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(54) Title: G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABA_B RECEPTORS

(57) Abstract: The present invention features G-protein fusion receptors and chimeric GABA_B receptors (GABA_BRs), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a GABA_B receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric GABA_BRs comprise at least one of a GABA_BR extracellular domain, a GABA_BR transmembrane domain, or a GABA_BR intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.



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G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABA_B RECEPTORSFIELD OF THE INVENTION

5 The present invention relates to a G-protein fusion receptors, chimeric GABA_B (γ-aminobutyric acid) receptors, nucleic acid encoding such receptors, and uses of such receptors and nucleic acid encoding such receptors.

BACKGROUND

10 The references cited herein are not admitted to be prior art to the claimed invention.

 Chimeric receptors made up of peptide segments from different receptors have different uses such as being used to assess the functions of different sequence regions and to assess the activity of different compounds at a particular receptor. Examples of using chimeric receptors to assess the activity of different compounds are provided by Dull *et al.*,
15 U.S. Patent No. 4,859,609, Dull *et al.*, U.S. Patent No. 5,030,576, and Fuller *et al.*, U.S. Patent No. 5,981,195.

 Dull *et al.* U.S. Patent No. 4,859,609, and Dull *et al.* U.S. Patent No. 5,030,576, indicate the production and use of chimeric receptors comprising a ligand binding domain of a predetermined receptor and a heterologous reporter polypeptide. The Dull *et al.* patents
20 provide as examples of chimerics: (1) a chimeric receptor made up of the insulin receptor extracellular α chain, and the EGF receptor transmembrane and cytoplasmic domains without any HIR B-chain sequence; and (2) a hybrid receptor made up of the v-erbB oncogene product intracellular domain fused to the EGF receptor extracellular and transmembrane domains.

25 Fuller *et al.* International Publication No. WO 97/05252 feature chimeric receptors made up of metabotropic glutamate receptor (mGluR) domains and calcium receptor (CaR) domains. The chimeric receptors allow the coupling of functional aspects of a mGluR with a CaR.

 An example of the use of chimeric receptors to assess the functions of different
30 sequence regions receptors are found in studies identifying regions of different guanine nucleotide-binding protein coupled receptors important for guanine nucleotide-binding protein coupling. (See, Kobilka *et al.*, *Science* 240:1310-1316, 1988; Wess *et al.*, *FEBS Lett.* 258:133-136, 1989; Cotecchia *et al.*, *Proc. Natl. Acad. Sci. USA* 87:2896-2900, 1990;

Lechleiter *et al.*, *EMBO J.* 9:4381-4390, 1990; Wess *et al.*, *Mol. Pharmacol.* 38:517-523, 1990; and Pin *et al.*, *EMBO J.* 13:342-348, 1994.)

SUMMARY OF THE INVENTION

5 The present invention features G-protein fusion receptors and chimeric GABA_B receptors (GABA_BRs), nucleic acid encoding such receptors, and the use of such receptors and nucleic acid. G-protein fusion receptors comprise at least one domain from a CaR, a mGluR, and/or a GABA_B receptor fused directly or through a linker to a guanine nucleotide-binding protein (G-protein). Chimeric GABA_BRs comprise at least one of a GABA_BR
10 extracellular domain, a GABA_BR transmembrane domain, or a GABA_BR intracellular domain and one or more domains from a mGluR subtype 8 (mGluR8) and/or a CaR.

G-proteins are peripheral membrane proteins made up of an α subunit, a β subunit, and a γ subunit. G-proteins interconvert between a GDP bound and a GTP bound form. Different types of G-proteins can affect different enzymes, such as adenylate cyclase and
15 phospholipase-C.

Thus, a first aspect of the present invention describes a G-protein fusion receptor comprising:

an extracellular domain comprising an amino acid sequence substantially similar to either an extracellular CaR amino acid sequence, an extracellular mGluR amino acid
20 sequence, or an extracellular GABA_B receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular domain, said transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to either a transmembrane CaR amino acid sequence, a transmembrane mGluR amino acid sequence, or a transmembrane GABA_B receptor amino
25 acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane domain comprising all or a portion of an intracellular amino acid sequence substantially similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino acid sequence, or an intracellular GABA_B receptor amino acid sequence, provided that said
30 portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular domain, where said optionally present linker is a polypeptide 3 to 30 amino acids in length,

wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and

a G-protein joined either to said intracellular domain or to said optionally present linker, provided that said G-protein is joined to said optionally present linker when said optionally present linker is present.

“Substantially similar” refers to at least 40% sequence similarity between respective polypeptide regions making up a domain. In preferred embodiments, substantially similar refers to at least 50%, at least 75%, at least 90%, at least 95% sequence similarity, or 100% (the same sequence), between polypeptide domains. The degree to which two polypeptide domains are substantially similar is determined by comparing the amino acid sequences located in corresponding domains. Sequence similarity is preferably determined using BLASTN (Altschul *et al.*, *J. Mol. Biol.* 215:403-410, 1990).

The different receptor components of the G-protein receptor can come from the same receptor protein or from a chimeric receptor made up of different receptor domains. By swapping different domains compounds able to effect different domains of a particular receptor can be identified and the activity of different compounds at different domains can be measured.

In different embodiments the CaR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian CaR, preferably the human CaR; mGluR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian mGluR, preferably a human mGluR; and GABA_BR region(s) present in the G-protein fusion are substantially similar to, comprise, or consist of portion(s) of a mammalian GABA_BR, preferably a human GABA_BR.

In preferred embodiments concerning GABA_BR regions that are present: the GABA_BR extracellular domain is substantially similar to a GABA_BR extracellular domain provided in SEQ. ID. NOs. 2-4; the GABA_BR transmembrane domain is substantially similar to the GABA_BR transmembrane domain provided in SEQ. ID. NOs. 7-9; and the GABA_BR intracellular domain is substantially similar to a GABA_BR intracellular domain provided in SEQ. ID. NOs. 12-14.

In preferred embodiments concerning CaR regions that are present: the CaR extracellular domain is substantially similar to the CaR extracellular provided in SEQ. ID. NO. 1; the CaR, transmembrane domain is substantially similar to the CaR transmembrane

domain provided in SEQ. ID. NO. 6; and the CaR intracellular domain is substantially similar to the CaR intracellular domain such as that provided in SEQ. ID. NO. 11.

Various different mGluR subtypes present in different organisms, including humans, are described in different patent publications as follows: mGluR₁ - WO 94/29449, EP 569 240 A1, WO 92/10583 and U.S. Patent No. 5,385,831; mGluR₂ - WO 94/29449, WO 96/06167, and EP 711 832 A2; mGluR₃ - WO 94/29449, and WO 95/22609; mGluR₄ - WO 95/08627, WO 95/22609, and WO 96/29404; mGluR₅ - WO 94/29449; mGluR₆ - WO 95/08627; mGluR₇ - U.S. Patent No. 5,831,047, WO 95/08627 and WO 96/29404; and mGluR₈ - U.S. Patent Nos. 6,051,688, 6,077,675, 6,084,084 and EP 816 498 A2. (Each of these references are hereby incorporated by reference herein.)

In preferred embodiments concerning mGluR regions that are present: the mGluR extracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; the mGluR transmembrane domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8; and the mGluR intracellular domain is substantially similar to either human mGluR 1, human mGluR 2, human mGluR 3, human mGluR 4, human mGluR 5, human mGluR 6, human mGluR 7, or human mGluR 8. Preferred embodiments also include any mGluR splice variant.

In preferred embodiments concerning the optionally present linker, said optionally present linker is a polypeptide 3 to 30 amino acids in length, wherein said amino acids of the optionally present linker are selected from the group consisting of alanine, proline, serine, and glycine; and more preferably, the optionally present linker is comprised of alanine amino acids.

Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a G-protein fusion receptor, and a cell where the G-protein fusion receptor is expressed. Preferably, the G-protein fusion receptor is functional in the cell.

Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a G-protein fusion receptor is expressed, and (b) a vector comprising nucleic acid encoding a G-protein fusion receptor and elements for introducing heterologous nucleic acid into the cell. Preferably, the G-protein fusion receptor is functional in the cell.

Another aspect of the present invention describes a process for the production of a G-protein fusion receptor. The process is performed by growing host cells comprising a G-protein fusion receptor.

Another aspect of the present invention describes a method of measuring the ability of a compound to affect G-protein fusion receptor activity.

Another aspect of the present invention describes a chimeric GABA_BR comprising an extracellular domain, a transmembrane domain and an intracellular domain, wherein at least one domain is from a GABA_BR and at least one domain is from CaR or mGluR8. The extracellular domain comprises an amino acid sequence substantially similar to a CaR extracellular domain (SEQ. ID. NO. 1), a GABA_BR1a extracellular domain (SEQ. ID. NO. 2), a GABA_BR1b extracellular domain (SEQ. ID. NO. 3), a GABA_BR2 extracellular domain (SEQ. ID. NO. 4), or a mGluR8 extracellular domain (SEQ. ID. NO. 5).

The transmembrane domain comprises an amino acid sequence substantially similar to a CaR transmembrane domain (SEQ. ID. NO. 6), a GABA_BR1a transmembrane domain (SEQ. ID. NO. 7), a GABA_BR1b transmembrane domain (SEQ. ID. NO. 8), a GABA_BR2 transmembrane domain (SEQ. ID. NO. 9), or a mGluR8 transmembrane domain (SEQ. ID. NO. 10).

The intracellular domain comprises an amino acid sequence substantially similar to a CaR intracellular domain (SEQ. ID. NO. 11), a GABA_BR1a intracellular domain (SEQ. ID. NO. 12), a GABA_BR1b intracellular domain (SEQ. ID. NO. 13), a GABA_BR2 intracellular domain (SEQ. ID. NO. 14), or a mGluR8 intracellular domain (SEQ. ID. NO. 15).

Preferred chimeric GABA_BRs contain at least one mGluR8 intracellular, transmembrane or extracellular domain, or at least one CaR intracellular, transmembrane or extracellular domain. More preferably, the chimeric GABA_BR contains at least one CaR domain.

In preferred embodiments concerning mGluR8 regions that are present: the mGluR8 extracellular domain is substantially similar to the mGluR8 extracellular domain provided in SEQ. ID. NO. 5; the mGluR8 transmembrane domain is substantially similar to the mGluR8 transmembrane domain provided in SEQ. ID. NO. 10; and the mGluR8 intracellular domain is substantially similar to the mGluR8 receptor intracellular provided in SEQ. ID. NO. 15.

Preferably, the domains are functionally coupled such that a signal from the binding of an extracellular ligand is transduced to the intracellular domain when the chimeric

receptor is present in a suitable host cell. A suitable host cell contains the elements for functional signal transduction for receptors coupled to a G-protein.

Another aspect of the present invention describes a nucleic acid comprising a nucleotide sequence encoding for a chimeric GABA_BR.

5 Another aspect of the present invention describes a recombinant cell comprising an expression vector encoding for a chimeric GABA_BR, and a cell where the chimeric GABA_BR is expressed. Preferably, the chimeric GABA_BR is functional in the cell.

Another aspect of the present invention describes a recombinant cell produced by combining (a) a cell where a chimeric GABA_BR is expressed, and (b) a vector comprising
10 nucleic acid encoding the chimeric GABA_BR and elements for introducing heterologous nucleic acid into the cell. Preferably, the chimeric GABA_BR is functional in the cell.

Another aspect of the present invention describes a process for the production of a chimeric receptor. The process is performed by growing host cells comprising a chimeric GABA_BR.

15 Another aspect of the present invention describes a method of measuring the ability of a compound to affect GABA_BR or mGluR activity. The method is performed by measuring the ability of a compound to affect chimeric GABA_BR or mGluR activity.

