minutes at 70°C). A final one minute extension of seven minutes at 70°C was done. Ten ul of each PCR reaction were gel purified using Geneclean II as described previously, and eluted in 10 ul dH_2O. Samples were digested with 10U each of EcoRI and HindIII in 20 ul reactions for 90 minutes at 37°C. Samples were gel purified again (Geneclean II) as described previously, and eluted in 10 ul dH_2O. Two ul of insert were ligated to 50 ng of NcoI/HindIII/phosphatased pSE420 vector in a 10 ul reaction as described previously. Transformation of competent DH5α cells and subsequent steps leading to final DNA sequence confirmation were done exactly as described above. Selected clones were then sequenced to verify the presence of the in frame EcoRI site as well as confirmation of the correct G-CSFR catalytic domain DNA sequence. Clones containing the predicted sequence were digested with EcoRI/HindIII as described previously and gel purified. Purified inserts of the hG-SCFR (EcoRI/HindIII) and hIL3L/hFlt3R (BamHI/EcoRI) fragments were ligated to BamHI/HindIII/phosphatased pcDNA 3.1 (-) vector (Invitrogen). Transformation of competent DH5α cells and subsequent steps leading to final DNA sequence confirmation were done as described above.

EXAMPLE 103

Additional genes encoding sequence rearranged Flt3 ligands were constructed using the dimer template intermediates previously described. For sequence rearranged flt3 receptor agonists having the fifteen amino acid linker $(GlyGlyGlySer)_3$GlyGlyGly SEQ ID NO:795, the dimer intermediates Flt4C.seq and Flt11N.seq were used as template. Breakpoints corresponding to Flt3 3 ligand amino acid residues 28/29, 34/35, 62/63, 94/95, and 98/99, were constructed using a PCR based approach using a PCR Optimizer kit (Invitrogen) and the following primer pairs; FL29For/FL29Rev, FL35For/FL35Rev, FL63For/FL63Rev, FL95For/FL95Rev, FL99For/FL99Rev as described IN Example 94. Amplification conditions were as follows: seven cycles of 94 °C for 1 min, 62 °C for 2 min, and 2.5 min at 70 °C; twelve cycles of 94 °C for 1 min, 68 °C for 2 min, and 70 °C for 2.5 min; followed by a final cycle of 7 min at 72 °C. PCR products corresponding to the predicted insert size were digested with NcoI and HindIII, and gel purified as described previously using Gene Clean II (Bio 101) following the manufacturer's suggested protocol. Samples were resuspended in 10 ul final volume with dH_2O. Inserts were cloned as single genes into the mammalian expression vector pMON3934 (NcoI/HindIII/SAP treated) and designated pMON35712, pMON35713, pMON35714, pMON35715, pMON35716, pMON35717 and pMON35718 respectively.

Genes encoding chimeric proteins comprising an IL-3 receptor agonist encoded by pMON13288 (WO 94/12638) herein referred to as "IL-3 receptor agonist I", and sequence rearranged Flt3 ligand were prepared by cloning the purified, restriction-digested PCR products of the 28/29, 34/35, 62/63, 94/95, and 98/99 breakpoint primer pairs into AflIII/HindIII/SAP-treated pMON30311. The resulting plasmids were designated pMON32398, pMON35700, pMON35702, pMON35704, and pMON35706 respectively. In addition, the same primer pairs were used in conjunction with the dimer template intermediates Flt7N.seq and Flt3C.seq to construct the ten amino acid linker $(GlyGlyGlySer)_2$GlyGly SEQ ID NO:793, forms of these IL-3 receptor agonist I/Flt3L chimeric proteins; pMON32397, pMON32399, pMON35701, pMON35703, and pMON35705 respectively.

EXAMPLE 104

Genes encoding IL-3 receptor agonist I/Flt3L chimeric proteins containing the 21 amino acid residue linker

$(GlyGlyGlySer)_5Gly$ SEQ ID NO:796 were constructed using a similar PCR approach using the dimer template intermediates Flt11N.seq and Flt10C.seq and the following primer pairs; Flt36/36Rev, Flt37/37Rev, Flt38/38Rev, Flt39/39Rev, Flt41/41Rev, Flt42/42Rev, and Flt43/43Rev. These primer pairs correspond to the following Flt3 ligand breakpoints 35/36; 36/37; 37/38; 38/39; 40/41; 41/42; and 42/43 (the 39/40 breakpoint was previously constructed as pMON32376) and were used for PCR amplification using the following cycle conditions: seven cycles of 94 °C for 1 min, 66 °C for 2 min, and 2.5 min at 70 ° C; fifteen cycles of 94 °C for 1 min, and 70 °C for 4 min; followed by a final cycle of 7 min at 72 °C using the Invitrogen PCR Optimizer kit (Buffer B). Following DNA sequence confirmation these constructs were designated pMON35733, pMON35734, pMON35735, pMON35736, pMON35738, pMON35739, pMON35740, pMON35741, pMON35742 and pMON35743 respectively. PCR incorporation errors resulted in two single amino acid substitutions of the sequence rearranged Flt3 chimeric partner (pMON35741, 35/36 breakpoint; and pMON35743, 42/43 breakpoint) and one construct (pMON35742, 38/39 breakpoint) containing two amino acid substitutions Q^{133} to R^{133} and Q^{100} to R^{100} and L^{112} to P^{112} in the Flt3L moiety, constructed and tested as part of this serieS.

Additional Flt3L/IL-3 receptor agonist I chimeric proteins in which the alternate Flt3L breakpoints corresponding to Flt3 ligand amino acid residues 28/29, 34/35, 62/63, 65/66, 89/90, 94/95, and 98/99 previously described were also constructed with the fifteen amino acid linker $(GlyGlyGlySer)_3GlyGlyGly$ templates FLt4C and FLt11N. PCR reaction mixtures were similar to those described in Example 103, except that reverse primers encoding the C-terminus of the sequence rearranged Flt3 moieties were modified by replacing the HindIII restriction site with a SnaBI recognition sequence. PCR amplification cycle parameters were as follows: seven cycles of 94 °C for 1 min, 66 °C for 2 min, and 2.5 min at 70 °C; fourteen cycles of 94 °C for 1 min, and 70 °C for 4 min; followed by a final cycle of 7 min at 72 °C. PCR clean up, restriction digestion and purification were done as described previously. Inserts were ligated to NcoI/SnaBI/SAP-treated pMON26431 (a BHK expression vector containing an IgG2b linker/IL-3 receptor agonist I moiety) as follows: 50ng treated vector, insert (10:1 insert:vector), 1 unit of T4 DNA ligase (Gibco BRL), and 1 ul 10X ligase buffer in a 10 ul reaction volume. Ligations were incubated for one hour at ambient temperature, then 2 ul of each ligation were removed and used to transform 100 ul of chemically competent DH10B (alternatively, DH5α) cells (Gibco BRL) following the manufacturer's suggested protocol. One fifth and 1/25th volumes of each transformation mixture were plated out on LB agar plates supplemented with the appropriate antibiotic markers and incubated overnight (14-16 hours) at 37 °C. Isolated colonies were picked, and DNA prepared using the Qiagen midiprep protocol as described previously.

Sequence analysis of selected clones were confirmed for 28/29 breakpoint (pMON35719), 34/35 breakpoint (pMON35720), 62/63 breakpoint (pMON35721), 65/66 breakpoint (pMON35722), 89/90 breakpoint (pMON35723), and 98/99 breakpoint (pMON35725). pMON35726 contains a single amino acid substitution (Leu94 to Phe94) for the 94/95 breakpoin. Flt3L/IL-3 receptor agonist I chimeric constructs with a Flt3L breakpoint of 39/40 and varying amino acid linker lengths of 10, 15, and 21 AA are represented by pMON35707, pMON35708, pMON35709, pMON35710 and pMON35711. These constructs were generated by PCR amplification of one of the following templates; pMON32373, pMON32375, or pMON32376, and the Flt3L-specific primer pair 39N TERM-1/SNAB1C TERM. Standard

PCR reaction mixtures were set up as previously described, and DNA product amplified using the following parameters: seven cycles of 94 °C for 1 min, 62 °C for 2 min, and 2.5 min at 70 °C; twelve cycles of 94 °C for 1 min, 68 °C for 2 min, and 70 °C for 2.5 min; followed by a final cycle of 7 min at 72 °C. PCR products corresponding to the predicted insert size were digested to completion with NcoI and SnaBI, gel purified, and cloned as described previously into the mammalian expression vector pMON26431 (NcoI/SnaBI/SAP treated) as Flt3L/IgG2b/IL-3 receptor agonist I chimeric proteins. Two of these constructs contained PCR incorporation errors in the sequence rearranged Flt3 chimeric partner which resulted in single amino acid substitutions F^{96} to L^{96}, and E^{58} to G^{58} (pMON35710 and pMON35711).

EXAMPLE 105

Another series of chimeric proteins, sequence rearranged Flt3L/IL-3 receptor agonist I with the breakpoints corresponding to Flt3 ligand amino acid residues 35/36, 36/37, 38/39, 40/41, 41/42, 42/43 and 65/66 previously described and a 21 amino acid linker were also constructed using selected IL-3 receptor agonist I/sequence rearranged Flt3L constructs as template (see Table 11 below). One exception was that a fifteen amino acid linker template (pMON35715) was used to construct the 65/66 breakpoint, pMON35771.

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Table 11

Flt3L/IL-3 receptor agonist I IL-3 receptor agonist I/Flt3L

Construct	template	Flt3L breakpoint	Primer Pair
pMON35744	pMON35733	35/36	Flt36/36Rev'
pMON35745	pMON35734	36/37	Flt37/37Rev'
pMON35746	pMON35735	37/38	Flt38/38Rev'
pMON35747	pMON35736	38/39	Flt39/39Rev'
pMON35748	pMON35738	40/41	Flt41/41Rev'
pMON35749	pMON35739	41/42	Flt42/42Rev'
pMON35750	pMON35740	42/43	Flt43/43Rev'
pMON35769	pMON35743	42/43	Flt43/43Rev'
pMON35771	pMON35715	65/66	65For/66SnaBI

Primer pairs encoding the same restriction sites as those used to construct pMON35719-35725 were utilized. The reverse primers 36Rev', 37 Rev', 38 Rev', 39 Rev', 41 Rev', 42 Rev', and 43 Rev', were used to create the in frame SnaBI site. The same forward primers Flt36, Flt37, Flt38, Flt39, Flt41, Flt42 and Flt43 were used. PCR reaction mixtures were identical to those described previously, however, with the exception of pMON35771, amplification conditions were modified as follows: 18 cycles of 94 °C for 1 min, 68 °C for 2 min, and 70 °C for 2.5 min; followed by a single extension cycle at 70 °C for 7 minutes. For pMON35771, amplification conditions were as follows: six cycles of 94 °C for 1 min, 66 °C for 2 min, and 2.5 min at 70 °C; fifteen cycles of 94 °C for 1 min, and 70 °C for 4 min; followed by a final cycle of 7 min at 72 °C. Flt3-specific PCR amplification products were restriction digested, purified, and cloned into pMON26431 (a BHK expression vector containing an IgG2b linker/IL-3 receptor agonist I moiety) as described in Example 104.

One variant, pMON32179, was constructed as a 34/40 breakpoint using the PCR primer pair Flt40/34Rev and dimer template intermediates Flt11N.seq and Flt10C.seq. PCR amplification conditions and subsequent cloning were identical to that used to clone pMON35771.

Three additional Flt3L/IL-3 receptor agonist I chimera (38/39 breakpoint) were designed and constructed to test the effects of alternate linker lengths and composition. Using pMON35709 as template, the GlySer linker length was expanded to encompass 29 amino acid residues with the motif $(GlyGlyGlySer)_7Gly$ using the primer pairs BamFor1/38Rev (reaction product referred to as PCR A) and Flt38/BamRev1 (reaction product referred to as PCR B). The amplification conditions were as follows: six cycles of 94 °C for 1 min, 66 °C for 2 min, and 2.5 min at 70 °C; fifteen cycles of 94 °C for 1 min, and 70 °C for 4 min; followed by a final cycle of 7 min at 72 °C. The resulting PCR products were cleaned up using a Promega PCR clean up kit, and digested with either NcoI/BamHI (PCR A) or BamHI/SnaBI (PCR B), gel purified and ligated to pMON26431 (a BHK expression vector containing an IgG2b linker/IL-3 receptor agonist I moiety) as described previously. The resulting construct was sequenced confirmed and designated pMON35774. In comparison, pMON35775 and 35776 different in that the GlySer linker was replaced by native Flt3L amino acid residues 140-154 (pMON35775) or 140-160 (pMON35776) containing a single amino acid substitution. PCR reaction conditions were identical as described for pMON35774, except the following primer pairs were used: 38For/Navfor and 38Rev/NavRevS (pMON35775); and 38For/Navfor and 38Rev/NavRevL (pMON35776). KasI was substituted for BamHI, otherwise the cloning steps of these PCR amplification products were identical to those employed for pMON35774. Sequence analysis revealed PCR induced errors in multiple isolates for both pMON35775 and 35776. To obtain the final correct sequences, it was necessary to redigest selected subclones with

NarI/SnaBI and NcoI/NarI, and use these gel purified fragments to reclone the desired constructs.

Several Flt3L dimer chimeric molecules were also constructed for testing as BHK transients. pMON32173, consisting of two native Flt3L molecules linked by an IgG2b linker, was assembled from two pre-existing molecules as follows: the NcoI/SnaBI Flt3L-containing insert from pMON32393 was ligated to gel purified, NcoI/SnaBI cut, pMON32377 in which the IL-3 receptor agonist I chimeric partner had been released. Similarly, pMON35727 (39/40 breakpoint, fifteen amino acid linker) was assembled using the Flt3L insert from pMON35708 (as an NcoI/SnaBI insert) to gel purified pMON32375 in which the IL-3 receptor agonist I chimeric partner had been excised. The third Flt3L dimer, pMON32168, (39/40 breakpoint, 21 amino acid linker) was assembled as follows: the NcoI/SnaBI insert from pMON32165 (E. coli equivalent of pMON35709, assembled by subcloning the NcoI/BamHI fragment from pMON32163 and the BamHI/HindIII fragment of pMON35709 into NcoI/HindIII-digested pMON5723). The NcoI/SnaBI insert from pMON32165 (Flt3L 1-139 (39/40)L21) and the SnaBI/HindIII insert (IgG2b/Flt3L 1-139 (39/40)L21) from pMON32376 were subcloned into the E. coli production vector pMON5723, creating pMON32167. The NcoI/HindIII insert from pMON32167 was then subcloned into pMON30304, and designated pMON32168.

EXAMPLE 106

A series of trimeric molecules, each consisting of two Flt3L moieties and a single copy of IL-3 receptor agonist I or IL-3 receptor agonist II (an IL-3 receptor agonist encoded by pMON13416 (WO 94/12638) herein referred to as "IL-3 receptor agonist II"), were also constructed from pre-existing molecules using restriction digested, gel purified fragments. pMON35728 was assembled using the NcoI/EcoRI (Flt3L/IgG2b/IL-3 receptor agonist I) insert from pMON32375 and the EcoRI/HindIII (IL-3 receptor agonist I/IgG2b/Flt3L) insert from pMON35708. The two fragments were then religated to NcoI/HindIII/SAP-treated mammalian expression vector pMON3934 and subcloned as described previously. pMON32205 (IL-3 receptor agonist II/IgG2B/Flt3 1-139/IgG2B/Flt3 1-139) was assembled by ligating the NcoI/HindIII fragment from pMON32173 into the AflIII/HindIII site of pMON30304. A similar approach was used to construct pMON32206 (IL-3 receptor agonist II/IgG2b/Flt3L (39/40)L21/IgG2b/Flt3L (39/40)L21). The NcoI/HindIII fragment from pMON32167 was gel and subcloned into the AflIII/Hind III-digested pMON30304 (which contains the IL-3 receptor agonist II/IgG2b-moiety). The plasmid pMON32207 (Flt3L (39/40)L21/IgG2b/Flt3L (39/40)L21)/G-CSF) was assembled by subcloning the gel purified NcoI/HindIII insert from pMON32170 into the intermediate pMON32198 (AflIII/HindIII).

pMON32208 (Flt3L 1-139/IgG2b/G-CSF/IgG2b/Flt3L1-139) was assembled by subcloning the gel purified SnaBI insert from pMON30320 (as IgG2b/G-CSF) into SnaBI-digested/SAP-treated pMON32173. pMON32204 was assembled by subcloning the NcoI/HindIII insert from pMON32173 into AflIII/HindIII-digested pMON30309 (which contains G-CSF/IgG2b). pMON32195 (Flt3L 1-139(39/40)L21/IgG2b/G-CSF/Flt3L 1-139(39/40)L21) was constructed by subcloning the NcoI/SacI insert from pMON32190 and the SacI/HindIII fragment from pMON32171 into NcoI/HindIII-digested pMON30304. pMON32196 (G-CSF/IgG2b/Flt3L 1-139(39/40)L21/IgG2b/Flt3L 1-139) was assembled by subcloning the NcoI/AflIII fragment from pMON30309 (as G-CSF/IgG2b) into NcoI/SAP-treated pMON32168 (Flt3L 1-139(39/40)L21/IgG2b/Flt3L 1-139), and confirming orientation by DNA sequence and restriction analysis. pMON32197 (G-CSF/IgG2b/Flt3L 1-139(39/40)L21/IgG2b/Flt3L 1-139 (39/40)L21) was constructed by subcloning the

NcoI/HindIII insert of pMON32167 (Flt3L 1-139(39/40)L21/IgG2b/Flt3L 1-139 (39/40)L21) into the AflIII/HindIII site of pMON30309 (G-CSF/IgG2b).

EXAMPLE 108

A series of Flt3L containing molecules was constructed as BHK transients by replacing IL-3 receptor agonist I or IL-3 receptor agonist II with G-CSF as the chimeric partner. For chimeric proteins expressed transiently and made using the BHK vector pMON3934, the G-CSF moiety could either encode Ser or Cys at position 17. For molecules used for either E. coli expression or expressed non-transiently in mammalian expression systems, position 17 of the G-CSF partner encoded Ser exclusively. Chimera of native Flt3L and G-CSF were made as BHK expression constructs in both orientations: G-CSF/IgG2b/Flt3L (pMON30329) and Flt3L/IgG2b/G-CSF (pMON32175). pMON30329 was assembled by subcloning the Flt3L 1-139 insert from pMON30238 (as a NcoI/Hind III digest) into pMON30309 (which contains G-CSF/IgG2b) digested with AflIII/HindIII, whereas pMON32175 was constructed using the gel-purified NcoI/SnaBI insert from pMON32393 to NcoI/SnaBI-digested pMON26420 (which contains the IgG2b/G-CSF gene). A third native G-CSF/Flt3L chimeric molecule, pMON32191, differs from pMON32175 in that it has a GlySer linker in place of the IgG2b chimeric linker and was designed for E.coli expression. pMON32191 was assembled using the same gel-purified NcoI/SnaBI insert from pMON32393 into NcoI/SnaBI-digested pMON31123 (which contains the GlySer/G-CSF gene). The BHK equivalent, pMON35767, was assembled by subcloning the gel-purified NcoI/HindIII chimeric gene from pMON32191 into the BHK vector pMON3934.

EXAMPLE 109

Two series of sequence rearranged Flt3L chimera were constructed by replacing the IL-3 receptor agonist I component with G-CSF. The first set, with the orientation G-CSF/IgG2B/ sequence rearranged Flt3L, were essentially assembled as follows: pMON30329 (G-CSF/IgG2B/Flt3L 1-139) was digested with SnaBI/HindIII, and the vector-containing G-CSF moiety gel-purified as described above. SnaBI/HindIII-digested inserts from the appropriate IL-3 receptor agonist I/Flt3L constructs shown below in Table !2were then subcloned into pMON30329 (SnaBI/HindIII).

Table 12

G-CSF/IgG2b/Flt3L constructs and their IL-3 receptor agonist I analogues

Flt3L breakpoint	pMON(G-CSF)	pMON(IL-3 receptor agonist I)
35/36L21	pMON32188	pMON35733
89/90L21	pMON32273	pMON32389
37/38L21	pMON35795	pMON35735
38/39L21	pMON35796	pMON35736
40/41L21	pMON35797	pMON35738
41/42L21	pMON35798	pMON35739
42/43L21	pMON35799	pMON35740

pMON32169 (G-CSF/IgG2b/Flt3L 1-139 (39/40)L21) was assembled using the NcoI/BamHI insert from pMON32163 and the BamHI/HindIII insert from pMON32370 subcloned into the AflIII/HindIII-digested pMON30309. Three molecules in this series have no direct IL-3 receptor agonist I counterparts. The first, pMON39914, was assembled using the BHK expression vector pMON30309 (which contains G-CSF/IgG2b) digested with AflIII/HindIII, and the Flt3 1-139 (39/40)L29 insert from pMON32243 (as NcoI/HindIII). For pMON39915, the Flt3L 1-154 (39/40) gene from pMON32242 (as a NcoI/HindIII insert) was subcloned into the parental vector pMON30309. pMON39916 was assembled exactly as for pMON39915, except that the Flt3L 1-160 (39/40) insert from pMON32252 was utilized. pMONs 32242, 32243, and 32252 are E. coli expression constructs containing a nonchimeric, sequence rearranged Flt3L gene (as NcoI/HindIII). Finally, the insert from pMON35799 was subcloned into pMON5723 (as an NcoI/HindIII fragment) for expression in E. coli. This E. coli production plasmid was designated pMON39904.

EXAMPLE 110

Many of the second series of G-CSF chimera with the orientation Flt3L/IgG2b/G-CSF were also constructed from their IL-3 receptor agonist I analogues as indicated below in Table 13.

Table 13

Flt3L /IgG2b/G-CSF constructs and their IL-3 receptor agonist I analogues

Flt3L breakpoint	pMON(G-CSF)	pMON(IL-3 receptor agonist I)
39/40L10	pMON35751	pMON35707
39/40L15	pMON35752	pMON35708
39/40L21	pMON35753	pMON35709
89/90L15	pMON35754	pMON35723
35/36L21	pMON35755	pMON35744
36/37L21	pMON35756	pMON35745
37/38L21	pMON35757	pMON35746
34/35L15	pMON35759	pMON35720
65/66L15	pMON35760	pMON35722
98/99L15	pMON35765	pMON35725

These constructs were assembled using NcoI/SnaBI-digested pMON36113 (a BHK vector containing the IgG2b/G-

CSF gene) and specific NcoI/SnaBI-digested sequence rearranged Flt3L inserts from the Flt3L/IL-3 receptor agonist I chimeric proteins in Table above. The resulting plasmids were designated pMON32170, pMON32871, pMON32271, pMON32172, pMON32174, pMON35751, pMON35752, pMON35753, pMON35754, pMON35755, pMON35756, pMON35757, pMON35758, pMON35759, pMON35760, pMON35761, pMON35762, pMON35763, pMON35764, pMON35765, pMON35766, pMON35767, pMON35768, pMON35770, pMON35772, pMON35773, pMON35777, pMON35778, pMON35779, pMON35780, pMON35782 and pMON39908

pMON35777 and pMON35778 were constructed by PCR and assembled from the same NcoI/NarI and NarI/SnaBI inserts as described for pMON35775 and pMON35776, except that NcoI/SnaBI-digested pMON35751 was used as the parental vector containing the IgG2b/G-CSF gene. To construct the 39/40 breakpoint equivalent of pMON35778, the primer pair Flt40/SnaBI C-term was used to re-amplify pMON35778 template. Amplification conditions were done as described previously for pMON35771, except the initial T_{anneal} was lowered from 66 to 55 °C. The resulting construct was designated pMON35782 (Flt3 1-160 (39/40)/IgG2b/G-CSF).

pMON32170 (Flt3L 1-139(39/40)L21/IgG2B/G-CSF) was assembled using the NcoI/SnaBI insert from pMON32165 ligated into NcoI/SnaBI-digested pMON26430 (which contains IgG2B/G-CSF). pMON35764 (Flt3L (38/39)L21/IgG2b/G-CSF) was cloned as follows: the sequence rearranged Flt3L insert was PCR amplified using as template pMON35736 and the primer pair Flt39/39Rev. Amplification conditions were identical to those employed for pMON35771, except the initial T_{anneal} was lowered from 66 to 56 °C. The NcoI/SnaBI digested PCR amplification was subcloned into NcoI/SnaBI-digested pMON35754 containing the IgG2b/G-CSF gene. pMON35768 (Flt3L (38/39)L21/IgG2b/G-CSF) has a mutation at residue

15 (Ser to Phe) of the Flt3 chimeric partner. pMON35762 (Flt3 template pMON35739), pMON35763 (Flt3 template 35738), pMON35758 (Flt3 template 35740), pMON35770 (pMON35743 as Flt3L template were constructed exactly as described for pMON35764. pMON35772 , a S^{125} to F^{125} mutant of the sequence rearranged Flt3 gene in pMON35760, was cloned by PCR using pMON35715 as Flt3 template and the primer pairs 65For/65SnaBI. PCR cycle conditions were identical to that used to amplify the Flt3 genes from pMON35733, pMON35734, pMON35735 and pMON35736 described previously. pMON35761 is a Q^{133} to R^{133} mutant of the sequence rearranged Flt3L gene in pMON35758. pMON35773 (Flt3L 1-139 (38/39)L29/IgG2B/G-CSF) was cloned as described previously for pMON35774, except pMON26430 (NcoI/SnaBI/SAP-treated) containing the IgG2b/G-CSF gene was used as parental vector.

To construct the 39/40 breakpoint equivalent, pMON35773 was used as template in a PCR amplification reaction with the primer pair Flt40/SnaBI C-term. Amplification was done exactly as described previously for pMON35771. The NcoI/SnaBI-digested amplification product was subcloned into pMON26430 (NcoI/SnaBI/SAP-treated), resulting in pMON35779 (Flt3L 1-139 (39/40)L29/IgG2B/G-CSF). pMON35780 is a variant of pMON35779 and encodes a single amino acid mutation (L^{60} to P^{60}) in the sequence rearranged Flt3 chimeric partner. pMON32190 (Flt3L 1-139 (39/40)L21/GS/G-CSF) contains an alternate GlySer chimeric linker which replaces the IgG2b linker of pMON32170. The NcoI/SnaBI fragment Flt3L gene from pMON32165 (Flt3L 1-139 (39/40)L21/IgG2b/IL-3 receptor agonist I in the E. coli expression vector pMON5723) was subcloned into NcoI/SnaBI-digested pMON31123. The BHK expression equivalent, pMON35766, was constructed by subcloning the entire Flt3L/GlySer/G-CSF chimeric insert as an NcoI/HindIII fragment into pMON3934.

pMON39908 is similar to pMON35779, except the Flt3L amino acid residues 133-160 have been replaced by the amino acid sequence, VETVFHRVSQDGLDLLTS SEQ ID NO:798, which is homologous to an alternate splice variant of Flt3L (Genbank accession number HSU29874). pMON32190 was used as a PCR template with the following sets of primer pairs Flt40/XbaRev and SnaBICterm/XbaFor. Amplification conditions were done as described previously for pMON35771, except the initial T_{anneal} was lowered from 66 to 64 °C. Both gel-purified PCR amplification products were digested with either NcoI/XbaI (Flt40/XbaRev PCR product) or XbaI/SnaBI (SnaBICterm/XbaFor PCR product) and subcloned into pMON26430 (NcoI/SnaBI/SAP-treated). pMON32273 (Flt3L 1-139 (39/40)L21/IgG2b/G-CSF) was constructed by PCR of pMON35777 with the primer pairs FltConNco/Grev to re-amplify the 38/39 Flt3L moiety as 39/40. The purified amplicon was digested with NcoI/SnaBI, and subcloned into the NcoI/SnaBI-digested pMON32191, and designated pMON32259 (for E. coli production). For BHK expression, the NcoI/HindIII insert from pMON32259 was subcloned into pMON3934 (NcoI/HindIII).

EXAMPLE 103

Another series of chimeric proteins were constructed in which the Flt3L partner contained one or two Cys mutations (Table XIA and XIB). pMON35790 (Flt3L 1-139($C^4 \rightarrow S^4$, $C^{85} \rightarrow S^{85}$)/GS/G-CSF (Ser17)), was constructed by PCR using pMON32191 as template and the primer pairs C1For/C3Rev and C3For/139Rev in two reactions. pMON35791 (Flt3L 1-139($C^{93} \rightarrow S^{93}$, $C^{132} \rightarrow S^{132}$)/GS/G-CSF (Ser17)), was also constructed by PCR using pMON32191 as template and the primer pairs C5For/C6Rev and C5Rev/N-term. Amplification conditions were done as described previously for pMON35771, except the initial T_{anneal} was lowered from 66 to 64 °C. A second round of PCR was done using the amplicons (10 ul each) from the first round, and the PCR products were then purified, digested with NcoI/SnaBI, and subcloned into NcoI/SnaBI -digested pMON32191. PCR amplification conditions for the second round were modified as follows: the initial T_{anneal} was increased to 68°C, and the number of cycles increased from 6 to 15. No additional amplification was required. These constructs, pMON35787 ($C^{4} \rightarrow S^{4}$, $C^{85} \rightarrow S^{85}$) and pMON35788 ($C^{93} \rightarrow S^{93}$, $C^{132} \rightarrow S^{132}$) were used for E. coli expression. The BHK expression equivalents, pMON35790 and 35791, were constructed by subcloning the correctly mutated Flt3L/GlySer/G-CSF chimeric inserts as NcoI/HindIII fragments into pMON3934. pMON35792 (Flt3L 1-132($C^{132} \rightarrow S^{132}$)/GlySer/G-CSF (Ser17)) was constructed by PCR using pMON32191 as template and the primer pair FLD1Rev/FltNTerm.

pMON39905 (Flt3L 1-139($C^{132} \rightarrow S^{132}$)/GlySer/G-CSF (Ser17)) was constructed by PCR using pMON32191 as template and the primer pair FLM1Rev/FltNTerm. pMON39906 (Flt3L 1-139($C^{127} \rightarrow S^{127}$/ $C^{32} \rightarrow S^{132}$)/GlySer/G-CSF (Ser17)) contains a single amino acid substitution at residue 127 of the sequence rearranged Flt3L partner, a result of a PCR induced error during the PCR amplification of pMON39905. pMON32276 (Flt3L 1-139 (39/40)L21($C^{4} \rightarrow S^{4}$/ $C^{85} \rightarrow S^{85}$)/GlySer/G-CSF (Ser17)) was constructed by two rounds of PCR. Three initial amplicons were generated: PCR1 (pMON32190 template and primer pairs G10L/85N); PCR 7 (pMON32190 template and primer pairs 4N/85S); and PCR 4 (pMON32198 template and primer pairs 4S/3605Rev). For the second round, PCR1, 4 and 7 were re-amplified in a combined mixture, resulting in PCR A. PCR A was purified, digested with NcoI/SnaBI, and subcloned in pMON30277 (GlySer/G-CSF). The next three constructs were generated in a similar manner. pMON32277 (G-CSF (Ser17)/IgG2B/Flt3L 1-139 (39/40)L21($C^{4} \rightarrow S^{4}$/ $C^{85} \rightarrow S^{85}$)) first round PCR generated three initial amplicons: PCR1 (pMON32190 template and primer pairs G10L/85N); PCR 7 (pMON32190 template and primer pairs 4N/85S); and PCR 6 (pMON32169 template and primer pairs 4S/3605Rev). For the second round, PCR1, 6 and 7 were re-amplified in a combined mixture, resulting in PCR B. PCR B was purified, digested with NcoI/HindIII, and subcloned into NcoI/HindIII-digested pMON30309 (G-CSF(Ser17)/IgG2B). pMON32278 (Flt3L 1-139 (39/40)L21($C^{93} \rightarrow S^{93}$/ $C^{132} \rightarrow S^{132}$)/GlySer/G-CSF (Ser17)) first round PCR generated three initial amplicons: PCR2 (pMON32190 template and primer pairs G10L/93N); PCR 8 (pMON32190 template and primer pairs 132N/93S); and PCR 3 (pMON32198 template and primer pairs 132S/3605Rev). For the second round, PCR2, 3 and 8 were re-amplified in a combined mixture, resulting in PCR C. PCR C was purified, digested with NcoI/SnaBI, and subcloned in pMON30277 (GlySer/G-CSF). pMON32279 G-CSF (Ser17)/IgG2B/Flt3L 1-139 (39/40)L21($C^{93} \rightarrow S^{93}$/ $C^{132} \rightarrow S^{132}$)) first round PCR generated three initial amplicons: PCR2 (pMON32190 template and primer pairs G10L/93N); PCR 8 (pMON32190 template and primer pairs 132N/93S); and PCR 5 (pMON32169 template and primer pairs 132S/3605Rev). For the second round, PCR2, 5 and 8 were re-amplified in a combined mixture, resulting in PCR D. PCR D was purified, digested with NcoI/HindIII, and subcloned into NcoI/HindIII-digested pMON30309 (G-CSF(Ser17)/IgG2B).

EXAMPLE 112

pMON39909 (Flt3L 1-139(39/40)L21/GS/G-CSF(Ser17)(133/132)) is one of two Flt3/G-CSF chimeric proteins in which both proteins the sequenced are rearranged. The NcoI/AflIII fragment from pMON32198 comprising the Flt3L 1-139(39/40)L21/GlySer gene was subcloned into NcoI/SAP-treated pMON25187 (E. coli production plasmid containing a single copy of G-CSF(Ser17)(133/132)). Following DNA sequence confirmation, the chimeric insert was subcloned into pMON3934 as an NcoI/HindIII fragment and designated pMON39909. pMON39910 (G-CSF(Ser17)(133/132/ IgG2B/Flt3L 1-139(39/40)L21) was constructed by PCR using pMON25187 as template and the primer pair GPFor1/GPRev2. Amplification conditions were identical to those utilized for pMON39908. NcoI/SnaBI-digested G-CSF(Ser17)(133/132) was subcloned into the NcoI/SnaBI site of pMON32376 containing the IgG2B/Flt3L 1-139 (39/40)L21 gene.

EXAMPLE 113

pMON40000 is the production plasmid modified from pC1neo (Promega) containing G-CSF(Ser17)/GlySer/Flt3L 1-139 (39/40)L21 for expression in NS0 cells (pMON32169 is the BHK equivalent). pMON40000 contains the CMV IE promoter/enhancer element, an IL-3 leader sequence immediately upstream of CSF(Ser17)/GlySer/Flt3L 1-139 (39/40)L21, truncated thymidine kinase promoter, SV40 late poly A signal sequence, and several DNAse 1 hypersensitive regions (part of IgH 3 min LCR).

EXAMPLE 114

Bioactivity of multi-functional chimeric hematopoietic receptor agonists

Table 14

IN VITRO MULTI-FUNCTIONAL CHIMERIC HEMATOPOIETIC RECEPTOR AGONISTS BIOASSAY

Clone	**BAF3/FLT3L Proliferation**[1]	**BAF3/FLT3L Proliferation**[2]	**CFU-GM Colonies**[3]
pMON30247	++	+	+
pMON32169		+++	+++
pMON32175		+++	
pMON32190		+++	
pMON32191		+++	+++
pMON32333	+		
pMON32342	++		
pMON32352	+		+
pMON32360	+		+
pMON35766	+		
pMON40000			+++
pMON40002[4]		++	+++

Legend:

+:	Decreased potency (right shifted) compared to control
++:	Equivalent potency to control (within 2 fold)
+++:	Increased potency (left shifted) compared to control

[1] Compared to control: pMON30247

[2] Compared to control: pMON32352

[3] Compared to appropriate coaddition control

[4] Analyzed in pool of clones pMON40000 and pMON40002

EXAMPLE 115

Bioactivity determination

Table15

EX VIVO MULTI-FUNCTIONAL CHIMERIC HEMATOPOIETIC

RECEPTOR AGONISTS BIOASSAY

Clone(s)	**Hematopoietic Ex Vivo Expansion** [1]			**Dendritic Cell Ex Vivo Expansion** [2]	
	Fold Expansion	Neutrophil Precursors	Mega-karyocyte Precursors	Fold Expansion	Function
pMON32175	+	+	+		
pMON32191	+	+	++	++	++
pMON32360	+	+	+	++	
Il-3 receptor agonist I, MFR agonist I, MFR agonist II	++	++	++		
Il-3 receptor agonist I, MFR agonist I, MFR agonist II, pMON30247	+++	++	+++		
Il-3 receptor agonist I, MFR agonist I, MFR agonist II, pMON32360	+++	++	++		
Il-3 receptor agonist I, MFR agonist I, MFR agonist II, pMON32333	++	++	++		
Il-3 receptor agonist I, MFR agonist I, MFR agonist II, pMON32191	+++	+++	+++		
Il-3 receptor agonist I, MFR agonist I, MFR	++	+++	+++		

agonist II, pMON32175					
MFR agonist II, pMON32191	+	+	+++		
pMON30247				+++	++
pMON32352				++	

[1] Legend:
+: Decreased activity compared to IL-3, IL-6, SCF,G-CSF (literature control)
++: Equivalent activity to IL-3, IL-6, SCF,G-CSF ((literature control)(within 20%))
+++: Increased activity compared to IL-3, IL-6, SCF,G-CSF (literature control)
Culture Condition: X-Vivo 10 Media, 37°C, 5% CO_2, 11 day incubation

[2] Legend:
+: Decreased activity compared to GM-CSF, TNFa, SCF (literature control)
++: Equivalent activity to GM-CSF, TNFa, SCF ((literature control)(within 20%))
+++: Increased activity compared to GM-CSF, TNFa, SCF (literature control)
Culture Condition: IMDM-20 Media supplemented with 100 ng/ml GM-CSF, 100 ng/ml TNFa, 20 ng/ml SCF, at 37°C/5% CO_2 for 18-22 days
MFR agonist I = pMON31140 (WO 95/21197)
MFR agonist II = pMON28571 (WO 97/12985)

Hematopoietic Ex Vivo Expansion Assay

$CD34^+$ enriched progenitor cells from human bone marrow were isolated and cultured at $5x10^4$ cells/ml in X-Vivo 10 + 1% HSA with test cytokines and controls to assess cytokine expansion potential. Cells were expanded and replated at $5x10^4$ cells/ml with new media and cytokines around day 5 depending on cell growth. On day 10 cells were harvested and characterized. Cells were collected from the plates and diluted to a concentration of $1x10^6$ cells/ml. Total cell expansion was determined and cells were characterized for hematopoietic progenitor cells by CFU Pre- and Post Expansion in methylcellulose (Stem Cell Technologies, MethocultHCC3534) . Expanded cells were also characterized by flow cytometry for lineage specific phenotyping: CD11b(PE)/CD15(FITC), CD34 (FITC), CD41a (FITC).

Dendritic Cell Ex Vivo Expansion Assay

CD34$^+$ enriched progenitor cells from human bone marrow were isolated and cultured at 2x10^5 cells/ml in IMDM/20% FCS with test cytokines and controls to assess expansion potential. Cells were expanded and replated at 5x10^4 cells/ml with new media and cytokines around day 5 depending on cell growth. On day 18-22 cells were harvested and characterized. Total cell expansion was determined expanded cells were characterized by flow cytometry for lineage specific phenotyping: HLA-DR+(PE)/CD1a+(FITC), CD86+(PE)/CD1a+(FITC), CD19-(FITC). Dendritic cell fold expansion was determined as the total cellular expansion x % HLA-DR+/CD1a+. The functional activity of the cells was determined using a 1-way mixed lymphocyte reaction. Washed, irradiated cultured dendritic cells were added in graded doses to allogeneic responder peripheral blood mononuclear cells in 96-well microtiter plates. The ability of the dendritic cells to serve as antigen presenting cells was determined by the degree of proliferation stimulated in the responding cell preparations, as measured by ^{3}H thymidine incorporation.

EXAMPLE 116
Receptor Binding

Table 16
Receptor Binding Analyses:

Compound	**Flt3-Fc**	**G-CSFR**	**IL-3R"**
	K_d (nM)	IC_{50} (nM)	IC_{50} (nM)
pMON32342	26 " 7	-	> 1000
pMON30247	36 " 7	-	6.6 " 0.5
pMON32360	45 " 17	-	26 (2)
pMON32352	56 " 5	-	13 " 4
pMON32191	37 " 14	0.33 " 0.01	-
Il-3 receptor agonist II	-	> 1000	1.3 " 0.2
Il-3 receptor agonist I	-	> 1000	3.7 " 0.6
G-CSF	-	0.69 " 0.08	> 100

Data are expressed as the mean " SEM from at least three experiments determined in triplicate,
except pMON 32360 where only (2) experiments have been completed.

The affinity of the Flt-3 agonist containing chimeric molecules was evaluated in receptor binding assays. BIACORE analysis was performed by directly immobilizing Flt3-Fc and the K_d value computed from determining the association and dissociation rate constants. Competitive binding assays were utilized for evaluating the interactions of the chimeric molecules with either the G-CSF receptor transfected in BaF3 cells or the " subunit of the IL-3 receptor expressed in BHK cells. The competition assays using these cells employed an agonist-specific radioligand and IC_{50} values were generated for the competing chimeras using logit-log analysis of dose-response curves.

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EXAMPLE 117

In vivo bioactivity

Table17

MURINE IN VIVO MULTI-FUNCTIONAL CHIMERIC HEMATOPOIETIC RECEPTOR AGONISTS ASSAY DATA

Clone	**Peripheral Blood**		**Spleen**		
	I-A^{b+}/CD11c^{+}	I-A^{b+}/CD8^{+}	I-A^{b+}/CD11c^{+}	I-A^{b+}/CD8^{+}	CFU-GM /Spleen
	DC cells/ul blood		DC cells/Spleen (x 10^{6})		Fold Increase
pMON30247	ND	ND	33.5	23.8	78
pMON32342	ND	ND	8.0	4.5	2
pMON32360	ND	ND	64.5	37.5	183
pMON32191	17,089	2,379	133.5	78.9	53

C57BL/6 mice were injected s.c. with pMON30247, pMON32342 or pMON32360 (150 ug/day) or pMON32191(200ug/day) or Mouse Serum Albumin (MSA, 200 ug/day) for 10 days. On Day 11 terminal bleeds were done via cardiac puncture. Leucocytes counts were obtained on whole blood. Peripheral blood leucocytes were obtained by gradient centrifugation (Histopaque) followed by ammonium chloride lysis to further remove erythrocytes. Cells were stained for flow cytometery using direct fluorescein or phycoerythrin conjugated monoclonal antibodies (Pharmingen). Prior to staining non-specific Fc receptor binding was blocked using FcBlock (Pharmingen). Cells were analyzed on a FacScan flow cytometer (Becton/Dickinson). Percent postive cells were determined by integration and phenotype enumeration was calculated based on WBC count. Spleens from treated animals were removed aseptically, teased apart, in RPMI media with needles. A cell suspension was obtained using the flat end of a 5cc syringe plunger followed by filtration through a cotton plug to remove clumps.

Erythrocytes were removed by ammonium chloride lysis, cells were washed, resuspended and counted using a Coulter counter (Coulter Electronics). Cells were prepared for flow cytometry as described above. Phenotype was expressed as number of cells/spleen based on the percent of cells with a postive phenotype and total spleen WBC count. CFU cultures were obtained by plating 1.5 x 10^5 splenic cells/1ml in triplicate wells of methylcellulose with murine cytokines w/o erythropoietin (Stem Cell Technologies). Cultures were incubated for 10 days at 37°C and counted on an inverted microscope. A CFU was defined as a colony of cells with >50 cells. The fold increase of CFU/spleen was determined (total number of CFU/Spleen of test compound/total number of CFU/Spleen of MSA control). MSA control values for peripheral blood were 15 and 347 cells/ul for I-A^{b+}/CD11c^+ and I-A^{b+}/CD8^+ respectively. MSA control values for the splenic leucocytes were 2 and 1 x 10^6 cells/spleen for I-A^{b+}/CD11c^+ and I-A^{b+}/CD8^+ respectively.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

More details concerning the molecular biology techniques, protein purification and bioassays can be found in WO 94/12639, WO 94/12638, WO 95/20976, WO 95/21197, WO 95/20977, WO 95/21254 and WO 96/23888, are hereby incorporated by reference in their entirety.

All references, patents or applications cited herein are incorporated by reference in their entirety as if written herein.

Various other examples will be apparent to the person skilled in the art after reading the present disclosure without departing from the spirit and scope of the invention. It is intended that all such other examples be included within the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: G. D. Searle

(ii) TITLE OF THE INVENTION: Multi-functional Chimeric Hematopoietic Receptor Agonists

(iii) NUMBER OF SEQUENCES: 865

(iv) CORRESPONDENCE ADDRESS:
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(F) ZIP: 60680

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
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(B) FILING DATE: 22-OCT-1997
(C) CLASSIFICATION:

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(B) FILING DATE: 25-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 34,547
(C) REFERENCE/DOCKET NUMBER: C-2994

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(A) TELEPHONE: 314-737-6986
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA    180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC    300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT    360
CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT    420
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    720
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC    780
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT    360
CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT    420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGGG AATTCGGCGG CAACATGGCG    480
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT    540
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC CTTTGCCTAC ACCTGTCCTG    600
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA    660
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    720
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC    780
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGGGCAGGA CCACAGCTCA CAAGGATCCC    840
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC    300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT    360
CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT    420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGGG AATTCGGCAA CATGGCGTCT    480
CCCGCTCCGC CTGCTTGTGA CCTCCGAGTC CTCAGTAAAC TGCTTCGTGA CTCCCATGTC    540
CTTCACAGCA GACTGAGCCA GTGCCCAGAG GTTCACCCTT TGCCTACACC TGTCCTGCTG    600
CCTGCTGTGG ACTTTAGCTT GGGAGAATGG AAAACCCAGA TGGAGGAGAC CAAGGCACAG    660
GACATTCTGG GAGCAGTGAC CCTTCTGCTG GAGGGAGTGA TGGCAGCACG GGACAACTG     720
GGACCCACTT GCCTCTCATC CCTCCTGGGG CAGCTTTCTG GACAGGTCCG TCTCCTCCTT    780
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 939 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT     900
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGG                           939G
AATTCGGCGG CAACATGGCG     480 TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA
AACTGCTTCG TGACTCCCAT     540 GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC
CTTTGCCTAC ACCTGTCCTG     600 CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC
AGATGGAGGA GACCAAGGCA     660 CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG
TGATGGCAGC ACGGGGACAA     720 CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT
CTGGACAGGT CCGTCTCCTC     780 CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC
CACAGGGCAG GACCACAGCT     840 CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC
TGCTCCGAGG AAAGGTGCGT     900 TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGG
939
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC CTTTGCCTAC ACCTGTCCTG     120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA     180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA     240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC     300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT     360
CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT     420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGGG AATTCGGCGG CAACGGCGGC     480
AACATGGCGT CCCCAGCGCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT     540
GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTCACCC TTTGCCTACA     600
CCTGTCCTGC TGCCTGCTGT GGACTTTAGC TTGGGAGAAT GGAAAACCCA GATGGAGGAG     660
ACCAAGGCAC AGGACATTCT GGGAGCAGTG ACCCTTCTGC TGGAGGGAGT GATGGCAGCA     720
CGGGGACAAC TGGGACCCAC TTGCCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC     780
CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC CTTGGAACCC AGCTTCCTCC ACAGGGCAGG     840
ACCACAGCTC ACAAGGATCC CAATGCCATC TTCCTGAGCT TCCAACACCT GCTCCGAGGA     900
AAGGTGCGTT TCCTGATGCT TGTAGGAGGG TCCACCCTCT GCGTCAGG                 948
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC      60
ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA     120
CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC     180
AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC     240
CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAACTGAC     300
GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAACTGCTC     360
TATAATGATC GATGAAATTA TACATCACTT AAAGAGACCA CCTGCACCTT TGCTGGACCC     420
GAACAACCTC AATGACGAAG ACGTCTCTAT CCTGATGGAC CGAAACCTTC GACTTCCAAA     480
CCTGGAGAGC TTCGTAAGGG CTGTCAAGAA CTTAGAAAAT GCATCAGGTA TTGAGGCAAT     540
TCTTCGTAAT CTCCAACCAT GTCTGCCCTC TGCCACGGCC GCACCCTCTC GACATCCAAT     600
CATCATCAAG GCAGGTGACT GGCAAGAATT CCGGGAAAAA CTGACGTTCT ATCTGGTTAC     660
CCTTGAGCAA GCGCAGGAAC AACAGTAC                                       688
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 712 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC    60
ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA   120
CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC   180
AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC   240
CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAACTGAC   300
GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG   360
CAGCGGCGGC GGTTCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG   420
ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT   480
GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA   540
AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC   600
GGCCGCACCC TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA   660
AAAACTGACG TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT AC           712
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC    60
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   120
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   180
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   240
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TAACTGCTCT   300
ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT GTACGTAGAG   360
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT   420
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC   480
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC   540
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC   600
TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA   660
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG   720
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG   780
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG   840
CAGGCCCTGG AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC   900
GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC   960
CTGCAGCCCT AATAA                                                    975
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG TCTGCCCTCT    60
GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG CAGGTGACTG GCAAGAATTC   120
CGGGAAAAAC TGACGTTCTA TCTGGTTACC CTTGAGCAAG CGCAGGAACA ACAGGGTGGT   180
GGCTCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA   240
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC   300
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA ATACGTAGAG   360
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT   420
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC   480
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC   540
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC   600
TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA   660
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG   720
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG   780
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG   840
CAGGCCCTGG AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC   900
GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC   960
CTGCAGCCCT AATAA                                                    975
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG     60
GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC    120
TCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT    180
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    240
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    300
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CTACGTAGAG    360
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT    420
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC    480
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC    540
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC    600
TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA    660
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG    720
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG    780
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG    840
CAGGCCCTGG AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC    900
GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC    960
CTGCAGCCCT AATAA                                                     975
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 975 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT     60
GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTAACTGCT CTATAATGAT CGATGAAATT    120
ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA    180
GACGTCTCTA TCCTGATGGA CCGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG    240
GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA    300
TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA GTACGTAGAG    360
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT    420
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC    480
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC    540
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC    600
TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA    660
GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG    720
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG    780
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG    840
CAGGCCCTGG AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC    900
GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC    960
CTGCAGCCCT AATAA                                                     975
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC     60
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA    120
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC    180
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG    240
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TGGCGGTGGC    300
AGCGGCGGCG GTTCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA    360
CCACCTGCAC CTTTGTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA    420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT    480
```

ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 540
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG 600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG 660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG 720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG 780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC 840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC 900
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG 960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA 999

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG TCTGCCCTCT 60
GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG CAGGTGACTG GCAAGAATTC 120
CGGGAAAAAC TGACGTTCTA TCTGGTTACC CTTGAGCAAG CGCAGGAACA ACAGGGTGGT 180
GGCTCTGGCG GTGGCAGCGG CGGCGGTTCT AACTGCTCTA TAATGATCGA TGAAATTATA 240
CATCACTTAA AGAGACCACC TGCACCTTTG CTGGACCCGA ACAACCTCAA TGACGAAGAC 300
GTCTCTATCC TGATGGACCG AAACCTTCGA CTTCCAAACC TGGAGAGCTT CGTAAGGGCT 360
GTCAAGAACT TAGAATACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA 420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT 480
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 540
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG 600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG 660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG 720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG 780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC 840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC 900
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG 960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA 999

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG 60
GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC 120
TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC TGCTCTATAA TGATCGATGA AATTATACAT 180
CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC 240
TCTATCCTGA TGGACCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC 300
AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG 360
CCCTCTGCCA CGGCCTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA 420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT 480
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 540
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG 600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG 660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG 720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG 780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC 840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC 900
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG 960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA 999

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 60
GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC 120
TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC ACCTTTGCTG 180
GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA CCTTCGACTT 240
CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC AGGTATTGAG 300
GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT 360
CCAATCATCA TCAAGTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA 420
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT 480
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 540
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG 600
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG 660
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG 720
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG 780
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC 840
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC 900
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG 960
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA 999

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT ACAAGCTGTG CCACCCCGAG 420
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC 480
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC 540
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA 600
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA 660
ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG 720
CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC 780
CGCGTTCTAC GCCACCTTGC GCAGCCCTCT GGCGGCTCTG GCGGCTCTCA GAGCTTCCTG 840
CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG 900
CTGTGTGCCA CCTAATAA 918

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC 480
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG 540
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG 600
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC 660
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG 720
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG 780
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC 840
CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG 900
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAA 960
TAA 963

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA     60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC    120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA    180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC    240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG    300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC    360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CCGAGTTGGG TCCCACCTTG    420
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA    480
CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT    540
TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG    600
TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG GCTCTGGCGG CTCTCAGAGC    660
TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA AAGATCCAGG GCGATGGCGC AGCGCTCCAG    720
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC    780
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA    840
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG    900
GAAGGGATAT CCTAATAA                                                  918
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA     60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC    120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA    180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC    240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG    300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC    360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA    420
TCTCATAAAT CTCCAAACAT GGCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG    480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT    540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA    600
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA    660
CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT    720
TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC    780
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC    840
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA    900
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCTAA    960
TAA                                                                  963
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA     60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC    120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA    180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC    240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG    300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC    360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA TGGCCCCTGC CCTGCAGCCC    420
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG    480
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG    540
```

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG 600
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG 660
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG 720
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC 780
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC 840
ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG 900
GAAGAACTGG GATAATAA 918

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG 480
CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG 540
CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CTCTGGCGGC 600
TCTGGCGGCT CTCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGAAA GATCCAGGGC 660
GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCGAGGAG 720
CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC 780
CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG 840
GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCCACCTT GGACACACTG 900
CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGATAA 960
TAA 963

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTCTGG CGGCTCTGGC 540
GGCTCTCAGA GCTTCCTGCT CAAGTCTTTA GAGCAAGTGA GAAAGATCCA GGGCGATGGC 600
GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG 660
CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC 720
CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC 780
CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG 840
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT 900
GCCCTGCAGC CCTAATAA 918

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 540
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC 600
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG 660
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT 720
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC 780
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA 840
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT 900
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA 960
TAA 963

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT CTGCTTTCCA GCGCCGGGCA 420
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA 480
CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT 540
TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC 600
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC 660
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA 720
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC 780
GAGTTGGGTC CCACCTTGGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC 840
TGGCAGCAGA TGGAAGAACT GGGAATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG 900
CCGGCCTTCG CCTAATAA 918

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT 480
GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG 540
CCCTCTGGCG GCTCTGGCGG CTCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA 600
AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC 660
CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC 720
TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT 780
TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC 840
TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA 900
GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTAA 960
TAA 963

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT ACAAGCTGTG CCACCCCGAG 420
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC 480
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC 540
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA 600
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA 660
ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG 720
CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC 780
CGCGTTCTAC GCCACCTTGC GCAGCCCACA CCATTGGGCC CTGCCAGCTC CCTGCCCCAG 840
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC 900
CAGGAGAAGC TGTGTGCCAC CTAATAA 927

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC 480
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG 540
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG 600
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC 660
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG 720
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG 780
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC 840
CTTGCGCAGC CCACACCATT GGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG 900
TCTTTAGAGC AAGTGAGAAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT 960
GCCACCTAAT AA 972

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CCGAGTTGGG TCCCACCTTG 420
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA 480
CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT 540
TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG 600
TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCACACCAT TGGGCCCTGC CAGCTCCCTG 660
CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA 720

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG 780
CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG 840
CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG 900
CAGGCCCTGG AAGGGATATC CTAATAA 927

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG 480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT 540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA 600
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA 660
CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG 720
CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG 780
CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG 840
GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC 900
TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG 960
ATATCCTAAT AA 972

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA TGGCCCCTGC CCTGCAGCCC 420
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 480
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG 540
CAGCCCACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA 600
GAGCAAGTGA GAAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC 660
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG 720
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC 780
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG 840
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG 900
CAGCAGATGG AAGAACTGGG ATAATAA 927

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG 480
CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG 540
CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CACACCATTG 600
GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG 660
ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC 720
CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC 780
TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC 840
CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG 900
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA 960
CTGGGATAAT AA 972

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCACACC ATTGGGCCCT 540
GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC AAGTCTTTAG AGCAAGTGAG AAAGATCCAG 600
GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG 660
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC 720
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC 780
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA 840
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA 900
ATGGCCCCTG CCCTGCAGCC CTAATAA 927

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 540
TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC 600
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG 660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC 720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG 780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG 840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC 900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG 960
CAGCCCTAAT AA 972

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA    60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC   120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT CTGCTTTCCA GCGCCGGGCA   420
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA   480
CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG   540
CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG   600
CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG   660
GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC   720
TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG   780
ATATCCCCCG AGTTGGGTCC CACCTTGGAC ACACTGCAGC TGGACGTCGC CGACTTTGCC   840
ACCACCATCT GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCCAG   900
GGTGCCATGC CGGCCTTCGC CTAATAA                                       927
```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA    60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC   120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420
TCTCATAAAT CTCCAAACAT GGCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT   480
GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG   540
CCCACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG   600
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC   660
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT   720
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT   780
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG   840
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG   900
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC   960
TTCGCCTAAT AA                                                       972
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG    60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTAAT GGACAATAAC   120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA   180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC   240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC   300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC   360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC   480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG   540
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC   600
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG   660
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT   720
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC   780
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA   840
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT   900
```

GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA 960
TAA 963

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC 120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC 240
ACGCGACATC CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC 300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 540
TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTGG GCCCTGCCAG CTCCCTGCCC 600
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG 660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC 720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG 780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG 840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC 900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG 960
CAGCCCTAAT AA 972

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC 120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC 240
ACGCGACATC CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC 300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 540
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC 600
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG 660
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT 720
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC 780
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA 840
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT 900
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA 960
TAA 963

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 970 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTAAT GGACAATAAC 120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC 240
GCGACATCCA ATCCATATCA AGGACGGTGA CTGGAATGAA TTCCGTCGTA AACTGACCTT 300

```
CTATCTGAAA ACCTTGGAGA ACGCGCAGGC TCAACAGTAC GTAGAGGGCG GTGGAGGCTC     360
CCCGGGTGAA CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC     420
TCATAAATCT CCAAACATGG CTACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA     480
GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA     540
CCGCGTTCTA CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA     600
GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT     660
CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG     720
ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT     780
GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC     840
CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC ACACTGCAGC TGGACGTCGC     900
CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA     960
GCCCTAATAA                                                            970
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT GCCTGCTGTG     480
GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA CCAAGGCACA GGACATTCTG     540
GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG ATGGCAGCAC GGGGACAACT GGGACCCACT     600
TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG     660
CAGAGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC     720
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT     780
GTAGGAGGGT CCACCCTCTG CGTCAGGGAA TTCGGCGGCA ACATGGCGTC TCCCGCTCCG     840
CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC     900
AGACTGAGCC AGTGCCCA                                                   918
```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG     480
GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC     540
CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC     600
CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT     660
GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC     720
CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC     780
ACCCTCTGCG TCAGGGAATT CGGCGGCAAC ATGGCGTCTC CCGCTCCGCC TGCTTGTGAC     840
CTCCGAGTCC TCAGTAAACT GCTTCGTGAC TCCCATGTCC TTCACAGCAG ACTGAGCCAG     900
TGCCCAGAGG TTCACCCT                                                   918
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA     480
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG     540
GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG     600
CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT     660
CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA     720
CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC     780
AGGGAATTCG GCGGCAACAT GGCGTCTCCC GCTCCGCCTG CTTGTGACCT CCGAGTCCTC     840
AGTAAACTGC TTCGTGACTC CCATGTCCTT CACAGCAGAC TGAGCCAGTG CCCAGAGGTT     900
CACCCTTTGC CTACACCT                                                   918
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG     480
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA     540
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG     600
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC     660
AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA     720
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC     780
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT     840
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT     900
ACACCTGTCC TGCTGCCT                                                   918
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC     480
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG     540
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT     600
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC     660
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG     720
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC     780
ATGGCGTCTC CCGCTCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC     840
TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT     900
GTCCTGCTGC CTGCTGTG                                                   918
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 907 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCGGTTAC CCTTGAGCAA GCGCAGGAAC AACAGTACGT AGAGGGCGGT GGAGGCTCCC    360
CGGGGAACCG TCTGGTCCAA TCTCTACTAT CAACCCGTCT CCTCCGTCTA AAGAATCTCA    420
TAAACTCCAA ACATGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT    480
CTGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA    540
CTTGCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT    600
GCAGGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC    660
AATGCATCTT CCTGAGCTTC CAACACCTGC TCCGAGGAAA GGTGCGTTTC CTGATGCTTG    720
TAGGGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC ATGGCGTCTC CCGCTCCGCC    780
TGCTGTGACC TCCGAGTCCT CAGTAAACTG CTTCGTGACT CCCATGTCCT TCACAGCAGA    840
CTGACCAGTG CCCAGAGGTT CACCCTTTGC CTACACCTGT CCTGCTGCCT GCTGTGGACT    900
TTAGTTG                                                              907
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA    480
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG    540
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC    600
CGAGGAAAGG TGCGTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC    660
GGCGGCAACA TGGCGTCTCC CGCTCCGCCT GCTTGTGACC TCCGAGTCCT CAGTAAACTG    720
CTTCGTGACT CCCATGTCCT TCACAGCAGA CTGAGCCAGT GCCCAGAGGT TCACCCTTTG    780
CCTACACCTG TCCTGCTGCC TGCTGTGGAC TTTAGCTTGG GAGAATGGAA AACCCAGATG    840
GAGGAGACCA AGGCACAGGA CATTCTGGGA GCAGTGACCC TTCTGCTGGA GGGAGTGATG    900
GCAGCACGGG GACAACT                                                   917
```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG    480
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG    540
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACAT GGCGTCTCCC    600
GCTCCGCCTG CTTGTGACCT CCGAGTCCTC AGTAAACTGC TTCGTGACTC CCATGTCCTT    660
```

CACAGCAGAC TGAGCCAGTG CCCAGAGGTT CACCCTTTGC CTACACCTGT CCTGCTGCCT 720
GCTGTGGACT TTAGCTTGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC 780
ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA 840
CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG 900
GCCCTGCAGA GCCTCCTT 918

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG 480
AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC 540
CTCTGCGTCA GGGAATTCGG CGGCAACATG GCGTCTCCCG CTCCGCCTGC TTGTGACCTC 600
CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC 660
CCAGAGGTTC ACCCTTTGCC TACACCTGTC CTGCTGCCTG CTGTGGACTT TAGCTTGGGA 720
GAATGGAAAA CCCAGATGGA GGAGACCAAG GCACAGGACA TTCTGGGAGC AGTGACCCTT 780
CTGCTGGAGG GAGTGATGGC AGCACGGGGA CAACTGGGAC CCACTTGCCT CTCATCCCTC 840
CTGGGGCAGC TTTCTGGACA GGTCCGTCTC CTCCTTGGGG CCCTGCAGAG CCTCCTTGGA 900
ACCCAGCTTC CTCCACAG 918

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC 480
CTGCTCCGAG GAAAGGTGCG TTTCCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG 540
GAATTCGGCG GCAACATGGC GTCTCCCGCT CCGCCTGCTT GTGACCTCCG AGTCCTCAGT 600
AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC 660
CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC 720
CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA 780
GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT 840
TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT 900
CCACAGGGCA GGACCACA 918

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA 480
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC 540
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT 600
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT 660
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG 720
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA 780
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG 840
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC 900
AGGACCACAG CTCACAAG 918

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG 480
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGGAATTCGG CGGCAACATG 540
GCGTCTCCCG CTCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC 600
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC 660
CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA CCCAGATGGA GGAGACCAAG 720
GCACAGGACA TTCTGGGAGC AGTGACCCTT CTGCTGGAGG GAGTGATGGC AGCACGGGGA 780
CAACTGGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA GGTCCGTCTC 840
CTCCTTGGGG CCCTGCAGAG CCTCCTTGGA ACCCAGCTTC CTCCACAGGG CAGGACCACA 900
GCTCACAAGG ATCCCAAT 918

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT GCCTGCTGTG 480
GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA CCAAGGCACA GGACATTCTG 540
GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG ATGGCAGCAC GGGGACAACT GGGACCCACT 600
TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG 660
CAGAGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 720
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT 780
GTAGGAGGGT CCACCCTCTG CGTCAGGGAA TTCGGCAACA TGGCGTCTCC CGCTCCGCCT 840
GCTTGTGACC TCCGAGTCCT CAGTAAACTG CTTCGTGACT CCCATGTCCT TCACAGCAGA 900
CTGAGCCAGT GCCCA 915

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG    480
GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC    540
CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC    600
CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT    660
GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC    720
CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC    780
ACCCTCTGCG TCAGGGAATT CGGCAACATG GCGTCTCCCG CTCCGCCTGC TTGTGACCTC    840
CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC    900
CCAGAGGTTC ACCCT                                                     915
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA    480
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG    540
GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG    600
CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT    660
CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA    720
CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC    780
AGGGAATTCG GCAACATGGC GTCTCCCGCT CCGCCTGCTT GTGACCTCCG AGTCCTCAGT    840
AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC    900
CCTTTGCCTA CACCT                                                     915
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG    480
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA    540
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG    600
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC    660
AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA    720
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC    780
AACATGGCGT CTCCCGCTCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT    840
GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTCACCC TTTGCCTACA    900
CCTGTCCTGC TGCCT                                                     915
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC    480
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG    540
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT    600
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC    660
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG    720
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCAACATG    780
GCGTCTCCCG CTCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC    840
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC    900
CTGCTGCCTG CTGTG                                                     915
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC    480
ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA    540
CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG    600
GCCCTGCAGA GCCTCCTTGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG    660
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG    720
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCAACATGGC GTCTCCCGCT    780
CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA TGTCCTTCAC    840
AGCAGACTGA GCCAGTGCCC AGAGGTTCAC CCTTTGCCTA CACCTGTCCT GCTGCCTGCT    900
GTGGACTTTA GCTTG                                                     915
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA    480
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG    540
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC    600
CGAGGAAAGG TGCGTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC    660
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GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT     720
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT     780
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG     840
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA     900
GCACGGGGAC AACTG                                                      915
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG     480
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG     540
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCAACATGGC GTCTCCCGCT     600
CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA TGTCCTTCAC     660
AGCAGACTGA GCCAGTGCCC AGAGGTTCAC CCTTTGCCTA CACCTGTCCT GCTGCCTGCT     720
GTGGACTTTA GCTTGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT     780
CTGGGAGCAG TGACCCTTCT GCTGGAGGGA GTGATGGCAG CACGGGGACA ACTGGGACCC     840
ACTTGCCTCT CATCCCTCCT GGGGCAGCTT TCTGGACAGG TCCGTCTCCT CCTTGGGGCC     900
CTGCAGAGCC TCCTT                                                      915
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG     480
AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC     540
CTCTGCGTCA GGGAATTCGG CAACATGGCG TCTCCCGCTC CGCCTGCTTG TGACCTCCGA     600
GTCCTCAGTA AACTGCTTCG TGACTCCCAT GTCCTTCACA GCAGACTGAG CCAGTGCCCA     660
GAGGTTCACC CTTTGCCTAC ACCTGTCCTG CTGCCTGCTG TGGACTTTAG CTTGGGAGAA     720
TGGAAAACCC AGATGGAGGA GACCAAGGCA CAGGACATTC TGGGAGCAGT GACCCTTCTG     780
CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA CTTGCCTCTC ATCCCTCCTG     840
GGGCAGCTTT CTGGACAGGT CCGTCTCCTC CTTGGGGCCC TGCAGAGCCT CCTTGGAACC     900
CAGCTTCCTC CACAG                                                      915
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT      60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT     120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
```

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC 480
CTGCTCCGAG GAAAGGTGCG TTTCCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG 540
GAATTCGGCA ACATGGCGTC TCCCGCTCCG CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA 600
CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGAGCC AGTGCCCAGA GGTTCACCCT 660
TTGCCTACAC CTGTCCTGCT GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG 720
ATGGAGGAGA CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 780
ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT 840
GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC TTGGAACCCA GCTTCCTCCA 900
CAGGGCAGGA CCACA 915

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA 480
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC 540
AACATGGCGT CTCCCGCTCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT 600
GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTCACCC TTTGCCTACA 660
CCTGTCCTGC TGCCTGCTGT GGACTTTAGC TTGGGAGAAT GGAAAACCCA GATGGAGGAG 720
ACCAAGGCAC AGGACATTCT GGGAGCAGTG ACCCTTCTGC TGGAGGGAGT GATGGCAGCA 780
CGGGGACAAC TGGGACCCAC TTGCCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC 840
CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC CTTGGAACCC AGCTTCCTCC ACAGGGCAGG 900
ACCACAGCTC ACAAG 915

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG 480
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGGAATTCGG CAACATGGCG 540
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT 600
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC CTTTGCCTAC ACCTGTCCTG 660
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA 720
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA 780
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGCAGCTTT CTGGACAGGT CCGTCTCCTC 840
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT 900
CACAAGGATC CCAAT 915

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
GACTTCCAAA CCTGGAGAGC TTCGTAAGGG CTGTCAAGAA CTTAGAAAAT GCATCAGGTA 180
TGAGGCAATT CTTCGTAATC TCCAACCATG TCTGCCCTCT GCCACGGCCG CACCCTCTCG 240
CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT 300
TGGTTACCCT TGAGCAAGCG CAGGAACAAC AGTACGTAGA GGGCGGTGGA GGCTCCCCGG 360
TAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA 420
TCTCCAAACA TGGAGGTTCA CCCTTTGCCT ACACCTGTCC TGCTGCCTGC TGTGGACTTT 480
AGCTTGGGAG AATGGAAAAC CCAGATGGAG GAGACCAAGG CACAGGACAT TCTGGGAGCA 540
GTGACCCTTC TGCTGGAGGG AGTGATGGCA GCACGGGGAC AACTGGGACC CACTTGCCTC 600
TCATCCCTCC TGGGGCAGCT TTCTGGACAG GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC 660
CTCCTTGGAA CCCAGCTTCC TCCACAGGGC AGGACCACAG CTCACAAGGA TCCCAATGCC 720
ATCTTCCTGA GCTTCCAACA CCTGCTCCGA GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA 780
GGGTCCACCC TCTGCGTCAG GGAATTCGGC GGCAACGGCG GCAACATGGC GTCCCCAGCG 840
CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AAACTGCTTC GTGACTCCCA TGTCCTTCAC 900
AGCAGACTGA GCCAGTGCCC A 921

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG 480
GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC 540
CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC 600
CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT 660
GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC 720
CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC 780
ACCCTCTGCG TCAGGGAATT CGGCGGCAAC GGCGGCAACA TGGCGTCCCC AGCGCCGCCT 840
GCTTGTGACC TCCGAGTCCT CAGTAAACTG CTTCGTGACT CCCATGTCCT TCACAGCAGA 900
CTGAGCCAGT GCCCAGAGGT TCACCCT 927

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA 480
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG 540
GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG 600
CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT 660
CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA 720
CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC 780
AGGGAATTCG GCGGCAACGG CGGCAACATG GCGTCCCCAG CGCCGCCTGC TTGTGACCTC 840
CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC 900
CCAGAGGTTC ACCCTTTGCC TACACCT 927

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG 480
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA 540
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG 600
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC 660
AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA 720
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC 780
GGCAACGGCG GCAACATGGC GTCCCCAGCG CCGCCTGCTT GTGACCTCCG AGTCCTCAGT 840
AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC 900
CCTTTGCCTA CACCTGTCCT GCTGCCT 927

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC 480
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG 540
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT 600
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC 660
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG 720
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC 780
GGCGGCAACA TGGCGTCCCC AGCGCCGCCT GCTTGTGACC TCCGAGTCCT CAGTAAACTG 840
CTTCGTGACT CCCATGTCCT TCACAGCAGA CTGAGCCAGT GCCCAGAGGT TCACCCTTTG 900
CCTACACCTG TCCTGCTGCC TGCTGTG 927

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC 480
ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA 540
CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG 600
GCCCTGCAGA GCCTCCTTGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG 660

GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG 720
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACGG CGGCAACATG 780
GCGTCCCCAG CGCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC 840
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC 900
CTGCTGCCTG CTGTGGACTT TAGCTTG 927

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA 480
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG 540
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC 600
CGAGGAAAGG TGCGTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC 660
GGCGGCAACG GCGGCAACAT GGCGTCCCCA GCGCCGCCTG CTTGTGACCT CCGAGTCCTC 720
AGTAAACTGC TTCGTGACTC CCATGTCCTT CACAGCAGAC TGAGCCAGTG CCCAGAGGTT 780
CACCCTTTGC CTACACCTGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA 840
ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG 900
GGAGTGATGG CAGCACGGGG ACAACTG 927

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG 480
GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG 540
ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACGG CGGCAACATG 600
GCGTCCCCAG CGCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC 660
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC 720
CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA CCCAGATGGA GGAGACCAAG 780
GCACAGGACA TTCTGGGAGC AGTGACCCTT CTGCTGGAGG GAGTGATGGC AGCACGGGGA 840
CAACTGGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA GGTCCGTCTC 900
CTCCTTGGGG CCCTGCAGAG CCTCCTT 927

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG 480
AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC 540
CTCTGCGTCA GGGAATTCGG CGGCAACGGC GGCAACATGG CGTCCCCAGC GCCGCCTGCT 600
TGTGACCTCC GAGTCCTCAG TAAACTGCTT CGTGACTCCC ATGTCCTTCA CAGCAGACTG 660
AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT ACACCTGTCC TGCTGCCTGC TGTGGACTTT 720
AGCTTGGGAG AATGGAAAAC CCAGATGGAG GAGACCAAGG CACAGGACAT TCTGGGAGCA 780
GTGACCCTTC TGCTGGAGGG AGTGATGGCA GCACGGGGAC AACTGGGACC CACTTGCCTC 840
TCATCCCTCC TGGGGCAGCT TTCTGGACAG GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC 900
CTCCTTGGAA CCCAGCTTCC TCCACAG 927

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC 480
CTGCTCCGAG GAAAGGTGCG TTTCCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG 540
GAATTCGGCG GCAACGGCGG CAACATGGCG TCCCCAGCGC CGCCTGCTTG TGACCTCCGA 600
GTCCTCAGTA AACTGCTTCG TGACTCCCAT GTCCTTCACA GCAGACTGAG CCAGTGCCCA 660
GAGGTTCACC CTTTGCCTAC ACCTGTCCTG CTGCCTGCTG TGGACTTTAG CTTGGGAGAA 720
TGGAAAACCC AGATGGAGGA GACCAAGGCA CAGGACATTC TGGGAGCAGT GACCCTTCTG 780
CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA CTTGCCTCTC ATCCCTCCTG 840
GGGCAGCTTT CTGGACAGGT CCGTCTCCTC CTTGGGGCCC TGCAGAGCCT CCTTGGAACC 900
CAGCTTCCTC CACAGGGCAG GACCACA 927

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA 480
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC 540
GGCAACGGCG GCAACATGGC GTCCCCAGCG CCGCCTGCTT GTGACCTCCG AGTCCTCAGT 600
AAACTGCTTC GTGACTCCCA TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTCAC 660
CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC 720
CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA 780
GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT 840
TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT 900
CCACAGGGCA GGACCACAGC TCACAAG 927

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG    480
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGGAATTCGG CGGCAACGGC    540
GGCAACATGG CGTCCCCAGC GCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT    600
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT    660
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG    720
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA    780
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG    840
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC    900
AGGACCACAG CTCACAAGGA TCCCAAT                                        927
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA    480
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC    540
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT    600
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT    660
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG    720
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA    780
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG    840
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGGGCAG GACCACAGCT    900
CACAAG                                                               906
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA     60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC    120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA    180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC    240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG    300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC    360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA    420
TCTCATAAAT CTCCAAACAT GTCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC    480
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG    540
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG    600
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC    660
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG    720
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG    780
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC    840
CTTGCGCAGC CCGGCGGCGG CTCTGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG    900
CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA    960
GCGCTCCAGG AGAAGCTGTG TGCCACCTAA TAA                                 993
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA    60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC   120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420
TCTCATAAAT CTCCAAACAT GTCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG   480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT   540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA   600
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA   660
CGCCACCTTG CGCAGCCCGG CGGCGGCTCT GACATGGCTA CACCATTAGG CCCTGCCAGC   720
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT   780
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG   840
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG   900
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG   960
CTCCTGCAGG CCCTGGAAGG GATATCCTAA TAA                                993
```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA    60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC   120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420
TCTCATAAAT CTCCAAACAT GTCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT   480
GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG   540
CCCGGCGGCG GCTCTGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC   600
TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG   660
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC   720
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA   780
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG   840
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC   900
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC   960
ACCCAGGGTG CCATGCCGGC CTTCGCCTAA TAA                                993
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA    60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC   120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA   180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC   240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG   300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC   360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA   420
TCTCATAAAT CTCCAAACAT GTCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG   480
```

CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG 540
CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CGGCGGCGGC 600
TCTGACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG 660
TCTTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT 720
GCCACCTACA AGCTGTGCCA CCCCGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC 780
CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC 840
CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC 900
CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC 960
ATCTGGCAGC AGATGGAAGA ACTGGGATAA TAA 993

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 993 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420
TCTCATAAAT CTCCAAACAT GTCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 480
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 540
TACCGCGTTC TACGCCACCT TGCGCAGCCC GGCGGCGGCT CTGACATGGC TACACCATTA 600
GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG 660
ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC 720
CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC 780
TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC 840
CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG 900
GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA 960
CTGGGAATGG CCCCTGCCCT GCAGCCCTAA TAA 993

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1027 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA 60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC 120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG 180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC 240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG 300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG 360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG 420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG 480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGG CGGCGGCTCT 540
GACATGGCTA CACCATTGGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT 600
TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC 660
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC 720
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA 780
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC 840
GAGTTGGGTC CCACCTTGGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC 900
TGGCAGCAGA TGGAAGAACT GGGAATGGCC CCTGCCCTGC AGCCCACCCA TCCTGGTTGC 960
TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC 1020
CTGATAA 1027

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT     60
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC CTTTGCCTAC ACCTGTCCTG    120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA    180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGCAGCTTT  CTGGACAGGT CCGTCTCCTC    300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT    360
CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT    420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGG                           459
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT     60
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC CTTTGCCTAC ACCTGTCCTG    120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA    180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGCAGCTTT  CTGGACAGGT CCGTCTCCTC    300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGGGCAGGA CCACAGCTCA CAAGGATCCC    360
AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT    420
GTAGGAGGGT CCACCCTCTG CGTCAGG                                        447
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
TCCCCAGCGC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT     60
GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCACC CTTTGCCTAC ACCTGTCCTG    120
CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA    180
CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA    240
CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGCAGCTTT  CTGGACAGGT CCGTCTCCTC    300
CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT    360
CACAAGGATC CCAATGCCAT CTTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT    420
TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGG                           459
```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
CCATGGCTAA CTGCTCTATA ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG     60
CACCTTTGCT GGACCCGAAC AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGATCGAA    120
ACCTTCGACT TCCAAACCTG GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT    180
CAGGTATTGA GGCAATTCTT CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC    240
CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA    300
CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAGAG GGCGGTGGAG    360
GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT CCGTCTAAAG    420
AATCTCATAA ATCTCCAAAC ATGTAAGGTA CCGCATGCAA GCTT                     464
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 419 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
CCATGGCTAA CTGCTCTATA ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG      60
CACCTTTGCT GGACCCGAAC AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGATCGAA     120
ACCTTCGACT TCCAAACCTG GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT     180
CAGGTATTGA GGCAATTCTT CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC     240
CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA     300
CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAGAG GGCGGTGGAG     360
GCTCCCCGGG TGGTGGTTCT GGCGGCGGCT CCAACATGTA AGGTACCGCA TGCAAGCTT      419
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
GCCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC      60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG     120
GACGAGGAGC TCTGCGGGGC GCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG     180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA     240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC     300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC     360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCC                     405
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
GCCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC      60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG     120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG     180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA     240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC     300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC     360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG     420
```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
GCCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC      60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG     120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG     180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA     240
CACTTTGTCA CCAAATGTGC CTTTCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC     300
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA     360
ACCCTG                                                                366
```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGAACTCAGG ATTGTTCTTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCC 405

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGTACCCAGG ATTGTTCTTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GCCACTCAGG ACTGTTCTTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCC 405