Another aspect of the present invention describes a fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused
20 to the intracellular domain of said receptor, provided that the receptor is not an adrenoceptor.

Various examples are described herein. These examples are not intended in any way to limit the claimed invention.

Other features and advantages of the invention will be apparent from the following
25 drawings, the description of the invention, the examples, and the claims.

BRIEF DESCRIPTION OF DRAWINGS

Figures 1a-1d illustrate the amino acid sequences of a human CaR extracellular domain (SEQ. ID. NO. 1), a human GABA_BR1a extracellular domain (SEQ. ID. NO. 2), a
30 human GABA_BR1b extracellular domain (SEQ. ID. NO. 3), a human GABA_BR2 extracellular domain (SEQ. ID. NO. 4), and a human mGluR8 extracellular domain (SEQ. ID. NO. 5).

Figures 2a-2b illustrate the amino acid sequences of a human CaR transmembrane domain (SEQ. ID. NO. 6), a human GABA_BR1a transmembrane domain (SEQ. ID. NO. 7), a human GABA_BR1b transmembrane domain (SEQ. ID. NO. 8), a human GABA_BR2 transmembrane domain (SEQ. ID. NO. 9), and a human mGluR8 transmembrane domain (SEQ. ID. NO. 10).

Figures 3a-3b illustrate the amino acid sequences of a human CaR intracellular domain (SEQ. ID. NO. 11), a human GABA_BR1a intracellular domain (SEQ. ID. NO. 12), a human GABA_BR1b intracellular domain (SEQ. ID. NO. 13), a human GABA_BR2 intracellular domain (SEQ. ID. NO. 14), and a human mGluR8 intracellular domain (SEQ. ID. NO. 15).

Figures 4a-4b illustrate the amino acid sequence of G₁₅ (SEQ. ID. NO. 16) and G₁₆ (SEQ. ID. NO. 17).

Figures 5a-5r illustrate the cDNA sequences encoding for human CaR (SEQ. ID. NO. 18), human GABA_BR1a (SEQ. ID. NO. 19), human GABA_BR1b (SEQ. ID. NO. 20), and human GABA_BR2 (SEQ. ID. NO. 21).

Figures 6a-6h illustrate the cDNA sequence for rat GABA_BR1a (SEQ. ID. NO. 22) and rat GABA_BR1b (SEQ. ID. NO. 23).

Figures 7a-7c illustrate the amino sequence for rat GABA_BR1a (SEQ. ID. NO. 24) and rat GABA_BR1b (SEQ. ID. NO. 25).

Figure 8 illustrates the ability of a chimeric CaR/GABA_BR2 (CaR extracellular and transmembrane domains, and intracellular GABA_BR2 domain) to transduce a signal. Signal production was measured by detecting an increase in the calcium-activated chloride current. The line in the middle of the increase signifies a wash step.

Figures 9a-9p illustrate the cDNA sequence for human mGluR2 (SEQ. ID. NO. 26), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 30), chimeric hmGluR2/hCaR (SEQ. ID. NO. 34), and chimeric hmGluR8/hCaR (SEQ. ID. NO. 38).

Figures 10a-10f illustrate the amino acid sequence for human mGluR2 (SEQ. ID. NO. 27), chimeric hCAR/hmGluR2 (SEQ. ID. NO. 31), chimeric hmGluR2/hCaR (SEQ. ID. NO. 35), chimeric hmGluR8/hCaR (SEQ. ID. NO. 39).

Figures 11a-11v illustrate the cDNA sequence for the phCaR/hmGluR2*Gq α i5 fusion construct (SEQ. ID. NO. 32), pmGluR2//CaR*Gq α i5 fusion construct (SEQ. ID. NO. 36), pmGluR2//CaR*Gq α i5+3Ala linker fusion construct (SEQ. ID. NO. 46), and the

mGluR8//CaR*G α _qi5 fusion construct (SEQ. ID. NO. 40).

Figures 12a-12h illustrate the amino acid sequence for the phCaR/hmGluR2*Gq_i5 fusion construct (SEQ. ID. NO. 33), pmGluR2//CaR*G α _qi5 fusion construct (SEQ. ID. NO. 37), pmGluR2//CaR*G α _qi5+3Ala linker fusion construct (SEQ. ID. NO. 47), and the
5 mGluR8//CaR*G α _qi5 fusion construct (SEQ. ID. NO. 41).

Figures 13a-13m illustrate the cDNA sequence for the GABA-R2*Gqo5 fusion construct (SEQ. ID. NO. 42) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 44).

Figures 14a-14e illustrate the amino acid sequence for the GABA-BR2*Gqo5 fusion
10 construct (SEQ. ID. NO. 43) and the GABA-BR1a*Gqo5 fusion construct (SEQ. ID. NO. 45).

Figure 15 illustrates the ability of different G-protein fusions to transduce signal resulting from ligand binding. mGluR2//CaR*Gq_i5 is shown by SEQ. ID. NO. 37, CaR/mGluR2*Gq_i5 is shown by SEQ. ID. NO. 33, mGluR8//CaR*Gq_i5 is shown by SEQ.
15 ID. NO. 41.

Figures 16a-16e illustrate the amino acid sequence for the ph8SPmGluR4 chimeric construct (SEQ. ID. NO.48), the amino acid sequence for the phmGluR4//CaR*AAA*G α _qi5 fusion construct (SEQ. ID. NO. 49), and the phmGluR8//CaR*AAA*G α _qi5 fusion construct (SEQ. ID. NO. 50).

Figures 17a-17c illustrate the nucleic acid sequence (SEQ ID NO. 51) and amino acid sequence (SEQ ID NO. 52) of ph2SPmGluR3 chimeric construct.

Figures 18a-18d illustrate the nucleic acid sequence (SEQ ID NO. 53) and amino acid sequence of ph2SPmGluR3//CaR*AAA*Gq_i5 fusion construct.

25 DETAILED DESCRIPTION OF THE INVENTION

The CaR, mGluR, and the GABA_BR are structurally similar in that they are each a single subunit membrane protein possessing an extracellular domain, a transmembrane domain comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain.
30 Signal transduction is activated by the extracellular binding of an agonist. The signal is transduced to the intracellular components of the receptor causing an intracellular effect.

Signal transduction from agonist binding to an extracellular region can be modulated by compounds acting at a downstream transmembrane domain or the intracellular domain. Downstream effects include antagonist actions of compounds and allosteric actions of compounds.

5 The transmembrane domain provides different types of target sites for compounds modulating receptor activity in different environments. As noted above, the transmembrane domain contains extracellular, transmembrane, and intracellular components.

Compounds modulating GABA_BR, CaR, or mGluR activity can be obtained, for example, by screening a group or library of compounds to identify those compounds having
10 the desired activity and then synthesizing such compound. Thus, included in the present invention is a method of making a GABA_BR, CaR, or mGluR active compound by first screening for a compound having desired properties and then chemically synthesizing that compound.

15 Metabotropic Glutamate Receptors (mGluRs)

mGluRs are G protein-coupled receptors capable of activating a variety of intracellular secondary messenger systems following the binding of glutamate (Schoepp *et al.*, *Trends Pharmacol. Sci.* 11:508, 1990; Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993, hereby incorporated by reference herein).

20 Activation of different mGluR subtypes *in situ* elicits one or more of the following responses: activation of phospholipase C, increases in phosphoinositide (PI) hydrolysis, intracellular calcium release, activation of phospholipase D, activation or inhibition of adenylyl cyclase, increases and decreases in the formation of cyclic adenosine monophosphate (cAMP), activation of guanylyl cyclase, increases in the formation of cyclic
25 guanosine monophosphate (cGMP), activation of phospholipase A₂, increases in arachidonic acid release, and increases or decreases in the activity of voltage- and ligand-gated ion channels (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Schoepp, *Neurochem. Int.* 24:439, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995, hereby incorporated by reference herein).

30 Eight distinct mGluR subtypes have been isolated. (Nakanishi, *Neuron* 13:1031, 1994; Pin and Duvoisin, *Neuropharmacology* 34:1, 1995; Knopfel *et al.*, *J. Med. Chem.* 38:1417; *Eur. J. Neuroscience* 7:622-629, 1995, each of these references is hereby incorporated by reference herein.) The different mGluRs possess a large amino-terminal extracellular

domain (ECD) followed by a seven putative transmembrane domain (7TMD) comprising seven putative membrane spanning helices connected by three intracellular and three extracellular loops, and an intracellular carboxy-terminal domain of variable length (cytoplasmic tail).

Human mGluR8 is described by Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084, and mouse mGluR8 is described by Duvoisin *et al.*, *J. Neurosci.* 15:3075-3083, 1995, (both of these references are hereby incorporated by reference herein). mGluR8 couples to G_i. Agonists of mGluR8 include L-glutamate and L-2-amino-4-phosphonobutyrate.

mGluR8 activity can be measured using standard techniques. For example, G_i negatively couples to adenylate cyclase to inhibit intracellular cAMP accumulation in a pertussis toxin-sensitive fashion. Thus, mGluR8 activity can be measured, for example, by measuring inhibition of forskolin-stimulated cAMP production as described by Duvoisin *et al.*, *J. Neurosci.* 15:3075-3083, 1995.

mGluRs have been implicated in a variety of neurological pathologies. Examples of such pathologies include stroke, head trauma, spinal cord injury, epilepsy, ischemia, hypoglycemia, anoxia, and neurodegenerative diseases such as Alzheimer's disease (Schoepp and Conn, *Trends Pharmacol. Sci.* 14:13, 1993; Cunningham *et al.*, *Life Sci.* 54: 135, 1994; Pin *et al.*, *Neuropharmacology* 34:1, 1995; Knopfel *et al.*, *J. Med. Chem.* 38:1417, 1995, each of which is hereby incorporated by reference herein).

Calcium Receptor

The CaR responds to changes of extracellular calcium concentration and also responds to other divalent and trivalent cations. The CaR is a G-protein coupled receptor containing an extracellular Ca²⁺ binding domain. Activation of the CaR, descriptions of CaRs isolated from different sources, and examples of CaR active compound are provided in Nemeth *NIPS* 10:1-5, 1995, Brown *et al.* U.S. Patent No. 5,688,938, Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, Brown E.M. *et al.*, *Nature* 366:575, 1993, Riccardi D., *et al.*, *Proc. Nat'l. Acad. Sci. USA* 92:131-135, 1995, and Garrett J.E., *et al.*, *J. Biol. Chem.* 31:12919-12925, 1995. (Each of these references are hereby incorporated by reference herein.) Brown *et al.* U.S. Patent No. 5,688,938 and Van Wagenen *et al.*, International Application Number PCT/US97/05558 International Publication Number WO 97/37967, describe different types

of compounds active at the CaR including compounds which appear to be allosteric modulators and CaR antagonists.

The CaR can be targeted to achieve therapeutic effects. Examples of target diseases are provided in Brown *et al.* U.S. Patent No. 5,688,938, and Van Wagenen *et al.*,

5 International Application Number PCT/US97/05558 International Publication Number WO 97/37967, and include hyperparathyroidism and osteoporosis.

γ -Aminobutyric acid Receptors (GABA_BRs)

GABA_BRs are G-protein coupled metabotropic receptors. GABA_BRs modulate
10 synaptic transmission by inhibiting presynaptic transmitter release and by increasing K⁺ conductance responsible for long-lasting inhibitory postsynaptic potentials. (See, Kaupmann *et al.*, *Nature* 386:239-246, 1997, hereby incorporated by reference herein.) GABA_BRs are found in the mammalian brain, in locations outside of the brain, and in lower species. Outside of the brain, GABA_BRs have been identified on axon terminals and
15 ganglion cell bodies of the autonomic nervous system, on fallopian tube and uterine intestinal smooth muscle cells, in the kidney cortex, urinary bladder muscle and on testicular interstitial cells. (See, Bowery, *Annu. Rev. Pharmacol. Toxicol.* 33:109-147, 1993, hereby incorporated by reference herein.)