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GCCACTCAGG ACTGCTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG    60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG   180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG   240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC   300
CTGTCTGGAG GTAACGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC   360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC   420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAG                   465
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG    60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG   180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG   240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC   300
CTGTCAGGCG GTAACGGCAG TGGAGGTAAT GGCACCCAGG ACTGCTCCTT CCAACACAGC   360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT   420
TACCCAGTCA CCGTGGCCTC CAACCTGCAG                                    450
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG    60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG   180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG   240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC   300
CTGTCTGGCG GCAACGGCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC   360
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG   420
GCCTCCAACC TGCAG                                                    435
```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA    60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC   120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC   180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGTCTGG AGGTAACGGA   240
TCCGGTGGCA ATGGGAGCGG CGGAAATGGA ACCCAGGACT GCTCCTTCCA ACACAGCCCC   300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC   360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG   420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGG                   465
```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA    60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC   120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC   180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGTCTGG AGGTAACGGA   240
TCCGGAGGTA ATGGCACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC   300
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC   360
TCCAACCTGC AGGACGAGGA GCTCTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC   420
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG                                    450
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA    60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC   120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC   180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGTCTGG CGGCAACGGC   240
ACGCAGGACT GCTCCTTCCA ACACAGCCCC ATCTCCTCCG ACTTCGCTGT CAAAATCCGT   300
GAGCTGTCTG ACTACCTGCT TCAAGATTAC CCAGTCACCG TGGCCTCCAA CCTGCAGGAC   360
GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC   420
AAGACTGTCG CTGGG                                                    435
```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC    60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG   120
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGTCTGGAG GTAACGGCAG TGGTGGCAAT   180
GGGAGCGGTG GAAATGGAAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC   240
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG   300
GCCTCCAACC TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG   360
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC   420
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCC                   465
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC    60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG   120
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGTCAGGCG GTAACGGCAG TGGAGGTAAT   180
GGCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC   240
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG   300
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG   360
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA   420
CACTTTGTCA CCAAATGTGC CTTTCAGCCC                                    450
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC    60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG   120
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGTCTGGCG GCAACGGCAC GCAGGACTGC   180
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC   240
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGGACGA GGAGCTCTGC   300
GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG AGCGGCTCAA GACTGTCGCT   360
GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA   420
TGTGCCTTTC AGCCC                                                    435
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG    60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG   180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG   240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC   300
CTGTCTGGAG GTAGTGGATC CGGAGGTTCT GGCAACCCAG GACTGCTCCT TCCAACACAG   360
CCCCATCTCC TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA   420
TTACCCAGTC ACCGTGGCCT CCAACCTGCA G                                  451
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG    60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG   180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG   240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC   300
CTGTCTGGAG GTAGTGGATC CGGTGGCAGT GGGAGCGGCG GATCTGGAAC CCAGGACTGC   360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC   420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAG                   465
```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
CCATGGCCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA    60
AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC   120
TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG   180
AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG   240
AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC   300
AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT   360
GGATCACTCG CCAGAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA   420
```

CCCTGGGCGG TGGATCC 437

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GGATCCGGAG GTACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC CGACTTCGCT 60
GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAAGATT ACCCAGTCAC CGTGGCCTCC 120
AACCTGCAGG ACGAGGAGCT CTGCGGGGGC CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG 180
ATGGAGCGGC TCAAGACTGT CGCTGGGTCC AAGATGCAAG GCTTGCTGGA GCGCGTGAAC 240
ACGGAGATAC ACTTTGTCAC CAAATGTGCC TTTCAGCCCC CCCCCAGCTG TCTTCGCTTC 300
GTCCAGACCA ACATCTCCCG CCTCCTGCAG GAGACCTCCG AGCAGCTGGT GGCGCTGAAG 360
CCCTGGATCA CTCGCCAGAA CTTCTCCCGG TGCCTGGAGC TGCAGTGTCA GCCCGACTCC 420
TCAACCCTGT AAGCTT 436

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCATGGCCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA 60
AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC 120
TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG 180
AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG 240
AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC 300
AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT 360
GGATCACTCG CCAGAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA 420
CCCTGGGCGG TGGGTCAGGA GGTGGATCC 449

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGATCCGGAG GTGGCACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC 60
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC 120
TCCAACCTGC AGGACGAGGA GCTCTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC 180
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG 240
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC 300
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG 360
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC 420
TCCTCAACCC TGTAAGCTT 439

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CCATGGCCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA 60
AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC 120
TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG 180
AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG 240

```
AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC    300
AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT    360
GGATCACTCG CCAGAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA    420
CCCTGGGCGG TGGGTCAGGA GGTGGGTCAG GAGGTGGATC C                        461
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 457 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC     60
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT    120
TACCCAGTCA CCGTGGCCTC CAACCTGCAG GACGAGGAGC TCTGCGGGGG CCTCTGGCGG    180
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA    240
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC    300
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC    360
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG    420
CTGCAGTGTC AGCCCGACTC CTCAACCCTG TAAGCTT                             457
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GATCCGGAGG TACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC    360
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC    420
GTGGCCTCCA ACCTGCAG                                                  438
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GATCCGGAGG TGGCACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC    360
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC    420
ACCGTGGCCT CCAACCTGCA G                                              441
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
```

CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGATCCGGA GGTACCCAGG ACTGCTCCTT CCAACACAGC 360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 420
TACCCAGTCA CCGTGGCCTC CAACCTGCAG 450

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GATCCGGAGG TGGCTCAGGG GGAGGTAGTG GTACCCAGGA CTGCTCCTTC 360
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG 420
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAG 459

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCAC CCAGGACTGC 360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAG 465

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGCCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAG 483

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT    60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT   120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC   480
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC   540
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGCGC TCTGGCGGCT GGTCCTGGCA   600
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG   660
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT   720
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG   780
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG   840
CCC                                                                 843
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT    60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT   120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC   480
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC   540
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGCGC TCTGGCGGCT GGTCCTGGCA   600
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG   660
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT   720
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG   780
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG   840
CCCGACTCCT CAACCCTG                                                 858
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT    60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT   120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG   480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG   540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC   600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG   660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT   720
CAGCCCGACT CCTCAACCCT GTCAGGCGGT AACGGCAGTG GAGGTAATGG CACCCAGGAC   780
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT   840
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAG                888
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG    480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG    540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC    600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG    660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT    720
CAGCCCGACT CCTCAACCCT GTCTGGAGGT AACGGATCCG GTGGCAATGG GAGCGGCGGA    780
AATGGAACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    840
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGTCTGGCG GCAACGGCAC GCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC    720
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG    780
GCCTCCAACC TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG    840
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGG                                 873
```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGTCTGGAG GTAACGGATC CGGAGGTAAT GGCACCCAGG ACTGCTCCTT CCAACACAGC    720
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT    780
TACCCAGTCA CCGTGGCCTC CAACCTGCAG GACGAGGAGC TCTGCGGGGG CCTCTGGCGG    840
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGG                 888
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 660
CTGTCTGGAG GTAACGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC 720
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 780
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGGACGA GGAGCTCTGC 840
GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG AGCGGCTCAA GACTGTCGCT 900
GGG 903

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC 480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG 540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GTCTGGCGGC 600
AACGGCACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 660
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 720
CAGGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 780
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 840
ATACACTTTG TCACCAAATG TGCCTTTCAG CCC 873

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC 480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG 540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GTCAGGCGGT 600

```
AACGGCAGTG GAGGTAATGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC    660
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC    720
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA    780
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG    840
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCC                 888
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC    480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG    540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GTCTGGAGGT    600
AACGGCAGTG GTGGTAATGG GAGCGGCGGA AATGGAACCC AGGACTGCTC CTTCCAACAC    660
AGCCCCATCT CCTCCGACTT CGCTGTCAAA ATCCGTGAGC TGTCTGACTA CCTGCTTCAA    720
GATTACCCAG TCACCGTGGC CTCCAACCTG CAGGACGAGG AGCTCTGCGG GGGCCTCTGG    780
CGGCTGGTCC TGGCACAGCG CTGGATGGAG CGGCTCAAGA CTGTCGCTGG GTCCAAGATG    840
CAAGGCTTGC TGGAGCGCGT GAACACGGAG ATACACTTTG TCACCAAATG TGCCTTTCAG    900
CCC                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC GACTCAGGAC TGTTCTTTCC AACACAGCCC CATCTCCTCC    480
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC    540
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA    600
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG    660
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT    720
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG    780
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG    840
CCC                                                                  843
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
```

```
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC AACCCAGGAC TGCTCTTTTC AACACAGCCC CATCTCCTCC    480
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC    540
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA    600
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG    660
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT    720
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG    780
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG    840
CCCGACTCCT CAACCCTG                                                  858
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
GCCACTCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG    180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA    240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC    300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC    360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCTACGT AGAGGGCGGT    420
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    480
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    540
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    600
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    660
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    720
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    780
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    840
CAG                                                                  843
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CCAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG    480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG    540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC    600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG    660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT    720
CAGCCCGACT CCTCAACCCT GTCAGGCGGT AACGGCAGTG GAGGTAATGG CACCCAGGAC    780
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT    840
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAG                 888
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
```

```
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG    480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG    540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC    600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG    660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT    720
CAGCCCGACT CCTCAACCCT GTCTGGAGGT AACGGATCCG GTGGCAATGG GAGCGGCGGA    780
AATGGAACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    840
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGTCTGGCG GCAACGGCAC GCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC    720
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG    780
GCCTCCAACC TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG    840
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGG                                 873
```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGTCTGGAG GTAACGGATC CGGAGGTAAT GGCACCCAGG ACTGCTCCTT CCAACACAGC    720
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT    780
TACCCAGTCA CCGTGGCCTC CAACCTGCAG GACGAGGAGC TCTGCGGGGG CCTCTGGCGG    840
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGG                 888
```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG   540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG   600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC   660
CTGTCTGGAG GTAACGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC   720
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC   780
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGGACGA GGAGCTCTGC   840
GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG AGCGGCTCAA GACTGTCGCT   900
GGG                                                                 903
```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC   480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG   540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GTCTGGCGGC   600
AACGGCACGC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA   660
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG   720
CAGGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG   780
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG   840
ATACACTTTG TCACCAAATG TGCCTTTCAG CCC                                873
```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC   480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG   540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GTCAGGCGGT   600
AACGGCAGTG GAGGTAATGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC   660
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC   720
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA   780
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG   840
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCC                888
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC   480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG   540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GTCTGGAGGT   600
AACGGCAGTG GTGGCAATGG GAGCGGCGGA AATGGAACCC AGGACTGCTC CTTCCAACAC   660
AGCCCCATCT CCTCCGACTT CGCTGTCAAA ATCCGTGAGC TGTCTGACTA CCTGCTTCAA   720
GATTACCCAG TCACCGTGGC CTCCAACCTG CAGGACGAGG AGCTCTGCGG GGGCCTCTGG   780
CGGCTGGTCC TGGCACAGCG CTGGATGGAG CGGCTCAAGA CTGTCGCTGG GTCCAAGATG   840
CAAGGCTTGC TGGAGCGCGT GAACACGGAG ATACACTTTG TCACCAAATG TGCCTTTCAG   900
CCC                                                                 903
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CCAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG   480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG   540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC   600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG   660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT   720
CAGCCCGACT CCTCAACCCT GTCTGGAGGT AGTGGATCCG GAGGTTCTGG CACCCAGGAC   780
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT   840
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAG                888
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG   480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG   540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC   600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG   660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT   720
CAGCCCGACT CCTCAACCCT GTCTGGAGGT AGTGGATCCG GTGGCAGTGG GAGCGGCGGA   780
```

TCTGGAACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 840
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 900
CAG 903

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GAACCGTCTG GTCCAATCTC TACTATCAAC 480
CCGTCTCCTC CGTCTAAAGA ATCTCATAAA TCTCCAAACA TGGCTAACTG CTCTATAATG 540
ATCGATGAAA TTATACATCA CTTAAAGAGA CCACCTAACC CTTTGCTGGA CCCGAACAAC 600
CTCAATTCTG AAGACATGGA TATCCTGATG GAACGAAACC TTCGAACTCC AAACCTGCTC 660
GCATTCGTAA GGGCTGTCAA GCACTTAGAA AATGCATCAG GTATTGAGGC AATTCTTCGT 720
AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT CTCGACATCC AATCATCATC 780
AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA AAACTGACGT TCTATCTGGT TACCCTTGAG 840
CAAGCGCAGG AACAACAG 858

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG 480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGA TCCGGAGGTA CCCAGGACTG CTCCTTCCAA 780
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT 840
CAAGATTACC CAGTCACCGT GGCCTCCAAC CTGCAG 876

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG 480

GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGA TCCGGAGGTG GCACCCAGGA CTGCTCCTTC 780
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG 840
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAG 879

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG 480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGG TCAGGAGGTG GATCCGGAGG TACCCAGGAC 780
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT 840
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAG 888

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG 480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGA TCCGGAGGTG GCTCAGGGGG AGGTAGTGGT 780
ACCCAGGACT GCTCCTTCCA ACACAGCCCC ATCTCCTCCG ACTTCGCTGT CAAAATCCGT 840
GAGCTGTCTG ACTACCTGCT TCAAGATTAC CCAGTCACCG TGGCCTCCAA CCTGCAG 897

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG 480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGG TCAGGAGGTG GGTCAGGAGG TGGATCCGGA 780
GGTGGCACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 840
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 900
CAG 903

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG 480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGG TCAGGAGGTG GGTCAGGAGG TGGATCCGGA 780
GGTGGCTCAG GGGGAGGTAG TGGTACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC 840
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC 900
ACCGTGGCCT CCAACCTGCA G 921

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 660
CTGGGCGGTG GATCCGGAGG TACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC 720
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC 780
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA 840
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGG 876

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGGGCGGTG GATCCGGAGG TGGCACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC    720
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC    780
ACCGTGGCCT CCAACCTGCA GGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG    840
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGG                           879
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGGGCGGTG GGTCAGGAGG TGGATCCGGA GGTACCCAGG ACTGCTCCTT CCAACACAGC    720
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT    780
TACCCAGTCA CCGTGGCCTC CAACCTGCAG GACGAGGAGC TCTGCGGGGG CCTCTGGCGG    840
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGG                 888
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    660
CTGGGCGGTG GATCCGGAGG TGGCTCAGGG GGAGGTAGTG GTACCCAGGA CTGCTCCTTC    720
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG    780
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAGG ACGAGGAGCT CTGCGGGGGC    840
CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG ATGGAGCGGC TCAAGACTGT CGCTGGG      897
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 660
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCAC CCAGGACTGC 720
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 780
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGGACGA GGAGCTCTGC 840
GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG AGCGGCTCAA GACTGTCGCT 900
GGG 903

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 480
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 540
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 600
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 660
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 720
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 780
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 840
CAGGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 900
CGGCTCAAGA CTGTCGCTGG G 921

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC 480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG 540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GGGCGGTGGA 600
TCCGGAGGTA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC 660
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC 720
CTGCAGGACG AGGAGCTCTG CGGGGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG 780
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG 840
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCC 876

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC   480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG   540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GGGCGGTGGA   600
TCCGGAGGTG GCACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC CGACTTCGCT   660
GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAAGATT ACCCAGTCAC CGTGGCCTCC   720
AACCTGCAGG ATGAGGAGCT CTGCGGGGGC CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG   780
ATGGAGCGGC TCAAGACTGT CGCTGGGTCC AAGATGCAAG GCTTGCTGGA GCGCGTGAAC   840
ACGGAGATAC ACTTTGTCAC CAAATGTGCC TTTCAGCCC                          879
```

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC   480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG   540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GGGCGGTGGG   600
TCAGGAGGTG GATCCGGAGG TACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC   660
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC   720
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA   780
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG   840
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCC                 888
```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC   480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG   540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GGGCGGTGGA   600
TCCGGAGGTG GCTCAGGGGG AGGTAGTGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC   660
```

```
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC    720
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG    780
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA GATGCAAGGC    840
TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCCTT TCAGCCC       897
```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC    480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG    540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GGGCGGTGGG    600
TCAGGAGGTG GGTCAGGAGG TGGATCCGGA GGTGGCACCC AGGACTGCTC CTTCCAACAC    660
AGCCCCATCT CCTCCGACTT CGCTGTCAAA ATCCGTGAGC TGTCTGACTA CCTGCTTCAA    720
GATTACCCAG TCACCGTGGC CTCCAACCTG CAGGACGAGG AGCTCTGCGG GGGCCTCTGG    780
CGGCTGGTCC TGGCACAGCG CTGGATGGAG CGGCTCAAGA CTGTCGCTGG GTCCAAGATG    840
CAAGGCTTGC TGGAGCGCGT GAACACGGAG ATACACTTTG TCACCAAATG TGCCTTTCAG    900
CCC                                                                 903
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC CAACATCTCC    480
CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT CACTCGCCAG    540
AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT GGGCGGTGGG    600
TCAGGAGGTG GGTCAGGAGG TGGATCCGGA GGTGGCTCAG GGGGAGGTAG TGGTACCCAG    660
GACTGCTCCT TCCAACACAG CCCCATCTCC TCCGACTTCG CTGTCAAAAT CCGTGAGCTG    720
TCTGACTACC TGCTTCAAGA TTACCCAGTC ACCGTGGCCT CCAACCTGCA GGACGAGGAG    780
CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG GCACAGCGCT GGATGGAGCG GCTCAAGACT    840
GTCGCTGGGT CCAAGATGCA AGGCTTGCTG GAGCGCGTGA ACACGGAGAT ACACTTTGTC    900
ACCAAATGTG CCTTTCAGCC C                                             921
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
```

```
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG    480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG    540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT    600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC    660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC    720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT    780
GGGTCAGGAG GTGGATCCGG AGGTACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC    840
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAA                 888
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG    480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG    540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT    600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC    660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC    720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT    780
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCA CCCAGGACTG CTCCTTCCAA    840
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT    900
CAA                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC    480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG    540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT    600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGATCC    780
GGAGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    840
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTG                 888
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAAGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC   480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG   540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT   600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG   660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC   720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA   780
GGAGGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC   840
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC   900
GTG                                                                 903
```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG   480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC   540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG   600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC   660
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGATCCGGAG GTACCCAGGA CTGCTCCTTC   720
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG   780
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAGG ACGAGGAGCT CTGCGGGGGC   840
CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG ATGGAGCGGC TCAAGACT                888
```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG   480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC   540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG   600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC   660
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCACC   720
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG   780
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG   840
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG   900
ACT                                                                 903
```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG 480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC 540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGATCC 600
GGAGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 660
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 720
CAGGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 780
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 840
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTT 888

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG 480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC 540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA 600
GGAGGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC 660
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC 720
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA 780
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG 840
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT 900
CTT 903

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAAGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG 480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGATCCGG AGGTACCCAG 600
GACTGCTCCT TCCAACACAG CCCCATCTCC TCCGACTTCG CTGTCAAAAT CCGTGAGCTG 660
TCTGACTACC TGCTTCAAGA TTACCCAGTC ACCGTGGCCT CCAACCTGCA GGACGAGGAG 720
CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG GCACAGCGCT GGATGGAGCG GCTCAAGACT 780
GTCGCTGGGT CCAAGATGCA AGGCTTGCTG GAGCGCGTGA ACACGGAGAT ACACTTTGTC 840
ACCAAATGTG CCTTTCAGCC CCCCCCCAGC TGTCTTCGCT TCGTCCAG 888

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG 480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGGTCAGG AGGTGGATCC 600
GGAGGTGGCA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC 660
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC 720
CTGCAGGACG AGGAGCTCTG CGGGGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG 780
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG 840
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC 900
CAG 903

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 780
GGATCCGGAG GTACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC CGACTTCGCT 840
GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAA 876

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 660

TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 780
GGATCCGGAG GTGGCACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC 840
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAA 879

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 780
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC 840
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAA 897

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 780
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCT CAGGGGGAGG TAGTGGTACC 840
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG 900
CTGTCTGACT ACCTGCTTCA A 921

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 869 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC 480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG 540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT 600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG 660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC 720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGATCCGG AGGTACTGCT 780
CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG CTGTCTGACT 840
ACCTGCTTCA AGATTACCCA GTCACCGTG 869

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC 480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG 540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT 600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG 660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC 720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGATCCGG AGGTGGCACT 780
GCTCCTTCCA ACACAGCCCC ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG 840
ACTACCTGCT TCAAGATTAC CCAGTCACCG TG 872

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 890 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC 480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG 540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT 600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG 660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC 720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGATCCGG AGGTGGCTCA 780
GGGGGAGGTA GTGGTACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA 840
AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG 890

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120

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CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC     480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG     540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT     600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG     660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC     720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA     780
GGAGGTGGAT CCGGAGGTGG CTCAGGGGGA GGTAGTGGTA GGACTGCTCC TTCCAACACA     840
GCCCCATCTC CTCCGACTTC GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG     900
ATTACCCAGT CACCGTG                                                    917
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(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT      60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT     120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG     480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC     540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG     600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC     660
TCCTCAACCC TGGGCGGTGG ATCCGGAGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC     720
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC     780
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG     840
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACT                               876
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(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT      60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT     120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG     480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC     540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG     600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC     660
TCCTCAACCC TGGGCGGTGG ATCCGGAGGT GGCACCCAGG ACTGCTCCTT CCAACACAGC     720
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT     780
TACCCAGTCA CCGTGGCCTC CAACCTGCAG GACGAGGAGC TCTGCGGGGG CCTCTGGCGG     840
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACT                            879
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG 480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC 540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG 600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC 660
TCCTCAACCC TGGGCGGTGG ATCCGGAGGT GGCTCAGGGG GAGGTAGTGG TACCCAGGAC 720
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT 780
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC 840
TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA CAGCGCTGGA TGGAGCGGCT CAAGACT 897

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG 480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC 540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG 600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC 660
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCTCA 720
GGGGGAGGTA GTGGTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC 780
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC 840
TCCAACCTGC AGGACGAGGA GCTCTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC 900
TGGATGGAGC GGCTCAAGAC T 921

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG 480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC 540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGATCCGG AGGTACCCAG 600
GACTGCTCCT TCCAACACAG CCCCATCTCC TCCGACTTCG CTGTCAAAAT CCGTGAGCTG 660
TCTGACTACC TGCTTCAAGA TTACCCAGTC ACCGTGGCCT CCAACCTGCA GGACGAGGAG 720
CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG GCACAGCGCT GGATGGAGCG GCTCAAGACT 780
GTCGCTGGGT CCAAGATGCA AGGCTTGCTG GAGCGCGTGA ACACGGAGAT ACACTTTGTC 840
ACCAAATGTG CCTTTCAGCC CCCCCCCAGC TGTCTT 876

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGATCCGG AGGTGGCACC    600
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG    660
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG    720
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG    780
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT    840
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTT                           879
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(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGATCCGG AGGTGGCTCA    600
GGGGGAGGTA GTGGTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC    660
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC    720
TCCAACCTGC AGGACGAGGA GCTCTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC    780
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG    840
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTT       897
```

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA    600
GGAGGTGGAT CCGGAGGTGG CTCAGGGGGA GGTAGTGGTA CCCAGGACTG CTCCTTCCAA    660
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT    720
CAAGATTACC CAGTCACCGT GGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC    780
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG    840
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT    900
```

CAGCCCCCCC CCAGCTGTCT T 921

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAAGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG 480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGATCCGGAG GTACCCAGGA CTGCTCCTTC 600
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG 660
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAGG ACGAGGAGCT CTGCGGGGGC 720
CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG ATGGAGCGGC TCAAGACTGT CGCTGGGTCC 780
AAGATGCAAG GCTTGCTGGA GCGCGTGAAC ACGGAGATAC ACTTTGTCAC CAAATGTGCC 840
TTTCAGCCCC CCCCCAGCTG TCTTCGCTTC GTCCAG 876

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAAGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG 480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGATCCGGAG GTGGCACCCA GGACTGCTCC 600
TTCCAACACA GCCCCATCTC CTCCGACTTC GCTGTCAAAA TCCGTGAGCT GTCTGACTAC 660
CTGCTTCAAG ATTACCCAGT CACCGTGGCC TCCAACCTGC AGGACGAGGA GCTCTGCGGG 720
GGCCTCTGGC GGCTGGTCCT GGCACAGCGC TGGATGGAGC GGCTCAAGAC TGTCGCTGGG 780
TCCAAGATGC AAGGCTTGCT GGAGCGCGTG AACACGGAGA TACACTTTGT CACCAAATGT 840
GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC TTCGTCCAG 879

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAAGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG 480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGATCCGGAG GTGGCTCAGG GGGAGGTAGT 600

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GGTACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     660
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG     720
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG     780
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA     840
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAG        897
```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

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GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT      60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT     120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG     480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG     540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGGTCAGG AGGTGGATCC     600
GGAGGTGGCT CAGGGGGAGG TAGTGGTACC CAGGACTGCT CCTTCCAACA CAGCCCCATC     660
TCCTCCGACT TCGCTGTCAA AATCCGTGAG CTGTCTGACT ACCTGCTTCA AGATTACCCA     720
GTCACCGTGG CCTCCAACCT GCAGGACGAG GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC     780
CTGGCACAGC GCTGGATGGA GCGGCTCAAG ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG     840
CTGGAGCGCG TGAACACGGA GATACACTTT GTCACCAAAT GTGCCTTTCA GCCCCCCCCC     900
AGCTGTCTTC GCTTCGTCCA G                                               921
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(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```
GGATCCACCA TGAGCCGCCT GCCCGTCCTG CTCCTGCTCC AACTCCTGGT CCGCCCCGCC      60
ATGTCTACAA ATCAAGATCT GCCTGTGATC AAGTGTGTTT TAATCAATCA TAAGAACAAT     120
GATTCATCAG TGGGGAAGTC ATCATCATAT CCCATGGTAT CAGAATCCCC GGAAGACCTC     180
GGGTGTGCGT TGAGACCCCA GAGCTCAGGG ACAGTGTACG AAGCTGCCGC TGTGGAAGTG     240
GATGTATCTG CTTCCATCAC ACTGCAAGTG CTGGTCGATG CCCCAGGGAA CATTTCCTGT     300
CTCTGGGTCT TTAAGCACAG CTCCCTGAAT TGCCAGCCAC ATTTTGATTT ACAAAACAGA     360
GGAGTTGTTT CCATGGTCAT TTTGAAAATG ACAGAAACCC AAGCTGGAGA ATACCTACTT     420
TTTATTCAGA GTGAAGCTAC CAATTACACA ATATTGTTTA CAGTGAGTAT AAGAAATACC     480
CTGCTTTACA CATTAAGAAG ACCTTACTTT AGAAAAATGG AAAACCAGGA CGCCCTGGTC     540
TGCATATCTG AGAGCGTTCC AGAGCCGATC GTGGAATGGG TGCTTTGCGA TTCACAGGGG     600
GAAAGCTGTA AAGAAGAAAG TCCAGCTGTT GTTAAAAAGG AGGAAAAAGT GCTTCATGAA     660
TTATTTGGGA TGGACATAAG GTGCTGTGCC AGAAATGAAC TGGGCAGGGA ATGCACCAGG     720
CTGTTCACAA TAGATCTAAA TCAAACTCCT CAGACCACAT TGCCACAATT ATTTCTTAAA     780
GTAGGGGAAC CCTTATGGAT AAGGTGCAAA GCTGTTCATG TGAACCATGG ATTCGGGCTC     840
ACCTGGGAAT TAGAAAACAA AGCACTCGAG GAGGGCAACT ACTTTGAGAT GAGTACCTAT     900
TCAACAAACA GAACTATGAT ACGGATTCTG TTTGCTTTTG TATCATCAGT GGCAAGAAAC     960
GACACCGGAT ACTACACTTG TTCCTCTTCA AAGCATCCCA GTCAATCAGC TTTGGTTACC    1020
ATCGTAGAAA AGGGATTTAT AAATGCTACC AATTCAAGTG AAGATTATGA AATTGACCAA    1080
TATGAAGAGT TTTGTTTTTC TGTCAGGTTT AAAGCCTACC CACAAATCAG ATGTACGTGG    1140
ACCTTCTCTC GAAAATCATT TCCTTGTGAG CAAAAGGGTC TTGATAACGG ATACAGCATA    1200
TCCAAGTTTT GCAATCATAA GCACCAGCCA GGAGAATATA TATTCCATGC AGAAAATGAT    1260
GATGCCCAAT TTACCAAAAT GTTCACGCTG AATATAAGAA GGAAACCTCA AGTGCTCGCA    1320
GAAGCATCGG CAAGTCAGGC GTCCTGTTTC TCGGATGGAT ACCCATTACC ATCTTGGACC    1380
TGGAAGAAGT GTTCAGACAA GTCTCCCAAC TGCACAGAAG AGATCACAGA AGGAGTCTGG    1440
AATAGAAAGG CTAACAGAAA AGTGTTTGGA CAGTGGGTGT CGAGCAGTAC TCTAAACATG    1500
AGTGAAGCCA TAAAAGGGTT CCTGGTCAAG TGCTGTGCAT ACAATTCCCT TGGCACATCT    1560
TGTGAGACGA TCCTTTTAAA CTCTCCAGGC CCCTTCCCTT TCATCCAAGA CAACGAATTC    1620
ATCATCCTGG GCCTGTTCGG CCTCCTGCTG TTGCTCACCT GCCTCTGTGG AACTGCCTGG    1680
CTCTGTTGCA GCCCCAACAG GAAGAATCCC CTCTGGCCAA GTGTCCCAGA CCCAGCTCAC    1740
AGCAGCCTGG GCTCCTGGGT GCCCACAATC ATGGAGGAGG ATGCCTTCCA GCTGCCCGGC    1800
CTTGGCACGC CACCCATCAC CAAGCTCACA GTGCTGGAGG AGGATGAAAA GAAGCCGGTG    1860
CCCTGGGAGT CCCATAACAG CTCAGAGACC TGTGGCCTCC CCACTCTGGT CCAGACCTAT    1920
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GTGCTCCAGG GGGACCCAAG AGCAGTTTCC ACCCAGCCCC AATCCCAGTC TGGCACCAGC 1980
GATCAGGTCC TTTATGGGCA GCTGCTGGGC AGCCCCACAA GCCCAGGGCC AGGGCACTAT 2040
CTCCGCTGTG ACTCCACTCA GCCCCTCTTG GCGGGCCTCA CCCCCAGCCC CAAGTCCTAT 2100
GAGAACCTCT GGTTCCAGGC CAGCCCCTTG GGGACCCTGG TAACCCCAGC CCCAAGCCAG 2160
GAGGACGACT GTGTCTTTGG GCCACTGCTC AACTTCCCCC TCCTGCAGGG GATCCGGGTC 2220
CATGGGATGG AGGCGCTGGG GAGCTTC 2247

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCC ACCCAGGACT GCTCCTTCCA ACACAGCCCC 660
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC 720
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG 780
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA GATGCAAGGC 840
TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCCTT TCAGCCCCCC 900
CCCAGCTGTC TTCGCTTCGT CCAGACCAAC ATCTCCCGCC TCCTGCAGGA GACCTCCGAG 960
CAGCTGGTGG CGCTGAAGCC CTGGATCACT CGCCAGAACT TCTCCCGGTG CCTGGAGCTG 1020
CAGTGTCAGC CCGACTCCTC AACCCTG 1047

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 942 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GCCACTCAGG ACTGCTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GAACCGTCTG GTCCAATCTC TACTATCAAC 480
CCGTCTCCTC CGTCTAAAGA ATCTCATAAA TCTCCAAACA TGGCTACCCA GGACTGCTCC 540
TTCCAACACA GCCCCATCTC CTCCGACTTC GCTGTCAAAA TCCGTGAGCT GTCTGACTAC 600
CTGCTTCAAG ATTACCCAGT CACCGTGGCC TCCAACCTGC AGGACGAGGA GCTCTGCGGG 660
GGCCTCTGGC GGCTGGTCCT GGCACAGCGC TGGATGGAGC GGCTCAAGAC TGTCGCTGGG 720
TCCAAGATGC AAGGCTTGCT GGAGCGCGTG AACACGGAGA TACACTTTGT CACCAAATGT 780
GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC TTCGTCCAGA CCAACATCTC CCGCCTCCTG 840
CAGGAGACCT CCGAGCAGCT GGTGGCGCTG AAGCCCTGGA TCACTCGCCA GAACTTCTCC 900
CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC TCCTCAACCC TG 942

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GCCACCCAGG ACTGCTCCTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60

CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCATGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GAACCGTCTG GTCCAATCTC TACTATCAAC 480
CCGTCTCCTC CGTCTAAAGA ATCTCATAAA TCTCCAAACA TGGCTACACC ATTAGGCCCT 540
GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC AAGTGCTTAG AGCAAGTGAG GAAGATCCAG 600
GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG 660
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC 720
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCCTCTAC 780
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA 840
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA 900
ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG 960
CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC 1020
CGCGTTTTAC GCCACCTTGC GCAGCCC 1047

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCC ACTCAGGACT GCTCTTTTCA ACACAGCCCC 660
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC 720
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG 780
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA GATGCAAGGC 840
TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCCTT TCAGCCCCCC 900
CCCAGCTGTC TTCGCTTCGT CCAGACCAAC ATCTCCCGCC TCCTGCAGGA GACCTCCGAG 960
CAGCTGGTGG CGCTGAAGCC CTGGATCACT CGCCAGAACT TCTCCCGGTG CCTGGAGCTG 1020
CAGTGTCAGC CCGACTCCTC AACCCTGTAC GTAGAGGGCG GTGGAGGCTC CCCGGGTGAA 1080
CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC TCATAAATCT 1140
CCAAACATGG CTACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC CGACTTCGCT 1200
GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAAGATT ACCCAGTCAC CGTGGCCTCC 1260
AACCTGCAGG ACGAGGAGCT CTGCGGGGGC CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG 1320
ATGGAGCGGC TCAAGACTGT CGCTGGGTCC AAGATGCAAG GCTTGCTGGA GCGCGTGAAC 1380
ACGGAGATAC ACTTTGTCAC CAAATGTGCC TTTCAGCCCC CCCCCAGCTG TCTTCGCTTC 1440
GTCCAGACCA ACATCTCCCG CCTCCTGCAG GAGACCTCCG AGCAGCTGGT GGCGCTGAAG 1500
CCCTGGATCA CTCGCCAGAA CTTCTCCCGG TGCCTGGAGC TGCAGTGTCA GCCCGACTCC 1560
TCAACCCTG 1569

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT 60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT 120
CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CACTCAGGAC TGCTCTTTTC AACACAGCCC CATCTCCTCC 480
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC 540

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GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA     600
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG     660
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT     720
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG     780
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG     840
CCCGACTCCT CAACCCTGTA CGTAGAGGGC GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT     900
CCAATCTCTA CTATCAACCC GTCTCCTCCG TCTAAAGAAT CTCATAAATC TCCAAACATG     960
GCTACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC    1020
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    1080
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG    1140
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA    1200
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC    1260
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC    1320
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG    1380
```

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```
GCCACTCAGG ACTGCTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC      60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG     120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG     180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA     240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC     300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC     360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG
1569    420 TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GAACCGTCTG GTCCAATCTC
TACTATCAAC    480 CCGTCTCCTC CGTCTAAAGA ATCTCATAAA TCTCCAAACA TGGCTACACC
ATTGGGCCCT    540 GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC AAGTCTTTAG AGCAAGTGAG
AAAGATCCAG    600 GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG
CCACCCCGAG    660 GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG
CTCCTGCCCC    720 AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT
TTTCCTCTAC    780 CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC
CTTGGACACA    840 CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA
AGAACTGGGA    900 ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC
TGCTTTCCAG    960 CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA GCTTCCTGGA
GGTGTCGTAC   1020 CGCGTTCTAC GCCACCTTGC GCAGCCCTAC GTAGAGGGCG GTGGAGGCTC
CCCGGGTGAA   1080 CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC
TCATAAATCT   1140 CCAAACATGG CTACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC
CGACTTCGCT   1200 GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAAGATT ACCCAGTCAC
CGTGGCCTCC   1260 AACCTGCAGG ACGAGGAGCT CTGCGGGGGC CTCTGGCGGC TGGTCCTGGC
ACAGCGCTGG   1320 ATGGAGCGGC TCAAGACTGT CGCTGGGTCC AAGATGCAAG GCTTGCTGGA
GCGCGTGAAC   1380 ACGGAGATAC ACTTTGTCAC CAAATGTGCC TTTCAGCCCC CCCCCAGCTG
TCTTCGCTTC   1440 GTCCAGACCA ACATCTCCCG CCTCCTGCAG GAGACCTCCG AGCAGCTGGT
GGCGCTGAAG   1500 CCCTGGATCA CTCGCCAGAA CTTCTCCCGG TGCCTGGAGC TGCAGTGTCA
GCCCGACTCC   1560 TCAACCCTG
1569
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```
GGCCACTCAG GACTGCTCTT TTCAACACAG CCCCATCTCC TCCGACTTCG CTGTCAAAAT      60
CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC ACCGTGGCCT CCAACCTGCA     120
GGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG GCACAGCGCT GGATGGAGCG     180
GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG GAGCGCGTGA ACACGGAGAT     240
ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC TGTCTTCGCT TCGTCCAGAC     300
CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG GTGGCGCTGA AGCCCTGGAT     360
CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT CAGCCCGACT CCTCAACCCT     420
GTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGGTGGTTCT GGCGGCGGCT CCAACATGGC     480
TACACCATTG GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA     540
AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA     600
GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC     660
```

CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG 720
CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG 780
TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA 840
GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT 900
CGCCTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT 960
CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCG 1003

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 780
GGGTCAGGAG GTGGATCCGG AGGTACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC 840
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAA 888

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 540
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 600
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 660
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 720
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 780
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCA CCCAGGACTG CTCCTTCCAA 840
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT 900
CAA 903

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240

```
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC     480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG     540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT     600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG     660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC     720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGATCC     780
GGAGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA     840
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTG                  888
```

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT      60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT     120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAAGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC     480
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG     540
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT     600
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG     660
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC     720
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA     780
GGAGGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC     840
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC     900
GTG                                                                   903
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT      60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT     120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT     180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT     240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC     300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC     360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG     480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC     540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG     600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC     660
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGATCCGGAG GTACCCAGGA CTGCTCCTTC     720
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG     780
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAGG ACGAGGAGCT CTGCGGGGGC     840
CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG ATGGAGCGGC TCAAGACT                  888
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG    480
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC    540
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG    600
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC    660
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCACC    720
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG    780
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG    840
GAGCTCTGCG GGGGCCTCTG GCGGCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG    900
ACT                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGATCC    600
GGAGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    660
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    720
CAGGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG    780
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    840
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTT                 888
```

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC CCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    480
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    540
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA    600
GGAGGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC    660
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC    720
GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA    780
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG    840
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT    900
CTT                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAAGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG   480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG   540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGATCCGG AGGTACCCAG   600
GACTGCTCCT TCCAACACAG CCCCATCTCC TCCGACTTCG CTGTCAAAAT CCGTGAGCTG   660
TCTGACTACC TGCTTCAAGA TTACCCAGTC ACCGTGGCCT CCAACCTGCA GGACGAGGAG   720
CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG GCACAGCGCT GGATGGAGCG GCTCAAGACT   780
GTCGCTGGGT CCAAGATGCA AGGCTTGCTG GAGCGCGTGA ACACGGAGAT ACACTTTGTC   840
ACCAAATGTG CCTTTCAGCC CCCCCCCAGC TGTCTTCGCT TCGTCCAG               888
```

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC CACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG   480
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG   540
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGGTCAGG AGGTGGATCC   600
GGAGGTGGCA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC   660
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC   720
CTGCAGGACG AGGAGCTCTG CGGGGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG   780
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG   840
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC   900
CAG                                                                903
```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT    60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT   120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT   180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT   240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC   300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC   360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT   420
CATAAATCTC CAAACATGGC TTCTAATCTG CAAGATGAAG AGCTGTGCGG GGGCCTCTGG   480
CGGCTGGTCC TGGCACAGCG CTGGATGGAG CGGCTCAAGA CTGTCGCTGG GTCCAAGATG   540
CAAGGCTTGC TGGAGCGCGT GAACACGGAG ATACACTTTG TCACCAAATG TGCCTTTCAG   600
CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC   660
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG   720
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA   780
GGTGGATCCG GAGGTGGCTC AGGGGGAGGT AGTGGTACCC AGGACTGCTC CTTCCAACAC   840
AGCCCCATCT CCTCCGACTT CGCTGTCAAA ATCCGTGAGC TGTCTGACTA CCTGCTTCAA   900
```

GATTACCCAG TCACCGTGGC C 921

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC CAACCTGCAA GATGAAGAGC TGTGTGGGGG CCTCTGGCGG 480
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA 540
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC 600
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC 660
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG 720
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GCGGTGGGT CAGGAGGTGG GTCAGGAGGT 780
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC 840
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 900
TACCCAGTCA CCGTGGCCTC C 921

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCTGCAGGAT GAGGAACTGT GCGGCGGCCT CTGGCGGCTG 480
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA GATGCAAGGC 540
TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCTTT TCAGCCCCCC 600
CCCAGCTGTC TTCGCTTCGT CCAGACCAAC ATCTCCCGCC TCCTGCAGGA GACCTCCGAG 660
CAGCTGGTGG CGCTGAAGCC CTGGATCACT CGCCAGAACT TCTCCCGGTG CCTGGAGCTG 720
CAGTGTCAGC CCGACTCCTC AACCCTGGGC GGTGGGTCAG GAGGTGGGTC AGGAGGTGGA 780
TCCGGAGGTG GCTCAGGGGG AGGTAGTGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC 840
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC 900
CCAGTCACCG TGGCCTCCAA C 921

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCAAGATGAA GAGCTGTGTG GTGGTCTCTG GCGGCTGGTC 480

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CTGGCACAGC GCTGGATGGA GCGGCTCAAG ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG    540
CTGGAGCGCG TGAACACGGA GATACACTTT GTCACCAAAT GTGCCTTTCA GCCCCCCCCC    600
AGCTGTCTTC GCTTCGTCCA GACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG    660
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG    720
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGGTCAGG AGGTGGATCC    780
GGAGGTGGCT CAGGGGGAGG TAGTGGTACC CAGGACTGCT CCTTCCAACA CAGCCCCATC    840
TCCTCCGACT TCGCTGTCAA AATCCGTGAG CTGTCTGACT ACCTGCTTCA AGATTACCCA    900
GTCACCGTGG CCTCCAACCT G                                              921
```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC TGAAGAACTG TGTGGTGGTC TGTGGCGGCT GGTCCTGGCA    480
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG    540
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT    600
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG    660
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG    720
CCCGACTCCT CAACCCTGGG CGGTGGGTCA GGAGGTGGGT CAGGAGGTGG ATCCGGAGGT    780
GGCTCAGGGG GAGGTAGTGG TACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC    840
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAAGATTA CCCAGTCACC    900
GTGGCCTCCA ACCTGCAGGA C                                              921
```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT    120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT    180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT    240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC    300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC    360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT    420
CATAAATCTC CAAACATGGC TGAGCTGTGT GGTGGCCTGT GGCGTCTGGT CCTGGCACAG    480
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC    540
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT    600
CGCTTCGTCC AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG    660
CTGAAGCCCT GGATCACTCG CCAAAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC    720
GACTCCTCAA CCCTGGGCGG TGGGTCAGGA GGTGGGTCAG GAGGTGGATC CGGAGGTGGC    780
TCAGGGGGAG GTAGTGGTAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC    840
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG    900
GCCTCCAACC TGCAGGACGA G                                              921
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT     60
```

TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCTGTGCGGT GGTCTGTGGC GTCTGGTCCT GGCACAGCGC 480
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG 540
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC 600
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG 660
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC 720
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCTCA 780
GGGGGAGGTA GTGGTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC 840
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC 900
TCCAACCTGC AGGACGAGGA G 921

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TTCTAATCTG CAAGATGAAG AGCTGTGCGG GGGCCTCTGG 480
CGGCTGGTCC TGGCACAGCG CTGGATGGAG CGGCTCAAGA CTGTCGCTGG GTCCAAGATG 540
CAAGGCTTGC TGGAGCGCGT GAACACGGAG ATACACTTTG TCACCAAATG TGCCTTTCAG 600
CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC 660
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG 720
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA 780
GGTGGATCCG GAGGTGGCTC AGGGGGAGGT AGTGGTACCC AGGACTGCTC CTTCCAACAC 840
AGCCCCATCT CCTCCGACTC CGCTGTCAAA ATCCGTGAGC TGTCTGACTA CCTGCTTCAA 900
GATTACCCAG TCACCGTGGC C 921

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCAAGATGAA GAACTGTGCG GTGGTCTCTG GCGGCTGGTC 480
CTGGCACAGC GCTGGATGGA GCGGCTCAAG ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG 540
CTGGAGCGCG TGAACACGGA GATACACTTT GTCACCAAAT GTGCCTTTCA GCCCCCCCCC 600
AGCTGTCTTC GCTTCGTCCA GACCAACATC TCCCGCCTCC TGCGGGAGAC CTCCGAGCAG 660
CCGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 720
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGGTCAGG AGGTGGATCC 780
GGAGGTGGCT CAGGGGGAGG TAGTGGTACC CAGGACTGCT CCTTCCAACA CAGCCCCATC 840
TCCTCCGACT TCGCTGTCAA AATCCGTGAG CTGTCTGACT ACCTGCTTCA AGATTACCCA 900
GTCACCGTGG CCTCCAACCT G 921

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTAACCCT 60
TTGCTGGACC CGAACAACCT CAATTCTGAA GACATGGATA TCCTGATGGA ACGAAACCTT 120
CGAACTCCAA ACCTGCTCGC ATTCGTAAGG GCTGTCAAGC ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TCTGTGCGGT GGTCTGTGGC GTCTGGTCCT GGCACAGCGC 480
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG 540
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC 600
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG 660
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCGGCCCGAC 720
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCTCA 780
GGGGGAGGTA GTGGTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC 840
GCTGTCAAGA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC 900
TCCAACCTGC AGGACGAGGA G 921

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGTA CGTAGAGGGC 480
GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG 540
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT 600
ATACATCACT TAAAGAGACC ACCTAACCCT TTGCTGGACC CGAACAACCT CAATTCTGAA 660
GACATGGATA TCCTGATGGA ACGAAACCTT CGAACTCCAA ACCTGCTCGC ATTCGTAAGG 720
GCTGTCAAGC ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA 780
TGTCTGCCCT CTGCCACGGC CGCACCCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC 840
TGGCAAGAAT TCCGGGAAAA ACTGACGTTC TATCTGGTTA CCCTTGAGCA AGCGCAGGAA 900
CAACAG 906

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GCGGATGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAGGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGATCCGGA GGTACCCAGG ACTGCTCCTT CCAACACAGC 360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 420
TACCCAGTCA CCGTGGCCTC CAACCTGCAG TACGTAGAGG GCGGTGGAGG CTCCCCGGGT 480
GAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA 540
TCTCCAAACA TGGCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA 600
CCACCTAACC CTTTGCTGGA CCCGAACAAC CTCAATTCTG AAGACATGGA TATCCTGATG 660
GAACGAAACC TTCGAACTCC AAACCTGCTC GCATTCGTAA GGGCTGTCAA GCACTTAGAA 720
AATGCATCAG GTATTGAGGC AATTCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG 780
GCCGCACCCT CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA 840
AAACTGACGT TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAACAG 888

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

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GCCGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGAAC CCAGGACTGC    360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC    420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

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GCAGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT    360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA    600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC    660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG    720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT    780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC    840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT    900
GAGCAAGCGC AGGAACAACA G                                              921
```

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```
GCGGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCCTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CCTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGAAC CCAGGACTGC    360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC    420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
```

```
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```
GCGGATGAGG AGCTGTGTGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGGG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT    360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA    600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC    660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG    720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT    780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC    840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT    900
GAGCAAGCGC AGGAACAACA G                                              921
```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```
GGCCGATTAC CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT     60
CTGGCGGCTG GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA    120
GATGCAAGGC TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCCTT    180
TCAGCCCCCC CCCAGCTGTC TTCGCTTCGT CCAGACCAAC ATCTCCCGCC TCCTGCAGGA    240
GACCTCCGAG CAGCTGGTGG CGCTGAAGCC CTGGATCACT CGCCAGAACT TCTCCCGGTG    300
CCTGGAGCTG CAGTGTCAGC CCGACTCCTC AACCCTGGGC GGTGGGTCAG GAGGTGGGTC    360
AGGAGGTGGA TCCGGAGGTG GCACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC    420
CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAATACG TAGAGGGCGG    480
TGGAGGCTCC CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC    540
TAAAGAATCT CATAAATCTC CAAACATGGC TAACTGCTCT ATAATGATCG ATGAAATTAT    600
ACATCACTTA AAGAGACCAC CTAACCCTTT GCTGGACCCG AACAACCTCA ATTCTGAAGA    660
CATGGATATC CTGATGGAAC GAAACCTTCG AACTCCAAAC CTGCTCGCAT TCGTAAGGGC    720
TGTCAAGCAC TTAGAAAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG    780
TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG CAGGTGACTG    840
GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC CTTGAGCAAG CGCAGGAACA    900
ACAG                                                                 904
```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```
GCCGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA     60
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG    120
```

```
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT    180
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG    240
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG    300
CCCGACTCCT CAACCCTGGG CGGTGGGTCA GGAGGTGGGT CAGGAGGTGG ATCCGGAGGT    360
GGCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC    420
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```
GCCGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT     60
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC    120
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC    180
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT    240
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCA CCCAGGACTG CTCCTTCCAA    300
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT    360
CAGGATTACC CAGTCACCGT GGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC    420
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA     60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC    120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC    180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGGGCGG TGGGTCAGGA    240
GGTGGGTCAG GAGGTGGATC CGGAGGTGGC ACCCAGGACT GCTCCTTCCA ACACAGCCCC    300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC    360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG    420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGCTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```
GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC     60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG    120
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA    180
GGTGGATCCG GAGGTGGCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC    240
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG    300
GCCTCCAACC TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG    360
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC    420
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```
GCCACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC     60
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    120
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CACCCAGGAC    180
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTYGCTG TCAAAATCCG TGAGCTGTCT    240
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC    300
TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA CAGCGCTGGA TGGAGCGGCT CAAGACTGTC    360
GCTGGGTCCA AGATGCAAGG CTTGCTGGAG CGCGTGAACA CGGAGATACA CTTTGTCACC    420
AAATGTGCCT TTCAGCCCCC CCCCAGCTGT CTTCGCTTCG TCCAGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```
GCCCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG     60
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG    120
CCCGACTCCT CAACCCTGGG CGGTGGGTCA GGAGGTGGGT CAGGAGGTGG ATCCGGAGGT    180
GGCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC    240
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    300
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG    360
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AACGCGTGAA CACGGAGATA    420
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTTTTTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```
GCTTCAAATC TGCAGGATGA AGAGCTGTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG      60
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC     120
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT     180
CGCTTCGTCC AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG     240
CTGAAGCCCT GGATCACTCG CCAGAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC     300
GACTCCTCAA CCCTGGGCGG TGGGTCAGGA GGTGGGTCAG GAGGTGGATC CGGAGGTGGC     360
TCAGGGGGAG GTAGTGGTAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC     420
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG     480
GCCTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC     540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA     600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC     660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG     720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT     780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC     840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT     900
GAGCAAGCGC AGGAACAACA G                                               921
```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```
GCTAATCTGC AAGATGAGGA GCTGTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC      60
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG     120
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC     180
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG     240
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC     300
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCTCA     360
GGGGGAGGTA GTGGTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC     420
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC     480
TCCTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC     540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA     600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC     660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG     720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT     780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC     840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT     900
GAGCAAGCGC AGGAACAACA G                                               921
```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```
GCGCTGCAGG ATGAAGAGCT GTGTGGCGGC CTCTGGCGGC TGGTCCTGGC ACAGCGCTTG      60
ATGGAGCGGC TCAAGACTGT CGCTGGGTCC AAGATGCAAG GCTTGCTGGA GCGCGTGAAC     120
ACGGAGATAC ACTTTGTCAC CAAATGTGCC TTTCAGCCCC CCCCCAGCTG TCTTCGCTTC     180
GTCCAGACCA ACATCTCCCG CCTCCTGCAG GAGACCTCCG AGCAGCTGGT GGCGCTGAAG     240
CCCTGGATCA CTCGCCAGAA CTTCTCCCGG TGCCTGGAGC TGCAGTGTCA GCCCGACTCC     300
TCAACCCTGG GCGGTGGGTC AGGAGGTGGG TCAGGAGGTG GATCCGGAGG TGGCTCAGGG     360
GGAGGTAGTG GTACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC CGACTTCGCT     420
GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAAGATT ACCCAGTCAC CGTGGCCTCC     480
AACTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC     540
```

AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA 600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC 660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG 720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT 780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC 840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 900
GAGCAAGCGC AGGAACAACA G 921

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GCGCAAGATG AGGAACTGTG TGGTGGTCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG 60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG 120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC 180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC 240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA 300
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CTCAGGGGGA 360
GGTAGTGGTA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC 420
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC 480
CTGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CCCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA 600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC 660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG 720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT 780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC 840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 900
GAGCAAGCGC AGGAACAACA G 921

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GCTGAAGAAC TGTGTGGTGG CCTGTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 60
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 120
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 180
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 240
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 300
GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT GGATCCGGAG GTGGCTCAGG GGGAGGTAGT 360
GGTACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 420
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 480
GACTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA 600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC 660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG 720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT 780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC 840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 900
GAGCAAGCGC AGGAACAACA G 921

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GCTCTGTGCG GTGGCCTGTG GCGTCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 60
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 120

GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 180
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 240
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 300
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCT CAGGGGGAGG TAGTGGTACC 360
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG 420
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA 600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC 660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG 720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT 780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC 840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 900
GAGCAAGCGC AGGAACAACA G 921

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GCACTGTGTG GTGGTCTGTG GCGTCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 60
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 120
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 180
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 240
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT 300
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCT CAGGGGGAGG TAGTGGTACC 360
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG 420
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA 600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC 660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG 720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT 780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC 840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 900
GAGCAAGCGC AGGAACAACA G 921

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GCTCTGTGTG GCGGTCTGTG GCGTCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 60
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 120
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 180
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 240
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCGGCCCG ACTCCTCAAC CCTGGGCGGT 300
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCT CAGGGGGAGG TAGTGGTACC 360
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA GATCCGTGAG 420
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG 480
GAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA 600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC 660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG 720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT 780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC 840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT 900
GAGCAAGCGC AGGAACAACA G 921

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA     60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC    120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC    180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGGGCGG TGGGTCAGGA    240
GGTGGGTCAG GAGGTGGATC CGGAGGTGGC ACCCAGGACT GCTCCTTCCA ACACAGCCCC    300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC    360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG    420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGCTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```
GCTCAAGATG ATGAGCTGTG TGGTGGTCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG     60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG    120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGCGGTGGTT CTGGCGGAGG ATCCGGCGGC    360
GGAAGCGGAG GTGGCTCTGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC    420
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT    480
TACCCAGTCA CCGTGGCCTC CAACCTGTAC GTAGAGGGCG GTGGAGGCTC CCCGGGTGAA    540
CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC TCATAAATCT    600
CCAAACATGG CTAACTGCTC TATAATGATC GATGAAATTA TACATCACTT AAAGAGACCA    660
CCTAACCCTT TGCTGGACCC GAACAACCTC AATTCTGAAG ACATGGATAT CCTGATGGAA    720
CGAAACCTTC GAACTCCAAA CCTGCTCGCA TTCGTAAGGG CTGTCAAGCA CTTAGAAAAT    780
GCATCAGGTA TTGAGGCAAT TCTTCGTAAT CTCCAACCAT GTCTGCCCTC TGCCACGGCC    840
GCACCCTCTC GACATCCAAT CATCATCAAG GCAGGTGACT GGCAAGAATT CCGGGAAAAA    900
CTGACGTTCT ATCTGGTTAC CCTTGAGCAA GCGCAGGAAC AACAG                    945
```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```
GCCCAAGATG AAGAACTGTG TGGTGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG     60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG    120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGCCGC CACCGTGGAG CCCGCGTCCA CTCGGCGCCA CCGCACCGAC CACCCAGGAC    360
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT    420
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA    600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC    660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT    720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT    780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG    840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA    900
CAG                                                                  903
```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```
GCCCAAGATG AAGAACTGTG TGGTGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG     60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG    120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGCCGC CACCGTGGAG CCCGCGTCCA CTCGGCGCCA CCGCACCGAC CGCTGGACAA    360
CCGCCTCTGA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC    420
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC    480
CTGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAA CTGCTCTATA    600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC    660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG    720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT    780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC    840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT    900
GAGCAAGCGC AGGAACAACA G                                              921
```

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG TCTGTGGCGG    660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA    720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC    780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC    840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG    900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT    960
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC   1020
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT   1080
TACCCAGTCA CCGTGGCCTC CAACCTGCAG                                    1110
```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
```

```
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCA AATCTGCAAG ACGAGGAGCT GTGCGGGGGC    660
CTCTGGCGGC TGGTCCTGGC ACAGCGCTGG ATGGAGCGGC TCAAGACTGT CGCTGGGTCC    720
AAGATGCAAG GCTTGCTGGA GCGCGTGAAC ACGGAGATAC ACTTTGTCAC CAAATGTGCC    780
TTTCAGCCCC CCCCCAGCTG TCTTCGCTTC GTCCAGATCA ACATCTCCCG CCTCCTGCAG    840
GAGACCTCCG AGCAGCTGGT GGCGCTGAAG CCCTGGATCA CTCGCCAGAA CTTCTCCCGG    900
TGCCTGGAGC TGCAGTGTCA GCCCGACTCC TCAACCCTGG GCGGTGGGTC AGGAGGTGGG    960
TCAGGAGGTG GATCCGGAGG TGGCTCAGGG GGAGGTAGTG GTACCCAGGA CTGCTCCTTC   1020
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG   1080
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC    660
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC    720
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG    780
GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT GGATCCGGAG GTGGCTCAGG GGGAGGTAGT    840
GGTACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC    900
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    960
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG   1020
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA   1080
CACTTTGTCA CCAAATGTGC CTTTCAGCCC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT CTGCAGGATG AGGAACTGTG CGGCGGCCTC    660
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG    720
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT    780
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    840
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC    900
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA    960
GGAGGTGGAT CCGGAGGTGG CTCAGGGGGA GGTAGTGGTA CCCAGGACTG CTCCTTCCAA   1020
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT   1080
CAAGATTACC CAGTCACCGT GGCCTCCAAC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT CAAGATGAAG AGCTGTGTGG TGGTCTCTGG    660
CGGCTGGTCC TGGCACAGCG CTGGATGGAG CGGCTCAAGA CTGTCGCTGG GTCCAAGATG    720
CAAGGCTTGC TGGAGCGCGT GAACACGGAG ATACACTTTG TCACCAAATG TGCCTTTCAG    780
CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC    840
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG    900
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA    960
GGTGGATCCG GAGGTGGCTC AGGGGGAGGT AGTGGTACCC AGGACTGCTC CTTCCAACAC   1020
AGCCCCATCT CCTCCGACTT CGCTGTCAAA ATCCGTGAGC TGTCTGACTA CCTGCTTCAA   1080
GATTACCCAG TCACCGTGGC CTCCAACCTG                                    1110
```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT GAAGAACTGT GTGGTGGTCT GTGGCGGCTG    660
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA GATGCAAGGC    720
TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCCTT TCAGCCCCCC    780
CCCAGCTGTC TTCGCTTCGT CCAGACCAAC ATCTCCCGCC TCCTGCAGGA GACCTCCGAG    840
CAGCTGGTGG CGCTGAAGCC CTGGATCACT CGCCAGAACT TCTCCCGGTG CCTGGAGCTG    900
CAGTGTCAGC CCGACTCCTC AACCCTGGGC GGTGGGTCAG GAGGTGGGTC AGGAGGTGGA    960
TCCGGAGGTG GCTCAGGGGG AGGTAGTGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC   1020
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC   1080
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
```

GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCT GAGCTGTGTG GTGGCCTGTG GCGTCTGGTC 660
CTGGCACAGC GCTGGATGGA GCGGCTCAAG ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG 720
CTGGAGCGCG TGAACACGGA GATACACTTT GTCACCAAAT GTGCCTTTCA GCCCCCCCCC 780
AGCTGTCTTC GCTTCGTCCA GACCAACATC TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG 840
CTGGTGGCGC TGAAGCCCTG GATCACTCGC CAGAACTTCT CCCGGTGCCT GGAGCTGCAG 900
TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT GGGTCAGGAG GTGGGTCAGG AGGTGGATCC 960
GGAGGTGGCT CAGGGGGAGG TAGTGGTACC CAGGACTGCT CCTTCCAACA CAGCCCCATC 1020
TCCTCCGACT TCGCTGTCAA AATCCGTGAG CTGTCTGACT ACCTGCTTCA AGATTACCCA 1080
GTCACCGTGG CCTCCAACCT GCAGGACGAG 1110

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCT CTGTGCGGTG GTCTGTGGCG TCTGGTCCTG 660
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 720
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 780
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 840
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 900
CAGCCCGACT CCTCAACCCT GGGCGGTGGG TCAGGAGGTG GGTCAGGAGG TGGATCCGGA 960
GGTGGCTCAG GGGGAGGTAG TGGTACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC 1020
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC 1080
ACCGTGGCCT CCAACCTGCA GGACGAGGAG 1110

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG GCTGTGGCGG 660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA 720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC 780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC 840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG 900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG CCGCCACCGT GGAGCCCGCG TCCACTCGGC 960
GCCACCGCAC CGACCACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC 1020
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC 1080
TCCAACCTGC AG 1092

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1134 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG GCTGTGGCGG    660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA    720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC    780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC    840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG    900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGCGGT    960
GGTTCTGGCG GAGGATCCGG CGGCGGAAGC GGAGGTGGCT CTGGGGGAGG TAGTGGTACC   1020
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG   1080
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAG         1134
```

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1110 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG GCTGTGGCGG    660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA    720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC    780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC    840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG    900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG CCGCCACCGT GGAGCCCGCG TCCACTCGGC    960
GCCACCGCAC CGACCGCTGG ACAACCGCCT CTGACCCAGG ACTGCTCCTT CCAACACAGC   1020
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT   1080
TACCCAGTCA CCGTGGCCTC CAACCTGCAG                                    1110
```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 465 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```
GCCGATTACC CAGTCACCGT GGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC     60
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACTGTCGC TGGGTCCAAG    120
ATGCAAGGCT TGCTGGAGCG CGTGAACACG GAGATACACT TTGTCACCAA ATGTGCCTTT    180
CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC CAGACCAACA TCTCCCGCCT CCTGCAGGAG    240
```

```
ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC TGGATCACTC GCCAGAACTT CTCCCGGTGC     300
CTGGAGCTGC AGTGTCAGCC CGACTCCTCA ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA     360
GGAGGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AACACAGCCC CATCTCCTCC     420
GACTTCGCTG TCAAAATCCG TGAGCTGTCT GACTACCTGC TTCAA                     465
```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
GCCGCCTCCA ACCTGCAGGA CGAGGAGCTC TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA      60
CAGCGCTGGA TGGAGCGGCT CAAGACTGTC GCTGGGTCCA AGATGCAAGG CTTGCTGGAG     120
CGCGTGAACA CGGAGATACA CTTTGTCACC AAATGTGCCT TTCAGCCCCC CCCCAGCTGT     180
CTTCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG     240
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG     300
CCCGACTCCT CAACCCTGGG CGGTGGGTCA GGAGGTGGGT CAGGAGGTGG ATCCGGAGGT     360
GGCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     420
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTG                     465
```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```
GCCGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT      60
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC     120
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC     180
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT     240
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCA CCCAGGACTG CTCCTTCCAA     300
CACAGCCCCA TCTCCTCCGA CTTCGCTGTC AAAATCCGTG AGCTGTCTGA CTACCTGCTT     360
CAAGATTACC CAGTCACCGT GGCCTCCAAC CTGCAGGACG AGGAGCTCTG CGGGGGCCTC     420
TGGCGGCTGG TCCTGGCACA GCGCTGGATG GAGCGGCTCA AGACT                     465
```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA      60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC     120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC     180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGGGCGG TGGGTCAGGA     240
GGTGGGTCAG GAGGTGGATC CGGAGGTGGC ACCCAGGACT GCTCCTTCCA ACACAGCCCC     300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC     360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG     420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGG                     465
```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```
GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC      60
```

TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG 120
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA 180
GGTGGATCCG GAGGTGGCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC 240
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG 300
GCCTCCAACC TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG 360
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC 420
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCC 465

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GCCCGCTTCG TCCAGACCAA CATCTCCCGC CTCCTGCAGG AGACCTCCGA GCAGCTGGTG 60
GCGCTGAAGC CCTGGATCAC TCGCCAGAAC TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG 120
CCCGACTCCT CAACCCTGGG CGGTGGGTCA GGAGGTGGGT CAGGAGGTGG ATCCGGAGGT 180
GGCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 240
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 300
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 360
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 420
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTT 465

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GCCACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC 60
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA 120
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CACCCAGGAC 180
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT 240
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC 300
TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA CAGCGCTGGA TGGAGCGGCT CAAGACTGTC 360
GCTGGGTCCA AGATGCAAGG CTTGCTGGAG CGCGTGAACA CGGAGATACA CTTTGTCACC 420
AAATGTGCCT TTCAGCCCCC CCCCAGCTGT CTTCGCTTCG TCCAG 465

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTGGGC 600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT GAGAAAGATC 660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1080

```
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                     1110
```

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```
GCAGATGAAG AACTGTGTGG GGGACTGTGG CGTCTGGTCC TGGCACAGCG CTGGATGGAG      60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG     120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG     180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG     240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC     300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT     360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA     420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG     480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC     540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC     600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC     660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC     720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC     780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC     840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC     900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG     960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC    1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG    1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                     1110
```

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```
GCTGATGAAG AACTGTGTGG TGGGCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG      60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG     120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG     180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG     240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC     300
CTGCCGCCAC CGTGGAGCCC GCGTCCACTC GGCGCCACCG CACCGACCGC TGGACAACCG     360
CCTCTGACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA     420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG     480
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GGTGGTTCTG GCGGCGGCTC CAACATGGCT     540
ACACCATTGG GCCCTGCCAG CTCCCTGCCC CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA     600
GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG     660
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC     720
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC     780
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT     840
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG     900
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC     960
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC    1020
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CG                       1062
```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1089 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```
GCTGATGAAG AACTGTGTGG TGGGCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG      60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG     120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG     180
```

ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGC GGTGGTTCTG GCGGAGGATC CGGCGGCGGA 360
AGCGGAGGTG GCTCTGGGGG AGGTAGTGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC 420
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC 480
CCAGTCACCG TGGCCTCCAA CCTGCAGTAC GTAGAGGGCG GTGGAGGCTC CCCGGGTGGT 540
GGTTCTGGCG GCGGCTCCAA CATGGCTACA CCATTGGGCC CTGCCAGCTC CCTGCCCCAG 600
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC 660
CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA 720
CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG 780
GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC 840
CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGGACA CACTGCAGCT GGACGTCGCC 900
GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG 960
CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC 1020
CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT 1080
GCGCAGCCG 1089

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GCTGATGAAG AACTGTGTGG TGGGCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGCCGCCAC CGTGGAGCCC GCGTCCACTC GGCGCCACCG CACCGACCAC CCAGGACTGC 360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGTACGTAGA GGGCGGTGGA 480
GGCTCCCCGG GTGGTGGTTC TGGCGGCGGC TCCAACATGG CTACACCATT GGGCCCTGCC 540
AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGRAA GATCCAGGGC 600
GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCGAGGAG 660
CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC 720
CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG 780
GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCCACCTT GGACACACTG 840
CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGAATG 900
GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC 960
CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT CTGCAGAGCT TCCTGGAGGT GTCGTACCGC 1020
GTTCTACGCC ACCTTGCGCA GCCG 1044

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1077 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GCGGATGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAGGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGATCCGGA GGTACCCAGG ACTGCTCCTT CCAACACAGC 360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 420
TACCCAGTCA CCGTGGCCTC CAACCTGCAG TACGTAGAGG GCGGTGGAGG CTCCCCGGGT 480
GAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA 540
TCTCCAAACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG CTTCCTGCTC 600
AAGTGCTTAG AGCAAGTGAG GAAGATCCAG GGCGATGGCG CAGCGCTCCA GGAGAAGCTG 660
TGTGCCACCT ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC 720
ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG 780
AGCCAACTCC ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC TGCAGGCCCT GGAAGGGATA 840
TCCCCCGAGT TGGGTCCCAC CTTGGACACA CTGCAGCTGG ACGTCGCCGA CTTTGCCACC 900
ACCATCTGGC AGCAGATGGA AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT 960
GCCATGCCGG CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC 1020
CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC GCAGCCC 1077

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GCCGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCAC CCAGGACTGC 360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGTACGT AGAGGGCGGT 480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC 600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG 660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC 720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG 780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG 840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC 900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG 960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG 1020
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC 1080
CTTGCGCAGC CC 1092

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCAGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC 600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC 660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1080
TACCGCGTTG TACGCCACCT TGCGCAGCCC 1110

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC 60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG 120
GAGCTGCAGT GTCAGCCCGA CTCCTCAACC CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA 180
GGTGGATCCG GAGGTGGCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC 240

```
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG     300
GCCTCCAACC TGCAGGACGA GGAGCTCTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG     360
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC     420
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCGTACGT AGAGGGCGGT     480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT     540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCGTGCCC     600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG     660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC     720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG     780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG     840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC     900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG     960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG    1020
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TATACGCCAC    1080
CTTGCGCAGC CC                                                        1092
```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```
GCTTCAAATC TGCAGGATGA AGAGCTGTGC GGGGGCCTCT GGCGGCTGGT CCTGGCACAG      60
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC     120
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT     180
CGCTTCGTCC AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG     240
CTGAAGCCCT GGATCACTCG CCAGAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC     300
GACTCCTCAA CCCTGGGCGG TGGGTCAGGA GGTGGGTCAG GAGGTGGATC CGGAGGTGGC     360
TCAGGGGGAG GTAGTGGTAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC     420
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG     480
GCCTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC     540
AACCCGTCTC ATCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC     600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC     660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC     720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC     780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC     840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC     900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG     960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC    1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG    1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                     1110
```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```
GCTAATCTGC AAGATGAGGA GCTGTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC      60
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG     120
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC     180
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG     240
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC     300
TCCTCAACCC TGGGCGGTGG GTCAGGAGGT GGGTCAGGAG GTGGATCCGG AGGTGGCTCA     360
GGGGGAGGTA GTGGTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC     420
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC     480
TCCTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC     540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC     600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC     660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC     720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC     780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC     840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC     900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG     960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC    1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG    1080
TACCGCGTTA TACGCCACCT TGCGCAGCCC                                     1110
```

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
GCGCTGCAGG ATGAAGAGCT GTGTGGCGGC CTCTGGCGGC TGGTCCTGGC ACAGCGCTTG     60
ATGGAGCGGC TCAAGACTGT CGCTGGGTCC AAGATGCAAG GCTTGCTGGA GCGCGTGAAC    120
ACGGAGATAC ACTTTGTCAC CAAATGTGCC TTTCAGCCCC CCCCCAGCTG TCTTCGCTTC    180
GTCCAGACCA ACATCTCCCG CCTCCTGCAG GAGACCTCCG AGCAGCTGGT GGCGCTGAAG    240
CCCTGGATCA CTCGCCAGAA CTTCTCCCGG TGCCTGGAGC TGCAGTGTCA GCCCGACTCC    300
TCAACCCTGG GCGGTGGGTC AGGAGGTGGG TCAGGAGGTG GATCCGGAGG TGGCTCAGGG    360
GGAGGTAGTG GTACCCAGGA CTGCTCCTTC CAACACAGCC CCATCTCCTC CGACTTCGCT    420
GTCAAAATCC GTGAGCTGTC TGACTACCTG CTTCAAGATT ACCCAGTCAC CGTGGCCTCC    480
AACTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC    600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC    660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC    720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC    780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC    840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC    900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG    960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC   1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG   1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```
GCACTGTGCG GTGGTCTGTG GCGTCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG     60
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT    120
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC    180
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC    240
CAGAACTTCT CCCGGTGCCT GGAGCTACAG TGTCAGCCCG ACTCCTCAAC CCTGGGCGGT    300
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCT CAGGGGGAGG TAGTGGTACC    360
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCGACT TCGCTGTCAA AATCCGTGAG    420
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG    480
GAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC    600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC    660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC    720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC    780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC    840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC    900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG    960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC   1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG   1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA     60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC    120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC    180
```

```
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGGGCGG TGGGTCAGGA     240
GGTGGGTCAG GAGGTGGATC CGGAGGTGGC ACCCAGGACT GCTCCTTCCA ACACAGCCCC     300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC     360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG     420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGCTACGT AGAGGGCGGT     480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT     540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC     600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG     660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC     720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG     780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG     840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC     900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG     960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG    1020
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC    1080
CTTGCGCAGC CC                                                        1092
```

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```
GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA      60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC     120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC     180
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGGGCGG TGGGTCAGGA     240
GGTGGGTCAG GAGGTGGATC CGGAGGTGGC ACCCAGGACT GCTCCTTCCA ACACAGCCCC     300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC     360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG     420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGCTACGT AGAGGGCGGT     480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT     540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC     600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG     660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC     720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG     780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG     840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC     900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG     960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG    1020
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC    1080
CTTGCGCAGC CC                                                        1092
```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```
GCGCTGTGTG GTGGTCTGTG GCGTCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG      60
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT     120
GTCACCAAAT GTGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC     180
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC     240
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCGGCCCG ACTCCTCAAC CCTGGGCGGT     300
GGGTCAGGAG GTGGGTCAGG AGGTGGATCC GGAGGTGGCT CAGGGGGAGG TAGTGGTACC     360
CAGGACTGCT CCTTCCAACA CAGCCCCATC TCCTCCAACT TCGCTGTCAA GATCCGTGAG     420
CTGTCTGACT ACCTGCTTCA AGATTACCCA GTCACCGTGG CCTCCAACCT GCAGGACGAG     480
GAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT TTTTACTATC     540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC     600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC     660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC     720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC     780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC     840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC     900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG     960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC    1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG    1080
```

TACCGCGTTC TACGCCACCT TGCGCAGCCC 1110

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GCTGAACTGT GTGGTGGTCT GTGGCGTCTG GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC 60
AAGACTGTCG CTGGGTCCAA GATGCAAGGC TTGCTGGAGC GCGTGAACAC GGAGATACAC 120
TTTGTCACCA AATGTGCCTT TCAGCCCCCC CCCAGCTGTC TTCGCTTCGT CCAGACCAAC 180
ATCTCCCGCC TCCTGCAGGA GACCTCCGAG CAGCTGGTGG CGCTGAAGCC CTGGATCACT 240
CGCCAGAACT TCTCCCGGTG CCTGGAGCTG CAGTGTCAGC CCGACTCCTC AACCCTGGGC 300
GGTGGGTCAG GAGGTGGGTC AGGAGGTGGA TCCGGAGGTG GCTCAGGGGG AGGTAGTGGT 360
ACCCAGGACT GCTCCTTCCA ACACAGCCCC ATCTCCTCCG ACTTCGCTGT CAAAATCCGT 420
GAGCTGTCTG ACTACCTGCT TCAAGATTAC CCAGTCACCG TGGCCTCCAA CCTGCAGGAC 480
GAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC 600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC 660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC 1110

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCTGAAGAAC TGTGTGGTGG CCTGTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 60
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 120
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 180
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 240
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 300
GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT GGATCCGGAG GTGGCTCAGG GGGAGGTAGT 360
GGTACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 420
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 480
GACTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC 600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC 660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC 1110

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GCTCAGGACG AGGAACTGTG TGGTGGTCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG 60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG 120

```
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CTCAGGGGGA    360
GGTAGTGGTA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC    420
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC    480
CTGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC    600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC    660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC    720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC    780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC    840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC    900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG    960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC   1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG   1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```
GCCACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC     60
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    120
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CACCCAGGAC    180
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTTGCTG TCAAAATCCG TGAGCTGTCT    240
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC    300
TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA CAGCGCTGGA TGGAGCGGCT CAAGACTGTC    360
GCTGGGTCCA AGATGCAAGG CTTGCTGGAG CGCGTGAACA CGGAGATACA CTTTGTCACC    420
AAATGTGCCT TTCAGCCCCC CCCCAGCTGT CTTCGCTTCG TCCAGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC    600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG    660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC    720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG    780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG    840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC    900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG    960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG   1020
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC   1080
CTTGCGCAGC CC                                                       1092
```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1065 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```
GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT    360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGGTGGTT CTGGCGGCGG CTCCAACATG    540
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG    600
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    660
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    720
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    780
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    840
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    900
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    960
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC   1020
```

TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCG 1065

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GCTCAAGATG AAGAACTGTG CGGTGGTCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG 60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG 120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC 180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC 240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA 300
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGCGGAT CCGGAGGTGG CTCAGGGGGA 360
GGTAGTGGTA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTCCGCTGTC 420
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC 480
CTGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC 600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC 660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC 1110

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GCGCTGTGTG GTGGCCTGTG GCGTCTGGTC CTGGCACAGC GCTGGATGGA GCGGCTCAAG 60
ACTGTCGCTG GGTCCAAGAT GCAAGGCTTG CTGGAGCGCG TGAACACGGA GATACACTTT 120
GTCACCAAAT ATGCCTTTCA GCCCCCCCCC AGCTGTCTTC GCTTCGTCCA GACCAACATC 180
TCCCGCCTCC TGCAGGAGAC CTCCGAGCAG CTGGTGGCGC TGAAGCCCTG GATCACTCGC 240
CAGAACTTCT CCCGGTGCCT GGAGCTGCAG TGTCGGCCCG ACTCCTCAAC CCTGGGCGGT 300
GGGTCAGGAG GTGGATCCGG AGGTGGCTCA GGGGGAGGTA GTGGTACCCA GGACTGCTCC 360
TTCCAACACA GCCCCATCTC CTCCGACTTC GCTGTCAAGA TCCGTGAGCT GTCTGACTAC 420
CTGCTTCAAG ATTACCCAGT CACCGTGGCC TCCAACCTGC AGGACGAGGA GTACGTAGAG 480
GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT 540
CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACAC CATTAGGCCC TGCCAGCTCC 600
CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA GAGCAAGTGA GGAAGATCCA GGGCGATGGC 660
GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG 720
CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC 780
CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC 840
CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG 900
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT 960
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA 1020
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA 1080
CGCCACCTTG CGCAGCCC 1098

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA 60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC 120

```
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC    180
TTCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTGGGCGG TGGGTCAGGA    240
GGTGGGTCAG GAGGTGGATC CGGAGGTGGC ACCCAGGACT GCTCCTTCCA ACACAGCCCC    300
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC    360
CCAGTCACCG TGGCCTCCAA CCTGCAGGAC GAGGAGCTCT GCGGGGGCCT CTGGCGGCTG    420
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGCTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC    600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG    660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC    720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG    780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG    840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC    900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG    960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG   1020
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC   1080
CTTGCGCAGC CC                                                      1092
```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
GCTCAAGACG AAGAACTGTG TGGTGGTCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG     60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG    120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGCGGTGGTT CTGGCGGAGG ATCCGGCGGC    360
GGAAGCGGAG GTGGCTCTGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC    420
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT    480
TACCCAGTCA CCGTGGCCTC CAACCTGTAC GTAGAGGGCG GTGGAGGCTC CCCGGGTGAA    540
CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC TCATAAATCT    600
CCAAACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG    660
TGCTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT    720
GCCACCTACA AGCTGTGCCA CCCCGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC    780
CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC    840
CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC    900
CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC    960
ATCTGGCAGC AGATGGAAGA ACTGGGAATG GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC   1020
ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT   1080
CTGCAGAGCT TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCC         1134
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1092 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
GCCCAAGATG AAGAACTGTG TGGTGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG     60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG    120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGCCGC CACCGTGGAG CCCGCGTCCA CTCGGCGCCA CCGCACCGAC CACCCAGGAC    360
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT    420
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGTACGT AGAGGGCGGT    480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    540
AAAGAATCTC ATAAATCTCC AAACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC    600
CAGAGCTTCC TGCTCAAGTG CTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG    660
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC    720
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG    780
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG    840
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC    900
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG    960
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG   1020
```

```
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC   1080
CTTGCGCAGC CC                                                       1092
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
GCCCAAGATG AAGAACTGTG TGGTGGCCTC TGGCGGCTGG TCCTGGCACA GCGCTGGATG     60
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG    120
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC    180
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC    240
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA    300
ACCCTGCCGC CACCGTGGAG CCCGCGTCCA CTCGGCGCCA CCGCACCGAC CGCTGGACAA    360
CCGCCTCTGA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC    420
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC    480
CTGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC    600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC    660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC    720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC    780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC    840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC    900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG    960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC   1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG   1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC                                    1110
```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```
GCTGATGAAG AACTGTGTGG TGGGCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGC GGTGGTTCTG GCGGAGGATC CGGCGGCGGA    360
AGCGGAGGTG GCTCTGGGGG AGGTAGTGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC    420
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC    480
CCAGTCACCG TGGCCTCCAA CCTGCAGTAC GTAGAGGGCG GTGGAGGCTC CCCGGGTGAA    540
CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC TCATAAATCT    600
CCAAACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG    660
TGCTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT    720
GCCACCTACA AGCTGTGCCA CCCCGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC    780
CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC    840
CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC    900
CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC    960
ATCTGGCAGC AGATGGAAGA ACTGGGAATG GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC   1020
ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT   1080
CTGCAGAGCT TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCC         1134
```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```
GCTGATGAAG AACTGTGTGG TGGGCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
```

CGGCCCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGC GGTGGTTCTG GCGGAGGATC CGGCGGCGGA 360
AGCGGAGGTG GCTCTGGGGG AGGTAGTGGT ACCCAGGACT GCTCCTTCCA ACACAGCCCC 420
ATCTCCTCCG ACTTCGCTGT CAAAATCCGT GAGCTGTCTG ACTACCTGCT TCAAGATTAC 480
CCAGTCACCG TGGCCTCCAA CCTGCAGTAC GTAGAGGGCG GTGGAGGCTC CCCGGGTGAA 540
CCGTCTGGTC CAATCTCTAC TATCAACCCG TCTCCTCCGT CTAAAGAATC TCATAAATCT 600
CCAAACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG 660
TGCTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT 720
GCCACCTACA AGCTGTGCCA CCCCGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC 780
CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC 840
CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC 900
CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC 960
ATCTGGCAGC AGATGGAAGA ACTGGGAATG GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC 1020
ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT 1080
CTGCAGAGCT TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCC 1134

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GCGGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGCCGCCAC CGTGGAGCCC GCGTCCACTC GGCGCCACCG CACCGACCGC TGGACAACCG 360
CCTCTGACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCACCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC 600
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC 660
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 720
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 780
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 840
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 900
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 960
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1020
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1080
TACCGCGTTC TACGCCACCT TGCGCAGCCC 1110

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GCTGATGAGG AGCTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGT AGAGACGGTG 300
TTTCACCGTG TCAGCCAGGA TGGTCTAGAT CTCCTGACCT CGACCCAGGA CTGCTCCTTC 360
CAACACAGCC CCATCTCCTC CGACTTCGCT GTCAAAATCC GTGAGCTGTC TGACTACCTG 420
CTTCAAGATT ACCCAGTCAC CGTGGCCTCC AACCTGCAGT ACGTAGAGGG CGGTGGAGGC 480
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC 540
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT 600
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACTAACAAGC TGTGCCACCC CGAGGAGCTG 660
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG 720
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG 780
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG 840
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC 900
CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG 960

```
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT   1020
CTACGCCACC TTGCGCAGCC G                                             1041
```

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```
GCTGATGAAG AACTGTGTGG TGGGCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC    360
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTGGGC    420
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT GAGAAAGATC    480
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC    540
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC    600
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC    660
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC    720
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG    780
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC    840
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG    900
TACCGCGTTC TACGCCACCT TGCGCAGCCC TACGTAGAGG GCGGTGGAGG CTCCCCGGGT    960
GAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA   1020
TCTCCAAACA TGGCAACCCA GGACTGCTCT TTTCAACACA GCCCCATCTC CTCCGACTTC   1080
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC   1140
TCCAACCTGC AG                                                       1152
```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1047 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```
GCCACCCAGG ACTGCTCCTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    120
GAGCCGAAGA GCCCGGACAC CCATACTAGT CCGCCATCTC CGACACCATT AGGCCCTGCC    180
AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGAAA GATCCAGGGC    240
GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCGAGGAG    300
CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC    360
CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG    420
GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GCCCCACCTT GGACACACTG    480
CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGAATG    540
GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC    600
CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT CTGCAGAGCT TCCTGGAGGT GTCGTACCGC    660
GTTCTACGCC ACCTTGCGCA GCCCTCTGCA GAACCGAAAT CTCCGGATAC TCATACCAGC    720
CCGCCATCCC CGGGTTCTAA TCTGCAAGAT GAAGAGCTGT GCGGGGGCCT CTGGCGGCTG    780
GTCCTGGCAC AGCGCTGGAT GGAGCGGCTC AAGACTGTCG CTGGGTCCAA GATGCAAGGC    840
TTGCTGGAGC GCGTGAACAC GGAGATACAC TTTGTCACCA AATGTGCCTT TCAGCCCCCC    900
CCCAGCTGCC TTCGCTTCGT CCAGACCAAC ATCTCCCGCC TCCTGCAGGA GACCTCCGAG    960
CAGCTGGTGG CGCTGAAGCC CTGGATCACT CGCCAGAACT TCTCCCGGTG CCTGGAGCTG   1020
CAGTGTCAGC CCGACTCCTC AACCCTG                                       1047
```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1043 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```
GCCACCCAGG ACTGCTCCTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     60
```

CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTGGCAGG GGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCCGAAG AGCCCGGACA CCCATACTAG TCCGCCATCT 300
CCGGGTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA 360
GAGCAAGTGA GAAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACT 420
ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG 480
CTCCCCTGAG CTCCTGCCCC AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC 540
ATAGCGGCCT TTTCCTCTAC CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT 600
TGGGTCCCAC CTTGGACACA CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC 660
AGCAGATGGA AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG 720
CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTTGCTAGC CATCTGCAGA 780
GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC GCAGCCCTCT GCAGAACCGA 840
AATCTCCGGA TACTCATACC AGCCCGCCAT CCCCGGGTAA GGCCTTTCAG CCCCCCCCCA 900
GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC 960
TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT 1020
GTCAGCCCGA CTCCTCAACC CTG 1043

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1065 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATC TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTCCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGGTGGTT CTGGCGGCGG CTCCAACATG 540
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 600
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACTAAC 660
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 720
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 780
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 840
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 900
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 960
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 1020
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCG 1065

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG TCTGTGGCGG 660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA 720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATCTGC CTTTCAGCCC 780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC 840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG 900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT 960
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTCCTCCTT CCAACACAGC 1020
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGCGAGCTGT CTGACTACCT GCTTCAAGAT 1080

TACCCAGTCA CCGTGGCCTC CAACCTGCAG 1110

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1065 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTCTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTA GAGCTGCAGT CTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGGTGGTT CTGGCGGCGG CTCCAACATG 540
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 600
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACTAAC 660
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 720
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 780
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 840
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 900
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 960
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 1020
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCG 1065

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 600
AAAGAATCTC ATAAATCTCC AAACATGGCA GATGAAGAAC TGTGTGGGGG CCTGTGGCGG 660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA 720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC 780
CCCCCCAGCT CTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC 840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG 900
CTGCAGTCTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT 960
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACTCAGG ACTGTTCTTT TCAACACAGC 1020
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 1080
TACCCAGTCA CCGTGGCCTC CAACCTGCAG 1110

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GCCACTCAGG ACTCCTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180

CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATCTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GGTGGTTCTG GCGGCGGCTC CAACATGGCT 480
ACACCATTGG GCCCTGCCAG CTCCCTGCCC CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA 540
GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACTAACAAG 600
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC 660
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC 720
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT 780
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG 840
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC 900
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC 960
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CG 1002

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GCCACTCAGG ACTGTTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT CTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTCTC AGCCCGACTC CTCAACCCTG 420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GGTGGTTCTG GCGGCGGCTC CAACATGGCT 480
ACACCATTGG GCCCTGCCAG CTCCCTGCCC CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA 540
GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG 600
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC 660
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC 720
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT 780
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG 840
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC 900
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC 960
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CG 1002

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 978 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GCCACTCAGG ACTGTTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTACG TAGAGGGCGG TGGAGGCTCC 420
CCGGGTGGTG GTTCTGGCGG CGGCTCCAAC ATGGCTACAC CATTGGGCCC TGCCAGCTCC 480
CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA GAGCAAGTGA GAAAGATCCA GGGCGATGGC 540
GCAGCGCTCC AGGAGAAGCT GTGTGCCACT AACAAGCTGT GCCACCCCGA GGAGCTGGTG 600
CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC 660
CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC 720
CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG 780
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT 840
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA 900
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA 960
CGCCACCTTG CGCAGCCG 978

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1002 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```
GCCACTCAGG ACTGTTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG    180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA    240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC    300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC    360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTCTC AGCCCGACTC CTCAACCCTG    420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GGTGGTTCTG GCGGCGGCTC CAACATGGCT    480
ACACCATTGG GCCCTGCCAG CTCCCTGCCC CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA    540
GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG    600
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC    660
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC    720
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT    780
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG    840
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC    900
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC    960
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CG                      1002
```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1001 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```
GCCACTCAGG ACTGTTCTTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC     60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG    120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG    180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA    240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC    300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC    360
ACTCGCCAGA ACTTCTCCCG GCGCCTGGAG CTGCAGTCTC AGCCCGACTC CTCAACCCTG    420
TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GGTGGTTCTG GCGGCGGCTC CAACATGGCT    480
ACACCATTGG GCCCTGCCAG CTCCCTGCCC CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA    540
GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACTAACAAG    600
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC    660
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC    720
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT    780
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG    840
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC    900
GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC    960
CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC C                       1001
```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```
GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG     60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG    120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG    180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG    240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC    300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT    360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA    420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG    480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGGTGGTT CTGGCGGCGG CTCCAACATG    540
GCTACTCAAG GTGCTATGCC AGCTTTTGCT TCTGCTTTTC AACGTCGTGC AGGTGGTGTT    600
CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT    660
GCGCAGCCCT CTGGCGGCTC TGGCGGCTCT CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA    720
```

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GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG     780
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC     840
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC     900
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT     960
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG    1020
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCC                              1056
```

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

```
GCTACTCAAG GTGCTATGCC AGCTTTTGCT TCTGCTTTTC AACGTCGTGC AGGTGGTGTT      60
CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT     120
GCGCAGCCCT CTGGCGGCTC TGGCGGCTCT CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA     180
GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG     240
CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC     300
CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC     360
GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT     420
CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG     480
ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCTACG TAGAGGGCGG TGGAGGCTCC     540
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT     600
CATAAATCTC CAAACATGGC CGACGAGGAG CTCTGCGGGG GCCTCTGGCG GCTGGTCCTG     660
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG     720
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC     780
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG     840
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT     900
CAGCCCGACT CCTCAACCCT GGGCGGTGGG TCAGGAGGTG GGTCAGGAGG TGGATCCGGA     960
GGTGGCTCAG GGGGAGGTAG TGGTACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC    1020
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC    1080
ACCGTGGCCT CCAACCTGCA G                                              1101
```

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1032 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

```
GCCGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG      60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG     120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG     180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG     240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC     300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGAAC CCAGGACTGC     360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC     420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGTACGT AGAGGGCGGT     480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT     540
AAAGAATCTC ATAAATCTCC AAACATGGCC GACGAGGAGC TCTGCGGGGG CCTCTGGCGG     600
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA     660
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC     720
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC     780
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG     840
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT     900
GGATCCGGAG GTGGCACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC     960
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC    1020
TCCAACCTGC AG                                                        1032
```

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 540
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC CCAGGACTGC 600
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 660
TACCTGCTTC AAAATTACCC AGTCACCGTG GCCTCCAACC TGCAGGACGA GGAGCTCTGC 720
GGGGGCCTCT GGCGGCTGGT CCTGGCACAG CGCTGGATGG AGCGGCTCAA GACTGTCGCT 780
GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA 840
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC 900
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC 960
TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC GACTCCTCAA CCCTG 1005

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGGTGGTT CTGGCGGCGG CTCCAACATG 540
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 600
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 660
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 720
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 780
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 840
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 900
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC 960
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC 1020
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT 1080
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 1140
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG TCTGTGGCGG 1200
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA 1260
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC 1320
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC 1380
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG 1440
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT 1500
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC 1560
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 1620
TACCCAGTCA CCGTGGCCTC CAACCTGCAG 1650

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1632 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG 60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC 120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT 180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT 240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG 300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG 360

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CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG TCTGTGGCGG    660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA    720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC    780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC    840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG    900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT    960
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC   1020
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT   1080
TACCCAGTCA CCGTGGCCTC CAACCTGCAG TACGTAGAGG GCGGTGGAGG CTCCCCGGGT   1140
GAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA   1200
TCTCCAAACA TGGCTACCCA GGACTGCTCC TTCCAACACA GCCCCATCTC CTCCGACTTC   1260
GCTGTCAAAA TCCGTGAGCT GTCTGACTAC CTGCTTCAAG ATTACCCAGT CACCGTGGCC   1320
TCCAACCTGC AGGACGAGGA GCTCTGCGGG GGCCTCTGGC GGCTGGTCCT GGCACAGCGC   1380
TGGATGGAGC GGCTCAAGAC TGTCGCTGGG TCCAAGATGC AAGGCTTGCT GGAGCGCGTG   1440
AACACGGAGA TACACTTTGT CACCAAATGT GCCTTTCAGC CCCCCCCCAG CTGTCTTCGC   1500
TTCGTCCAGA CCAACATCTC CCGCCTCCTG CAGGAGACCT CCGAGCAGCT GGTGGCGCTG   1560
AAGCCCTGGA TCACTCGCCA GAACTTCTCC CGGTGCCTGG AGCTGCAGTG TCAGCCCGAC   1620
TCCTCAACCC TG                                                       1632
```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1695 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```
GCTACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG     60
CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC    120
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT    180
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT    240
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCGAGTTG    300
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG    360
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC    420
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC    480
TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTACGT AGAGGGCGGT    540
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT    600
AAAGAATCTC ATAAATCTCC AAACATGGCT GATGAAGAAC TGTGTGGTGG TCTGTGGCGG    660
CTGGTCCTGG CACAGCGCTG GATGGAGCGG CTCAAGACTG TCGCTGGGTC CAAGATGCAA    720
GGCTTGCTGG AGCGCGTGAA CACGGAGATA CACTTTGTCA CCAAATGTGC CTTTCAGCCC    780
CCCCCCAGCT GTCTTCGCTT CGTCCAGACC AACATCTCCC GCCTCCTGCA GGAGACCTCC    840
GAGCAGCTGG TGGCGCTGAA GCCCTGGATC ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG    900
CTGCAGTGTC AGCCCGACTC CTCAACCCTG GGCGGTGGGT CAGGAGGTGG GTCAGGAGGT    960
GGATCCGGAG GTGGCTCAGG GGGAGGTAGT GGTACCCAGG ACTGCTCCTT CCAACACAGC   1020
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT   1080
TACCCAGTCA CCGTGGCCTC CAACCTGCAG TACGTAGAGG GCGGTGGAGG CTCCCCGGGT   1140
GAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA   1200
TCTCCAAACA TGGCTGATGA AGAACTGTGT GGTGGTCTGT GGCGGCTGGT CCTGGCACAG   1260
CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC   1320
GTGAACACGG AGATACACTT TGTCACCAAA TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT   1380
CGCTTCGTCC AGACCAACAT CTCCCGCCTC CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG   1440
CTGAAGCCCT GGATCACTCG CCAGAACTTC TCCCGGTGCC TGGAGCTGCA GTGTCAGCCC   1500
GACTCCTCAA CCCTGGGCGG TGGGTCAGGA GGTGGGTCAG GAGGTGGATC CGGAGGTGGC   1560
TCAGGGGGAG GTAGTGGTAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC   1620
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG   1680
GCCTCCAACC TGCAG                                                    1695
```

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```
GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT     60
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT    120
```

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT 180
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCTCT 240
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC 300
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC 360
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 420
CATAAATCTC CAAACATGGC TGATGAAGAA CTGTGTGGTG GTCTGTGGCG GCTGGTCCTG 480
GCACAGCGCT GGATGGAGCG GCTCAAGACT GTCGCTGGGT CCAAGATGCA AGGCTTGCTG 540
GAGCGCGTGA ACACGGAGAT ACACTTTGTC ACCAAATGTG CCTTTCAGCC CCCCCCCAGC 600
TGTCTTCGCT TCGTCCAGAC CAACATCTCC CGCCTCCTGC AGGAGACCTC CGAGCAGCTG 660
GTGGCGCTGA AGCCCTGGAT CACTCGCCAG AACTTCTCCC GGTGCCTGGA GCTGCAGTGT 720
CAGCCCGACT CCTCAACCCT GGGCGGTGGG TCAGGAGGTG GGTCAGGAGG TGGATCCGGA 780
GGTGGCTCAG GGGGAGGTAG TGGTACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC 840
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC 900
ACCGTGGCCT CCAACCTGCA GTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT 960
GGTCCAATCT CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC 1020
ATGGCTGATG AAGAACTGTG TGGTGGTCTG TGGCGGCTGG TCCTGGCACA GCGCTGGATG 1080
GAGCGGCTCA AGACTGTCGC TGGGTCCAAG ATGCAAGGCT TGCTGGAGCG CGTGAACACG 1140
GAGATACACT TTGTCACCAA ATGTGCCTTT CAGCCCCCCC CCAGCTGTCT TCGCTTCGTC 1200
CAGACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC 1260
TGGATCACTC GCCAGAACTT CTCCCGGTGC CTGGAGCTGC AGTGTCAGCC CGACTCCTCA 1320
ACCCTGGGCG GTGGGTCAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CTCAGGGGGA 1380
GGTAGTGGTA CCCAGGACTG CTCCTTCCAA CACAGCCCCA TCTCCTCCGA CTTCGCTGTC 1440
AAAATCCGTG AGCTGTCTGA CTACCTGCTT CAAGATTACC CAGTCACCGT GGCCTCCAAC 1500
CTGCAG 1506

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 600
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 660
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 720
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 780
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 840
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 900
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 960
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 1020
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGGTGGTT CTGGCGGCGG CTCCAACATG 540
GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 600
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 660
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 720
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 780
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 840
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 900
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 960
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 1020
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 1080
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCTAC ACCATTAGGC 1140
CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTGCT TAGAGCAAGT GAGGAAGATC 1200
CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC 1260
GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCT GGGCTCCCCT GAGCTCCTGC 1320
CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC 1380
TACCAGGGGC TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC 1440
ACACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT GGAAGAACTG 1500
GGAATGGCCC CTGCCCTGCA GCCCACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC 1560
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG 1620
TACCGCGTTC TACGCCACCT TGCGCAGCCC TGATAAGGAT CCGAATTCGG CAGC 1674

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GCCGACGAGG AGCTGTGCGG TGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60

CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGAAC CCAGGACTGC 360
TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC 420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAGTACGT AGAGGGCGGT 480
GGAGGCTCCC CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT 540
AAAGAATCTC ATAAATCTCC AAACATGGCT AACTGCTCTA TAATGATCGA TGAAATTATA 600
CATCACTTAA AGAGACCACC TAACCCTTTG CTGGACCCGA ACAACCTCAA TTCTGAAGAC 660
ATGGATATCC TGATGGAACG AAACCTTCGA ACTCCAAACC TGCTCGCATT CGTAAGGGCT 720
GTCAAGCACT TAGAAAATGC ATCAGGTATT GAGGCAATTC TTCGTAATCT CCAACCATGT 780
CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAGGC AGGTGACTGG 840
CAAGAATTCC GGGAAAAACT GACGTTCTAT CTGGTTACCC TTGAGCAAGC GCAGGAACAA 900
CAGTACGTAG AGGGCGGTGG AGGCTCCCCG GGTGAACCGT CTGGTCCAAT CTCTACTATC 960
AACCCGTCTC CTCCGTCTAA AGAATCTCAT AAATCTCCAA ACATGGCCGA CGAGGAGCTC 1020
TGCGGGGGCC TCTGGCGGCT GGTCCTGGCA CAGCGCTGGA TGGAGCGGCT CAAGACTGTC 1080
GCTGGGTCCA AGATGCAAGG CTTGCTGGAG CGCGTGAACA CGGAGATACA CTTTGTCACC 1140
AAATGTGCCT TTCAGCCCCC CCCCAGCTGT CTTCGCTTCG TCCAGACCAA CATCTCCCGC 1200
CTCCTGCAGG AGACCTCCGA GCAGCTGGTG GCGCTGAAGC CCTGGATCAC TCGCCAGAAC 1260
TTCTCCCGGT GCCTGGAGCT GCAGTGTCAG CCCGACTCCT CAACCCTGGG CGGTGGGTCA 1320
GGAGGTGGGT CAGGAGGTGG ATCCGGAGGT GGCACCCAGG ACTGCTCCTT CCAACACAGC 1380
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT 1440
TACCCAGTCA CCGTGGCCTC CAACCTGCAG 1470

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GCTGATGAAG AACTGTGTGG TGGTCTGTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG 60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG 120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG 180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG 240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC 300
CTGGGCGGTG GGTCAGGAGG TGGGTCAGGA GGTGGATCCG GAGGTGGCTC AGGGGGAGGT 360
AGTGGTACCC AGGACTGCTC CTTCCAACAC AGCCCCATCT CCTCCGACTT CGCTGTCAAA 420
ATCCGTGAGC TGTCTGACTA CCTGCTTCAA GATTACCCAG TCACCGTGGC CTCCAACCTG 480
CAGGAATTCA AGCTTGAGCC CAGAGGGCCC ACAATCAAGC CCTGTCCTCC ATGCAAATGC 540
CCAGCACCTA ACCTCTTGGG TGGACCATCC GTCTTCATCT TCCCTCCAAA GATCAAGGAT 600
GTACTCATGA TCTCCCTGAG CCCCATAGTC ACATGTGTGG TGGTGGATGT GAGCGAGGAT 660
GACCCAGATG TCCAGATCAG CTGGTTTGTG AACAACGTGG AAGTACACAC AGCTCAGACA 720
CAAACCCATA GAGAGGATTA CAACAGTACT CTCCGGGCGG TCAGTGCCCT CCCCATCCAG 780
CACCAGGACT GGATGAGTGG CAAGGAGTTC AAATGCAAGG TCAACAACAA AGACCTCCCA 840
GCGCCCATCG AGAGAACCAT CTCAAAACCC AAAGGGTCAG TAAGAGCTCC ACAGGTATAT 900
GTCTTGCCTC CACCAGAAGA AGAGATGACT AAGAAACAGG TCACTCTGAC CTGCATGGTC 960
ACAGACTTCA TGCCTGAAGA CATTTACGTG GAGTGGACCA ACAACGGGAA AACAGAGCTA 1020
AACTACAAGA ACACTGAACC AGTCCTGGAC TCTGATGGTT CTTACTTCAT GTACAGCAAG 1080
CTGAGAGTGG AAAAGAAGAA CTGGGTGGAA AGAAATAGCT ACTCCTGTTC AGTGGTCCAC 1140
GAGGGTCTGC ACAATCACCA CACGACTAAG AGCTTCTCCC GGACTCCGGG TAAA 1194

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GCCACCCAGG ACTGCTCCTT TCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC 60
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG 120
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCCTGG CACAGCGCTG GATGGAGCGG 180
CTCAAGACTG TCGCTGGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA 240
CACTTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTTCGCTT CGTCCAGACC 300
AACATCTCCC GCCTCCTGCA GGAGACCTCC GAGCAGCTGG TGGCGCTGAA GCCCTGGATC 360
ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420
GAATTCAAGC TTGAGCCCAG AGGGCCCACA ATCAAGCCCT GTCCTCCATG CAAATGCCCA 480
GCACCTAACC TCTTGGGTGG ACCATCCGTC TTCATCTTCC CTCCAAAGAT CAAGGATGTA 540

CTCATGATCT CCCTGAGCCC CATAGTCACA TGTGTGGTGG TGGATGTGAG CGAGGATGAC 600
CCAGATGTCC AGATCAGCTG GTTTGTGAAC AACGTGGAAG TACACACAGC TCAGACACAA 660
ACCCATAGAG AGGATTACAA CAGTACTCTC CGGGCGGTCA GTGCCCTCCC CATCCAGCAC 720
CAGGACTGGA TGAGTGGCAA GGAGTTCAAA TGCAAGGTCA ACAACAAAGA CCTCCCAGCG 780
CCCATCGAGA GAACCATCTC AAAACCCAAA GGGTCAGTAA GAGCTCCACA GGTATATGTC 840
TTGCCTCCAC CAGAAGAAGA GATGACTAAG AAACAGGTCA CTCTGACCTG CATGGTCACA 900
GACTTCATGC CTGAAGACAT TTACGTGGAG TGGACCAACA ACGGGAAAAC AGAGCTAAAC 960
TACAAGAACA CTGAACCAGT CCTGGACTCT GATGGTTCTT ACTTCATGTA CAGCAAGCTG 1020
AGAGTGGAAA AGAAGAACTG GGTGGAAAGA AATAGCTACT CCTGTTCAGT GGTCCACGAG 1080
GGTCTGCACA ATCACCACAC GACTAAGAGC TTCTCCCGGA CTCCGGGTAA A 1131

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

ACGTCCATGG CNTCNCCNGC NCCNCCTGCT TGTGCACTCC GAGTC 45

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

ATGCACGAAT TCCCTGACGC AGAGGGTGGA 30

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

TGACAAGCTT ACCTGACGCA GAGGGTGGAC CCT 33

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTCGGCAA 10

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

CATGTTGCCG 10

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATTCGGCGG CAA 13

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

CATGTTGCCG CCG 13

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

AATTCGGCGG CAACGGCGGC AA 22

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

CATGTTGCCG CCGTTGCCGC CG 22

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

CGATCCATGG AGGTTCACCC TTTGCCT 27

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GATCAAGCTT ATGGGCACTG GCTCAGTCT 29

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGATACATGT TGCCTACACC TGTCCTG 27

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GATCAAGCTT AAGGGTGAAC CTCTGGGCA 29

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

CGATCCATGG TCCTGCTGCC TGCTGTG 27

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GATCAAGCTT AAGGTGTAGG CAAAGGGTG 29

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

CGATCCATGG CTGTGGACTT TAGCTTGGGA 30

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GATCAAGCTT AAGGCAGCAG GACAGGTGT 29

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

CGATCCATGG ACTTTAGCTT GGGAGAA 27

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GATCAAGCTT ACACAGCAGG CAGCAGGAC 29

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

CGATCCATGG GAGAATGGAA AACCCAG 27

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GATCAAGCTT ACAAGCTAAA GTCCACAGC 29

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

CGATCCATGG GACCCACTTG CCTCTCA 27

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GATCAAGCTT ACAGTTGTCC CCGTGCTGC 29

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CAGTCCATGG GAACCCAGCT TCCTCCA 27

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GATCAAGCTT AAAGGAGGCT CTGCAGGGC 29

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CGATCCATGG GCAGGACCAC AGCTCAC 27

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GATCAAGCTT ACTGTGGAGG AAGCTGGGTT 30

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

CGATCCATGG CTCACAAGGA TCCCAATGCC 30

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GATCAAGCTT ATGTGGTCCT GCCCTGTGG 29

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

CGATCCATGG ATCCCAATGC CATCTTCCTG 30

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GATCAAGCTT ACTTGTGAGC TGTGGTCCT 29

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CGATCCATGG CCATCTTCCT GAGCTTCCAA 30

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GATCAAGCTT AATTGGGATC CTTGTGAGCT GT 32

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT 60
ACGTAGAGGG CGGTGGAGGC TCC 83

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

CCGGGGAGCC TCCACCGCCC TCTACGTACT GTTGAGCCTG CGCGTTCTCC AAGGTTTTCA 60
GATAGAAGGT CAGTTTACGA CGG 83

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAACTGCTC TATAATGAT 59

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGATCATTAT AGAGCAGTTA GAGCCACCAC CCTGTTGTTC CTGCGCTTGC TCAAGG 56

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG CAGCGGCGGC 60
GGTTCTAACT GCTCTATAAT GAT 83

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

CGATCATTAT AGAGCAGTTA GAACCGCCGC CGCTGCCACC GCCAGAGCCA CCACCCTGTT 60
GTTCCTGCGC TTGCTCAAGG 80

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GATCGACCAT GGCTCTGGAC CCGAACAACC TC 32

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

CTCGATTACG TACAAAGGTG CAGGTGGT 28

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

GATCGACCAT GGCTAATGCA TCAGGTATTG AG 32

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

CTCGATTACG TATTCTAAGT TCTTGACA 28

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GATCGACCAT GGCTGCACCC TCTCGACATC CA 32

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

CTCGATTACG TAGGCCGTGG CAGAGGGC 28

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GATCGACCAT GGCTGCAGGT GACTGGCAAG AA 32

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

CTCGATTACG TACTTGATGA TGATTGGA 28

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GCTCTGAGAG CCGCCAGAGC CGCCAGAGGG CTGCGCAAGG TGGCGTAGAA CGCG 54

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAG 54

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGGCTGCGCA AGGTGGCG 18

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

ACACCATTGG GCCCTGCCAG C 21

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GATCGACCAT GGCTTACAAG CTGTGCCACC CC 32

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

CGATCGAAGC TTATTAGGTG GCACACAGCT TCTCCT 36

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GATCGACCAT GGCTCCCGAG TTGGGTCCCA CC 32

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

CGATCGAAGC TTATTAGGAT ATCCCTTCCA GGGCCT 36

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GATCGACCAT GGCTATGGCC CCTGCCCTGC AG 32

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

CGATCGAAGC TTATTATCCC AGTTCTTCCA TCTGCT 36

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GATCGACCAT GGCTACCCAG GGTGCCATGC CG 32

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA 36

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GATCGACCAT GGCTTCTGCT TTCCAGCGCC GG 32

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

CGATCGAAGC TTATTAGGCG AAGGCCGGCA TGGCAC 36

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GTAGAGGGCG GTGGAGGCTC C 21

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

CCGGGGAGCC TCCACCGCCC TCTAC 25

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

TTCTACGCCA CCTTGCGCAG CCCGGCGGCG GCTCTGACAT GTCTACACCA TTG 53

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

CAATGGTGTA GACATGTCAG AGCCGCCGCC GGGCTGCGCA AGGTGGCGTA GAA 53

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GTCAGACCAT GGCCGATTAC CCAGTCACCG TGGCCTC 37

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GTCAGCCCAT GGCCGCCTCC AACCTGCAGG ACGAGGA 37

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GTCAGACCAT GGCCGTCGCT GGGTCCAAGA TGCAAGGC 38

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GTCAGACCAT GGCCCGCTTC GTCCAGACCA ACATCTCC 38

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GTCAGACCAT GGCCACCAAC ATCTCCCGCC TCCTGCAG 38

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

TCTGACAAGC TTATTGAAGC AGGTAGTCAG ACAGCTCAC 39

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TCTGACAAGC TTACACGGTG ACTGGGTAAT CTTGAAGC 38

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

TCTGACAAGC TTAAGTCTTG AGCCGCTCCA TCCAGCG 37

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GTCAAGAAGC TTACGGCTGA AAGGCACATT TG 32

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

TCTGACAAGC TTAAAGACAG CTGGGGGGGG GCTGAA 36

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

CTCGACAAGC TTACTGGACG AAGCGAAGAC AGCTGGG 37

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GTTGCCATGG CNTCNAAYCT GCARGAYGAR GARCTGTGCG GGGGCCTCTG GCGGCTG 57

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GTTGCCATGG CNAAYCTGCA RGAYGARGAR CTGTGYGGGG GCCTCTGGCG GCTGGTC 57

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GTTGCCATGG CNCTGCARGA YGARGARCTG TGYGGYGGCC TCTGGCGGCT GGTCCTG 57

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GTTGCCATGG CNCARGAYGA RGARCTGTGY GGYGGYCTCT GGCGGCTGGT CCTGGCA 57

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GTTGCCATGG CNGAYGARGA RCTGTGYGGY GGYCTCTGGC GGCTGGTCCT GGCACAG 57

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GTTGCCATGG CNGARGARCT GTGYGGYGGY CTCTGGCGGC TGGTCCTGGC ACAGCGC 57

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

GTTGCCATGG CNGARCTGTG YGGYGGYCTG TGGCGYCTGG TCCTGGCACA GCGCTGG 57

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GTTGCCATGG CNCTGTGYGG YGGYCTGTGG CGYCTGGTCC TGGCACAGCG CTGGATG 57

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GTTGCCATGG CWGATGAAGA ACTGTGTGGN GGNCTGTGGC GG 42

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

TATGCAAGCT TAGGCCACGG TGACTGGGTA 30

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

TATGCAAGCT TAGGAGGCCA CGGTGACTGG 30

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

TATGCAAGCT TAGTTGGAGG CCACGGTGAC 30

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

TATGCAAGCT TACAGGTTGG AGGCCACGGT 30

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TATGCAAGCT TAGTCCAGGT TGGAGGCCAC 30

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

TATGCAAGCT TACTCGTCCA GGTTGGAGGC 30

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

TATGCAAGCT TACTCCTCGT CCAGGTTGGA 30

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GACTAGCCAT GGCNGAYGAR GARCTGTGYG GTGGCCTCTG GCGG 44

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GACTAGTACG TACTGCAGGT TGGAGGCCAC GG 32

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GCAGGTTACG TATTGAAGCA GGTAGTCAGA CAGCTC 36

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GCAGGTTACG TACACGGTGA CTGGGTAATC TTGAAG 36

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GCAGGTTACG TAAGTCTTGA GCCGCTCCAT CCAGC 35

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GCAGGTTACG TAGCCAGCGA CAGTCTTGAG CCGCTC 36

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GTCAAGCCAT GGCNCCRCCR AGCTGTCTRC GCTTCGTTCA GACCAACTC 49

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GCAGGTTACG TACGGCTGAA AGGCACATTT GGTGACAA 38

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GCAGGTTACG TAAAGACAGC TGGGGGGGGG 30

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GCAGGTTACG TACTGGACGA AGCGAAGACA GCTG 34

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

TATGCTACGT AGGCCACGGT GACTGGGTA 29

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

TATGCTACGT AGGAGGCCAC GGTGACTGG 29

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

TATGCTACGT AGTTGGAGGC CACGGTGAC 29

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

TATGCTACGT ACAGGTTGGA GGCCACGGT 29

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

TATGCTACGT AGTCCAGGTT GGAGGCCAC 29

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

TATGCTACGT ACTCGTCCAG GTTGGAGGC 29

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

TATGCTACGT ACTCCTCGTC CAGGTTGGA 29

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

TCAGTTGGAT CCGGCGGCGG AAGCGGAGGT GGCTCTGGGG GAGGTA 46

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

TCAGTTGGAT CCTCCGCCAG AACCACCGCC TGACCCACCT CCTGACCC 48

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GTCTGAGGCG CCACCGCACC GACCGCTGGA CAACCGCCTC TGACCCAGGA CTGCTCCTTC 60

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GTCTGAGGCG CCACCGCACC GACCACCCAG GACTGCTCCT TCCAAC 46

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GTCTGAGGCG CCGAGTGGAC GCGGGCTCCA CGGTGGCGGC AGGGTTGAGG AGTCGGGCTG 60

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GTTGCCATGG CNTCNAAYCT GCARGAYGAR GARCTGTGCG GGGGCCTCTG GCGGCTG 57

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GTTGCCATGG CNAAYCTGCA RGAYGARGAR CTGTGYGGGG GCCTCTGGCG GCTGGTC 57

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GTTGCCATGG CNCTGCARGA YGARGARCTG TGYGGYGGCC TCTGGCGGCT GGTCCTG 57

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GTTGCCATGG CNCARGAYGA RGARCTGTGY GGYGGYCTCT GGCGGCTGGT CCTGGCA 57

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GTTGCCATGG CNGAYGARGA RCTGTGYGGY GGYCTCTGGC GGCTGGTCCT GGCACAG 57

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GTTGCCATGG CNGARGARCT GTGYGGYGGY CTCTGGCGGC TGGTCCTGGC ACAGCGC 57

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GTTGCCATGG CNGARCTGTG YGGYGGYCTG TGGCGYCTGG TCCTGGCACA GCGCTGG 57

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GTTGCCATGG CNCTGTGYGG YGGYCTGTGG CGYCTGGTCC TGGCACAGCG CTGGATG 57

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

TATGCAAGCT TAGGCCACGG TGACTGGGTA 30

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

TATGCAAGCT TAGGAGGCCA CGGTGACTGG 30

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

TATGCAAGCT TAGTTGGAGG CCACGGTGAC 30

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

TATGCAAGCT TACAGGTTGG AGGCCACGGT 30

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

TATGCAAGCT TACTGCAGGT TGGAGGCCAC 30

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

TATGCAAGCT TAGTCCTGCA GGTTGGAGGC 30

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

TATGCAAGCT TACTCGTCCT GCAGGTTGGA 30

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

```
TATGCAAGCT TACTCCTCGT CCTGCAGGTT                                  30
```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```
GCTACGTCTA GATCTCCTGA CCTCGACCCA GGACTGCTCC TTCCAAC               47
```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```
GCTAGTTCTA GACCATCCTG GCTGACACGG TGAAACACCG TCTCTACGGG CTGACACTGC  60
AGCTCCAG                                                          68
```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```
GTCAGTACTA GTATGGGTGT CCGGGCTCTT CGGCTCCTGC AGGTTGGAGG CCACGG      56
```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```
GTCAGTACTA GTCCGCCATC TCCGACACCA TTAGGCCCTG CCAGC                 45
```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```
GTCAGTTCCG GAGATTTCGG TTCTGCAGAG GGCTGCGCAA GGTGGCGTA             49
```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GTCAGTTCCG GATACTCATA CCAGCCCGCC ATCCCCGGGT TCTAATCTGC AAGATGAAGA 60
GCTG 64

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GTCAGTACTA GTATGGGTGT CCGGGCTCTT CGGAAAGGCA CATTTGGTGA CAAAGTGTAT 60
C 61

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GTCAGTACTA GTCCGCCATC TCCGGGTACA CCATTAGGCC CTGCCAGC 48

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GTCAGTTCCG GATACTCATA CCAGCCCGCC ATCCCCGGGT AAGGCCTTTC AGCCCCCCCC 60
CAG 63

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GTCAGACCAT GGCCACTCAG GACTCCTCTT TTC 33

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

CACTTTGTCA CCAAATCTGC CTTTCAG 27

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

CTGAAAGGCA GATTTGGTGA CAAAGTG 27

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GCCCCCCCCC AGCTCTCTTC G 21

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

CGAAGAGAGC TGGGGGGGGG C 21

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GTCAGTTACG TACAGGGTTG AAGGAGTCGG GCTGAGACTG C 41

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTCAGTCCAT GGCTACTCAA GGTGCTATGC 30

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```
GTAGCATACG TAGGGCTGCA GGGCAGGGGC C                                   31
```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

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

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

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

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

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

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

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

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

```
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
 1               5                  10                  15
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
```

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

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

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

```
    210                 215                 220
Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu
225                 230                 235                 240
Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val
                245                 250                 255
Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro
            260                 265                 270
Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
        275                 280                 285
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val
    290                 295                 300
Gly Gly Ser Thr Leu Cys Val Arg
305                 310
```

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

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

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

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

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

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

Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu
180 185 190
Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
195 200 205
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln
210 215 220
Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
225 230 235 240
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val
245 250 255
Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly
260 265 270
Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile
275 280 285
Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
290 295 300

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

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

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

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

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

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

```
                165                 170                 175
Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
            180                 185                 190
Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln
        195                 200                 205
Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
    210                 215                 220
Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
225                 230                 235                 240
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu
                245                 250                 255
Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
            260                 265                 270
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
        275                 280                 285
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe
    290                 295                 300
Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

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

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

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

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

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

```
Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
145                 150                 155                 160
Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
                165                 170                 175
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
            180                 185                 190
Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
        195                 200                 205
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu
    210                 215                 220
Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
225                 230                 235                 240
Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln
                245                 250                 255
Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
            260                 265                 270
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
        275                 280                 285
Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

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

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

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

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

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

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

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

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

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

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

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

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

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

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

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

```
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
    290                 295                 300
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
305                 310                 315                 320
```

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

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

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

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

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

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

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

```
                245                 250                 255
Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu
            260                 265                 270
Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
        275                 280                 285
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln
    290                 295                 300
Pro
305
```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

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

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
 1               5                  10                  15
```

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

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

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

```
Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
    210                 215                 220
Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
225                 230                 235                 240
Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln
                245                 250                 255
Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
            260                 265                 270
Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
        275                 280                 285
Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
    290                 295                 300
Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala
305                 310                 315                 320
```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

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

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

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

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

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

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

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

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

```
305                 310                 315                 320
Pro
```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

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

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

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

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

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

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

```
Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
225                 230                 235                 240
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
                245                 250                 255
Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
            260                 265                 270
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
        275                 280                 285
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
    290                 295                 300
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
305                 310                 315                 320
Leu Gly Met Ala Pro Ala Leu Gln Pro
                325
```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

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

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

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

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

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

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

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

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

```
305                 310                 315                 320
Thr Gln Gly Ala Met Pro Ala Phe Ala
                325
```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

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

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1               5                  10                  15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
            20                  25                  30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
        35                  40                  45
```

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

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

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

```
Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser
225                 230                 235                 240
Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu
                245                 250                 255
Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
            260                 265                 270
Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro
        275                 280                 285
Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
    290                 295                 300
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

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

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

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

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

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

```
                165             170                     175
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro
            180                 185                 190
Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
        195                 200                 205
Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
    210                 215                 220
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu
225                 230                 235                 240
Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
                245                 250                 255
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
            260                 265                 270
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
        275                 280                 285
Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
    290                 295                 300
Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
305                 310                 315                 320
Gln Pro
```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

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

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

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

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

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

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

         (2) INFORMATION FOR SEQ ID NO:512:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 306 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: None

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

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

```
Leu Pro
305
```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

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

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

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

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

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

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

260 265 270
Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile
275 280 285
Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly
290 295 300
Gln Leu
305

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

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

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
1 5 10 15
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val
20 25 30

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

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

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

```
Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr
225                 230                 235                 240
Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
                245                 250                 255
Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys
            260                 265                 270
Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu
        275                 280                 285
Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
    290                 295                 300
Thr Thr
305
```

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

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

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

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

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

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

```
            180                 185                 190
Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln
        195                 200                 205
Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu
    210                 215                 220
Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro
225                 230                 235                 240
Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg
                245                 250                 255
Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly
            260                 265                 270
Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
        275                 280                 285
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys
    290                 295                 300
Pro
305
```

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

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

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

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

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

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

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

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

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

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

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

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

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

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

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

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

```
    290                 295                 300
Leu
305
```

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

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

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

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

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

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

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

```
Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu
            260                 265                 270
Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln
        275                 280                 285
Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His
    290                 295                 300
Lys
305
```

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

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

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

```
Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 1               5                  10                  15
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val
```

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

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

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

```
    210                 215                 220
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
225                 230                 235                 240
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
                245                 250                 255
Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Gly Gly
            260                 265                 270
Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
        275                 280                 285
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys
    290                 295                 300
Pro Glu Val His Pro
305
```