Different GABA_BRs subtypes exist. Kaupmann *et al.*, *Nature* 386:239-246, 1997,
20 indicate that they cloned GABA_BRs. Nucleic acid encoding two GABA_BR proteins were indicated to be cloned from rat brain: GABA_BR1a and GABA_BR1b. GABA_BR1a differs from GABA_BR1b in that the N-terminal 147 residues are replaced by 18 amino acids. GABA_BR1a and GABA_BR1b appear to be splice variants. The cloned GABA_BRs were indicated to negatively couple adenylyl cyclases and show sequence similarity to the
25 metabotropic receptors for L-glutamate (mGluR). Northern blot analysis indicated that GABA_BR1a and GABA_BR1b is present in brain and testis, but not in kidney, skeletal muscle, liver, lung, spleen, or heart.

Kaupmann *et al.*, International Application Number PCT/EP97/01370, International Publication Number WO 97/46675, indicate that they have obtained rat GABA_BR clones,
30 GABA_BR1a and GABA_BR1b; and humans GABA_BR clones, GABA_BR1a/b (representing a partial receptor clone) and GABA_BR1b (representing a full-length receptor clone). Amino acid sequence information, and encoding cDNA sequence information, is provided for the different GABA_BR clones.

Another GABA_BR subtype is GABA_BR2. Northern blot analysis reveals that an approximately 6.3 Kb human GABA_BR2 transcript is abundantly expressed in the human brain. Expression is not detected in the heart, placenta, lung, liver, skeletal muscle, kidney and pancreas under conditions where GABA_BR2 transcript was identified in the human
5 brain. Within the human brain GABA_BR2 is broadly expressed at variable levels.

GABA_BR functions as a heterodimer of the subunits GABA_BR1 or GABA_BR2.
(Jones *et al. Nature* 396:674-679, 1998, hereby incorporated by reference herein.)

GABA_BRs have been targeted to achieve therapeutic effects. Kerr and Ong, DDT 1:371-380, 1996, describe different compounds indicated to be GABA_BR agonists and
10 GABA_BR antagonists. Kerr and Ong also review therapeutic implications of affecting GABA_BR activity including, spasticity and motor control, analgesia, epilepsy, cognitive effects, psychiatric disorders, alcohol dependence and withdrawal, feeding behavior, cardiovascular and respiratory functions, and peripheral functions.

Bittiger *et al., Tips* 4:391-394, 1993, review therapeutic applications of GABA_BR
15 antagonists. Potential therapeutic applications noted by Bittiger *et al.* include cognitive processes, epilepsy, and depression.

G-Protein Fusion Receptors

Examples of some different types of G-protein fusion receptors, and advantages of
20 some receptors, are provided below. Using the present application as guide additional G-protein receptors fusion can be constructed.

G-protein fusion receptors contain an intracellular domain of a receptor fused to a G-protein α subunit (G_{α}). G_{α} fusions to adrenoreceptors have been reported by Bertin *et al., Receptors and Channels* 5:41-51, 1997; Wise and Milligan, *Journal of Biological Chemistry*
25 39:24673-24678, 1997; and Bertin *et al., Proc. Natl. Acad. Sci. USA* 91:8827-8831, 1994 (each of which are hereby incorporated by reference herein). These studies were indicated to produce a functional chimeric by fusing the α_{2A} -adrenoreceptor to the $G_{i1\alpha}$, or the β_2 -adrenoreceptor to the $G_{s\alpha}$.

The G-protein fusion receptors described by the present invention include a G-
30 protein fused to an intracellular domain, where the intracellular domain when present in a wild type receptor does not interact with that type of G-protein. Thus, the present invention also describes swapping of signals by fusing an intracellular domain to a G_{α} normally not coupled to that intracellular domain. The use of such fusion proteins, while applicable to

chimeric GABA_BRs, is not limited to chimeric GABA_BRs. Indeed, such technology can be applied to receptors containing an extracellular domain, transmembrane domain and intracellular domain of a wild type receptor.

Preferred G-proteins fusion receptors contain an intracellular domain fused to a promiscuous G_α that couples to phospholipase C resulting in the mobilization of intracellular calcium. Increases in intracellular calcium can be conveniently measured through the use of dyes. Such techniques are well known in the art and are described, for example by Brown *et al.* U.S. Patent No. 5,688,938.

In an embodiment G-proteins fusions can also be used to decrease receptor desensitization.

Examples of promiscuous G_α's coupling to phospholipase C include naturally occurring G-proteins such as G_{α15} and G_{α16}, and chimeric G-protein such as Gqo5 and Gqi5. Gqo5 and Gqi5 are made of a Gq portion where the five amino acids at the C-terminal are from either G_o or G_i, respectively (Conklin *et al.*, *Nature* 363:274-277, 1993, hereby incorporated by reference herein). The Gq portion of such chimeric receptors provides for phospholipase C coupling while the terminal G_o or G_i portion allows the chimeric G-protein to couple to different receptor proteins that are normally involved in inhibitor effects on adenylate cyclase.

In an embodiment of the present invention the employed G-protein is from a human source or is made up of different G-protein components each from a human source.

G-proteins fusions can be created, for example, by fusing directly or indirectly the intracellular domain of a receptor protein to a polypeptide having an amino acid sequence substantially similar to G_{α15}, G_{α16}, Gqo5 or Gqi5. In different embodiments, the receptor is fused directly or indirectly to a G-protein consisting of the amino acid sequence of G_{α15}, G_{α16}, Gqo5 or Gqi5.

The intracellular domain portion of a receptor protein fused directly or indirectly to a G-protein should be at least about 1 amino acid in length. In different embodiments the portion is at least about 10 amino acids, is at least about 50 amino acids, at least about 100 amino acids, or the full length of an intracellular domain.

The intracellular domain can be directly linked to a G-protein or can be indirectly linked through an optionally present linker. Optionally present linkers are preferably about

3 to about 30 amino acids in length. Preferred linkers are made up of alanine, glycine, or a combination thereof.

Chimeric Receptors

5 Examples of some different types of chimeric receptors, and advantages of some receptors, are provided below. Using the present application as guide additional chimeric receptors can be constructed.

Chimeric GABA_BR Extracellular Domain

10 Chimeric GABA_BRs containing a GABA_BR extracellular domain are particularly useful for studying the importance of the GABA_BR extracellular domain and assaying for compounds active at the extracellular domain. Preferably chimeric GABA_BRs containing a GABA_BR extracellular domain also contain a CaR intracellular domain.

15 A variety of different activities have been generally attributed to GABA_BR subtypes. (*E.g.*, Kerr and Ong, DDT 1:371-380, 1996.) Kaupmann *et al.*, *Nature* 386:239-246, 1997, report that in preliminary experiments involving GABA_BR1a they did not detect positive coupling to the adenylyl cyclase or coupling to the phospholipase effector system.

20 An intracellular CaR domain can be used to couple with G-proteins which activate phospholipase C and mobilize intracellular calcium. Mobilization of intracellular calcium is readily detected, for example, by fluorescent indicators of intracellular Ca²⁺.

 An additional advantage of using the intracellular CaR domain is that CaR G-protein activation is not rapidly desensitized. Thus, the intracellular CaR domain can be used to produce a stronger intracellular signal than a signal produced from a receptor which is desensitized rapidly.

25 More preferably, the chimeric GABA_BR contains an intracellular CaR domain, and also contains either a CaR or a GABA_BR transmembrane domain. Advantages of using a CaR transmembrane domain include separating the effects occurring at a GABA_BR extracellular domain from effects occurring at a transmembrane domain; and providing additional intracellular elements, present on transmembrane intracellular loops, useful for
30 coupling to G-protein.

 A GABA_BR transmembrane domain is useful for examining whether the transmembrane GABA_BR can be targeted to affect GABA_BR activity, and obtaining

compounds active at the GABA_BR transmembrane domain. For example, a transmembrane GABA_BR can be used to screen for transmembrane allosteric modulators and antagonists.

Chimeric GABA_BR Transmembrane Domain

5 Chimeric GABA_BRs containing a GABA_BR transmembrane are particularly useful for studying the importance of the GABA_BR transmembrane domain and assaying for compounds active at the transmembrane domain. Preferably Chimeric GABA_BRs containing a GABA_BR transmembrane domain contain an extracellular domain which is either mGluR8 or CaR, and an intracellular CaR domain.

10 More preferably, the chimeric GABA_BR contains an extracellular domain from either mGluR8 or CaR, a GABA_BR transmembrane, and an intracellular CaR domain. A chimeric GABA_BR containing extracellular mGluR8 or CaR domains can readily be stimulated using mGluR8 or CaR ligands.

Chimeric GABA_BR Intracellular Domain

15 Chimeric GABA_BRs containing a GABA_BR intracellular domain are particularly useful for studying the importance of the GABA_BR intracellular domain and assaying for compounds active at the intracellular domain. Preferably, the chimeric receptors contain an extracellular domain from either mGluR8 or CaR. The extracellular mGluR8 or CaR domains can readily be activated using mGluR8 or CaR ligands.

Receptor Domains

25 Domains of a G-protein fusion receptor, a chimeric receptor, and G_α, substantially similar to a particular sequence can be readily produced using the disclosure provided herein in conjunction with information well known in the art. Substantially similar sequences can be obtained taking into account sequence information for a particular type of receptor obtained from different sources, different types of amino acids which are to some extent interchangeable, and the ease of experimentation with which functional receptor activity can be assayed.

30 Substantially similar sequences includes amino acid alterations such as deletions, substitutions, additions, and amino acid modifications. A "deletion" refers to the absence of one or more amino acid residue(s) in the related polypeptide. An "addition" refers to the presence of one or more amino acid residue(s) in the related polypeptide. Additions and

deletions to a polypeptide may be at the amino terminus, the carboxy terminus, and/or internal. Amino acid "modification" refers to the alteration of a naturally occurring amino acid to produce a non-naturally occurring amino acid. A "substitution" refers to the replacement of one or more amino acid residue(s) by another amino acid residue(s) in the polypeptide. Derivatives can contain different combinations of alterations including more than one alteration and different types of alterations.

The sequences of polypeptides can be compared from different sources to help identify variable amino acids not essential for receptor activity. For example, Figure 7 provides the rat GABA_BR1a and GABA_BR1b amino acid sequences. The rat GABA_BR1a and GABA_BR1b amino acid sequences can be compared with the human GABA_BR1a and GABA_BR1b sequences to identify conserved and variable amino acids. Derivatives can then be produced where a variable amino acid is changed, and receptor activity can be readily tested.

Similarly, the amino acid sequences for CaR, mGluR8, and G-proteins from different sources are either known in the art or can readily be obtained. Examples of such references are provided above.

While the effect of an amino acid change varies depending upon factors such as phosphorylation, glycosylation, intra-chain linkages, tertiary structure, and the role of the amino acid in the active site or a possible allosteric site, it is generally preferred that a substituted amino acid is from the same group as the amino acid being replaced. To some extent the following groups contain amino acids which are interchangeable: the basic amino acids lysine, arginine, and histidine; the acidic amino acids aspartic and glutamic acids; the neutral polar amino acids serine, threonine, cysteine, glutamine, asparagine and, to a lesser extent, methionine; the nonpolar aliphatic amino acids glycine, alanine, valine, isoleucine, and leucine (however, because of size, glycine and alanine are more closely related and valine, isoleucine and leucine are more closely related); and the aromatic amino acids phenylalanine, tryptophan, and tyrosine. In addition, although classified in different categories, alanine, glycine, and serine seem to be interchangeable to some extent, and cysteine additionally fits into this group, or may be classified with the polar neutral amino acids.