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

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

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

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

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

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

```
Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu
            180                 185                 190
Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser
        195                 200                 205
Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
    210                 215                 220
Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys
225                 230                 235                 240
Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu
                245                 250                 255
Phe Gly Gly Asn Gly Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys
            260                 265                 270
Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His
        275                 280                 285
Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
    290                 295                 300
Leu Leu Pro Ala Val
305
```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

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

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

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

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

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

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

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

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

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

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

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

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

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

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

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

```
Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala
    290                 295                 300
His Lys Asp Pro Asn
305
```

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

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

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

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

```
65                  70                  75                  80
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
                85                  90                  95
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
            100                 105                 110
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
        115                 120                 125
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
    130                 135                 140
Val Gly Gly Ser Thr Leu Cys Val Arg
145                 150
```

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

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

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

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

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

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

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

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

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```
Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
 1               5                  10                  15
```

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

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

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

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

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

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

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

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

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

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

```
Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 1               5                  10                  15
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
```

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

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

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

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

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

```
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        115                 120                 125
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    130                 135                 140
Gln
145
```

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

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

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

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

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

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

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

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

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

```
Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
 1               5                  10                  15
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
```

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

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

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

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

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

```
Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
        115                 120                 125
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
    130                 135                 140
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

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

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

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

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

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

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

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

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

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

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

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

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

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

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

```
Pro Asp Ser Ser Thr Leu
145                 150
```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

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

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

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

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

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

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

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

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

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

```
    50                  55                  60
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65                  70                  75                  80
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
                85                  90                  95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Ser Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
        115                 120                 125
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
    130                 135                 140
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

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

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

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

```
Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
    130                 135                 140
Asn Met Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
145                 150                 155                 160
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
                165                 170                 175
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
            180                 185                 190
Ala Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
        195                 200                 205
Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
    210                 215                 220
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
225                 230                 235                 240
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
                245                 250                 255
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
            260                 265                 270
Arg Cys Leu Glu Leu Gln Cys Gln Pro
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

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

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

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

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

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

```
                165                 170                 175
Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys
            180                 185                 190
Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn
        195                 200                 205
Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys
    210                 215                 220
Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys
225                 230                 235                 240
Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn
                245                 250                 255
Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
            260                 265                 270
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro
        275                 280                 285
Val Thr Val Ala Ser Asn Leu Gln
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

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

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

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

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

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

Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys
180 185 190
Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn
195 200 205
Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys
210 215 220
Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys
225 230 235 240
Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn
245 250 255
Gly Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro
260 265 270
Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu
275 280 285
Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
290 295 300

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

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

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

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

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

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

```
            180                 185                 190
Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser
        195                 200                 205
Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
    210                 215                 220
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
225                 230                 235                 240
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys
                245                 250                 255
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu
            260                 265                 270
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn
        275                 280                 285
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

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

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

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

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

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

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

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

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

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

```
Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 1               5                  10                  15
Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met
```

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

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

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

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

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

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

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

```
Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 1               5                  10                  15
Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met
            20                  25                  30
```

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

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

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

```
Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg
                245                 250                 255
Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly
            260                 265                 270
Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe
    275                 280                 285
Val Thr Lys Cys Ala Phe Gln Pro
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

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

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

```
Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 1               5                  10                  15
Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met
            20                  25                  30
Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe
```

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

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

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

```
                245                 250                 255
Gly Ser Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro
            260                 265                 270
Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu
        275                 280                 285
Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

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

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

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

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

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

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

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 292 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

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

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 293 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

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

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

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

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

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

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

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

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

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

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

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

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

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

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

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

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

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

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

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

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

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

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

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

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

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

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

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

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

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

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

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 296 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

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

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

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

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

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

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

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

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

(2) INFORMATION FOR SEQ ID NO:622:

```
(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 296 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:
```

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

```
  (2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 301 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:
```

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

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

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

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

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

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

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

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

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

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

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

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

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

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

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

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

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

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

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

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

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

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

Asn Met Ala Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu
145   150   155   160
Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met
                165   170   175
Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu
            180   185   190
Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
        195   200   205
Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu
    210   215   220
Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg
225   230   235   240
Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser
                245   250   255
Thr Leu Gly Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln His
            260   265   270
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp
        275   280   285
Tyr Leu Leu Gln
    290

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

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

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

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

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

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

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

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

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

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

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

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

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

Asn Met Ala Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu
145 150 155 160
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val
165 170 175
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
180 185 190
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg
195 200 205
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln
210 215 220
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys
225 230 235 240
Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser
245 250 255
Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe Gln
260 265 270
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser
275 280 285
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val
290 295

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

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

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

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

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 293 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

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

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

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

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

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

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

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

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

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

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

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

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

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

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

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

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

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

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

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

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

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

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

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

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

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

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

```
Gly Ser Thr Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu
1               5                   10                  15
Val Arg Pro Ala Met Ser Thr Asn Gln Asp Leu Pro Val Ile Lys Cys
            20                  25                  30
Val Leu Ile Asn His Lys Asn Asn Asp Ser Ser Val Gly Lys Ser Ser
        35                  40                  45
Ser Tyr Pro Met Val Ser Glu Ser Pro Glu Asp Leu Gly Cys Ala Leu
    50                  55                  60
Arg Pro Gln Ser Ser Gly Thr Val Tyr Glu Ala Ala Ala Val Glu Val
65                  70                  75                  80
Asp Val Ser Ala Ser Ile Thr Leu Gln Val Leu Val Asp Ala Pro Gly
                85                  90                  95
Asn Ile Ser Cys Leu Trp Val Phe Lys His Ser Ser Leu Asn Cys Gln
            100                 105                 110
Pro His Phe Asp Leu Gln Asn Arg Gly Val Val Ser Met Val Ile Leu
        115                 120                 125
Lys Met Thr Glu Thr Gln Ala Gly Glu Tyr Leu Leu Phe Ile Gln Ser
    130                 135                 140
Glu Ala Thr Asn Tyr Thr Ile Leu Phe Thr Val Ser Ile Arg Asn Thr
145                 150                 155                 160
Leu Leu Tyr Thr Leu Arg Arg Pro Tyr Phe Arg Lys Met Glu Asn Gln
                165                 170                 175
Asp Ala Leu Val Cys Ile Ser Glu Ser Val Pro Glu Pro Ile Val Glu
            180                 185                 190
Trp Val Leu Cys Asp Ser Gln Gly Glu Ser Cys Lys Glu Glu Ser Pro
        195                 200                 205
Ala Val Val Lys Lys Glu Glu Lys Val Leu His Glu Leu Phe Gly Met
    210                 215                 220
Asp Ile Arg Cys Cys Ala Arg Asn Glu Leu Gly Arg Glu Cys Thr Arg
225                 230                 235                 240
Leu Phe Thr Ile Asp Leu Asn Gln Thr Pro Gln Thr Thr Leu Pro Gln
                245                 250                 255
Leu Phe Leu Lys Val Gly Glu Pro Leu Trp Ile Arg Cys Lys Ala Val
            260                 265                 270
His Val Asn His Gly Phe Gly Leu Thr Trp Glu Leu Glu Asn Lys Ala
        275                 280                 285
Leu Glu Glu Gly Asn Tyr Phe Glu Met Ser Thr Tyr Ser Thr Asn Arg
    290                 295                 300
Thr Met Ile Arg Ile Leu Phe Ala Phe Val Ser Ser Val Ala Arg Asn
305                 310                 315                 320
Asp Thr Gly Tyr Tyr Thr Cys Ser Ser Ser Lys His Pro Ser Gln Ser
                325                 330                 335
Ala Leu Val Thr Ile Val Glu Lys Gly Phe Ile Asn Ala Thr Asn Ser
            340                 345                 350
Ser Glu Asp Tyr Glu Ile Asp Gln Tyr Glu Glu Phe Cys Phe Ser Val
        355                 360                 365
Arg Phe Lys Ala Tyr Pro Gln Ile Arg Cys Thr Trp Thr Phe Ser Arg
    370                 375                 380
Lys Ser Phe Pro Cys Glu Gln Lys Gly Leu Asp Asn Gly Tyr Ser Ile
385                 390                 395                 400
Ser Lys Phe Cys Asn His Lys His Gln Pro Gly Glu Tyr Ile Phe His
                405                 410                 415
Ala Glu Asn Asp Asp Ala Gln Phe Thr Lys Met Phe Thr Leu Asn Ile
            420                 425                 430
Arg Arg Lys Pro Gln Val Leu Ala Glu Ala Ser Ala Ser Gln Ala Ser
        435                 440                 445
Cys Phe Ser Asp Gly Tyr Pro Leu Pro Ser Trp Thr Trp Lys Lys Cys
    450                 455                 460
Ser Asp Lys Ser Pro Asn Cys Thr Glu Glu Ile Thr Glu Gly Val Trp
465                 470                 475                 480
Asn Arg Lys Ala Asn Arg Lys Val Phe Gly Gln Trp Val Ser Ser Ser
                485                 490                 495
Thr Leu Asn Met Ser Glu Ala Ile Lys Gly Phe Leu Val Lys Cys Cys
            500                 505                 510
Ala Tyr Asn Ser Leu Gly Thr Ser Cys Glu Thr Ile Leu Leu Asn Ser
        515                 520                 525
```

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

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

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

```
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
    290                 295                 300
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
305                 310                 315                 320
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
                325                 330                 335
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

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

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

```
Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
1               5                   10                  15
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro
```

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

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 523 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

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

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

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

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

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

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 523 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

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

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

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

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

```
        195                 200                 205
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    210                 215                 220
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
225                 230                 235                 240
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                245                 250                 255
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            260                 265                 270
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        275                 280                 285
Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    290                 295                 300
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
305                 310                 315                 320
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

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

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

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

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

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

```
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile
            180                 185                 190
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg
        195                 200                 205
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln
    210                 215                 220
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys
225                 230                 235                 240
Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser
                245                 250                 255
Gly Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro
            260                 265                 270
Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu
        275                 280                 285
Leu Gln Asp Tyr Pro Val Thr Val
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

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

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

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

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

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

```
            180                 185                 190
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
        195                 200                 205
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
    210                 215                 220
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr
225                 230                 235                 240
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
                245                 250                 255
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr
            260                 265                 270
Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg
        275                 280                 285
Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

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

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

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

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

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

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

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

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

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

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

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

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

180 185 190
Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val
195 200 205
Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val
210 215 220
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu
225 230 235 240
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly
245 250 255
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr
260 265 270
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val
275 280 285
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr
290 295 300
Val Ala Ser
305

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

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

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

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

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

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

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

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

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

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

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

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

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

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

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

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

290 295 300
Ser Asn Leu
305

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

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

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

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

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

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

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

```
Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr
        275                 280                 285
Leu Glu Gln Ala Gln Glu Gln Gln
    290                 295
```

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

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

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

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

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

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

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

```
            260                 265                 270
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
        275                 280                 285
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

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

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

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

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

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

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

```
Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
            260                 265                 270
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
        275                 280                 285
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

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

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

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

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

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

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

```
            260                 265                 270
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
        275                 280                 285
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

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

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

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

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

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

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

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
275 280 285
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
290 295 300
Glu Gln Gln
305

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

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

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

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

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

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

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

225 230 235 240
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
245 250 255
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
260 265 270
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
275 280 285
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
290 295 300
Glu Gln Gln
305

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

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

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

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

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

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

```
Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
        195                 200                 205
Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser
    210                 215                 220
Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
225                 230                 235                 240
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile
                245                 250                 255
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
            260                 265                 270
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
        275                 280                 285
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
    290                 295                 300
Glu Gln Gln
305
```

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

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

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

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

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

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

```
                165                 170                 175
Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro
            180                 185                 190
Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Asn Cys Ser Ile
    195                 200                 205
Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn Pro Leu
    210                 215                 220
Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu Met Glu
225                 230                 235                 240
Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala Val Lys
                245                 250                 255
His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln
            260                 265                 270
Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile
        275                 280                 285
Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
    290                 295                 300
Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

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

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

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

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

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

```
Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Tyr
                165                 170                 175
Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser
            180                 185                 190
Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn
        195                 200                 205
Met Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala
    210                 215                 220
Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln
225                 230                 235                 240
Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys
                245                 250                 255
Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile
            260                 265                 270
Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro
        275                 280                 285
Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln
    290                 295                 300
Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
305                 310                 315                 320
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser
                325                 330                 335
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
            340                 345                 350
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
        355                 360                 365
Leu Gln
    370
```

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

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

```
Ile Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala
        275                 280                 285
Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu
    290                 295                 300
Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly
305                 310                 315                 320
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln
                325                 330                 335
Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys
            340                 345                 350
Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val
        355                 360                 365
Ala Ser
    370
```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

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

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 370 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

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

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 370 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

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

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

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

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

```
                165                 170                 175
Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser
            180                 185                 190
Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn
        195                 200                 205
Met Ala Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
    210                 215                 220
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
225                 230                 235                 240
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
                245                 250                 255
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
            260                 265                 270
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
        275                 280                 285
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
    290                 295                 300
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
305                 310                 315                 320
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe
                325                 330                 335
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
            340                 345                 350
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
        355                 360                 365
Gln Asp
    370
```

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

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

```
    290                 295                 300
Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
305                 310                 315                 320
Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe Gln
                325                 330                 335
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser
            340                 345                 350
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
        355                 360                 365
Asp Glu
    370
```

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

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

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

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

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

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

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

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

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

```
Met Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala
    210                 215                 220
Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln
225                 230                 235                 240
Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys
                245                 250                 255
Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile
            260                 265                 270
Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro
        275                 280                 285
Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln
    290                 295                 300
Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly
305                 310                 315                 320
Ala Thr Ala Pro Thr Ala Gly Gln Pro Pro Leu Thr Gln Asp Cys Ser
                325                 330                 335
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
            340                 345                 350
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
        355                 360                 365
Leu Gln
    370
```

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

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

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

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

```
65                  70                  75                  80
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu
                85                  90                  95
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly
            100                 105                 110
Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln
        115                 120                 125
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser
    130                 135                 140
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val
145                 150                 155
```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

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

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

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

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

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

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

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

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

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

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

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

```
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
            340                 345                 350
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
        355                 360                 365
Gln Pro
    370
```

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

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

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

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

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

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

115 120 125
Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
130 135 140
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
145 150 155 160
Pro Val Thr Val Ala Ser Asn Leu Gln Tyr Val Glu Gly Gly Gly Gly
165 170 175
Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Pro Leu
180 185 190
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu
195 200 205
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu
210 215 220
Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
225 230 235 240
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
245 250 255
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe
260 265 270
Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu
275 280 285
Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
290 295 300
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln
305 310 315 320
Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
325 330 335
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val
340 345 350
Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
355 360

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

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

```
        260                     265                 270
Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
        275                 280                 285
Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
    290                 295                 300
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
305                 310                 315                 320
Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
                325                 330                 335
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

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

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

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

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

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

```
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe
        115                 120                 125
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
    130                 135                 140
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
145                 150                 155                 160
Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
                165                 170                 175
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
            180                 185                 190
Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
        195                 200                 205
Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
    210                 215                 220
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
225                 230                 235                 240
Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
                245                 250                 255
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
            260                 265                 270
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
        275                 280                 285
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
    290                 295                 300
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
305                 310                 315                 320
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
                325                 330                 335
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
            340                 345                 350
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Val Arg His Leu Ala
        355                 360                 365
Gln Pro
    370
```

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

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

```
Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu
225                 230                 235                 240
Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
                245                 250                 255
Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
            260                 265                 270
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
        275                 280                 285
Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
    290                 295                 300
Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
305                 310                 315                 320
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
                325                 330                 335
Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
            340                 345                 350
Val Ser Tyr Arg Val Ile Arg His Leu Ala Gln Pro
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

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

```
Gln Pro
    370
```

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

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

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

```
Ala Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu
```

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

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

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

130 135 140
Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu
145 150 155 160
Glu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
165 170 175
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
180 185 190
Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
195 200 205
Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
210 215 220
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
225 230 235 240
Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
245 250 255
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
260 265 270
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
275 280 285
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
290 295 300
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
305 310 315 320
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
325 330 335
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
340 345 350
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
355 360 365
Gln Pro
370

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

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

260 265 270
Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
275 280 285
Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
290 295 300
Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
305 310 315 320
Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
325 330 335
Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
340 345 350
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
355 360

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

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

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

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

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

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

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

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

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

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

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

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

```
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
                325                 330                 335
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
            340                 345                 350
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
        355                 360                 365
Gln Pro
    370
```

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

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

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

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

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

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

```
        115                 120                 125
Phe Gln His Ser Pro Ile Ser Ser Asp Ser Ala Val Lys Ile Arg Glu
    130                 135                 140
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
145                 150                 155                 160
Leu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
                165                 170                 175
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
            180                 185                 190
Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
        195                 200                 205
Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
    210                 215                 220
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
225                 230                 235                 240
Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
                245                 250                 255
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
            260                 265                 270
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
        275                 280                 285
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
    290                 295                 300
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
305                 310                 315                 320
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
                325                 330                 335
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His
            340                 345                 350
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
        355                 360                 365
Gln Pro
    370
```

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

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

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

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

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

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

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

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

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

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

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

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

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

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

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

```
Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
                325                 330                 335
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala
            340                 345                 350
Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser
        355                 360                 365
Tyr Arg Val Leu Arg His Leu Ala Gln Pro
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

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

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

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

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

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

```
                85                  90                  95
Val Glu Thr Val Phe His Arg Val Ser Gln Asp Gly Leu Asp Leu Leu
            100                 105                 110
Thr Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
        115                 120                 125
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
    130                 135                 140
Pro Val Thr Val Ala Ser Asn Leu Gln Tyr Val Glu Gly Gly Gly Gly
145                 150                 155                 160
Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Pro Leu
                165                 170                 175
Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu
            180                 185                 190
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu
        195                 200                 205
Cys Ala Thr Asn Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
    210                 215                 220
His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
225                 230                 235                 240
Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe
                245                 250                 255
Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu
            260                 265                 270
Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
        275                 280                 285
Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln
    290                 295                 300
Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
305                 310                 315                 320
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val
                325                 330                 335
Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
            340                 345
```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

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

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

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

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

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

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

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

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

```
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
                85                  90                  95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Ser Ser Phe
        115                 120                 125
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
    130                 135                 140
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
145                 150                 155                 160
Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
                165                 170                 175
Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln
            180                 185                 190
Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
        195                 200                 205
Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Asn Lys Leu Cys His
    210                 215                 220
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
225                 230                 235                 240
Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
                245                 250                 255
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
            260                 265                 270
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
        275                 280                 285
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
    290                 295                 300
Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
305                 310                 315                 320
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
                325                 330                 335
His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
            340                 345                 350
Ala Gln Pro
        355
```

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

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

```
Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln
225                 230                 235                 240
Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Ser
                245                 250                 255
Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile
            260             265                     270
Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro
        275                 280                 285
Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln
    290                 295                 300
Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
305                 310                 315                 320
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln Asp Ser Ser
                325                 330                 335
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu
            340                 345                 350
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn
        355                 360                 365
Leu Gln
    370

          (2) INFORMATION FOR SEQ ID NO:759:

       (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 355 amino acids
         (B) TYPE: amino acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: None

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

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

```
Ala Gln Pro
        355
```

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

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

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

```
Ala Thr Gln Asp Ser Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe
```

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

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

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

```
            180                 185                 190
Glu Lys Leu Cys Ala Thr Asn Lys Leu Cys His Pro Glu Glu Leu Val
        195                 200                 205
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    210                 215                 220
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
225                 230                 235                 240
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                245                 250                 255
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            260                 265                 270
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        275                 280                 285
Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    290                 295                 300
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
305                 310                 315                 320
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

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

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

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

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

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

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

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

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

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

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

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

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

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

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

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

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

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

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

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

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

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

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

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

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

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

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

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

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

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

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

```
145                 150                 155                 160
Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly
                165                 170                 175
Gly Ser Asn Met Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu
            180                 185                 190
Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser
        195                 200                 205
Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val
    210                 215                 220
Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln
225                 230                 235                 240
Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala
                245                 250                 255
Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu
            260                 265                 270
Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly
        275                 280                 285
Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Thr Gln
    290                 295                 300
Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys
305                 310                 315                 320
Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val
                325                 330                 335
Ala Ser Asn Leu Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu
            340                 345                 350
Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
        355                 360                 365
Ser His Lys Ser Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser
    370                 375                 380
Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile
385                 390                 395                 400
Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
                405                 410                 415
Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile
            420                 425                 430
Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
        435                 440                 445
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
    450                 455                 460
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp
465                 470                 475                 480
Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
                485                 490                 495
Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
            500                 505                 510
Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu
        515                 520                 525
Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
    530                 535                 540
Arg His Leu Ala Gln Pro Ser Thr Pro Ser Thr Pro Gly Ser Glu Phe
545                 550                 555                 560
Gly Ser
```

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

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

```
                85                  90                  95
Asp Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
            100                 105                 110
Ser Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
        115                 120                 125
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
    130                 135                 140
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Tyr Val Glu Gly Gly
145                 150                 155                 160
Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
                165                 170                 175
Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Asn Cys
            180                 185                 190
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn
        195                 200                 205
Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu
    210                 215                 220
Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala
225                 230                 235                 240
Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
                245                 250                 255
Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
            260                 265                 270
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
        275                 280                 285
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu
    290                 295                 300
Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile
305                 310                 315                 320
Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
                325                 330                 335
Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg
            340                 345                 350
Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu
        355                 360                 365
Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe
    370                 375                 380
Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg
385                 390                 395                 400
Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile
                405                 410                 415
Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp
            420                 425                 430
Ser Ser Thr Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
        435                 440                 445
Gly Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
    450                 455                 460
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
465                 470                 475                 480
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln
                485                 490
```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

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

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

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

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

```
    210                 215                 220
Asp Tyr Asn Ser Thr Leu Arg Ala Val Ser Ala Leu Pro Ile Gln His
225                 230                 235                 240
Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
                245                 250                 255
Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
            260                 265                 270
Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
        275                 280                 285
Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
    290                 295                 300
Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
305                 310                 315                 320
Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
                325                 330                 335
Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
            340                 345                 350
Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
        355                 360                 365
Lys Ser Phe Ser Arg Thr Pro Gly Lys
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

```
Gly Gly Gly Ser
 1
```

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

```
Gly Gly Gly Ser Gly Gly Gly Ser
 1               5
```

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

```
Ser Gly Gly Ser Gly Gly Ser
 1               5
```

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

```
Glu Phe Gly Asn Met
 1               5
```

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

```
Glu Phe Gly Gly Asn Met
 1               5
```

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

```
Glu Phe Gly Gly Asn Gly Gly Asn Met
 1               5
```

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

```
Gly Gly Ser Asp Met Ala Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

```
Ser Gly Gly Asn Gly
 1               5

          (2) INFORMATION FOR SEQ ID NO:787:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: None

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly
 1               5                  10

          (2) INFORMATION FOR SEQ ID NO:788:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: None

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly
 1               5                  10                  15

          (2) INFORMATION FOR SEQ ID NO:789:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: None

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
 1               5                  10

          (2) INFORMATION FOR SEQ ID NO:790:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: None

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
 1               5                  10                  15

          (2) INFORMATION FOR SEQ ID NO:791:

      (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: None

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

Gly Gly Gly Ser Gly Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

```
Gly Gly Gly Ser Gly Gly Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1               5                  10                  15
Gly Gly Gly Ser Gly
            20
```

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

```
Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr Ala
 1               5                  10                  15
Gly Gln Pro Pro Leu
            20
```

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

```
Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

```
Val Glu Thr Val Phe His Arg Val Ser Gln Asp Gly Leu Leu Thr Ser
 1               5                  10                  15
```

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

```
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
 1               5                  10                  15
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
            20                  25                  30
Gly Gly Gly Ser
        35
```

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

```
Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
1               5                   10                  15
Ser Lys Glu Ser His Lys Ser Pro
            20
```

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```
Ile Glu Gly Arg Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
1               5                   10                  15
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

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

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

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

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

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

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

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

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```
CTGACCATGG CNACCCAGGA CTGCTCCTTC CAA                                  33
```

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

ACTGAAGCTT AGGGCTGACA CTGCAGCTCC AG 32

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

ACTGAAGCTT ACAGGGTTGA GGAGTCGGGC TG 32

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC 46

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC 46

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

TGTCCAAACT CATCAATGTA TC 22

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

CATGGCCATG GCCGACGAGG AGCTCTGCGG GGGCCTCT 38

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GCTAGAAGCT TACTGCAGGT TGGAGGCCAC GGTGAC 36

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

CATGGCCATG GCCTCCAAGA TGCAAGGCTT GCTGGAGC 38

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GCTAGAAGCT TACCCAGCGA CAGTCTTGAG CCGCTC 36

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

CATGGCCATG GCCCCCCCCA GCTGTCTTCG CTTCGT 36

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GCTAGAAGCT TAGGGCTGAA AGGCACATTT GGTGACA 37

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

CCCTGTCTGG CGGCAACGGC ACCCAGGACT GCTCCTTCCA AC 42

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

GCGGTAACGG CAGTGGAGGT AATGGCACCC AGGACTGCTC CTTCCAAC 48

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

ACGGCAGTGG TGGCAATGGG AGCGGCGGAA ATGGAACCCA GGACTGCTCC TTCCAAC 57

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GTGCCGTTGC CGCCAGACAG GGTTGAGGAG TCGGGCTG 38

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

ATTACCTCCA CTGCCGTTAC CGCCTGACAG GGTTGAGGAG TCGGGCTG 48

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GCTCCCATTG CCACCACTGC CGTTACCTCC AGACAGGGTT GAGGAGTCGG GCTG 54

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GATGAGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC TCCTTCCACC 60

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GATGACGGAT CCGTTACCTC CAGACAGGGT TGAGGAGTCG GGCTG 45

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GATGACGGAT CCGGAGGTAA TGGCACCCAG GACTGCTCCT TCCAAC 46

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GACTGCCATG GCCGACGAGG AGCTCTGCG 29

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GACTCAAGCT TACTGCAGGT TGGAGGCC 28

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GACTCGGGAT CCGGAGGTTC TGGCACCCAG GACTGCTCC 39

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GACTGGGATC CGGTGGCAGT GGGAGCGGCG GATCTGGAAC C 41

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GACTTGGGAT CCACTACCTC CAGACAGGGT TGAGGAGTC 39

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

ACTGACGGAT CCACCGCCCA GGGTTGAGGA GTCGGGCTG 39

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

ACTGACGGAT CCACCTCCTG ACCCACCGCC CAGGGTTGAG GAGTCGGGCT G 51

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

ACTGACGGAT CCACCTCCTG ACCCACCTCC TGACCCACCG CCCAGGGTTG AGGAGTCGGG 60
CTG 63

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ACGTAAAGCT TACAGGGTTG AGGAGTCG 28

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GTCAGTGGAT CCGGAGGTAC CCAGGACTGC TCCTTCCAAC 40

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GTCAGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AAC 43

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

TCAGTGGATC CGGAGGTGGC TCAGGGGGAG GTAGTGGTAC CCAGGACTGC TCCTTCCAAC 60

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

TAGTCCATGG CCACCCAGGA CTGCTCC 27

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GCATTACGTA GGGCTGACAC TGCAGCTCCA G 31

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GCATTACGTA CAGGGTTGAG GAGTCGGGCT G 31

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GTCAGACCAT GGCCGATTAC CCAGTCACCG TGGCCTC 37

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

TCTGACAAGC TTATTGAAGC AGGTAGTCAG ACAGCTCAC 39

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GTCAGCCCAT GGCCGCCTCC AACCTGCAGG ACGAGGA 37

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

TCTGACAAGC TTACACGGTG ACTGGGTAAC TTGAAGC 37

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GTCAGACCAT GGCCGTCGCT GGGTCCAAGA TGCAAGGC 38

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

TCTGACAAGC TTAAGTCTTG AGCCGCTCCA TCCAGCG 37

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GTCAGACCAT GGCCCGCTTC GTCCAGACCA ACATCTCC 38

(2) INFORMATION FOR SEQ ID NO:850:

745

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

TCTGACAAGC TTAAAGACAG CTGGGGGGGG GCTGAA 36

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

GTCAGACCAT GGCCACCAAC ATCTCCCGCC TCCTGCAG 38

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

CTCGACAAGC TTACTGGACG AAGCGAAGAC AGCTGGG 37

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GATCACATGT CTACAAATCA AGATCTGCCT GTG 33

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

GATCGAATTC GTTGTCTTGG ATGAAAGGGA 30

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

ACTTGAATTC ATCATCCTGG GCCTGTTCGG GC 32

746

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

```
ACTCAAGCTT AGAAGCTCCC CAGCGCCTCC                                  30
```

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

```
GGATCCACCA TGAGCCGCCT GCCCGTCCTG CTCCTGCTCC AACTCCTGGT CCGCCCCGCC  60
ATGG                                                               64
```

(2) INFORMATION FOR SEQ ID NO: 858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:2
(D) OTHER INFORMATION:/note= "Xaa at position 2 is Pro or Leu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:3
(D) OTHER INFORMATION:/note= "Xaa at position 3 is Leu, Arg, Tyr or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:13
(D) OTHER INFORMATION:/note= "Xaa at position 13 is Phe, Ser, His, Thr or Pro;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:16
(D) OTHER INFORMATION:/note= "Xaa at position 16 is Lys, Pro, Ser, thr or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:17
(D) OTHER INFORMATION:/note= "Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site

```
          (B) LOCATION:18
          (D) OTHER INFORMATION:/note= "Xaa at position 18 is Leu,
                Thr, Pro, His, Ile or Cys;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:22
          (D) OTHER INFORMATION:/note= "Xaa at position 22 is Arg,
                Tyr, Ser, Thr or Ala;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:24
          (D) OTHER INFORMATION:/note= "Xaa at position 24 is Ile,
                Pro, Tyr or Leu;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:27
          (D) OTHER INFORMATION:/note= "Xaa at position 27 is Asp,
                or Gly;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:30
          (D) OTHER INFORMATION:/note= "Xaa at position 30 is Ala,
                Ile, Leu or Gly;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:34
          (D) OTHER INFORMATION:/note= "Xaa at position 34 is Lys
                or Ser;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:36
          (D) OTHER INFORMATION:/note= "Xaa at position 36 is Cys
                or Ser;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:42
          (D) OTHER INFORMATION:/note= "Xaa at position 42 is Cys
                or Ser;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:43
          (D) OTHER INFORMATION:/note= "Xaa at position 43 is His,
                Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:44
          (D) OTHER INFORMATION:/note= "Xaa at position 44 is Pro,
                Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:46
          (D) OTHER INFORMATION:/note= "Xaa at position 46 is Glu,
                Arg, Phe, Arg, Ile or Ala;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:47
          (D) OTHER INFORMATION:/note= "Xaa at position 47 is Leu
                or Thr;"

    (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:49
          (D) OTHER INFORMATION:/note= "Xaa at position 49 is Leu,
                Phe, Arg or Ser;"

    (ix) FEATURE:
```

(A) NAME/KEY: Modified-site
(B) LOCATION:50
(D) OTHER INFORMATION:/note= "Xaa at position 50 is Leu, Ile, His, Pro or Tyr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:54
(D) OTHER INFORMATION:/note= "Xaa at position 54 is Leu or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:64
(D) OTHER INFORMATION:/note= "Xaa at position 64 is Cys or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:67
(D) OTHER INFORMATION:/note= "Xaa at position 67 is Gln, Lys, Leu or Cys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:70
(D) OTHER INFORMATION:/note= "Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:74
(D) OTHER INFORMATION:/note= "Xaa at position 74 is Cys or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:104
(D) OTHER INFORMATION:/note= "Xaa at position 104 is Asp, Gly or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:108
(D) OTHER INFORMATION:/note= "Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:115
(D) OTHER INFORMATION:/note= "Xaa at position 115 is Thr, His, Leu or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:120
(D) OTHER INFORMATION:/note= "Xaa at position 120 is Gln, Gly, Arg, Lys or His"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:123
(D) OTHER INFORMATION:/note= "Xaa at position 123 is Glu, Arg, Phe or Thr"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:144
(D) OTHER INFORMATION:/note= "Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or Glu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:146
(D) OTHER INFORMATION:/note= "Xaa at position146 is Arg or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:147
(D) OTHER INFORMATION:/note= "Xaa ap position 147 is Arg or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:156
(D) OTHER INFORMATION:/note= "Xaa at position 156 is His, Gly or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:159
(D) OTHER INFORMATION:/note= "Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:162
(D) OTHER INFORMATION:/note= "Xaa at position 162 is Glu, Leu, Gly or Trp;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:163
(D) OTHER INFORMATION:/note= "Xaa at position 163 is Val, Gly, Arg or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:169
(D) OTHER INFORMATION:/note= "Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:170
(D) OTHER INFORMATION:/note= "Xaa at position 170 is His, Arg or Ser;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858:

```
Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa Leu Leu Xaa


Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly Ala Xaa Leu Gln
            20                  25                  30

Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa Xaa Glu Xaa Xaa Val
        35                  40                  45

Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp Ala Pro Leu Ser Ser Xaa
    50                  55                  60

Pro Ser Xaa Ala Leu Xaa Leu Ala Gly Xaa Leu Ser Gln Leu His Ser
65                  70                  75                  80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85                  90                  95

Pro Glu Leu Gly Pro Thr Leu Xaa Thr Leu Gln Xaa Asp Val Ala Asp
            100                 105                 110

Phe Ala Xaa Thr Ile Trp Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro
        115                 120                 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa
    130                 135                 140

Gln Xaa Xaa Ala Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe
145                 150                 155                 160

Leu Xaa Xaa Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro
```

(2) INFORMATION FOR SEQ ID NO: 859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:17
(D) OTHER INFORMATION:/note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:18
(D) OTHER INFORMATION:/note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:19
(D) OTHER INFORMATION:/note= "Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:20
(D) OTHER INFORMATION:/note= "Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:21
(D) OTHER INFORMATION:/note= "Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:22
(D) OTHER INFORMATION:/note= "Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:23
(D) OTHER INFORMATION:/note= "Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:24
(D) OTHER INFORMATION:/note= "Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, Leu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:25
(D) OTHER INFORMATION:/note= "Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:26
(D) OTHER INFORMATION:/note= "Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, Trp;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:27
(D) OTHER INFORMATION:/note= "Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:28
(D) OTHER INFORMATION:/note= "Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:29
(D) OTHER INFORMATION:/note= "Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:30
(D) OTHER INFORMATION:/note= "Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or L..."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:31
(D) OTHER INFORMATION:/note= "Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:32
(D) OTHER INFORMATION:/note= "Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:33
(D) OTHER INFORMATION:/note= "Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:34
(D) OTHER INFORMATION:/note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:35
(D) OTHER INFORMATION:/note= "Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:36
(D) OTHER INFORMATION:/note= "Xaa at position 36 is Asp, Leu, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:37
(D) OTHER INFORMATION:/note= "Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:38
(D) OTHER INFORMATION:/note= "Xaa at position 38 is Asn, or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:40
(D) OTHER INFORMATION:/note= "Xaa at position 40 is Leu, Trp, or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:41

(D) OTHER INFORMATION:/note= "Xaa at position 41 is Asn,
Cys, Arg, Leu, His, Met, or pro;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:42
(D) OTHER INFORMATION:/note= "Xaa at position 42 is Gly,
Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile,
Met
or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:43
(D) OTHER INFORMATION:/note= "Xaa at position 43 is Glu,
Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly, or
Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:44
(D) OTHER INFORMATION:/note= "Xaa at position 44 is Asp,
Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or
Pro;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:45
(D) OTHER INFORMATION:/note= "Xaa at position 45 is Gln,
Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser,
Ala, Ile, Glu or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:46
(D) OTHER INFORMATION:/note= "Xaa at position 46 is Asp,
Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile,
Val
or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:47
(D) OTHER INFORMATION:/note= "Xaa at position 47 is Ile,
Gly, Val, Ser, Arg, Pro, or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:48
(D) OTHER INFORMATION:/note= "Xaa at position 48 is Leu,
Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val
or
Asn;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:49
(D) OTHER INFORMATION:/note= "Xaa at position 49 is Met,
Arg, Ala, Gly, Pro, Asn, His, or Asp;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:50
(D) OTHER INFORMATION:/note= "Xaa at position 50 is Glu,
Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe,
Met
or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:51
(D) OTHER INFORMATION:/note= "Xaa at position 51 is Asn,
Arg, Met, Pro, Ser, Thr, or his;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:52

(D) OTHER INFORMATION:/note= "Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:53
(D) OTHER INFORMATION:/note= "Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or M..."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:54
(D) OTHER INFORMATION:/note= "Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:55
(D) OTHER INFORMATION:/note= "Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:56
(D) OTHER INFORMATION:/note= "Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val

or Lys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:57
(D) OTHER INFORMATION:/note= "Xaa at position 57 is Asn or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:58
(D) OTHER INFORMATION:/note= "Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:59
(D) OTHER INFORMATION:/note= "Xaa at position 59 is Glu, Tyr, His, Leu, Pro, or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:60
(D) OTHER INFORMATION:/note= "Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:61
(D) OTHER INFORMATION:/note= "Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:62
(D) OTHER INFORMATION:/note= "Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:63
(D) OTHER INFORMATION:/note= "Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:64
(D) OTHER INFORMATION:/note= "Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;"

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:65
      (D) OTHER INFORMATION:/note= "Xaa at position 65 is Val,
            Thr, Pro, His, Leu, Phe, or Ser;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:66
      (D) OTHER INFORMATION:/note= "Xaa at position 66 is Lys,
            Ile, Arg, Val, Asn, Glu, or Ser;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:67
      (D) OTHER INFORMATION:/note= "Xaa at postion 67 is Ser,
            Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:68
      (D) OTHER INFORMATION:/note= "Xaa at position 68 is Leu,
            Val, Trp, Ser, Ile, Phe, Thr, or His;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:69
      (D) OTHER INFORMATION:/note= "Xaa at position 69 is Gln,
            Ala, Pro, Thr, Glu, Arg, Trp, Gly, or L..."

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:70
      (D) OTHER INFORMATION:/note= "Xaa at position 70 is Asn,
            Leu, Val, Trp, pro, or Ala;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:71
      (D) OTHER INFORMATION:/note= "Xaa at position 71 is Ala,
            Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:72
      (D) OTHER INFORMATION:/note= "Xaa at position 72 is Ser,
            Glu, Met, Ala, His, Asn, Arg, or Asp;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:73
      (D) OTHER INFORMATION:/note= "Xaa at position 73 is Ala,
            Glu, Asp, Leu, Ser, Gly, Thr, or Arg;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:74
      (D) OTHER INFORMATION:/note= "Xaa at position 74 is Ile,
            Met, Thr, Pro, Arg, Gly, Ala;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:75
      (D) OTHER INFORMATION:/note= "Xaa at position 75 is Glu,
            Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;"

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:76
      (D) OTHER INFORMATION:/note= "Xaa at position 76 is Ser,
            Val, Ala, Asn, Trp, Glu, Pro, Gly, or A..."

(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION:77
      (D) OTHER INFORMATION:/note= "Xaa at position 77 is Ile,
            Ser, Arg, Thr, or Leu;"
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(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:78
       (D) OTHER INFORMATION:/note= "Xaa at position 78 is Leu,
             Ala, Ser, Glu, Phe, Gly, or Arg;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:79
       (D) OTHER INFORMATION:/note= "Xaa at position 79 is Lys,
             Thr, Asn, Met, Arg, Ile, Gly, or Asp;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:80
       (D) OTHER INFORMATION:/note= "Xaa position at 80 is Asn,
             Trp, Val, Gly, Thr, Leu, Glu, or Arg;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:81
       (D) OTHER INFORMATION:/note= "Xaa at position 81 is Leu,
             Gln, Gly, Ala, Trp, Arg, Val, or Lys;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:82
       (D) OTHER INFORMATION:/note= "Xaa at position 82 is Leu,
             Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr,
            Phe, Ile, Met or Val;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:83
       (D) OTHER INFORMATION:/note= "Xaa at position 83 is Pro,
             Ala, Thr, Trp, Arg, or Met;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:84
       (D) OTHER INFORMATION:/note= "Xaa at position 84 is Cys,
             Glu, Gly, Arg, Met, or Val;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:85
       (D) OTHER INFORMATION:/note= "Xaa at position 85 is Leu,
             Asn, Val, or Gln;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:86
       (D) OTHER INFORMATION:/note= "Xaa at position 86 is Pro,
             Cys, Arg, Ala, or Lys;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:87
       (D) OTHER INFORMATION:/note= "Xaa at position 87 is Leu,
             Ser, Trp, or Gly;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:88
       (D) OTHER INFORMATION:/note= "Xaa at position 88 is Ala,
             Lys, Arg, Val, or Trp;"

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:89
       (D) OTHER INFORMATION:/note= "Xaa at position 89 is Thr,
             Asp, Cys, Leu, Val, Glu, His, Asn, or S..."

(ix) FEATURE:
       (A) NAME/KEY: Modified-site
       (B) LOCATION:90
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        (D) OTHER INFORMATION:/note= "Xaa at position 90 is Ala,
              Pro, Ser, Thr, Gly, Asp, Ile, or ,Met;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:91
        (D) OTHER INFORMATION:/note= "Xaa at position 91 is Ala,
              Pro, Ser, Thr, Phe, Leu, Asp, or His;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:92
        (D) OTHER INFORMATION:/note= "Xaa at position 92 is Pro,
              Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:93
        (D) OTHER INFORMATION:/note= "Xaa at position 93 is Thr,
              Asp, Ser, Asn, Pro, Ala, Leu, or Arg;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:94
        (D) OTHER INFORMATION:/note= "Xaa at position 94 is Arg,
              Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:95
        (D) OTHER INFORMATION:/note= "Xaa at position 95 is His,
              Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp,
              Phe, Ile, or Tyr;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:96
        (D) OTHER INFORMATION:/note= "Xaa at position 96 is Pro,
              Lys, Tyr, Gly, Ile, or Thr;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:97
        (D) OTHER INFORMATION:/note= "Xaa at position 97 is Ile,
              Val, Lys, Ala, or Asn;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:98
        (D) OTHER INFORMATION:/note= "Xaa at position 98 is His,
              Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val,
              Lys, Arg, Tyr, or Pro;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:99
        (D) OTHER INFORMATION:/note= "Xaa at position 99 is Ile,
              Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:100
        (D) OTHER INFORMATION:/note= "Xaa at position 100 is Lys,
              Tyr, Leu, His, Arg, Ile, Ser, Gln, or ..."

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:101
        (D) OTHER INFORMATION:/note= "Xaa at position is Asp,
              Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly,
              Ile, Leu, or Gln;"

    (ix) FEATURE:
        (A) NAME/KEY: Modified-site
        (B) LOCATION:102
        (D) OTHER INFORMATION:/note= "Xaa at position 102 is Gly,
              Leu, Glu, Lys, Ser, Tyr, or Pro;"
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     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:103
          (D) OTHER INFORMATION:/note= "Xaa at position 103 is Asp,
                or Ser;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:104
          (D) OTHER INFORMATION:/note= "Xaa at position 104 is Trp,
                Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or
Gly;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:105
          (D) OTHER INFORMATION:/note= "Xaa at position 105 is Asn,
                Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or
His;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:106
          (D) OTHER INFORMATION:/note= "Xaa at position 106 is Glu,
                Ser, Ala, Lys, Thr, Ile, Gly, or Pro;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:108
          (D) OTHER INFORMATION:/note= "Xaa at position 108 is Arg,
                Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:109
          (D) OTHER INFORMATION:/note= "Xaa at position 109 is Arg,
                Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:110
          (D) OTHER INFORMATION:/note= "Xaa at position 110 is Lys,
                Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:111
          (D) OTHER INFORMATION:/note= "Xaa at position 111 is Leu,
                Ile, Arg, Asp, or Met;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:112
          (D) OTHER INFORMATION:/note= "Xaa at position 112 is Thr,
                Val, Gln, Tyr, Glu, His, Ser, or Phe;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:113
          (D) OTHER INFORMATION:/note= "Xaa at position 113 is Phe,
                Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or
Asn;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:114
          (D) OTHER INFORMATION:/note= "Xaa at position 114 is Tyr,
                Cys, His, Ser, Trp, Arg, or Leu;"

     (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION:115
          (D) OTHER INFORMATION:/note= "Xaa at position 115 is Leu,
                Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;"

     (ix) FEATURE:
```

(A) NAME/KEY: Modified-site
(B) LOCATION:116
(D) OTHER INFORMATION:/note= "Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:117
(D) OTHER INFORMATION:/note= "Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:118
(D) OTHER INFORMATION:/note= "Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:119
(D) OTHER INFORMATION:/note= "Xaa at position 119 is Glu, Ser, Lys, Pro, leu, Thr, Tyr, or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:120
(D) OTHER INFORMATION:/note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:121
(D) OTHER INFORMATION:/note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:122
(D) OTHER INFORMATION:/note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:123
(D) OTHER INFORMATION:/note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859:

```
Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys
1               5                   10                  15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85                  90                  95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa
            100                 105                 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu
        115                 120                 125

Ser Leu Ala Ile Phe
    130
```

(2) INFORMATION FOR SEQ ID NO: 860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:112
(D) OTHER INFORMATION:/note= "position 112 is deleted or Leu, Ala,VAl, Ile, Pro, Phe, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:113
(D) OTHER INFORMATION:/note= "positoin 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:114
(D) OTHER INFORMATION:/note= "position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION:115
(D) OTHER INFORMATION:/note= "positon 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or Asn"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860:

```
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
1               5                   10                  15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
            20                  25                  30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
        35                  40                  45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
    50                  55                  60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
65                  70                  75                  80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
                85                  90                  95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Xaa
            100                 105                 110

Xaa Xaa Xaa Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
        115                 120                 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
    130                 135                 140

Val Gly Gly Ser Thr Leu Cys Val Arg
145                 150
```

(2) INFORMATION FOR SEQ ID NO: 861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "where x=(glyglyglyser)n and where n is an integer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

Xaa
1

(2) INFORMATION FOR SEQ ID NO: 862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "where x=(glyglyglyglyser)n and where n is an integer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:

Xaa
1

(2) INFORMATION FOR SEQ ID NO: 863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION:1
(D) OTHER INFORMATION:/note= "where x= (glyglyglyglyglyser)n and where n is an integer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

Xaa
1

(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein

```
          (B) LOCATION:1
          (D) OTHER INFORMATION:/note= "where x= (gly n ser)n and
                where n is an integer"


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864:

    Xaa
    1

(2) INFORMATION FOR SEQ ID NO: 865:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein


    (ix) FEATURE:
          (A) NAME/KEY: Protein
          (B) LOCATION:1
          (D) OTHER INFORMATION:/note= "where x=(alaglyser)n and
                where n is an integer"


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

    Xaa
```

WHAT IS CLAIMED IS:

1. A hematopoietic protein comprising; an amino acid sequence of the formula:

$$R_1\text{-}L_1\text{-}R_2,\ R_2\text{-}L_1\text{-}R_1,\ R_1\text{-}R_2,\ \text{or}\ R_2\text{-}R_1$$

wherein R_1 and R_2 are independently selected from the group consisting of;

(I) A human EPO receptor agonist polypeptide, comprising; a modified EPO amino acid sequence of the Formula:

```
AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys
                       10                          20

GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr
                       30                          40

ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla
                       50                          60

ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu
                       70                          80

LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer
                       90                          100

GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer
                       110                         120

ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys
                       130                         140

LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla
                       150                         160

CysArgThrGlyAspArg SEQ ID NO:464
          166
```

wherein 1-6 amino acids from the N-terminus and/or 1-5 from the C-terminus are optionally deleted from said EPO receptor agonist polypeptide;

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the

N-terminus to the C-terminus and having new C- and N-termini at amino acids;

23-24
24-25
25-26
26-27
27-28
28-29
29-30
30-31
31-32
32-33
33-34
34-35
35-36
36-37
37-38
38-39
39-40
40-41
41-42
42-43
43-44
44-45
45-46
46-47
47-48
48-49
49-50
50-51
51-52
52-53
53-54
54-55
55-56
56-57
57-58
77-78
78-79
79-80
80-81
81-82
82-83
84-85
85-86
86-87
87-88
88-89
108-109
109-110
110-111
111-112
112-113
113-114
114-115
115-116
116-117
117-118
118-119
119-120
120-121
121-122
122-123
123-124
124-125
125-126
126-127
127-128
128-129
129-130
130-131
131-132
respectively;

(II) A human stem cell factor receptor agonist polypeptide, comprising; a modified stem cell factor amino acid sequence of the Formula:

```
GluGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeuValAla
                                        10                      20

AsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyMetAspValLeuPro
                                        30                      40

SerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeu
```

50 60

AspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleIleAspLysLeuVal
70 80

AsnIleValAspAspLeuValGluCysValLysGluAsnSerSerLysAspLeuLysLys
90 100

SerPheLysSerProGluProArgLeuPheThrProGluGluPhePheArgIlePheAsn
110 120

ArgSerIleAspAlaPheLysAspPheValValAlaSerGluThrSerAspCysValVal
130 140

SerSerThrLeuSerProGluLysAspSerArgValSerValThrLysProPheMetLeu
150 160

ProProValAlaAla SEQ ID NO:465
165

wherein 1-23 amino acids are optionally deleted from the C-terminus of said stem cell factor receptor agonist polypeptide; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

23-24
24-25
25-26
26-27
27-28
28-29
29-30
30-31
31-32
32-33
33-34
34-35
35-36
36-37
39-40
40-41
64-65
65-66
66-67
67-68
68-69
69-70
70-71
89-90
90-91
91-92
92-93
93-94
96-97
97-98
98-99
99-100
100-101
101-102
102-103
103-104
104-105
105-106
106-107
107-108
108-109
109-110

37-38
38-39
94-95
95-96
110-111
respectively;

(III) A human flt-3 receptor agonist polypeptide, comprising; a modified flt-3 ligand amino acid sequence of the Formula:

ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
10 20

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
30 40

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
50 60

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
70 80

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
90 100

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
110 120

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
130 SEQ ID NO:466

wherein 1-7 amino acids are optionally deleted from the C-terminus of said flt3 receptor agonist polypeptide; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

28-29
29-30
30-31
31-32
32-33
34-35
36-37
37-38
42-43
64-65
65-66
66-67
86-87
87-88
88-89
89-90
93-94
94-95
95-96
96-97
97-98
98-99
99-100
100-101

38-39
39-40
40-41
41-42
90-91
91-92
92-93
101-102
102-103
respectively;

(IV) A polypeptide comprising; a modified human G-CSF amino acid sequence of the formula:

1 10
Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa

20
Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly

30 40
Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa

50
Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp

60 70
Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly

80
Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu

90 100
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu

110
Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp

120 130
Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr

140
Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala

150 160
Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa

170
Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro SEQ ID NO:858

wherein

Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
Xaa at position 2 is Pro or Leu;
Xaa at position 3 is Leu, Arg, Tyr or Ser;
Xaa at position 13 is Phe, Ser, His, Thr or Pro;
Xaa at position 16 is Lys, Pro, Ser, Thr or His;
Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or

Arg;
Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
Xaa at position 24 is Ile, Pro, Tyr or Leu;
Xaa at position 27 is Asp, or Gly;
Xaa at position 30 is Ala, Ile, Leu or Gly;
Xaa at position 34 is Lys or Ser;
Xaa at position 36 is Cys or Ser;
Xaa at position 42 is Cys or Ser;
Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;
Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;
Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
Xaa at position 47 is Leu or Thr;
Xaa at position 49 is Leu, Phe, Arg or Ser;
Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
Xaa at position 54 is Leu or His;
Xaa at position 64 is Cys or Ser;
Xaa at position 67 is Gln, Lys, Leu or Cys;
Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
Xaa at position 74 is Cys or Ser;
Xaa at position 104 is Asp, Gly or Val;
Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or Gly;
Xaa at position 115 is Thr, His, Leu or Ala;
Xaa at position 120 is Gln, Gly, Arg, Lys or His
Xaa at position 123 is Glu, Arg, Phe or Thr
Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or Glu;
Xaa at position 146 is Arg or Gln;
Xaa at position 147 is Arg or Gln;
Xaa at position 156 is His, Gly or Ser;
Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
Xaa at position 162 is Glu, Leu, Gly or Trp;
Xaa at position 163 is Val, Gly, Arg or Ala;
Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
Xaa at position 170 is His, Arg or Ser;

wherein 1-11 amino acids from the N-terminus and/or 1-5 amino acids from the C-terminus are optionally deleted from said modified human G-CSF amino acid sequence; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

38-39
39-40
40-41
41-42
62-63
63-64
64-65
65-66
123-124
124-125
125-126
126-127

42-43
43-44
45-46
48-49
49-50
52-53
53-54
54-55
55-56
56-57
57-58
58-59
59-60
60-61
61-62
66-67
67-68
68-69
69-70
70-71
71-72
91-92
92-93
93-94
94-95
95-96
96-97
97-98
98-99
99-100
128-129
128-129
129-130
130-131
131-132
132-133
133-134
134-135
135-136
136-137
137-138
138-139
139-140
140-141
141-142
or 142-143
respectively;

(V) A polypeptide comprising; a modified human IL-3 amino acid sequence of the formula:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 85 90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
95 100 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
110 115 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe SEQ ID NO:859
125 130

wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;
Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;
Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;
Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;
Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;
Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;
Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;
Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
Xaa at position 36 is Asp, Leu, or Val;
Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
Xaa at position 38 is Asn, or Ala;
Xaa at position 40 is Leu, Trp, or Arg;
Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;

770

Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly or Ser;

Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;

Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;

Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;

Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;

Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;

Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;

Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;

Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;

Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;

Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;

Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;

Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;

Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;

Xaa at position 57 is Asn or Gly;

Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;

Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;

Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;

Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;

Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;

Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;

Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;

Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;

Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;

Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;

Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;

Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;

Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;

Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;

Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;

Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;

Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;

Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;

Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;

Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;

Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;

Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;

Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;

Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;

Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;

Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;

Xaa at position 85 is Leu, Asn, Val, or Gln;

Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;

Xaa at position 87 is Leu, Ser, Trp, or Gly;

Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;

Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;

Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;

Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His;

Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;

Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;

Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;

Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;

Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;

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Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;

Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;

Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;

Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;

Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;

Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;

Xaa at position 103 is Asp, or Ser;

Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;

Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;

Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;

Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;

Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;

Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;

Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;

Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;

Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;

Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;

Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;

Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;

Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;

Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;

Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg;

Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;

Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;

Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;

Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein from 1 to 14 amino acids are optionally deleted from the N-terminus and/or from 1 to 15 amino acids are optionally deleted from the C-terminus of said modified human IL-3 amino acid sequence; wherein from 0 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2), capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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87-88
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89-90
90-91
91-92
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97-98
98-99
99-100
100-101
101-102
102-103
or 103-104
respectively;

(VI) A polypeptide comprising; a modified human c-mpl ligand amino acid sequence of the formula:

```
SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
1           5                   10                  15

HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
20                  25                  30                  35

ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
    40                  45                  50                  55
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ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
        60                  65                  70                  75

AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
            80                  85                  90                  95

GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
                100                 105                 110

XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
115                 120                 125                 130

LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
    135                 140                 145                 150

Arg SEQ ID NO:860
153
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wherein;

Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro, Phe, Trp, or Met;
Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;
Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;
Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or Asn; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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119-120
120-121
121-122

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47-48
48-49
50-51
83-84
84-85
85-86
86-87
87-88
88-89
122-123
123-124
124-125
125-126
126-127
or 127-128
respectively;

(VII) A polypeptide comprising; a modified human IL-3 amino acid sequence of the formula:

```
Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1               5                   10                  15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20                  25                  30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
                35                  40                  45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                50                  55                  60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                65                  70                  75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                80                  85                  90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                95                  100                 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                110                 115                 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe SEQ ID NO:859
                125                 130
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wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;

Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;

Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;

Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;

Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;

Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;

Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;

Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;

Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;

Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;

Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;

Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;

Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;

Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;

Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;

Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;

Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;

Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;

Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;

Xaa at position 36 is Asp, Leu, or Val;

Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;

Xaa at position 38 is Asn, or Ala;

Xaa at position 40 is Leu, Trp, or Arg;

Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;

Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;

Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly or Ser;

Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;

Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;

Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;

Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;

Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;

Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;

Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;

Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;

Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;

Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;

Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;

Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;

Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;

Xaa at position 57 is Asn or Gly;

Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;

Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;

Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;

Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;

Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;

Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;

Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;

Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;

Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;

Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;

Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;

Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;

Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;

Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;

Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;

Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;

Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;

Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;

Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;

Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;

Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;

Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;

Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;

Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;

Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;

Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;

Xaa at position 85 is Leu, Asn, Val, or Gln;

Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;

Xaa at position 87 is Leu, Ser, Trp, or Gly;

Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;

Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;

Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;

Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His;

Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;

Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;

Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;

Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;

Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;

Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;

Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;

Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;

Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;

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Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;

Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;

Xaa at position 103 is Asp, or Ser;

Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;

Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;

Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;

Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;

Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;

Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;

Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;

Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;

Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;

Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;

Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;

Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;

Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;

Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;

Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg;

Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;

Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;

Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;

Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein from 1 to 14 amino acids are optionally deleted from the N-terminus and/or from 1 to 15 amino acids are optionally deleted from the C-terminus of said modified human IL-3 amino acid sequence; and wherein from 1 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

(VIII) a factor selected from the group consisting of: a colony stimulating factor, a cytokine, a lymphokine, an interleukin, and a hematopoietic growth factor; and

wherein L_1 is a linker capable of linking R_1 to R_2;

said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1});

with the proviso that at least R_1 or R_2 is selected from the polypeptide of formula (I) , (II), or (III); and.

2. A hematopoietic protein comprising; an amino acid sequence of the formula:

R_1-L_1-R_2, R_2-L_1-$R_{1,}$ R_1-$R_{2,}$ or R_2-R_1

wherein R_1 and R_2 are independently selected from the group consisting of;

(I) A human EPO receptor agonist polypeptide, comprising; a modified EPO amino acid sequence of the Formula:

AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys
10 20

GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr
30 40

ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla
50 60

ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu
70 80

LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer
90 100

GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer
110 120

ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys
130 140

LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla
150 160

CysArgThrGlyAspArg SEQ ID NO:464
166

wherein 1-6 amino acids from the N-terminus and/or 1-5 from the C-terminus are optionally deleted from said EPO receptor agonist polypeptide; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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124-125
125-126

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45-46
46-47
84-85
85-86
86-87
87-88
88-89
108-109
126-127
127-128
128-129
129-130
130-131
131-132
respectively;

(II) A human stem cell factor receptor agonist polypeptide, comprising; a modified stem cell factor amino acid sequence of the Formula:

GluGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeuValAla
10 20

AsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyMetAspValLeuPro
30 40

SerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeu
50 60

AspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleIleAspLysLeuVal
70 80

AsnIleValAspAspLeuValGluCysValLysGluAsnSerSerLysAspLeuLysLys
90 100

SerPheLysSerProGluProArgLeuPheThrProGluGluPhePheArgIlePheAsn
110 120

ArgSerIleAspAlaPheLysAspPheValValAlaSerGluThrSerAspCysValVal
130 140

SerSerThrLeuSerProGluLysAspSerArgValSerValThrLysProPheMetLeu
150 160

ProProValAlaAla SEQ ID NO:465
165

wherein 1-23 amino acids are optionally deleted from the C-terminus of said stem cell factor receptor agonist polypeptide; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the

N-terminus to the C-terminus and having new C- and N-termini at amino acids;

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24-25
25-26
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27-28
28-29
29-30
30-31
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69-70
70-71
89-90
90-91
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92-93
93-94
94-95
95-96
96-97
97-98
98-99
99-100
100-101
101-102
102-103
103-104
104-105
105-106
106-107
107-108
108-109
109-110
110-111
respectively;

(III) A human flt-3 receptor agonist polypeptide, comprising a modified flt-3 ligand amino acid sequence of the Formula:

```
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
                            10                            20

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
                            30                            40

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
                            50                            60

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
                            70                            80

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
                            90                           100

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
```

110 120

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu

130 SEQ ID NO:466

wherein 1-7 amino acids are optionally deleted from the C-terminus of said flt3 receptor agonist polypeptide; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

28-29
29-30
30-31
31-32
32-33
34-35
36-37
37-38
38-39
39-40
40-41
41-42
42-43
64-65
65-66
66-67
86-87
87-88
88-89
89-90
90-91
91-92
92-93
93-94
94-95
95-96
96-97
97-98
98-99
99-100
100-101
101-102
102-103
respectively;

(IV) A polypeptide comprising; a modified human IL-3 amino acid sequence of the formula:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn

1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa

35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50 55 60

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                65                  70                  75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                80                  85                  90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                95                  100                 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                110                 115                 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe SEQ ID NO:859
                125                 130
```

wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;
Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;
Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;
Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;
Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;
Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;
Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;

Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;

Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;

Xaa at position 36 is Asp, Leu, or Val;

Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;

Xaa at position 38 is Asn, or Ala;

Xaa at position 40 is Leu, Trp, or Arg;

Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;

Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;

Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly or Ser;

Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;

Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;

Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;

Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;

Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;

Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;

Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;

Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;

Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;

Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;

Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;

Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;

Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;

Xaa at position 57 is Asn or Gly;

Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;

Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;

Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

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Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;
Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;
Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;
Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;
Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;
Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;
Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;
Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;
Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;
Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;
Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;
Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;
Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;
Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
Xaa at position 85 is Leu, Asn, Val, or Gln;
Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
Xaa at position 87 is Leu, Ser, Trp, or Gly;
Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;
Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;

Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His;

Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;

Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;

Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;

Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;

Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;

Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;

Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;

Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;

Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;

Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;

Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;

Xaa at position 103 is Asp, or Ser;

Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;

Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;

Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;

Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;

Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;

Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;

Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;

Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;

Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;

Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;

Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;

Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;
Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg;
Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;
Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;
Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein from 1 to 14 amino acids are optionally deleted from the N-terminus and/or from 1 to 15 amino acids are optionally deleted from the C-terminus of said modified human IL-3 amino acid sequence; and wherein from 1 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3;

(V) a factor selected from the group consisting of: a colony stimulating factor, a cytokine, a lymphokine, an interleukin, and a hematopoietic growth factor;

wherein L_1 is a linker capable of linking R_1 to R_2; and

wherein said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1});

with the proviso that at least R_1 or R_2 is selected from the polypeptide of formula (I) , (II), or (III).

3. The hematopoietic protein as recited in claim 2 wherein the polypeptide of (IV) is selected from the from the group consisting of;

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu
Asp Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
Glu Gln Ala Gln Glu Gln Gln SEQ ID NO:803;

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
Glu Gln Ala Gln Glu Gln Gln SEQ ID NO:804;

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu
Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
Leu Ala Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
Glu Gln Ala Gln Glu Gln Gln SEQ ID NO:805; and

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln SEQ ID NO:806.

4. A hematopoietic protein comprising; an amino acid sequence of the formula:

$R_1-L_1-R_2$, $R_2-L_1-R_{1,}$ $R_1-R_{2,}$ or R_2-R_1

wherein R_1 is a polypeptide, comprising; a modified flt-3 ligand amino acid sequence of the Formula:

```
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
                          10                            20

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
                          30                            40

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
                          50                            60

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
                          70                            80

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
                          90                            100

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
                          110                           120

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeu
                          130                 SEQ ID NO:466
```

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

28-29
29-30
30-31
31-32
32-33
34-35
36-37
37-38
38-39
39-40
40-41
41-42
42-43
64-65
65-66
66-67
86-87
87-88
88-89
89-90
90-91
91-92
92-93
93-94
94-95
95-96
96-97
97-98
98-99
99-100
100-101
101-102
102-103
respectively;

wherein R_2 is a polypeptide comprising; a modified human IL-3 amino acid sequence of the formula:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 85 90

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
95 100 105

Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
110 115 120

Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe SEQ ID NO:859
125 130

wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;
Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn,

Thr, Ser or Val;

Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;

Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;

Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;

Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;

Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;

Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;

Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or Trp;

Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;

Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys;

Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;

Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu;

Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;

Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;

Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;

Xaa at position 36 is Asp, Leu, or Val;

Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;

Xaa at position 38 is Asn, or Ala;

Xaa at position 40 is Leu, Trp, or Arg;

Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;

Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met or Ala;

Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly or Ser;

Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;

Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;

Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val or Gly;

Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;

Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or Asn;

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Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp;

Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met or Gln;

Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;

Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;

Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met;

Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;

Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;

Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val or Lys;

Xaa at position 57 is Asn or Gly;

Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;

Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;

Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;

Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;

Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;

Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;

Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;

Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;

Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;

Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;

Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;

Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu;

Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;

Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;

Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp;

Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg;

Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;

Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;

Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp;

Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp;
Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg;
Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys;
Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
Xaa at position 85 is Leu, Asn, Val, or Gln;
Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
Xaa at position 87 is Leu, Ser, Trp, or Gly;
Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser;
Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met;
Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His;
Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;
Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg;
Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;
Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;
Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro;
Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
Xaa at position 103 is Asp, or Ser;
Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,

Gln, Lys, Ala, Phe, or Gly;
Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;
Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;
Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;
Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;
Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;
Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or Phe;
Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;
Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;
Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;
Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg;
Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;
Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;
Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;

wherein from 1 to 14 amino acids are optionally deleted from the N-terminus and/or from 1 to 15 amino acids optionally deleted from the C-terminus of said modified human interleukin-3 amino acid sequence; and wherein from 1 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

wherein L_1 is a linker capable of linking R_1 to R_2; and

said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1}).

5. The hematopoeitic protein of claim 4 wherein R$_2$ is selected from the group consisting of;

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu
Asp Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
Glu Gln Ala Gln Glu Gln Gln SEQ ID NO:803;

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
Glu Gln Ala Gln Glu Gln Gln SEQ ID NO:804;

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu
Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
Leu Ala Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
Glu Gln Ala Gln Glu Gln Gln SEQ ID NO:805; and
Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln SEQ ID NO:806.

6. A hematopoietic protein comprising; an amino acid sequence of the formula:

$$R_1-L_1-R_2,\ R_2-L_1-R_1,\ R_1-R_2,\ \text{or}\ R_2-R_1$$

wherein R_1 is a polypeptide comprising; a modified flt-3 ligand amino acid sequence of the Formula:

```
ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
                                     10                      20

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
                                     30                      40

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
                                     50                      60

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
                                     70                      80

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
                                     90                     100

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
                                    110                     120

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsrSerSerThrLeu
                                    130          SEQ ID NO:466
```

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

28-29 42-43 93-94

29-30
30-31
31-32
32-33
34-35
36-37
37-38
38-39
39-40
40-41
41-42
64-65
65-66
66-67
86-87
87-88
88-89
89-90
90-91
91-92
92-93
94-95
95-96
96-97
97-98
98-99
99-100
100-101
101-102
102-103
respectively;

wherein R_2 is a factor selected from the group consisting of: a colony stimulating factor, a cytokine, a lymphokine, an interleukin, and a hematopoietic growth factor;

wherein L_1 is a linker capable of linking R_1 to R_2; and

said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1}).

7. A hematopoietic protein comprising; an amino acid sequence of the formula:

$$R_1-L_1-R_2,\ R_2-L_1-R_{1,}\ R_1-R_{2,}\ \text{or}\ R_2-R_1$$

wherein R_1 is a polypeptide comprising; a modified flt-3 ligand amino acid sequence of the Formula:

ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg
10 20

GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp
30 40

GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
50 60

LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
70 80

PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn
90 100

IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr
110 120

ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAsrSerSerThrLeu
130 SEQ ID NO:466

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

28-29
29-30
30-31
31-32
32-33
34-35
36-37
37-38
38-39
39-40
40-41
41-42
42-43
64-65
65-66
66-67
86-87
87-88
88-89
89-90
90-91
91-92
92-93
93-94
94-95
95-96
96-97
97-98
98-99
99-100
100-101
101-102
102-103
respectively;

wherein R_2 is a polypeptide, comprising; a modified human G-CSF amino acid sequence of the formula:

1 10
Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa

20
Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly

30 40
Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa

50
Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp

60 70
Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly

80
Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu

90 100

```
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu

                        110
Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp

    120                                     130
Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr

                        140
Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala

    150                                     160
Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa

                        170
Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro SEQ ID NO:858
```

wherein

Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
Xaa at position 2 is Pro or Leu;
Xaa at position 3 is Leu, Arg, Tyr or Ser;
Xaa at position 13 is Phe, Ser, His, Thr or Pro;
Xaa at position 16 is Lys, Pro, Ser, Thr or His;
Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;
Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
Xaa at position 24 is Ile, Pro, Tyr or Leu;
Xaa at position 27 is Asp, or Gly;
Xaa at position 30 is Ala, Ile, Leu or Gly;
Xaa at position 34 is Lys or Ser;
Xaa at position 36 is Cys or Ser;
Xaa at position 42 is Cys or Ser;
Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;
Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;
Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
Xaa at position 47 is Leu or Thr;
Xaa at position 49 is Leu, Phe, Arg or Ser;
Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
Xaa at position 54 is Leu or His;
Xaa at position 64 is Cys or Ser;
Xaa at position 67 is Gln, Lys, Leu or Cys;
Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
Xaa at position 74 is Cys or Ser;
Xaa at position 104 is Asp, Gly or Val;
Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or Gly;
Xaa at position 115 is Thr, His, Leu or Ala;
Xaa at position 120 is Gln, Gly, Arg, Lys or His
Xaa at position 123 is Glu, Arg, Phe or Thr
Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or Glu;
Xaa at position 146 is Arg or Gln;

Xaa at position 147 is Arg or Gln;
Xaa at position 156 is His, Gly or Ser;
Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
Xaa at position 162 is Glu, Leu, Gly or Trp;
Xaa at position 163 is Val, Gly, Arg or Ala;
Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
Xaa at position 170 is His, Arg or Ser;

wherein 1-11 amino acids from the N-terminus and/or 1-5 amino acids from the C-terminus are optionally deleted from said modified human G-CSF amino acid sequence; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L_2) capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids;

38-39
39-40
40-41
41-42
42-43
43-44
45-46
48-49
49-50
52-53
53-54
54-55
55-56
56-57
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59-60
60-61
61-62
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64-65
65-66
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67-68
68-69
69-70
70-71
71-72
91-92
92-93
93-94
94-95
95-96
96-97
97-98
98-99
99-100
123-124
124-125
125-126
126-127
128-129
128-129
129-130
130-131
131-132
132-133
133-134
134-135
135-136
136-137
137-138
138-139
139-140
140-141
141-142
or 142-143

respectively;

wherein L_1 is a linker capable of linking R_1 to R_2; and

said hematopoietic protein can optionally be immediately preceded by (methionine^{-1}), (alanine^{-1}) or (methionine^{-2}, alanine^{-1}).

8. The hematopoietic protein as recited in claim 1, 2, 3, 4, 5, 6 or 7 wherein said linker (L_2) is selected from the group consisting of;

Ser;
Asn;
Gly;
Thr;
GlySer;
AlaAla;
GlySerGly;
GlyGlyGly;
GlyAsnGly;
GlyAlaGly;
GlyThrGly;
AlaSerAla;
AlaAlaAla;
GlyGlyGlySer SEQ ID NO:778;
GlyGlyGlySerGlyGlyGlySer SEQ ID NO:779;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySer SEQ ID NO:780;
SerGlyGlySerGlyGlySer SEQ ID NO:781;
GluPheGlyAsnMet SEQ ID NO:782;
GluPheGlyGlyAsnMet SEQ ID NO:783;
GluPheGlyGlyAsnGlyGlyAsnMet SEQ ID NO:784;
GlyGlySerAspMetAlaGly SEQ ID NO:785;
SerGlyGlyAsnGly SEQ ID NO:786;
SerGlyGlyAsnGlySerGlyGlyAsnGly SEQ ID NO:787;
SerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGlyAsnGly SEQ ID NO:788;
SerGlyGlySerGlySerGlyGlySerGly SEQ ID NO:789;
SerGlyGlySerGlySerGlyGlySerGlySerGlyGlySerGly SEQ ID NO:790;
GlyGlyGlySerGlyGly SEQ ID NO:791;
GlyGlyGlySerGlyGlyGly SEQ ID NO:792;
GlyGlyGlySerGlyGlyGlySerGlyGly SEQ ID NO:793;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly SEQ ID NO:794;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGly

SEQ ID NO:795;
GlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGly
GlyGlySerGly SEQ ID NO:796;

ProProProTrpSerProArgProLeuGlyAlaThrAlaProThrAlaGly
GlnProProLeu SEQ ID NO:797;
ProProProTrpSerProArgProLeuGlyAlaThrAlaProThr
SEQ ID NO:798; and
ValGluThrValPheHisArgValSerGlnAspGlyLeuLeuThrSer
SEQ ID NO:799.

9. The hematopoietic protein as recited in claim 1 wherein said protein is selected from the group consisting of;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:581;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAsp
CysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGluLeuSer
AspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:582;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAsp
PheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrVal
AlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGln
ArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID NO:583;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaSerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGln
ThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrp
IleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThr
LeuSerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSer
ProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAsp
TyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly SEQ ID
NO:584;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeu
AlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeu
GluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSer
CysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeu
ValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCys
GlnProAspSerSerThrLeuSerGlyGlyAsnGlySerGlyGlyAsnGlySerGlyGly
AsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
Gln SEQ ID NO:585;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLys
IleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeu
GlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGlu
ArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGlu
IleHisPheValThrLysCysAlaPheGlnPro SEQ ID NO:586;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHisSerProIleSerSer
AspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProValThr
ValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAla
GlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeuLeuGlu
ArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnPro SEQ ID
NO:587;

AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
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ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
HisLysSerProAsnMetAlaProProSerCysLeuArgPheValGlnThrAsnIleSer
ArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGln
AsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuSerGlyGly
AsnGlySerGlyGlyAsnGlySerGlyGlyAsnGlyThrGlnAspCysSerPheGlnHis
SerProIleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGln
AspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeuCysGlyGlyLeuTrp
ArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMet
GlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGln
Pro SEQ ID NO:588;

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ThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArg
CysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGly
GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGlyGly
GlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSer
LeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyr
LysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeu
SerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThr
LeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAla
ProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeu
AlaGlnPro SEQ ID NO:743;

AlaThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGlu
LeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAspGluGluLeu
CysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGly
SerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPhe
GlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSer
GluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGln
CysGlnProAspSerSerThrLeuTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGly
GlyGlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLys
SerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThr
TyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaPro
LeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeu
PheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAsp
ThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMet
AlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAla
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LeuAlaGlnPro SEQ ID NO:659;

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ProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysPro
SerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGly
LeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAsp
ValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGln
ProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuVal
AlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProTyr
ValGluGlyGlyGlyGlySerProGlyGluProSerGlyProIleSerThrIleAsnProSerPro
ProSerLysGluSerHisLysSerProAsnMetAlaAspGluGluLeuCysGlyGlyLeuTrpArg
LeuValLeuAlaGlnArgTrpMetGluArgLeuLysThrValAlaGlySerLysMetGlnGlyLeu
LeuGluArgValAsnThrGluIleHisPheValThrLysCysAlaPheGlnProProProSerCys
LeuArgPheValGlnThrAsnIleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeu
LysProTrpIleThrArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSer
ThrLeuGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
GlyThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArgGlu
LeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGln SEQ ID
NO:705;

AlaAspGluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu
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ThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsnIleSerArgLeu
LeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThrArgGlnAsnPheSerArg
CysLeuGluLeuGlnCysGlnProAspSerSerThrLeuGlyGlyGlySerGlyGlyGlySerGly
GlyGlySerGlyGlyGlySerGlyGlyGlySerGlyThrGlnAspCysSerPheGlnHisSerPro
IleSerSerAspPheAlaValLysIleArgGluLeuSerAspTyrLeuLeuGlnAspTyrProVal
ThrValAlaSerAsnLeuGlnTyrValGluGlyGlyGlyGlySerProGlyGlyGlySerGlyGly
GlySerAsnMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSer
LeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyr
LysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeu
SerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThr
LeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAla
ProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGly
GlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeu
AlaGlnPro SEQ ID NO:743.

11. The hematopoietic protein of claim 1, 2 or 6, wherein said colony stimulating factor is selected from the group consisting of GM-CSF, G-CSF, G-CSF Ser^{17}, c-mpl ligand (TPO), M-CSF, erythropoietin (EPO), IL-1, IL-4, IL-2, IL-3, IL-5, IL 6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-15, LIF, flt3/flk2 ligand, human growth hormone, B-cell growth factor, B-cell differentiation factor, eosinophil differentiation factor and stem cell factor (SCF).

12. The hematopoietic protein of claim 11 wherein said colony stimulating factor is selected from the group consisting of G-CSF, G-CSF Ser^{17}, G-CSF Ala^{17} and c-mpl ligand (TPO).

13. A nucleic acid molecule encoding said hematopoietic protein of claim 1.

14. A nucleic acid molecule encoding said hematopoietic protein of claim 2.

15. A nucleic acid molecule encoding said hematopoietic protein of claim 3.

16. A nucleic acid molecule encoding said hematopoietic protein of claim 4.

17. A nucleic acid molecule encoding said hematopoietic protein of claim 5.

18. A nucleic acid molecule encoding said hematopoietic protein of claim 6.

19. A nucleic acid molecule encoding said hematopoietic protein of claim 7.

20. A nucleic acid molecule encoding said hematopoietic protein of claim 8.

21. A nucleic acid molecule encoding said hematopoietic protein of claim 9.

22. A nucleic acid molecule encoding said hematopoietic protein of claim 10.

23. A nucleic acid molecule encoding said hematopoietic protein of claim 11.

24. The nucleic acid molecule according to claim 13 selected from group consisting of;

GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACC
ACCTGCACCTTTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTA
TCCTGATGGACCGAAACCTTCGACTTCCAAACCTGGAGAGCTTCGTAAGG
GCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAGGCAATTCTTCGTAA
TCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCCAA
TCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGG
TGGAGGCTCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGT
CTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGCCGACGAGGAG
CTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCG
GCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGA
ACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGC
TGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTC
CGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCC
GGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGTCAGGCGGT

AACGGCAGTGGAGGTAATGGCACCCAGGACTGCTCCTTCCAACACAGCCC
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TCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCCAA
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TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGG
TGGAGGCTCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGT
CTCCTCCGTCTAAAGAATCTCATAAATCTCCAAACATGGCCGACGAGGAG
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GGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGTCTGGAGGT
AACGGATCCGGTGGCAATGGGAGCGGCGGAAATGGAACCCAGGACTGCTC
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CAG SEQ ID NO:122;

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TCCTGATGGACCGAAACCTTCGACTTCCAAACCTGGAGAGCTTCGTAAGG
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TCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCCAA
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TGGAGGCTCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGT
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CCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGG
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CTCCTCAACCCTGTCTGGCGGCAACGGCACGCAGGACTGCTCCTTCCAAC
ACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGAC
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TCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCCAA
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TGGAGGCTCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGT
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CCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGG
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CTCCTCAACCCTGTCTGGAGGTAACGGATCCGGAGGTAATGGCACCCAGG
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CGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTC
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GTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCCTGCCCTGCAG
CCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGAGGGGTCCTGGTT
GCTAGCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCGCAGCCCTAC
GTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCT
CCGTCTAAAGAATCTCATAAATCTCCAAACATGGCTGATGAAGAACTGTGTGGTGGTCTGTGGCGG
CTGGTCCTGGCACAGCGCTGGATGGAGCGGCTCAAGACTGTCGCTGGGTCCAAGATGCAAGGCTTG
CTGGAGCGCGTGAACACGGAGATACACTTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGT
CTTCGCTTCGTCCAGACCAACATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTG
AAGCCCTGGATCACTCGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCA
ACCCTGGGCGGTGGGTCAGGAGGTGGGTCAGGAGGTGGATCCGGAGGTGGCTCAGGGGGAGGTAGT
GGTACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGTGAG
CTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAG SEQ ID
NO:244;

GCTGATGAAGAACTGTGTGGTGGTCTGTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
AAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACACTTTGTC
ACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAACATCTCCCGCCTC
CTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACTCGCCAGAACTTCTCCCGG
TGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGGGCGGTGGGTCAGGAGGTGGGTCAGGA
GGTGGATCCGGAGGTGGCTCAGGGGGAGGTAGTGGTACCCAGGACTGCTCCTTCCAACACAGCCCC
ATCTCCTCCGACTTCGCTGTCAAAATCCGTGAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTC
ACCGTGGCCTCCAACCTGCAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGGTGGTTCTGGCGGC
GGCTCCAACATGGCTACACCATTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTCT
TTAGAGCAAGTGAGAAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTAC
AAGCTGTGCCACCCCGAGGAGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTG
AGCTCCTGCCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGCGGCCTTTTC
CTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATATCCCCCGAGTTGGGTCCCACCTTGGACACA
CTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCTTTCCAGCGCCGGGCAGGA
GGGGTCCTGGTTGCTAGCCATCTGCAGAGCTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTT
GCGCAGCCG SEQ ID NO:282.

25. A method of producing a hematopoietic protein comprising: growing under suitable nutrient conditions,

a host cell transformed or transfected with a replicable vector comprising a nucleic acid molecule of claim 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23 or 24 in a manner allowing expression of said hematopoietic protein and recovering said hematopoietic protein.

26. A pharmaceutical composition comprising; the hematopoietic protein according to claim 1, 2, 3, 4, 5, 6, 7, 9, or 10; and a pharmaceutically acceptable carrier.

27. A method of stimulating the production of hematopoietic cells in a patient comprising the step of; administering an effective amount of the hematopoietic protein as recited in claim 1, 2, 3, 4, 5, 6, 7, 9 or 10 to said patient.

28. A method for selective ex vivo expansion of hematopoietic cells, comprising the steps of;

(a) culturing said hematopoietic cells in a culture medium comprising; the hematopoietic protein of claim 1; and

(b) harvesting said cultured cells.

29. A method for selective ex vivo expansion of hematopoietic cells, comprising the steps of;

(a) separating hematopoietic cells from other cells;

(b) culturing said separated hematopoietic cells in a culture medium comprising; the hematopoietic protein of claim 1; and

(c) harvesting said cultured cells.

30. A method for treatment of a patient having a hematopoietic disorder, comprising the steps of;

(a) removing hematopoietic cells from said patient;

(b) culturing said hematopoietic cells in a culture medium comprising; the hematopoietic protein of claim 1;

(c) harvesting said cultured cells; and

(d) transplanting said cultured cells into said patient.