While proline is a nonpolar neutral amino acid, its replacement represents difficulties because of its effects on conformation. Thus, substitutions by or for proline are not preferred, except when the same or similar conformational results can be obtained. The

conformation conferring properties of proline residues may be obtained if one or more of these is substituted by hydroxyproline (Hyp).

Examples of modified amino acids include the following: altered neutral nonpolar amino acids such as ω -amino acids of the formula $H_2N(CH_2)_nCOOH$ where n is 2-6, sarcosine (Sar), t-butylalanine (t-BuAla), t-butylglycine (t-BuGly), N-methyl isoleucine (N-MeIle), and norleucine (Nleu); altered neutral aromatic amino acids such as phenylglycine; altered polar, but neutral amino acids such as citrulline (Cit) and methionine sulfoxide (MSO); altered neutral and nonpolar amino acids such as cyclohexyl alanine (Cha); altered acidic amino acids such as cysteic acid (Cya); and altered basic amino acids such as ornithine (Orn).

Preferred derivatives have one or more amino acid alteration(s) which do not significantly affect the receptor activity of the related receptor protein. In regions of receptor domains not necessary for receptor activity, amino acids may be deleted, added or substituted with less risk of affecting activity. In regions required for receptor activity, amino acid alterations are less preferred as there is a greater risk of affecting receptor activity.

Derivatives can be produced using standard chemical techniques and recombinant nucleic acid techniques. Modifications to a specific polypeptide may be deliberate, as through site-directed mutagenesis and amino acid substitution during solid-phase synthesis, or may be accidental such as through mutations in hosts which produce the polypeptide. Polypeptides including derivatives can be obtained using standard techniques such as those described by Sambrook *et al.*, *Molecular Cloning*, Cold Spring Harbor Laboratory Press (1989). For example, Chapter 15 of Sambrook describes procedures for site-directed mutagenesis of cloned DNA.

Receptor Nucleic Acid

G-protein fusion and chimeric receptor nucleic acid can be produced based on the information provided herein along with standard recombinant nucleic acid techniques. Examples of references describing recombinant nucleic acid techniques include *Molecular Cloning*, Sambrook *et al.*, Cold Spring Harbor Laboratory Press (1989); and *Current Protocols in Molecular Biology*, Frederick *et al.*, John Wiley & Sons, Inc. (1995).

Due to the degeneracy of the genetic code different nucleic acid sequences can encode for a particular polypeptide. Thus, a large number of nucleic acids encoding for a receptor having the same amino acid sequence can be produced.

5 An embodiment of the present invention uses human nucleic acid encoding for the domains from CaR, GABA_BR1A, GABA_BR1B, GABA_BR2 and/or mGluR8. The amino acid sequences of different domains is provided in Figures 1-3.

Recombinant Cells

10 Nucleic acid expressing a functional G-Protein fusion or a chimeric receptor can be used to create transfected cells lines expressing such receptors. Such cell lines have a variety of uses such as being used for high-throughput screening for compounds modulating receptor activity; being used to assay binding to the receptor; and as factories to produce large amounts of a receptor.

15 A variety of cell lines can couple exogenously expressed receptors to endogenous functional responses. Cell lines such as NIH-3T3, HeLa, NG115, CHO, HEK 293 and COS7 which are expected to lack CaR, mGluR8, and GABA_BR can be tested to confirm that they lack these receptors.

20 Production of stable transfectants can be accomplished by transfection of an appropriate cell line with, for example, an expression vector such as pMSG vector, in which the coding sequence for the G-protein fusion or chimeric GABA_BR cDNA has been cloned. Expression vectors containing a promoter region, such as the mouse mammary tumor virus promoter (MMTV), drive high-level transcription of cDNAs in a variety of mammalian cells. In addition, these vectors contain genes for selecting cells stably expressing cDNA of interest. The selectable marker in the pMSG vectors encode an enzyme, xanthine-guanine
25 phosphoribosyl transferase (XGPRT), conferring resistance to a metabolic inhibitor that is added to the culture to kill nontransfected cells.

The most effective method for transfection of eukaryotic cell lines with plasmid DNA varies with the given cell type. The expression construct will be introduced into cultured cells by the appropriate technique, such as Ca²⁺ phosphate precipitation, DEAE-
30 dextran transfection, lipofection or electroporation. Expression of the receptor cDNA in cell lines can be assessed by solution hybridization and Northern blot analysis.

Binding Assays

The present invention also includes using G-protein fusion receptors or chimeric GABA_BR in a binding assay. G-protein fusion receptors or chimeric GABA_BRs having a particular GABA_BR domain can be used, for example to facilitate obtaining compounds able to bind to that particular receptor domain; and to determine whether a compound which
5 binds to a particular domain. For example, in a complete chimeric GABA_BR containing extracellular, transmembrane, and intracellular domains, the presence of one or more domains from CaR or mGluR are useful to present GABA_BR domain(s) to a binding agent in a form more like the GABA_BR domain(s) in the wild type receptor compared to an incomplete GABA_BR receptor fragment lacking one or more domains.

10 Binding assays can be carried out using techniques well known in the art. Binding assays preferably employ radiolabeled binding agents.

An example of a binding procedure is carried out by first attaching chimeric GABA_BR to a solid-phase support to create an affinity matrix. The affinity matrix is then contacted with potential GABA_BR binding agents. A large library of compounds may be
15 used to determine those compounds binding to the affinity matrix. Bound compounds can be eluted from the column.

Therapeutic Modulation

As pointed out above, different types of diseases and disorders can be treated using
20 compounds modulating CaR, mGluR, or GABA_BR activity. Additionally, such compounds can be used prophylactically. Compounds modulating GABA_BR2 activity can be administered to patients who would benefit from such treatment. Patients are mammals, preferably humans.

Modulators of CaR, mGluR, or GABA_BR activity can be administered to a patient
25 using standard techniques. Techniques and formulations generally may be found in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, 1990 (hereby incorporated by reference herein).

Suitable dosage forms, in part, depend upon the use or the route of entry, for example, oral, transdermal, transmucosal, or by injection (parenteral). Such dosage forms should allow the
30 therapeutic agent to reach a target cell whether the target cell is present in a multicellular host or in culture. For example, pharmacological compounds or compositions injected into the blood stream should be soluble. Other factors are well known in the art, and include

considerations such as toxicity and dosage forms which retard the therapeutic agent from exerting its effect.

Therapeutic compounds can be formulated as pharmaceutically acceptable salts and complexes thereof. Pharmaceutically acceptable salts are non-toxic salts in the amounts and concentrations at which they are administered. The preparation of such salts can facilitate the pharmacological use by altering the physical characteristics of the compound without preventing it from exerting its physiological effect. Useful alterations in physical properties include lowering the melting point to facilitate transmucosal administration and increasing the solubility to facilitate administering higher concentrations of the drug.

The pharmaceutically acceptable salt of a compound may be present as a complex. Examples of complexes include an 8-chlorotheophylline complex (analogous to, *e.g.*, dimenhydrinate:diphenhydramine 8-chlorotheophylline (1:1) complex; Dramamine) and various cyclodextrin inclusion complexes.

Pharmaceutically acceptable salts include acid addition salts such as those containing sulfate, hydrochloride, fumarate, maleate, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluene-sulfonate, cyclohexylsulfamate and quinate.

Pharmaceutically acceptable salts can be obtained from acids such as hydro-chloric acid, maleic acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid, lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, *p*-toluenesulfonic acid, cyclohexyls-ulfamic acid, fumaric acid, and quinic acid.

Pharmaceutically acceptable salts also include basic addition salts such as those containing benzathine, chlorprocaine, choline, diethanolamine, ethylenediamine, meglumine, procaine, aluminum, calcium, lithium, magnesium, potassium, sodium, ammonium, alkylamine, and zinc, when acidic functional groups, such as carboxylic acid or phenol are present. For example, see Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, p. 1445, 1990. Such salts can be prepared using the appropriate corresponding bases.

Carriers or excipients can also be used to facilitate administration of therapeutic agents. Examples of carriers include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents. Examples of

physiologically compatible solvents include sterile solutions of water for injection (WFI), saline solution and dextrose.

GABA_BR modulating compounds can be administered by different routes including intravenous, intraperitoneal, subcutaneous, intramuscular, oral, topical (transdermal), or transmucosal administration. For systemic administration, oral administration is preferred. For oral administration, for example, the compounds can be formulated into conventional oral dosage forms such as capsules, tablets, and liquid preparations such as syrups, elixirs, and concentrated drops.

Alternatively, injection (parenteral administration) may be used, *e.g.*, intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, compounds are formulated in liquid solutions, preferably, in physiologically compatible buffers or solutions, such as saline solution, Hank's solution, or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms can also be produced.

Systemic administration can be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are well known in the art, and include, for example, for transmucosal administration, bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration, for example, may be through nasal sprays, rectal suppositories, or vaginal suppositories.

For topical administration, compounds can be formulated into ointments, salves, gels, or creams, as is well known in the art.

The amounts of various GABA_BR modulating compounds to be administered can be determined by standard procedures taking into account factors such as the compound IC₅₀, EC₅₀, the biological half-life of the compound, the age, size and weight of the patient, and the disease or disorder associated with the patient. The importance of these and other factors to be considered are well known to those of ordinary skill in the art. Generally, the amount is expected to preferably be between about 0.01 and 50 mg/kg of the animal to be treated.

EXAMPLES

Examples are provided below illustrating different aspects and embodiments of the present invention. The examples include techniques that can be used to produce and use G-protein fusion receptors and chimeric receptors. These examples are not intended to limit
5 the claimed invention.

Example 1: Construction of G-Protein Fusions

This example illustrates different G-protein fusion receptor constructs and techniques used to produce different G-protein fusion receptor constructs. Numbering of
10 nucleotide position for all the following constructs is such that nucleotide number 1 corresponds to the A of the ATG start codon of the nucleotide sequence encoding the designated protein.

I. FULL-LENGTH CONSTRUCTS

A. phCaR

The cDNA encoding the human CaR (Garrett et al., (1995) J. Biol. Chem.270:12919) is harbored in the Bluescript SK(-) plasmid (Stratagene). This construct is referred to as phCaR.

B. phmGluR2

A full length human mGluR2 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR2 cDNA sequence (Genbank Accession # 4504136). The obtained PCR fragment was subcloned into the pT7Blue TA vector (Novagen). A Hind III-Not I fragment containing the human
25 mGluR2 cDNA was then subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR2.

C. phG α_q

A full length human G α_q cDNA was amplified from human cerebral cortex Quick-
30 Clone cDNA (Clontech) using PCR primers based on the human G α_q cDNA sequence (Genbank Accession # 4504044). The obtained PCR fragment was subcloned into the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phG α_q .

D. phmGluR8

The cDNA encoding the full length human mGluR8 cDNA (Stormann *et al.*, U.S. Patent Nos. 6,051,688, 6,077,675, and 6,084,084) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as phmGluR8.

E. ph8SPmGluR4

A full length human mGluR4 cDNA was amplified from human cerebellum MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR4 cDNA sequence (Genbank Accession #X80818). The obtained PCR fragment was cloned into the pT7Blue TA vector (Novagen). A 2977 bp BamHI fragment containing the human mGluR4 cDNA was then subcloned into the vector pcDNA3.1/Hygro+ (Invitrogen). This construct is referred to as phmGluR4.