31. A method for treatment of a patient having a hematopoietic disorder, comprising the steps of;

(a) removing hematopoietic cells from said patient;

(b) separating hematopoietic cells from other cells;

(c) culturing said separated hematopoietic cells in a culture medium comprising; the hematopoietic protein of claim 1;

(d) harvesting said cultured cells; and

(e) transplanting said cultured cells into said patient.

32. A method of human gene therapy, comprising the steps of;

(a) removing hematopoietic cells from a patient;

(b) separating said hematopoietic cells from other cells;

(c) culturing said separated hematopoietic cells in a culture medium comprising; the hematopoietic protein of claim 1;

(d) introducing DNA into said cultured cells;

(e) harvesting said transduced cells; and

(f) transplanting said transduced cells into said patient.

33. The method according to claim 28, 29, 30, 31 or 32 wherein said hematopoietic cells are CD34+ cells.

34. The method according to claim 28, 29, or 30, 31 or 32 wherein said hematopoietic cells are peripheral blood cells.

35. A method for the production of dendritic cells comprising the steps of;

a) separating hematopoietic progenitor cells or CD34+ cells from other cells; and

b) culturing said hematopoietic progenitor cells or CD34+ cells in a growth medium, comprising the hematopoietic protein of claim 1, 2, 3 or 4.

36. The method of claim 35, further comprising the step of;

c) pulsing said culturing hematopoietic progenitor cells or CD34+ cells with an antigen.

37. The method of claim 35, wherein said growth medium, further comprises; one or more factor selected from the group consisting of; GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

38. The method of claim 36, wherein said growth medium, further comprises; one or more factor selected from the group consisting of; GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

39. A method for treating a human having a tumor, infection or auto-immune disease, comprising the step

of; administering the hematopoietic protein of claim 1, 2, 3, or 4, to said human.

40. The method of claim 39, further comprising; administrating one or more factor selected from the group consisting of; GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

41. The method of claim 39, further comprising the step of; administering an antigen to said patient.

42. The method of claim 40, further comprising the step of; administering an antigen to said patient.

43. A method for treating a human having a tumor, infection or auto-immune disease, comprising the step of;

a) mobilizing dendritic cell progenitors or mature dendritic cells by administering the hematopoietic protein of claim 1 to said human;

b) removing said dendritic cell precursors or mature dendritic cells by a blood draw or pheresis;

c) pulsing said dendritic cell precursors or mature dendritic cells with an antigen; and

d) returning said antigen pulsed dendritic cell precursors or mature dendritic cells to said human.

44. The method of claim 43, further comprising; administering in step a), one or more factor selected from the group consisting of; GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant,

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an IL-3 variant fusion protein, and a multi-functional receptor agonist.

45. The method of claim 43, further comprising the step of; culturing said dendritic cell precursors or mature dendritic cells from step b), in a growth medium, comprising; the hematopoietic protein of claim 1, 2, 3 or 4.

46. The method of claim 44, further comprising the step of; culturing said dendritic cell precursors or mature dendritic cells from step b), in a growth medium, comprising; the hematopoietic protein of claim 1, 2, 3 or 4.

47. The method of claim 45, wherein said growth medium, further comprises one or more factor selected from the group consisting of; GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

48. The method of claim 46, wherein said growth medium, further comprises one or more factor selected from the group consisting of; GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

49. A method for treating a human having a tumor, infection or auto-immune disease, comprising the step of;

a) removing hematopoietic progenitor cells or CD34+ cells from said human by a blood draw or pheresis;

b) culturing said hematopoietic progenitor cells or CD34+ cells in a growth medium, comprising the hematopoietic protein of claim 1 to produce dendritic cell precursors or mature dendritic cells;

c) returning said dendritic cell precursors or mature dendritic cells to said human.

50. A method for treating a human having a tumor, infection or auto-immune disease, comprising the step of;

a) removing hematopoietic progenitor cells or CD34+ cells from said patient by a blood draw or pheresis;

b) culturing said hematopoietic progenitor cells or CD34+ cells in a growth medium, comprising; the hematopoietic protein of claim 1 to produce dendritic cell precursors or mature dendritic cells;

c) pulsing said dendritic cell precursors or mature dendritic cells with an antigen; and

d) returning said antigen pulsed dendritic cell precursors or mature dendritic cells to said human.

51. The method of claim 49, further comprising the step of; separating said hematopoietic progenitor cells or CD34+ cells from other cells prior to culturing.

52. The method of claim 50, further comprising the step of; separating said hematopoietic progenitor cells or CD34+ cells from other cells prior to culturing.

53. The method of claim 51, wherein said culture medium further comprises; one or more factor selected from the group consisting of: GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant,

an IL-3 variant fusion protein, and a multi-functional receptor agonist.

54. The method of claim 50, wherein said culture medium further comprises; one or more factor selected from the group consisting of: GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

55. The method of claim 51, wherein said culture medium further comprises; one or more factor selected from the group consisting of: GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

56. The method of claim 52, wherein said culture medium further comprises; one or more factor selected from the group consisting of: GM-CSF, IL-4, TNF-α, stem cell factor (SCF), flt-3 ligand, IL-3, an IL-3 variant, an IL-3 variant fusion protein, and a multi-functional receptor agonist.

FIG.1

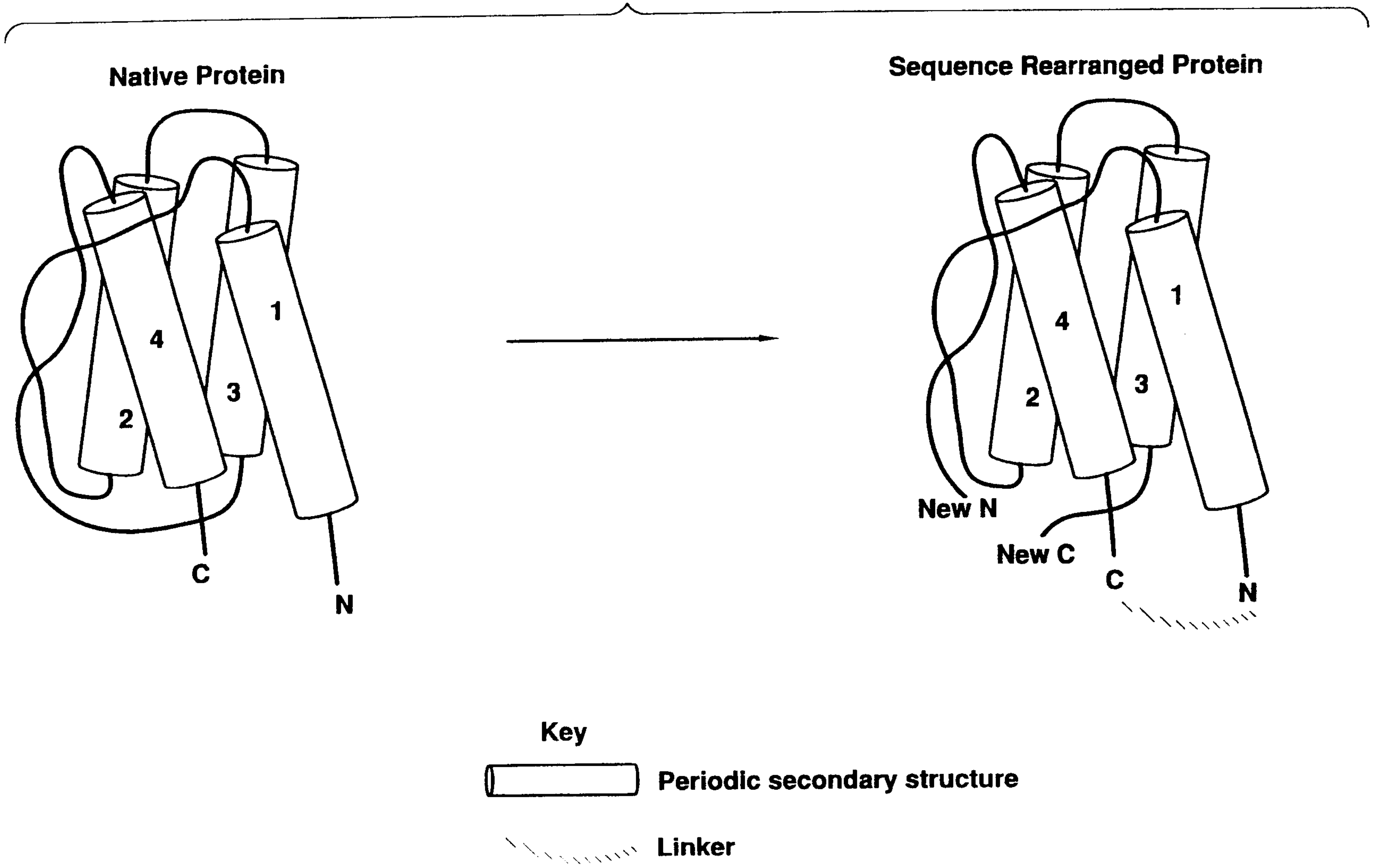

Native Protein
1
4
3
2
C
N
Sequence Rearranged Protein
1
4
3
2
New N
New C
C
N
Key
Periodic secondary structure
Linker

FIG.2

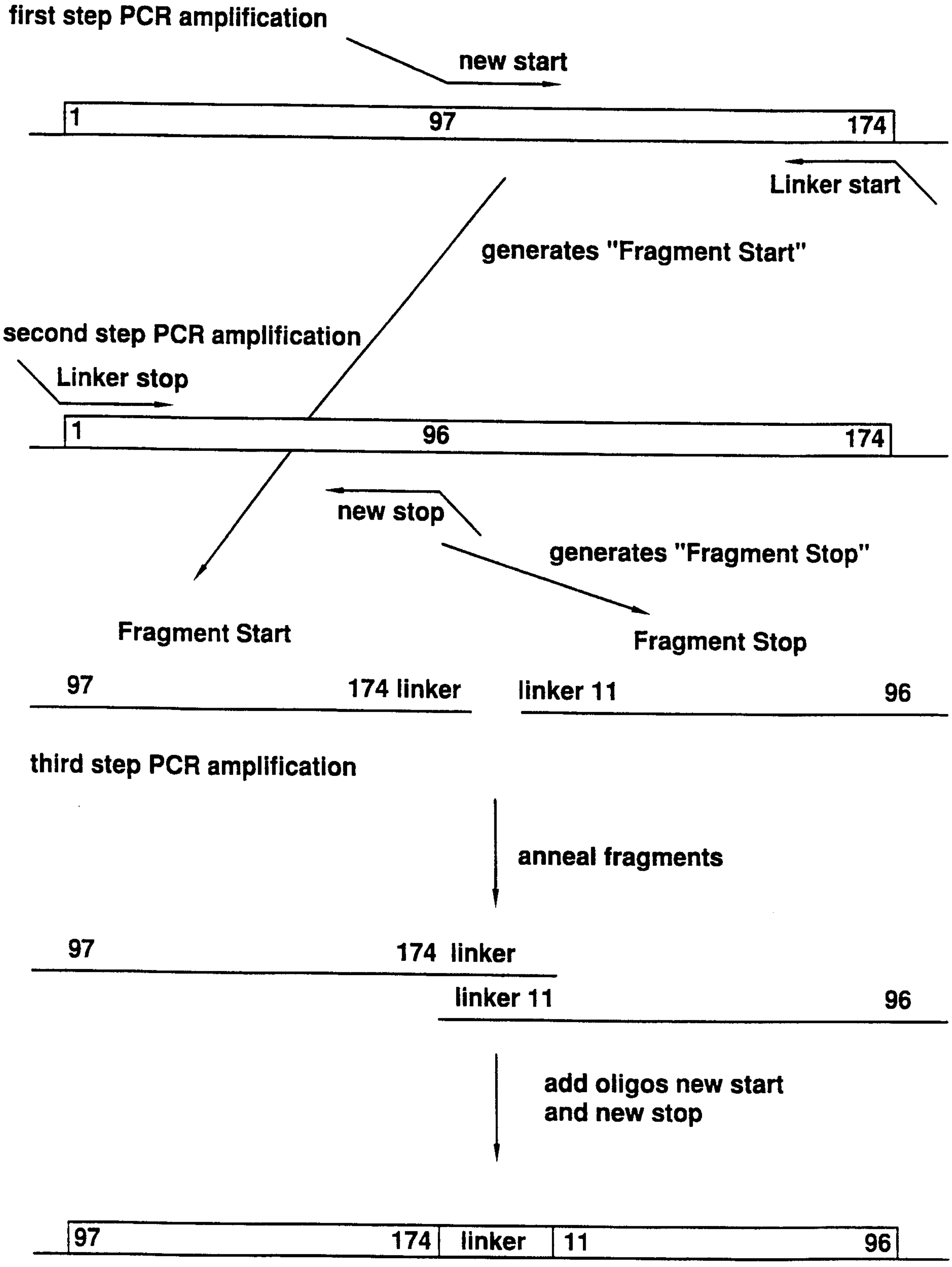

first step PCR amplification
new start
1
97
174
Linker start
generates "Fragment Start"
second step PCR amplification
Linker stop
1
96
174
new stop
generates "Fragment Stop"
Fragment Start
Fragment Stop
97
174 linker
linker 11
96
third step PCR amplification
anneal fragments
97
174 linker
linker 11
96
add oligos new start
and new stop
97
174
linker
11
96

FIG.3

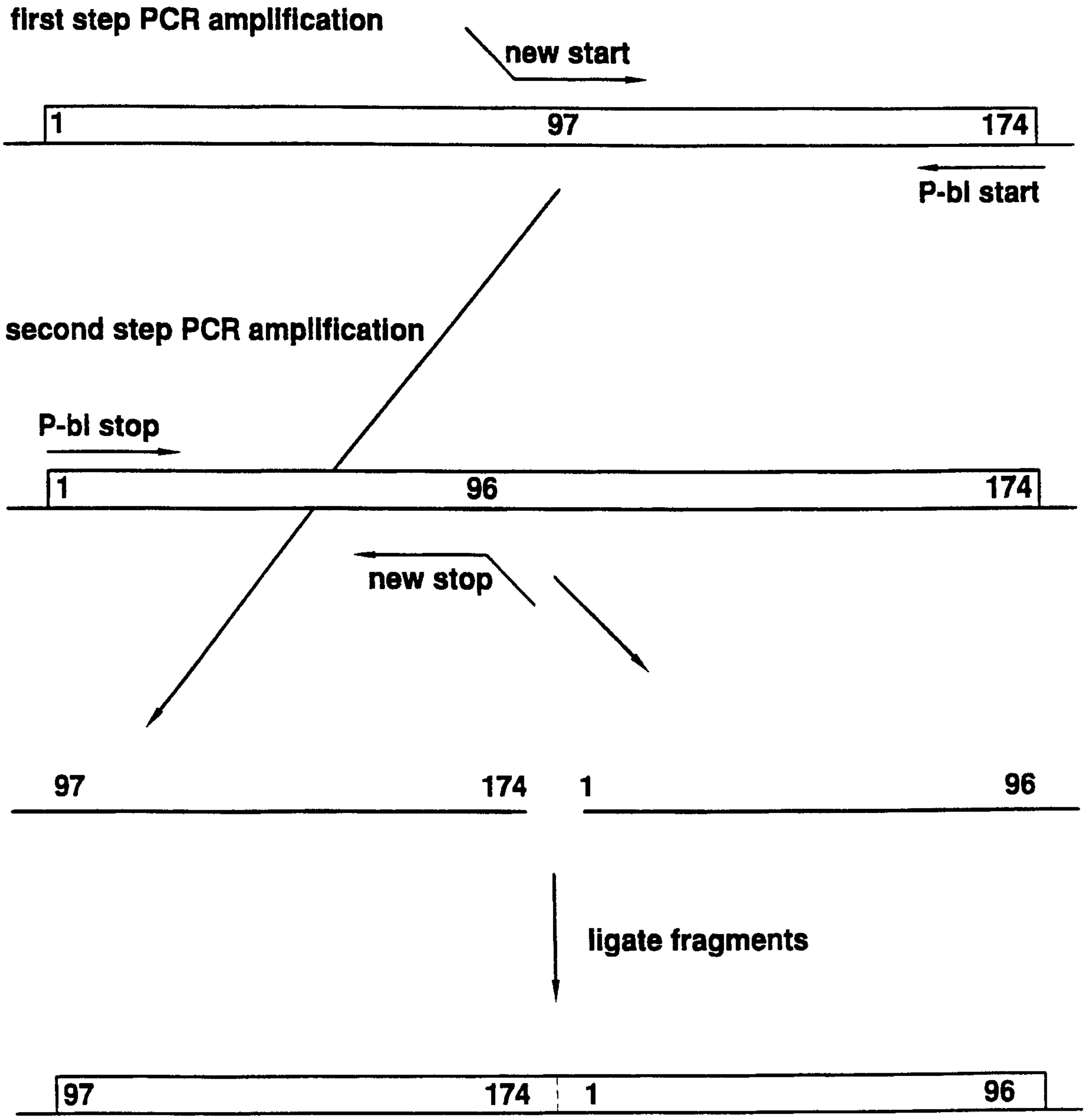

first step PCR amplification
new start
1
97
174
P-bl start
second step PCR amplification
P-bl stop
1
96
174
new stop
97
174
1
96
ligate fragments
97
174
1
96

FIG.4

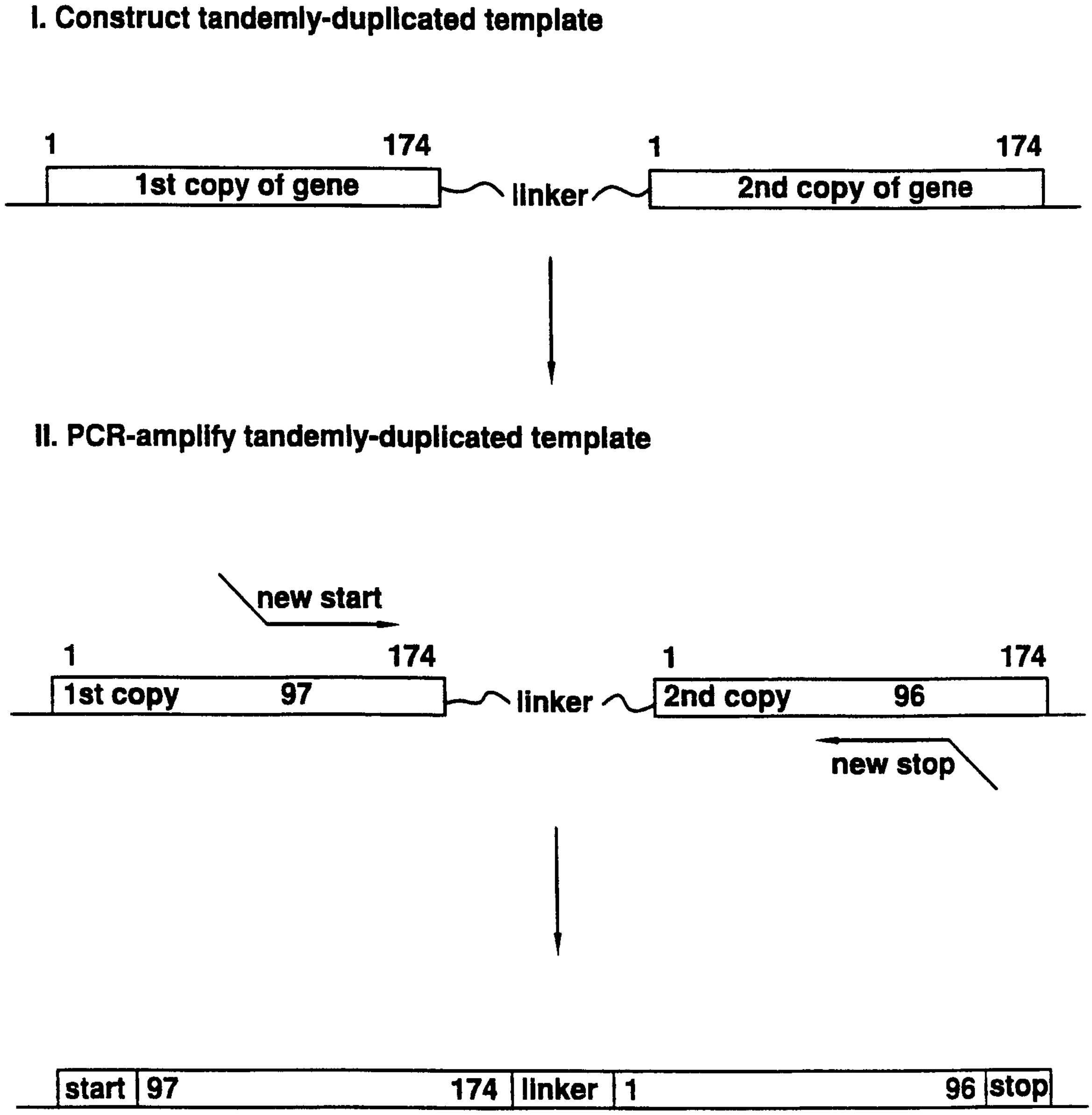
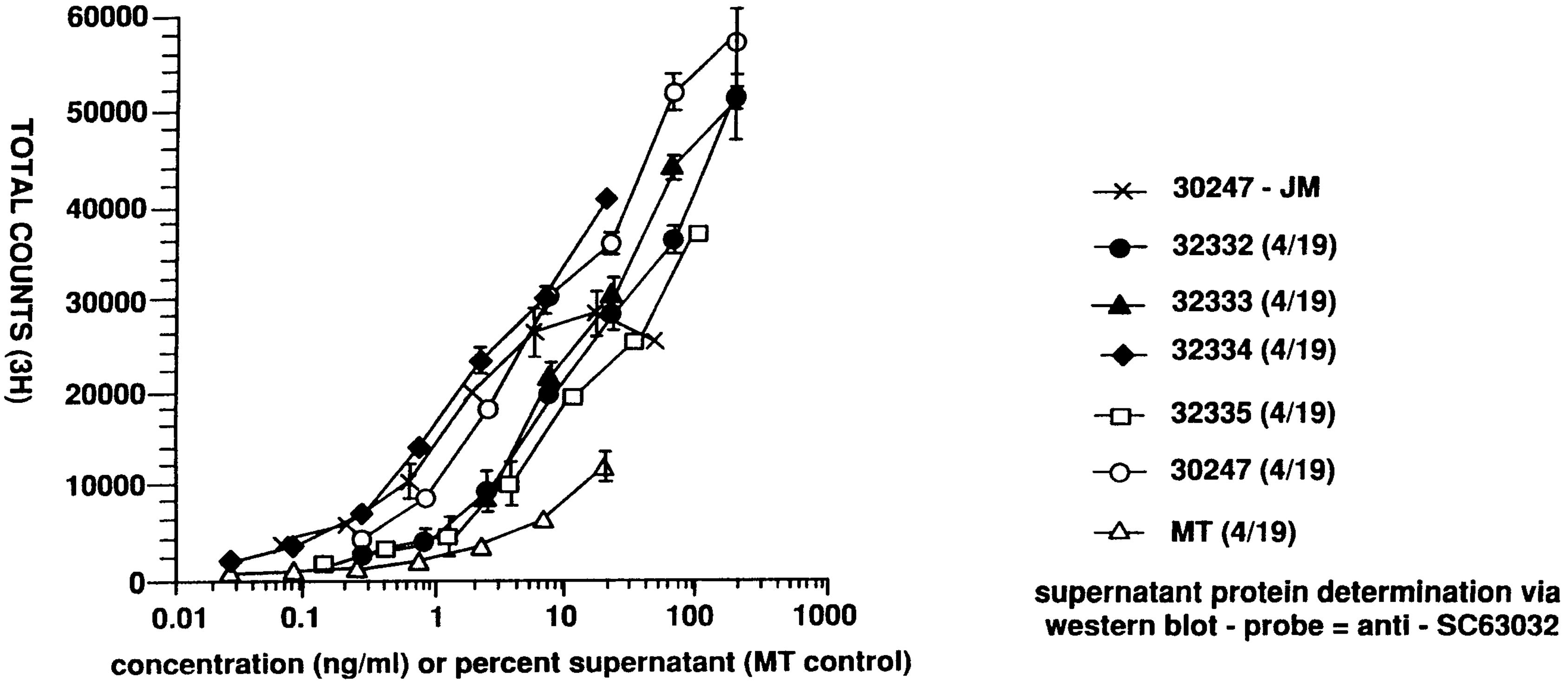

I. Construct tandemly-duplicated template
1
174
1st copy of gene
linker
1
174
2nd copy of gene
II. PCR-amplify tandemly-duplicated template
new start
1
174
1st copy
97
linker
1
174
2nd copy
96
new stop
start
97
174
linker
1
96
stop

FIG.5



supernatant protein determination via western blot - probe = anti - SC63032

FIG.6A

```
    GCCCCACCACGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAG
  1 ---------+---------+---------+---------+---------+---------+ 60
    CGGGGTGGTGCGGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTC
    AlaProProArgLeuIleCysAspSerArgValLeuGluArgTyrLeuLeuGluAlaLys

    GAGGCCGAGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACT
 61 ---------+---------+---------+---------+---------+---------+ 120
    CTCCGGCTCTTATAGTGCTGCCCGACACGACTTGTGACGTCGAACTTACTCTTATAGTGA
    GluAlaGluAsnIleThrThrGlyCysAlaGluHisCysSerLeuAsnGluAsnIleThr

    GTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGATGGAGGTCGGGCAGCAGGCC
121 ---------+---------+---------+---------+---------+---------+ 180
    CAGGGTCTGTGGTTTCAATTAAAGATACGGACCTTCTCCTACCTCCAGCCCGTCGTCCGG
    ValProAspThrLysValAsnPheTyrAlaTrpLysArgMetGluValGlyGlnGlnAla

    GTAGAAGTCTGGCAGGGCCTGGCCCTGCTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTG
181 ---------+---------+---------+---------+---------+---------+ 240
    CATCTTCAGACCGTCCCGGACCGGGACGACAGCCTTCGACAGGACGCCCCGGTCCGGGAC
    ValGluValTrpGlnGlyLeuAlaLeuLeuSerGluAlaValLeuArgGlyGlnAlaLeu

    TTGGTCAACTCTTCCCAGCCGTGGGAGCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGT
241 ---------+---------+---------+---------+---------+---------+ 300
    AACCAGTTGAGAAGGGTCGGCACCCTCGGGGACGTCGACGTACACCTATTTCGGCAGTCA
    LeuValAsnSerSerGlnProTrpGluProLeuGlnLeuHisValAspLysAlaValSer
```

FIG.6B

```
    GGCCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGAGCCCAGAAGGAAGCCATCTCC
301 ---------+---------+---------+---------+---------+---------+ 360
    CCGGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCTCGGGTCTTCCTTCGGTAGAGG
    GlyLeuArgSerLeuThrThrLeuLeuArgAlaLeuGlyAlaGlnLysGluAlaIleSer

    CCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTTCCGCAAA
361 ---------+---------+---------+---------+---------+---------+ 420
    GCAGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGCGTTT
    ProProAspAlaAlaSerAlaAlaProLeuArgThrIleThrAlaAspThrPheArgLys

    CTCTTCCGAGTCTACTCCAATTTCCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCC
421 ---------+---------+---------+---------+---------+---------+ 480
    GAGAAGGCTCAGATGAGGTTAAAGGAGGCCCCTTTCGACTTCGACATGTGTCCCCTCCGG
    LeuPheArgValTyrSerAsnPheLeuArgGlyLysLeuLysLeuTyrThrGlyGluAla

    TGCAGGACAGGGGACAGATGA
481 ---------+---------+- 501
    ACGTCCTGTCCCCTGTCTACT
    CysArgThrGlyAspArg
```

FIG.7A -1

```
    GAAGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTGGCA
  1 ---------+---------+---------+---------+---------+---------+ 60
    CTTCCCTAGACGTCCTTAGCACACTGATTATTACATTTTCTGCAGTGATTTAACCACCGT

    GluGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeuValAla

    AATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGATGGATGTTTTGCCA
 61 ---------+---------+---------+---------+---------+---------+ 120
    TTAGAAGGTTTTCTGATGTACTATTGGGAGTTTATACAGGGGCCCTACCTACAAAACGGT

    AsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyMetAspValLeuPro

    AGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTG
121 ---------+---------+---------+---------+---------+---------+ 180
    TCAGTAACAACCTATTCGCTCTACCATCATGTTAACAGTCTGTCGAACTGACTAGAAGAC

    SerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeu

    GACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGTG
181 ---------+---------+---------+---------+---------+---------+ 240
    CTGTTCAAAAGTTTATAAAGACTTCCGAACTCATTAATAAGGTAGTATCTGTTTGAACAC

    AspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleIleAspLysLeuVal
```

FIG.7A-2

```
    AATATAGTCGATGACCTTGTGGAGTGCGTCAAAGAAAACTCATCTAAGGATCTAAAAAAA
241 ---------+---------+---------+---------+---------+---------+ 300
    TTATATCAGCTACTGGAACACCTCACGCAGTTTCTTTTGAGTAGATTCCTAGATTTTTTT

    AsnIleValAspAspLeuValGluCysValLysGluAsnSerSerLysAspLeuLysLys

    TCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAAT
301 ---------+---------+---------+---------+---------+---------+ 360
    AGTAAGTTCTCGGGTCTTGGGTCCGAGAAATGAGGACTTCTTAAGAAATCTTAAAAATTA

    SerPheLysSerProGluProArgLeuPheThrProGluGluPhePheArgIlePheAsn

    AGATCCATTGATGCCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTT
361 ---------+---------+---------+---------+---------+---------+ 420
    TCTAGGTAACTACGGAAGTTCCTGAAACATCACCGTAGACTTTGATCACTAACACACCAA

    ArgSerIleAspAlaPheLysAspPheValValAlaSerGluThrSerAspCysValVal

    TCTTCAACATTAAGTCCTGAGAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTA
421 ---------+---------+---------+---------+---------+---------+ 480
    AGAAGTTGTAATTCAGGACTCTTTCTAAGGTCTCAGTCACAGTGTTTTGGTAAATACAAT

    SerSerThrLeuSerProGluLysAspSerArgValSerValThrLysProPheMetLeu
```

FIG.7B -1

```
    CCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCAGTAATAGGAAGGCCAAA
481 ---------+---------+---------+---------+---------+---------+ 540
    GGGGGACAACGTCGGTCGAGGGAATCCTTACTGTCGTCATCGTCATTATCCTTCCGGTTT

    ProProValAlaAlaSerSerLeuArgAsnAspSerSerSerSerAsnArgLysAlaLys

    AATCCCCCTGGAGACTCCAGCCTACACTGGGCAGCCATGGCATTGCCAGCATTGTTTTCT
541 ---------+---------+---------+---------+---------+---------+ 600
    TTAGGGGGACCTCTGAGGTCGGATGTGACCCGTCGGTACCGTAACGGTCGTAACAAAAGA

    AsnProProGlyAspSerSerLeuHisTrpAlaAlaMetAlaLeuProAlaLeuPheSer

    CTTATAATTGGCTTTGCTTTTGGAGCCTTATACTGGAAGAAGAGACAGCCAAGTCTTACA
601 ---------+---------+---------+---------+---------+---------+ 660
    GAATATTAACCGAAACGAAAACCTCGGAATATGACCTTCTTCTCTGTCGGTTCAGAATGT

    LeuIleIleGlyPheAlaPheGlyAlaLeuTyrTrpLysLysArgGlnProSerLeuThr
```

FIG.7B-2

```
    AGGGCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAAGTATGTTGCAAGAG
661 ---------+---------+---------+---------+---------+---------+ 720
    TCCCGTCAACTTTTATATGTTTAATTACTTCTCCTATTACTCTATTCATACAACGTTCTC

    ArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleSerMetLeuGlnGlu

    AAAGAGAGAGAGTTTCAAGAAGTGTAA
721 ---------+---------+------- 747
    TTTCTCTCTCTCAAAGTTCTTCACATT

    LysGluArgGluPheGlnGluValEnd
```

FIG.8A

```
    GAAGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTGGCA
  1 ---------+---------+---------+---------+---------+---------+ 60
    CTTCCCTAGACGTCCTTAGCACACTGATTATTACATTTTCTGCAGTGATTTAACCACCGT

    GluGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeuValAla

    AATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGATGGATGTTTTGCCA
 61 ---------+---------+---------+---------+---------+---------+ 120
    TTAGAAGGTTTTCTGATGTACTATTGGGAGTTTATACAGGGGCCCTACCTACAAAACGGT

    AsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyMetAspValLeuPro

    AGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTG
121 ---------+---------+---------+---------+---------+---------+ 180
    TCAGTAACAACCTATTCGCTCTACCATCATGTTAACAGTCTGTCGAACTGACTAGAAGAC

    SerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeu

    GACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGTG
181 ---------+---------+---------+---------+---------+---------+ 240
    CTGTTCAAAAGTTTATAAAGACTTCCGAACTCATTAATAAGGTAGTATCTGTTTGAACAC

    AspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleIleAspLysLeuVal
```

FIG.8B

```
    AATATAGTCGATGACCTTGTGGAGTGCGTCAAAGAAAACTCATCTAAGGATCTAAAAAAA
241 ---------+---------+---------+---------+---------+---------+ 300
    TTATATCAGCTACTGGAACACCTCACGCAGTTTCTTTTGAGTAGATTCCTAGATTTTTTT

    AsnIleValAspAspLeuValGluCysValLysGluAsnSerSerLysAspLeuLysLys

    TCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAAT
301 ---------+---------+---------+---------+---------+---------+ 360
    AGTAAGTTCTCGGGTCTTGGGTCCGAGAAATGAGGACTTCTTAAGAAATCTTAAAAATTA

    SerPheLysSerProGluProArgLeuPheThrProGluGluPhePheArgIlePheAsn

    AGATCCATTGATGCCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTT
361 ---------+---------+---------+---------+---------+---------+ 420
    TCTAGGTAACTACGGAAGTTCCTGAAACATCACCGTAGACTTTGATCACTAACACACCAA

    ArgSerIleAspAlaPheLysAspPheValValAlaSerGluThrSerAspCysValVal
```

FIG.8C

```
    TCTTCAACATTAAGTCCTGAGAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTA
421 ---------+---------+---------+---------+---------+---------+ 480
    AGAAGTTGTAATTCAGGACTCTTTCTAAGGTCTCAGTCACAGTGTTTTGGTAAATACAAT

    SerSerThrLeuSerProGluLysAspSerArgValSerValThrLysProPheMetLeu

    CCCCCTGTTGCAGCC
481 ---------+----- 495
    GGGGGACAACGTCGG

    ProProValAlaAla
```

FIG.9A -1

```
    ACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGT
  1 ---------+---------+---------+---------+---------+---------+ 60
    TGGGTCCTGACGAGGAAGGTTGTGTCGGGGTAGAGGAGGCTGAAGCGACAGTTTTAGGCA

    ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg

    GAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGAC
 61 ---------+---------+---------+---------+---------+---------+ 120
    CTCGACAGACTGATGGACGAAGTTCTAATGGGTCAGTGGCACCGGAGGTTGGACGTCCTG

    GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp

    GAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
121 ---------+---------+---------+---------+---------+---------+ 180
    CTCCTCGAGACGCCCCCGGAGACCGCCGACCAGGACCGTGTCGCGACCTACCTCGCCGAG

    GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu

    AAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACAC
181 ---------+---------+---------+---------+---------+---------+ 240
    TTCTGACAGCGACCCAGGTTCTACGTTCCGAACGACCTCGCGCACTTGTGCCTCTATGTG

    LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
```

FIG.9A-2

```
    TTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAAC
241 ---------+---------+---------+---------+---------+---------+ 300
    AAACAGTGGTTTACACGGAAAGTCGGGGGGGGGTCGACAGAAGCGAAGCAGGTCTGGTTG

    PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn

    ATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACT
301 ---------+---------+---------+---------+---------+---------+ 360
    TAGAGGGCGGAGGACGTCCTCTGGAGGCTCGTCGACCACCGCGACTTCGGGACCTAGTGA

    IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr

    CGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCCGACTCCTCAACCCTGCCA
361 ---------+---------+---------+---------+---------+---------+ 420
    GCGGTCTTGAAGAGGGCCACGGACCTCGACGTCACAGTCGGGCTGAGGAGTTGGGACGGT

    ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnProAspSerSerThrLeuPro

    CCCCCATGGAGTCCCCGGCCCCTGGAGGCCACAGCCCCGACAGCCCCGCAGCCCCCTCTG
421 ---------+---------+---------+---------+---------+---------+ 480
    GGGGGTACCTCAGGGGCCGGGGACCTCCGGTGTCGGGGCTGTCGGGGCGTCGGGGGAGAC

    ProProTrpSerProArgProLeuGluAlaThrAlaProThrAlaProGlnProProLeu
```

FIG.9B

```
     CTCCTCCTACTGCTGCTGCCCGTGGGCCTCCTGCTGCTGGCCGCTGCCTGGTGCCTGCAC
481  ---------+---------+---------+---------+---------+---------+ 540
     GAGGAGGATGACGACGACGGGCACCCGGAGGACGACGACCGGCGACGGACCACGGACGTG

     LeuLeuLeuLeuLeuLeuProValGlyLeuLeuLeuLeuAlaAlaAlaTrpCysLeuHis

     TGGCAGAGGACGCGGCGGAGGACACCCCGCCCTGGGGAGCAGGTGCCCCCCGTCCCCAGT
541  ---------+---------+---------+---------+---------+---------+ 600
     ACCGTCTCCTGCGCCGCCTCCTGTGGGGCGGGACCCCTCGTCCACGGGGGGCAGGGGTCA

     TrpGlnArgThrArgArgArgThrProArgProGlyGluGlnValProProValProSer

     CCCCAGGACCTGCTGCTTGTGGAGCACTGA
601  ---------+---------+---------+ 630
     GGGGTCCTGGACGACGAACACCTCGTGACT

     ProGlnAspLeuLeuLeuValGluHisEnd
```

FIG.10A

```
    ACCCAGGACTGCTCCTTCCAACACAGCCCCATCTCCTCCGACTTCGCTGTCAAAATCCGT
  1 ---------+---------+---------+---------+---------+---------+ 60
    TGGGTCCTGACGAGGAAGGTTGTGTCGGGGTAGAGGAGGCTGAAGCGACAGTTTTAGGCA

    ThrGlnAspCysSerPheGlnHisSerProIleSerSerAspPheAlaValLysIleArg

    GAGCTGTCTGACTACCTGCTTCAAGATTACCCAGTCACCGTGGCCTCCAACCTGCAGGAC
 61 ---------+---------+---------+---------+---------+---------+ 120
    CTCGACAGACTGATGGACGAAGTTCTAATGGGTCAGTGGCACCGGAGGTTGGACGTCCTG

    GluLeuSerAspTyrLeuLeuGlnAspTyrProValThrValAlaSerAsnLeuGlnAsp

    GAGGAGCTCTGCGGGGGCCTCTGGCGGCTGGTCCTGGCACAGCGCTGGATGGAGCGGCTC
121 ---------+---------+---------+---------+---------+---------+ 180
    CTCCTCGAGACGCCCCCGGAGACCGCCGACCAGGACCGTGTCGCGACCTACCTCGCCGAG

    GluGluLeuCysGlyGlyLeuTrpArgLeuValLeuAlaGlnArgTrpMetGluArgLeu

    AAGACTGTCGCTGGGTCCAAGATGCAAGGCTTGCTGGAGCGCGTGAACACGGAGATACAC
181 ---------+---------+---------+---------+---------+---------+ 240
    TTCTGACAGCGACCCAGGTTCTACGTTCCGAACGACCTCGCGCACTTGTGCCTCTATGTG

    LysThrValAlaGlySerLysMetGlnGlyLeuLeuGluArgValAsnThrGluIleHis
```

FIG.10B

```
    TTTGTCACCAAATGTGCCTTTCAGCCCCCCCCCAGCTGTCTTCGCTTCGTCCAGACCAAC
241 ---------+---------+---------+---------+---------+---------+ 300
    AAACAGTGGTTTACACGGAAAGTCGGGGGGGGGTCGACAGAAGCGAAGCAGGTCTGGTTG

    PheValThrLysCysAlaPheGlnProProProSerCysLeuArgPheValGlnThrAsn

    ATCTCCCGCCTCCTGCAGGAGACCTCCGAGCAGCTGGTGGCGCTGAAGCCCTGGATCACT
301 ---------+---------+---------+---------+---------+---------+ 360
    TAGAGGGCGGAGGACGTCCTCTGGAGGCTCGTCGACCACCGCGACTTCGGGACCTAGTGA

    IleSerArgLeuLeuGlnGluThrSerGluGlnLeuValAlaLeuLysProTrpIleThr

    CGCCAGAACTTCTCCCGGTGCCTGGAGCTGCAGTGTCAGCCC
361 ---------+---------+---------+---------+-- 402
    GCGGTCTTGAAGAGGGCCACGGACCTCGACGTCACAGTCGGG

    ArgGlnAsnPheSerArgCysLeuGluLeuGlnCysGlnPro
```