Next, the predicted signal peptide of mGluR4 was replaced with the predicted signal peptide and 87 bp of 5' UTR from phmGluR8 using a recombinant PCR strategy similar to those described above. The first reaction used a phmGluR8 construct with two primers, 3.1-535F (sense 21-mer, complementary to vector sequence upstream of the hmGluR8 insert; sequence 5'-ggcattatgccagtagcatga-3'), and the hybrid primer 8/4RP (antisense 42-mer, containing 21 nucleotides complementary to human mGluR8 and 21 nucleotides complementary human mGluR4; sequence 5'-caagcctctcttcccaggcattttctccacaggtggtattgc-3'). These primers were used to amplify a 469 bp PCR fragment of human mGluR8.

In a separate PCR reaction using phmGluR4 as template, a 472 bp fragment of human mGluR4 was amplified using a hybrid primer 4/8RP (sense 42-mer, exactly complementary to primer 8/4RP) and oligo mG4-472R, (antisense 18-mer, complementary to the human mGluR4 cDNA; sequence 5'-ctgaagcaccgatgacac-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-472R and 3.1-535F, and Turbo Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with NarI and NheI (New England Biolabs) and subcloned into phmGluR4 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4, was verified by ABI automated DNA sequence analysis.

The replacement of the predicted signal peptide of mGluR4 with that of mGluR8

greatly increased the activity of this receptor in *in vitro* assays

F. ph2SPmGluR3

A full length human mGluR3 cDNA was amplified from human hippocampus
5 MarathonReady cDNA (Clontech) using PCR primers based on the human mGluR3 cDNA
sequence (Genbank Accession #NM 000840) and cloned into the pBluescript SKII(-)
plasmid (Stratagene). This construct is referred to as phmGluR3/pSK.

The predicted signal peptide of mGluR was replaced with the predicted signal
peptide and 40 bp of 5' UTR from phmGluR2 using a recombinant PCR strategy exactly
10 analogous to that described above. The first reaction used a phmGluR2 construct with two
primers, 3.1-535F (sense 21-mer, complementary to vector sequence upstream of the
hmGluR2 insert; sequence 5'-ggcattatgccccagtagcatga-3'), and the hybrid primer SP2/3RP
(antisense 42-mer, containing 21 nucleotides complementary to human mGluR2 and 21
nucleotides complementary human mGluR3; sequence 5'-

15 tagaaagtattgtcccctaagccacagcaccacacagcag-3'). These primers were used to amplify an
approximately 500 bp PCR fragment of human mGluR2.

In a separate PCR reaction using phmGluR3//CaR in pcDNA3.1/Hygro(+) (See
construction of this chimeric construct, phmGluR3//CaR, below) as template, an
approximately 1000 bp fragment of human mGluR3 was amplified using a hybrid primer
20 3/SP2RP (sense 42-mer, exactly complementary to primer SP2/3RP) and oligo 3-1086R,
(antisense 19-mer, complementary to the human mGluR3 cDNA; sequence 5'-
ctggaggctgcactgaaac-3'). The two PCR products generated from the above two reactions
were annealed together in equimolar ratios in the presence of the external primers 3-1086R
and 3.1-535F, and Turbo Pfu DNA polymerase (Stratagene).

25 The resulting chimeric PCR product was digested with NarI and NheI (New England
Biolabs) and subcloned into phmGluR3//CaR digested with the same two restriction
enzymes. The sequence of the resultant chimeric construct, ph2SPmGluR3//CaR, was
verified by ABI automated DNA sequence analysis.

The replacement of the predicted signal peptide of mGluR3 with that of mGluR2
30 greatly increased the activity of the chimeric receptor in *in vitro* assays.

The full-length mGluR3 receptor construct with the signal peptide and 5'UTR of
mGluR2 was then constructed by replacing the 3' half of ph2SPmGluR3//CaR with that
from phmGluR3/pSK. Specifically, a 1002 nt fragment digested with Bsu36I (at position

1691 in mGluR3 coding DNA sequence (CDS)) and NotI (in vector) was subcloned in place of a 1484 nt fragment dropped from the ph2SPmGluR3//CaR plasmid digested with the same restriction enzymes. The sequence of the resultant construct, ph2SPmGluR3 in pcDNA3.1/Hygro(+), was verified by ABI automated DNA sequence analysis.

5

II. G α _{qi5}

The cDNA encoding the human G α _{qi5} cDNA (Conklin et al (1993) Nature 363:274-77) is harbored in the Bluescript SKII(-) plasmid (Stratagene). This construct is referred to as G α _{qi5}. The nucleic acid and amino acid sequences for G α _{qi5} are provided by SEQ. ID. NOs. 28 and 29 respectively.

10

III. phCaR/hmGluR2

This chimera contains the extracellular domain of the human CaR and transmembrane domain and intracellular cytoplasmic tail of human mGluR2. The chimeric junction between the CaR and hmGluR2 was created using a recombinant PCR strategy similar to those described above.

15

The first reaction used two primers, CA1156 (sense 19-mer, corresponding to nucleotides 1156-1174 of human CaR), and the hybrid primer CA/2 (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 1774-1794 of human CaR and 21 nucleotides complementary to nucleotides 1660-1680 of the human mGluR2). These primers were used to amplify a 659 bp PCR fragment of human CaR.

20

In a separate PCR reaction using phmGluR2 as template, a 692 bp fragment of the human mGluR2 was amplified using a hybrid primer 2/CA (sense 42-mer, exactly complementary to primer CA/2) and oligo 2-2330m, (antisense 23-mer, complementary to nucleotides 2309-2331 of the human mGluR2 cDNA). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CA1156 and 2-2330m, and the Pfu DNA polymerase (Stratagene).

25

The resulting chimeric PCR product was digested with SexA1 (Boehringer Mannheim) and BamHI (New England Biolabs) and subcloned into phCaR digested with the same two restriction enzymes. In the final cloning step, the 3' end of human mGluR2 was subcloned into this construct using the restriction enzymes BsrGI and BamHI (both

30

New England Biolabs). The sequence of the resultant chimeric construct, phCaR/hmGluR2, was verified by ABI automated DNA sequence analysis.

IV. phCaR/hmGluR2*Gqi5

5 This construct contains the phCaR/hmGluR2 chimeric receptor fused to human $G\alpha_{qi5}$. A HindIII-BamHI fragment containing the phCaR/hmGluR2 construct was subcloned into pcDNA3.1/Hygro(+) (Invitrogen) to aid in constructing this fusion protein. The chimeric junction between the C-terminus of phCaR/hmGluR2 and the N-terminus of $G\alpha_{qi5}$ was created using a recombinant PCR strategy similar to those described above.

10 The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to nucleotides 1710-1730 of human mGluR2) and the hybrid primer 2/Q (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2596-2616 of human mGluR2, and 21 nucleotides complementary to nucleotides 1-21 of p $G\alpha_{qi5}$). These primers were used to amplify a 927 bp PCR fragment of phCaR/hmGluR2. In a separate PCR reaction all of $G\alpha_{qi5}$ was amplified using a hybrid primer Q/2 (sense 42-mer, exactly complementary to primer 2/Q) and the and the T3 primer commercially available from Stratagene.

15 These two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with Bsu361 and BamHI (New England Biolabs) and subcloned into phCaR/hmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, phCaR/hmGluR2* $G\alpha_{qi5}$, was verified by DNA sequence analysis.

V. phmGluR2//CaR Construct

25 This chimera contains the extracellular and transmembrane domains of human mGluR2 linked to the intracellular cytoplasmic tail domain of the human CaR. The chimeric junction was created using three separate PCR reactions.

30 The first reaction used two primers, 2-1713 (sense 21-mer, corresponding to nucleotides 1710-1730 of human mGluR2, Genbank Accession # 4504136) and the hybrid primer 2/CT (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 2452 – 2472 of human mGluR2 and 21 nucleotides complementary to nucleotides 2602-2622 of the human CaR). These primers were used to amplify a 783 bp PCR fragment of

human mGluR2. In a separate PCR reaction using phCaR in the BlueScript SK⁻ plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CT/2 (sense 42-mer, exactly complementary to primer 2/CT) and the T3 primer commercially available from Stratagene.

5 The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 2-1713 and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Not I (New England Biolabs) and subcloned into pmGluR2 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct,
10 pmGluR2//CaR, was verified by ABI automated DNA sequence analysis.

VI. pmGluR2//CaR*Gα_qi5 Construct

This construct contains the hmGluR2//CaR chimeric receptor fused to human Gα_qi5. The chimeric junction between the C-terminus of hmGluR2//CaR and the N-
15 terminus of Gα_qi5 was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer CaRQ (antisense 42-mer, containing 21 nucleotides complementary to nucleotides 3214– 3234 phCaR, and 21
20 nucleotides complementary to nucleotides 1-21 of pGα_qi5). These primers were used to amplify a 443 bp PCR fragment of hmGluR2//CaR. In a separate PCR reaction, all of Gα_qi5 was amplified using a hybrid primer QCaR (sense 42-mer, exactly complementary to primer CaRQ) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed
25 together in equimolar ratios in the presence of the external primers CRP10A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BstE II and Not I (New England Biolabs) and subcloned into pmGluR2//CaR digested with the same two restriction enzymes. The sequence of the resultant chimeric fusion construct, pmGluR2//CaR*Gα_qi5, was verified by ABI automated DNA sequence analysis.

VII. Fusion Receptor Protein Linker Addition Constructs

A. phmGluR2//CaR*AAA*G α _qi5

A linker encoding three alanine residues was incorporated into the phmGluR2//CaR*G α _qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit). A sense 40-mer, 2CQ+LP, contained 16 nucleotides corresponding to 3219-3234 of human CaR, followed by the 9 nucleotide sequence (GCGGCCGCC) encoding three alanine residues and a NotI restriction enzyme site, and then 15 nucleotides corresponding to nucleotides 1-15 of G α _qi5. 2CQ+LP was annealed to an antisense 40-mer, 2CQ+LM, the exact complement of 2CQ+LP. These oligos were used in the mutagenesis reaction according to the manufacturer's protocol. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9 nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR2//CaR and the N-terminus of G α _qi5. This construct was designated phmGluR2//CaR*AAA*G α _qi5.

B. Human GABA_BR2*AAA*G α _qo5 and human GABA_BR1a*AAA*G α _qo5

These constructs contain the human GABA_BR2 (hGABA_BR2: Genbank Accession # AJ 012188) and human GABA_BR1a (hGABA_BR1a: Genbank Accession # AJ 012185) fused at their C-terminus to the N-terminus of human G α _qo5 (hG α _qo5: *Nature* 363:274-276, 1993). Human GABA_BR2, hGABA_BR1a, and hG α _qo5 were cloned into the plasmid pcDNA3.1/Hygro+ (Invitrogen) and are designated phGABA_BR2, phGABA_BR1a, and phG α _qo5. The first reaction used two primers, XcmI-R2 (sense 20-mer, corresponding to nucleotides 2650-2669 of phGABA_BR2) and the hybrid primer R2/Go5(-) (antisense 45-mer, containing 18 nucleotides complementary to nucleotides 2806-2823 of phGABA_BR2 and 18 nucleotides complementary to nucleotides 1-18 of hG α _qo5). These two complementary areas flank a 9 nucleotide sequence coding for 3 alanine sequences with a unique NotI restriction site. These primers were used to amplify a 200 base-pair PCR fragment.

In a separate PCR reaction, part of hG α _qo5 was amplified using a hybrid primer R2/G α _qo5(+) (sense 45-mer), exactly complementary to R2/Go5(-) and XbaI-Go5 primer (22-mer containing 22 nucleotides complementary to nucleotides 873-895 of hG α _qo5). These primers were used to amplify a 914 base-pair PCR product. The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers; XcmI-R2 and XbaI-Go5, and Pfu polymerase (Stratagene).

The resulting chimeric PCR product was digested with the restriction endonucleases XcmI and XbaI (New England Biolabs) and subcloned into phGABA_BR2 digested with the same two restriction enzymes. The resulting clone was then digested with HindIII and XbaI and subcloned into phGα_qo5 cut with HindIII and XbaI resulting in the chimeric hGABA_BR*AAA*Gα_qo5. The chimeric junction between the C-terminus hGABA_BR1a, the Ala linker, and the N-terminus of hGα_qo5 was created using a recombinant PCR strategy similar to those described above.

To construct hGABA_BR1a*AAA*Gqo5, the first reaction used a commercially available T7 primer (Novagen) and the NtI hGBR1 primer (CAGAGTCATGGCGGCCGCTTATAAAGCAAATGCACTCG) corresponding to nucleotide numbers 1-9 of hGα_qo5 and nucleotide numbers 2863-2883 of hGABA_BR1a.

C. phmGluR8//CaR*AAA*Gα_qi5

A linker encoding three alanine residues was incorporated into the phmGluR8//CaR*Gα_qi5 construct by mutagenesis (Stratagene QuickChange Mutagenesis Kit), exactly as described in Section A, above to create phmGluR2//CaR*AAA*Gα_qi5. The same primers, 2CQ+LP and 2CQ+LM, were used for this mutagenesis. Restriction enzyme analysis and DNA sequence analysis confirmed the insertion of the 9-nucleotide linker (GCGGCCGCC) between the C-terminus of phmGluR8//CaR and the N-terminus of Gα_qi5. This construct was designated phmGluR8//CaR*AAA*Gα_qi5.

D. ph8SPmGluR4//CaR*AAA*Gα_qi5

This chimera contains the extracellular and transmembrane domains of the human 8SPmGluR4 construct and intracellular cytoplasmic tail of human CaR fused to Gα_qi5 through the three alanine residue linker.

The chimeric junction between the human 8SPmGluR4 and hCaR was created using a recombinant PCR strategy similar to those previously described. The first reaction used two primers, mG4-2028R (sense 19-mer, corresponding to nucleotides of human 8SPmGluR4; sequence 5'-catctaccgcatcttcgag-3'), and the hybrid primer 4CT (antisense 42-mer, containing 21 nucleotides complementary to human 8SPmGluR4 and 21 nucleotides

complementary human CaR; sequence 5'-acgcacctcctcgatgggtgttctgctccgggtggaaggat-3'). These primers were used to amplify a 549 bp PCR fragment from human 8SPmGluR4.

In a separate PCR reaction, using phmGluR2//CaR*AAA*G α _qi5 as a template, a 743 bp fragment of the human CaR*AAA*G α _qi5 was amplified using the hybrid primer CT4 (sense 42-mer, exactly complementary to primer 4CT) and oligo Gaqi58R, (antisense 21-mer, complementary to G α _qi5 cDNA; sequence 5'-ctcgatctcgtcgttgatccg-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers mG4-2028R and Gaqi58R, and Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested sequentially with KpnI and NotI (New England Biolabs) and subcloned into ph8SPmGluR4 prepared with the same two restriction enzymes. This intermediate construct was known as ph8SPmGluR4//CaR(no stop). In the final cloning step, a fragment containing the G α _qi5 cDNA was released from phmGluR8//CaR*AAA*G α _qi5 using the restriction enzymes ApaI and NotI (both New England Biolabs) and subcloned into the ph8SPmGluR4//CaR(no stop) construct, which was prepared with the same restriction enzymes. The sequence of the resultant chimeric construct, ph8SPmGluR4//CaR*AAA*G α _qi5, was verified by ABI automated DNA sequence analysis.

E. ph2SPmGluR3//CaR*AAA*G α _qi5

This chimera contains the extracellular and transmembrane domains of the human 2SPmGluR3 construct and intracellular cytoplasmic tail of human CaR fused to G α _qi5 through the three alanine residue linker.

The chimeric junction between the human mGluR3 and hCaR was created using a recombinant PCR strategy similar to those previously described. The first reaction used two primers, 3-2032 (sense 18-mer, corresponding to nucleotides of human mGluR3; sequence 5'-ccaaaattcatcagcccc-3'), and the hybrid primer 3/CT (antisense 42-mer, containing 21 nucleotides complementary to human mGluR3 and 21 nucleotides complementary human CaR; sequence 5'-gcaacgcacctcctcgatgggtattcttctggggtgaaacag-3'). These primers were used to amplify a 479 bp PCR fragment from human mGluR3.

In a separate PCR reaction, using human CaR in pBluescript SK(-) as a template, a 756 bp fragment of the human CaR was amplified using the hybrid primer CT/3 (sense 42-

mer, exactly complementary to primer 3/CT) and oligo T3, (antisense 20-mer, complementary to vector sequence; sequence 5'-attaaccctcactaaaggga-3'). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers 3-2032 and T3, and Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with AccI and NotI (New England Biolabs) and subcloned into hmGluR3 prepared with the same two restriction enzymes. This construct was known as phmGluR3//CaR.

As detailed under the Full-length Constructs Examples, the 5' UTR and signal peptide of hmGluR2 was then added to this chimeric construct to produce ph2SPmGluR3//CaR.

Next, mutagenesis was performed (Stratagene QuickChange Mutagenesis Kit) to replace the stop codon of ph2SPmGluR3//CaR with a three alanine linker (also creating a Not I site) to facilitate addition of the $G\alpha_{i5}$ coding sequence. The two mutagenic primers used were CNOTP (sense 42mer, sequence 5'-gaaaacgtagtgaattcagcgccgcaatggaaggagaagac-3') and CNOTM (antisense 42mer, complementary to CNOTP). This intermediate construct was known as ph2SPmGluR3//CaR(no stop).

In the final cloning step, a fragment containing the $G\alpha_{i5}$ cDNA was released from phmGluR8//CaR*AAA* $G\alpha_{i5}$ using the restriction enzymes ApaI and NotI (both New England Biolabs) and subcloned into the ph2SPmGluR3//CaR(no stop) construct, which was prepared with the same restriction enzymes. The sequence of the resultant chimeric construct, ph2SPmGluR3//CaR*AAA* $G\alpha_{i5}$, was verified by ABI automated DNA sequence analysis.

VIII. phmGluR8//CaR Construct

This chimera contains the extracellular and transmembrane domains of human mGluR8 linked to the intracellular cytoplasmic tail domain of the human CaR. The chimeric junction between hmGluR8 and the CaR was created using a recombinant PCR strategy similar to those described above.

The first reaction used two primers, CH5A (sense 19-mer, corresponding to nucleotides 2187-2205 of human mGluR8, Stormann *et al.*, U.S. Patent Nos. 6,051,688,

6,077,675, and 6,084,084) and the hybrid primer CH5B (antisense 40-mer, containing 22 nucleotides complementary to nucleotides 2523 – 2544 of human mGluR8, and 18 nucleotides complementary to nucleotides 2602-2619 of the human CaR). These primers were used to amplify a 375 bp PCR fragment of human mGluR8. In a separate PCR reaction using phCaR in the BlueScript SK(-) plasmid as template, a 750 bp fragment of the human CaR was amplified using a hybrid primer CH5C (sense 40-mer, exactly complementary to primer CH5B) and the T3 primer commercially available from Stratagene.

The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CH5A and T3, and the Pfu DNA polymerase (Stratagene). The resulting chimeric PCR product was digested with BsrG I and Xba I (New England Biolabs) and subcloned into pmGluR8 digested with the same two restriction enzymes. The sequence of the resultant chimeric construct, pmGluR8//CaR, was verified by DNA sequence analysis.

IX. mGluR8//CaR*G α qi5 Construct

This construct contains the hmGluR8//CaR chimeric receptor fused to human G α qi5. The chimeric junction between the C-terminus of hmGluR8//CaR and the N-terminus of G α qi5 was created using a recombinant PCR strategy similar to that described above for the construction of phmGluR2//CaR*G α qi5.

The first reaction used two primers, CRP10A (sense 18-mer, corresponding to nucleotides 2812-2829 of phCaR) and the hybrid primer Gqi5/CaR (antisense 40-mer, containing 21 nucleotides complementary to nucleotides 3214-3234 phCaR, and 19 nucleotides complementary to nucleotides 1-19 of pG α qi5). These primers were used to amplify a 441 bp PCR fragment of hmGluR8//CaR.

In a separate PCR reaction all of G α qi5 was amplified using a hybrid primer CaR/Gqi5 (sense 40-mer, exactly complementary to primer Gqi5/CaR) and the Apa I-mut primer (20-mer). The two PCR products generated from the above two reactions were annealed together in equimolar ratios in the presence of the external primers CRP10A and Apa I-mut, and the Pfu DNA polymerase (Stratagene).

The resulting chimeric PCR product was digested with BstE II and Apa I (New England Biolabs) and subcloned into pmGluR8//CaR digested with the same two restriction

enzymes. The sequence of the resultant chimeric fusion construct, pmGluR8//CaR*G α q15, was verified by DNA sequence analysis.

Example 2: Functional Expression of CaR/GABA_BR2

5 In vitro transcribed RNA (7 ng) encoding a chimeric CaR/GABA_BR2 (CaR extracellular and transmembrane domains, and intracellular GABA_BR2 domain) was co-injected with *in vitro* transcribed RNA (2 ng) encoding G α 15 into *Xenopus* oocytes. Following a 72-hour incubation, the oocytes were voltage-clamped using standard electrophysiological techniques (Hille, B., Ionic Channels of Excitable Membranes, pp.30-
10 33, Sinauer Associates, Inc., Sunderland, Ma., 1992). Activation of the chimeric receptor was detected by increases in the calcium-activated chloride current.

Application of the CaR activator 100 μ M Gd³⁺, resulted in reversible, oscillatory increases in the calcium-activated chloride current as shown in Figure 8. These data demonstrate the functional response of the chimeric CaR/GABA_BR2 receptor upon
15 activation via a site within the CaR extracellular domain. In this assay, the G α 15 subunit acts to promote signal transduction through intracellular pathways that mobilize intracellular Ca⁺⁺.

Example 3: Expression of Different G-Protein Fusion Receptors

20 The ability of different G-protein fusions to transduce signal resulting from ligand binding is shown in Figure 15. The different G-protein fusion receptors used in this example were as follows: mGluR2//CaR*Gqi5 (SEQ. ID. NO. 37), CaR/mGluR2*Gqi5 (SEQ. ID. NO. 33), and mGluR8//CaR*Gqi5 SEQ. ID. NO. 41.

Oocytes suitable for injection were obtained from adult female *Xenopus laevis* toads
25 using procedures described in C. J. Marcus-Sekura and M. J. M. Hitchcock, *Methods in Enzymology*, Vol. 152 (1987).

Receptor fusion cRNAs were dissolved in water and 50 nl (12.5 ng/oocyte) were injected into individual oocytes. Following injection, oocytes were incubated at 16°C in MBS containing 1 mM CaCl₂ for 2 to 7 days prior to electrophysiological recording.

30 Test substances were applied by superfusion at a flow rate of about 5 ml/min. Receptor fusion activation was determined by measuring the increase in calcium-activated chloride current (I_{Cl}). Increases in I_{Cl} were quantified by measuring the peak inward current stimulated by activating agent, relative to the holding current at -60 mV. Application of 100

μM L-glutamate elicited a response from the mGluR2//CaR*G α qi5 and mGluR8//CaR*G α qi5. Application of 100 μM Gd³⁺ activated the CaR/mGluR2*Gqi5.

Example 4: Expression of Different G-Protein Fusion Receptors in Mammalian Cells

5

HEK293 cells were transiently transfected with the p8SPhmGluR4//CaR*AAA*G α qi5 or phmGluR8//CaR*G α qi5 plasmid DNAs using the following protocol. Initially, 150 cm² tissue culture flasks containing HEK293 cells at 75% confluence were transfected with 24 μg of plasmid DNA using Gibco BRL Life Technologies' Lipofectamine reagent. Following liposomal gene delivery the cells were allowed to recover for 24 hours. They were then plated overnight at 100,000 cells per well in black, clear bottom, Collagen I coated 96-well plates (Becton Dickinson, Biocoat) using DMEM supplemented with 10% fetal bovine serum (Hyclone Laboratories). The cells were assayed for function 48 hours after transient transfection.

10

15

On the day of the assay, tissue culture medium was aspirated from the wells of a 96-well plate and 80 μL of Assay Buffer (Assay Buffer is: 20 mM HEPES, 146 mM NaCl, 5 mM KCl, 1 mM MgCl₂, 1 mM CaCl₂, 1 mg/ml BSA, 1 mg/ml glucose, pH 7.4) supplemented with 6 μM of the Ca²⁺-sensitive dye, Fluo-3 AM (Molecular Probes) and 0.025% Pluronic (Molecular Probes) was added to each well.

20

The plate was then incubated in the dark for 1 hour at room temperature to efficiently load the cells with Fluo-3. At the end of the incubation, extracellular Fluo-3 was removed by washing the plate with Assay Buffer. Assay Buffer was added back to each well (final volume = 160 μL) prior to beginning the assay. The plate was loaded into a fluorescence imaging plate reader (FLIPR) robotic device (Molecular Devices) with the laser setting at 0.8 Watts. At a time of 15 seconds after initiation of the assay, 40 μL of Assay Buffer containing 150 μM L-AP4 was added to the 160 μL of Assay Buffer in each well of the plate to yield a final concentration of 30 μM L-AP4.

25

Relative fluorescence intensity (excitation λ = 488 nm / emission λ = 510 nm) was monitored at relevant time intervals throughout the assay period to measure L-AP4-induced receptor activation.

30

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

5 One skilled in the art would readily appreciate that the present invention is well adapted to obtain the ends and advantages mentioned, as well as those inherent therein. The methods, variances, and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are
10 encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims.

15 The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of
20 description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification
25 and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that
30 the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Also, unless indicated to the contrary, where various numerical values are provided for embodiments, additional embodiments are described by taking any 2 different values as

the endpoints of a range. Such ranges are also within the scope of the described invention.

Thus, additional embodiments are within the scope of the invention and within the following claims.

Claims

1. A G-protein fusion receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence
substantially similar to either an extracellular CaR amino acid sequence, an extracellular
mGluR amino acid sequence, or an extracellular GABA_B receptor amino acid sequence;

a transmembrane domain joined to the carboxy terminus of said extracellular
domain, said transmembrane domain comprising a transmembrane domain amino acid
sequence substantially similar to either a transmembrane CaR amino acid sequence, a
transmembrane mGluR amino acid sequence, or a transmembrane GABA_B receptor amino
acid sequence;

an intracellular domain joined to the carboxy terminus of said transmembrane
domain comprising all or a portion of an intracellular amino acid sequence substantially
similar to either an intracellular CaR amino acid sequence, an intracellular mGluR amino
acid sequence, or an intracellular GABA_B receptor amino acid sequence, provided that said
portion is at least about 10 amino acids;

an optionally present linker joined to the carboxy terminus of said intracellular
domain; and

a G-protein joined either to said intracellular domain or to said optionally present
linker, provided that said G-protein is joined to said optionally present linker when said
optionally present linker is present.

2. The G-protein fusion receptor of claim 1, wherein said extracellular domain
consists of said extracellular domain amino acid sequence, said transmembrane domain
consists of said transmembrane domain amino acid sequence; and said intracellular domain
consists of said transmembrane domain amino acid sequence.

3. The G-protein fusion receptor of claim 2, wherein said optionally present
linker is present and is a polypeptide 3 to 30 amino acids in length.

4. The G-protein fusion receptor of claim 2, wherein said optionally present
linker is not present.

5. The G-protein fusion receptor of claim 3 or 4, wherein said G-protein is selected from the group consisting of: $G_{\alpha 15}$, $G_{\alpha 16}$, Gqo5, and Gqi5

6. The G-protein fusion of claim 5, wherein any of said CaR sequence present is
5 a human CaR sequence, any of said mGluR sequence present is from a human mGluR, and any of said GABA_B receptor sequence present is from human mGluR.

7. A nucleic acid comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6.

10

8. An expression vector comprising a nucleotide sequence encoding for the G-protein fusion of any one of claims 1-6 transcriptionally coupled to a promoter.

9. A recombinant cell comprising the expression vector of claim 8 and a cell
15 wherein the G-protein fusion is expressed and is functional.

10. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 9 and elements for introducing heterologous nucleic acid into a cell wherein the G-protein fusion receptor is expressed, and said cell.

20

11. A process for the production of a G-protein fusion receptor comprising:
growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence
expressing the G-protein fusion receptor of any one of claims 1-6, under suitable nutrient
conditions allowing for cell growth.

25

12. A method of measuring the ability of a compound to effect G-protein fusion activity comprising the steps of:

a) providing said compound to a cell expressing the G-protein fusion receptor of any one of claims 1-6, and

30 b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect G-protein fusion receptor activity.

13. A chimeric receptor comprising

an extracellular domain comprising an extracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4 and SEQ ID NO: 5;

5 a transmembrane domain comprising a transmembrane domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, and SEQ ID NO: 10; and

an intracellular cytoplasmic domain comprising an intracellular domain amino acid sequence substantially similar to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14;

10 wherein at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14; and at least one domain is present which comprises an amino acid sequence substantially similar to a sequence selected from the
15 group consisting of: SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 11, and SEQ ID NO: 15.

14. The chimeric receptor of claim 13 wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group
20 consisting of SEQ ID NOs: 2, 3, and 4; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs:
11 and 15.

25 15. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 2; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least
30 90% with the amino acid sequence of SEQ ID NO: 11.

16. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 3; said

transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

5 17. The chimeric receptor of claim 14, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence SEQ ID NO: 4; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

10 18. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4 and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of
15 SEQ ID Nos: 7, 8, and 9; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 12, 13, 14, and 15.

20 19. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 11.

25 20. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

30 21. The chimeric receptor of claim 18, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO 11.

22. The chimeric receptor of claim 13, wherein said extracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 4, and 5; said transmembrane domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID Nos: 6, 7, 8, 9, and 10; and said intracellular domain has a sequence similarity of at least 90% with an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 13, and 14.

23. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

24. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 7; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 12.

25. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 8; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

26. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid

sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 13.

27. The chimeric receptor of claim 22, wherein said extracellular domain has a
5 sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 9; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

10 28. The chimeric receptor of claim 22, wherein said extracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 1; said transmembrane domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 6; and said intracellular domain has a sequence similarity of at least 90% with the amino acid sequence of SEQ ID NO: 14.

15

29. The chimeric receptor of any one of claims 13-28, wherein said receptor functional couples to a G-protein.

30. The chimeric receptor of any one of claims 13-28, wherein said chimeric
20 receptor consists of said extracellular domain, said transmembrane domain, said intracellular domain, and an optionally present G-protein α subunit covalently joined to said intracellular domain.

31. The chimeric receptor of claim 30, wherein said chimeric receptor consists of
25 said extracellular domain, said transmembrane domain, and said intracellular domain.

32. The chimeric receptor of claim 30, wherein said G-protein α subunit consists of the amino acid sequence of SEQ ID Nos: 16 or 17.

30 33. A nucleic acid comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32.

34. An expression vector comprising a nucleotide sequence encoding for the chimeric receptor of any one of claims 13-32 transcriptionally coupled to a promoter.

5 35. A recombinant cell comprising the expression vector of claim 34 and a cell wherein the chimeric receptor is expressed and is functional.

36. A recombinant cell produced by combining a vector comprising the nucleic acid of claim 33 and elements for introducing heterologous nucleic acid into a cell wherein the chimeric receptor is expressed, and said cell.

10

37. A process for the production of a chimeric receptor comprising:
growing procaryotic or eukaryotic host cells comprising a nucleic acid sequence expressing the chimeric receptor of any one of claims 13-32, under suitable nutrient conditions allowing for cell growth.

15

38. A method of measuring the ability of a compound to effect GABA_BR or mGluR activity comprising the steps of:
a) providing said compound to a cell expressing the chimeric receptor of any one of claims 13-32, and
20 b) measuring the ability of said compound to affect the activity of said receptor as an indication of the ability of said compound to effect GABA_BR or mGluR activity.

39. The method of claim 38, wherein said method measures activity at a GABA_BR.

25 40. The method of claim 38, wherein said method measures activity at a mGluR.

41. A fusion receptor polypeptide comprising a receptor and a G-protein α subunit, wherein said G-protein α subunit is fused to the intracellular domain of said receptor, provided that said receptor is not an adrenoceptor.

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ClustalW Formatted Alignments

SEQ ID 1 M A F Y S C C W V L L A L T W H T S A Y G P D Q R
SEQ ID 2 M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ ID 3 M G P G A P F A R V G W P L P L L V V M A A G V A
SEQ ID 4 M A S P R S S G Q P G P X P P P P P P P A R L L L
SEQ ID 5 M V C E G K R S A S C P C F F L L T A K F Y W I L

SEQ ID 1 A Q K K G D I I L G G L F P I H F G V A A K D Q D
SEQ ID 2 T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ ID 3 P V W A S H S P H L P R P H S R V P P H P S S E R
SEQ ID 4 L L L L P L L L P L A P G A W G W A R G A P R P P
SEQ ID 5 T M M Q R T H S Q E Y A H S I R V D G D I I L G G

SEQ ID 1 L K S R P E S V E C I R Y N F R G F R W L Q A M I
SEQ ID 2 V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ ID 3 R A V Y I G A L F P M S G G W P G G Q A C Q P A V
SEQ ID 4 P S S P P L S I M G L M P L T K E V A K G S I G R
SEQ ID 5 L F P V H A K G E R G V P C G E L K K E K G I H R

SEQ ID 1 F A I E E I N S S P A L L P N L T L G Y R I F D T
SEQ ID 2 P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ ID 3 E M A L E D V N S R R D I L P D Y E L K L I H H D
SEQ ID 4 G V L P A V E L A I E Q I R N E S L L R P Y F L D
SEQ ID 5 L E A M L Y A I D Q I N K D P D L L S N I T L G V

SEQ ID 1 C N T V S K A L E A T L S F V A Q N K I D S L N L
SEQ ID 2 S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ ID 3 S K C D P G Q A T K Y L Y E L L Y N D P I K I I L
SEQ ID 4 L R L Y D T E C D N A K G L K A F Y D A I K Y G P
SEQ ID 5 R I L D T C S R D T Y A L E Q S L T F V Q A L I E

SEQ ID 1 D E F C N C S E H I P S T I A V V G A T G S G V S
SEQ ID 2 R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ ID 3 M P G C S S V S T L V A E A A R M W N L I V L S Y
SEQ ID 4 N H L M V F G G V C P S V T S I I A E S L Q G W N
SEQ ID 5 K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ ID 1 T A V A N L L G L F Y I P Q V S Y A S S S R L L S
SEQ ID 2 S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ ID 3 G S S S P A L S N R Q R F P T F F R T H P S A T L
SEQ ID 4 L V Q L S F A A T T P V L A D K K K Y P Y F F R T
SEQ ID 5 I G A A A S S V S I M V A N I L R L F K I P Q I S

FIG. 1a.

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SEQ ID 1 NKNQFKSFLRTIPNDEHQATAMADI
 SEQ ID 2 FPMSSGGWPGGQACQPAVEMALEDVN
 SEQ ID 3 HNPTRVKLF EKWGWKKIATIQQTTTE
 SEQ ID 4 VPSDNAVNPAILKLLKH YQWKRVGT
 SEQ ID 5 YASTAPELS DNTRYDFFSRVVPD S

SEQ ID 1 IEYFRWNWVGTIAADDDYGRPGIEK
 SEQ ID 2 SRRDILPDYELKLIHHDSKCDPGQA
 SEQ ID 3 VFTSTLDDLEERVKEAGIEITFRQS
 SEQ ID 4 LTQDVQRFSEVRNDLTGVLYGEDIE
 SEQ ID 5 YQAQAMVDIVTALGWN YVSTLASEG

SEQ ID 1 FREEAEERDICI DFSELISQYSDEE
 SEQ ID 2 TKYLYELLYNDPIKII LMPGCSSVS
 SEQ ID 3 FFSDPAVPVKNLKRQDARIIVGLFY
 SEQ ID 4 ISDTESFSNDPCTSVKKLKGNDVRI
 SEQ ID 5 NYGESGVEAFTQISREIGGVCI AQ S

SEQ ID 1 EIQHVVEVIQNSTAKVIVVFSSGPD
 SEQ ID 2 TLVAEAAARMWNLIVLSYGSSSPALS
 SEQ ID 3 ETEARKVFCEVYKERLFGKKYVWFL
 SEQ ID 4 ILGQFDQNMAAKVFCCAYEENMYGS
 SEQ ID 5 QKIPREPRPGEF EKIIKRLLLETPNA

SEQ ID 1 LEPLIKEIVRRNITGKIWLASEAWA
 SEQ ID 2 NRQRFPTFFRTHPSATLHNPTRVKL
 SEQ ID 3 IGWYADNWFKIYDPSINCTVDEMTE
 SEQ ID 4 KYQWII PGWYEP SWWEQVHTEANSS
 SEQ ID 5 RAVIMFANEDDIRRILEAAKKLNQS

SEQ ID 1 SSSLIAMPQYFHVVG GTIGFALKAG
 SEQ ID 2 FEKWGWKKIATIQQTTTEVFTSTLDD
 SEQ ID 3 AVEGHITTEIVMLNPANTRSISNMT
 SEQ ID 4 RCLRKNLLAAMEGYIGVDFEPLSSK
 SEQ ID 5 GHFLWIGSDSWGSK IAPVYQQEEIA

SEQ ID 1 QIPGFREFLKKVHPRKSVHNGFAKE
 SEQ ID 2 LEERVKEAGIEITFRQSF FSDPAVP
 SEQ ID 3 SQEFVEKLTKRRLKRHP EETGGFQEA
 SEQ ID 4 QIKTISGKTPQQYEREYNNKRSGVG
 SEQ ID 5 EGAVTILPKRASIDGFDRYFRSRTL

FIG. 1b.

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SEQ ID 1 F W E E T F N C H L Q E G A K G P L P V D T F L R
 SEQ ID 2 V K N L K R Q D A R I I V G L F Y E T E A R K V F
 SEQ ID 3 P L A Y D A I W A L A L A L N K T S G G G G R S G
 SEQ ID 4 P S K F H G Y A Y D G I W V I A K T L Q R A M E T
 SEQ ID 5 A N N R R N V W F A E F W E E N F G C K L G S H G

SEQ ID 1 G H E E S G D R F S N S S T A F R P L C T G D E N
 SEQ ID 2 C E V Y K E R L F G K K Y V W F L I G W Y A D N W
 SEQ ID 3 V R L E D F N Y N N Q T I T D Q I Y R A M N S S S
 SEQ ID 4 L H A S S R H Q R I Q D F N Y T D H T L G R I I L
 SEQ ID 5 K R N S H I K K C T G L E R I A R D S S Y E Q E G

SEQ ID 1 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
 SEQ ID 2 F K I Y D P S I N C T V D E M T E A V E G H I T T
 SEQ ID 3 F E G V S G H V V F D A S G S R M A W T L I E Q L
 SEQ ID 4 N A M N E T N F F G V T G Q V V F R N G E R M G T
 SEQ ID 5 K V Q F V I D A V Y S M A Y A L H N M H K D L C P

SEQ ID 1 S I A H A L Q D I Y T C L P G R G L F T N G S C A
 SEQ ID 2 E I V M L N P A N T R S I S N M T S Q E F V E K L
 SEQ ID 3 Q G G S Y K K I G Y Y D S T K D D L S W S K T D K
 SEQ ID 4 I K F T Q F Q D S R E V K V G E Y N A V A D T L E
 SEQ ID 5 G Y I G L C P R M S T I D G K E L L G Y I R A V N

SEQ ID 1 D I K K V E A W Q V L K H L R H L N F T N N M G E
 SEQ ID 2 T K R L K R H P E E T G G F Q E A P L A Y D A I W
 SEQ ID 3 W I G G S P P A D Q T L V I K T F R F L S Q K
 SEQ ID 4 I I N D T I R F Q G S E P P K D K T I I L E Q L R
 SEQ ID 5 F N G S A G T P V T F N E N G D A P G R Y D I F Q

SEQ ID 1 Q V T F D E C G D L V G N Y S I I N W H L S P E D
 SEQ ID 2 A L A L A L N K T S G G G G R S G V R L E D F N Y
 SEQ ID 3
 SEQ ID 4 K I S L P
 SEQ ID 5 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E

SEQ ID 1 G S I V F K E V G Y Y N V Y A K K G E R L F I N E
 SEQ ID 2 N N Q T I T D Q I Y R A M N S S S F E G V S G H V
 SEQ ID 3
 SEQ ID 4
 SEQ ID 5 D M Q W A H R E H T H P A S V C S L P C K P G E R

FIG. 1c.

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SEQ ID 1 E K I L W S G F S R E V P F S N C S R D C L A G T
SEQ ID 2 V F D A S G S R M A W T L I E Q L Q G G S Y K K I
SEQ ID 3
SEQ ID 4
SEQ ID 5 K K T V K G V P C C W H C E R C E G Y N Y Q V D E

SEQ ID 1 R K G I I E G E P T C C F E C V E C P D G E Y S D
SEQ ID 2 G Y Y D S T K D D L S W S K T D K W I G G S P P A
SEQ ID 3
SEQ ID 4
SEQ ID 5 L S C E L C P L D Q R P N M N R T G C Q L I P I I

SEQ ID 1 E T D A S A C N K C P D D F W S N E N H T S C I A
SEQ ID 2 D Q T L V I K T F R F L S Q K
SEQ ID 3
SEQ ID 4
SEQ ID 5 K L E W H S P W

SEQ ID 1 K E I E F L S W T E P F
SEQ ID 2
SEQ ID 3
SEQ ID 4
SEQ ID 5

FIG. 1d.

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SEQ ID 6 G I A L T L F A V L G I F L T A F V L G V F I K F R N T P I
 SEQ ID 7 L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
 SEQ ID 8 L F I S V S V L S S L G I V L A V V C L S F N I Y N S H V R
 SEQ ID 9 L Y S I L S A L T I L G M I M A S A F L F F N I K N R N Q K
 SEQ ID 10 A V V P V F V A I L G I I A T T F V I V T F V R Y N D T P I

SEQ ID 6 V K A T N R E L S Y L L L F S L L C C F S S S L F F I G E P
 SEQ ID 7 Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
 SEQ ID 8 Y I Q N S Q P N L N N L T A V G C S L A L A A V F P L G L D
 SEQ ID 9 L I K M S S P Y M N N L I I L G G M L S Y A S I F L F G L D
 SEQ ID 10 V R A S G R E L S Y V L L T G I F L C Y S I T F L M I A A P

SEQ ID 6 Q D W T C R L R Q P A F G I S F V L C I S C I L V K T N R V
 SEQ ID 7 G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
 SEQ ID 8 G Y H I G R N Q F P F V C Q A R L W L L G L G F S L G Y G S
 SEQ ID 9 G S F V S E K T F E T L C T V R T W I L T V G Y T T A F G A
 SEQ ID 10 D T I I C S F R R V F L G L G M C F S Y A A L L T K T N R I

SEQ ID 6 L L V F E A K I P T S F H R K W W G L N L Q F L L V F L C T
 SEQ ID 7 M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
 SEQ ID 8 M F T K I W W V H T V F T K K E E K K E W R K T L E P W K L
 SEQ ID 9 M F A K T W R V H A I F K N V K M K K K I I K D O K L L V I
 SEQ ID 10 H R I F E Q G K K S V T A P K F I S P A S Q L V I T F S L I

SEQ ID 6 F M Q I V I C V I W L Y T A P P S S Y R N Q E L E D E I I F
 SEQ ID 7 Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
 SEQ ID 8 Y A T V G L L V G M D V L T L A I W Q I V D P L H R T I E T
 SEQ ID 9 V G G M L L I D L C I L I C W Q A V D P L R R T V E K Y S M
 SEQ ID 10 S V Q L L G V F V W F V V D P P H I I I D Y G E O R T L D P

SEQ ID 6 I T C H E G S L M A L G F L I G Y T C L L A A I C F F F A F
 SEQ ID 7 F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
 SEQ ID 8 F A K E E P K E D I D V S I L P Q L E H C S S R K M N T W L
 SEQ ID 9 E P D P A G R D I S I R P L L E H C E N T H M T I W L G I V
 SEQ ID 10 E K A R G V L K C D I S D L S L I C S L G Y S I L L M V T C

SEQ ID 6 K S R K L P E N F N E A K F I T F S M L I F F I V W I S F I
 SEQ ID 7 G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
 SEQ ID 8 G I F Y G Y K G L L L L L G I F L A Y E T K S V S T E K I N
 SEQ ID 9 Y A Y K G L L M L F G C F L A W E T R N V S I P A L N D S K
 SEQ ID 10 T V Y A I K T R G V P E T F N E A K P I G F T M Y T T C I I

FIG. 2a.

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SEQ ID 6 P A Y A S T Y G K F V S A V E V I A I L A A S F G L L A C I
SEQ ID 7 D H R A V G M A I Y N V A V L C L I T A P V T M I L S S Q Q
SEQ ID 8 D H R A V G M A I Y N V A V L C L I T A P V T M I L S S Q Q
SEQ ID 9 Y I G M S V Y N V G I M C I I G A A V S F L T R D Q P N V Q
SEQ ID 10 W L A F I P I F F G T A Q S A E K M Y I Q T T T L T V S M S

SEQ ID 6 F F N K I Y I I L F
SEQ ID 7 D A A F A F A S L A I V F S S Y I T L V V L F V P K M
SEQ ID 8 D A A F A F A S L A I V F S S Y I T L V V L F V P K M
SEQ ID 9 F C I V A L V I I F C S T I T L C L V F V P K L
SEQ ID 10 L S A S V S L G M L Y M P K V Y I I I F

FIG. 2b.

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SEQ ID 11 K P S R N T I E E V R C S T A A H A F K V A A R A T L R R S
 SEQ ID 12 R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E E K
 SEQ ID 13 R R L I T R G E W Q S E A Q D T M K T G S S T N N N E E E E K
 SEQ ID 14 I T L R T N P D A A T Q N R R F Q F T Q N Q K K E D S K T S
 SEQ ID 15 H P E Q N V Q K R K R S F K A V V T A A T M Q S K L I Q K G

SEQ ID 11 N V S R K R S S S L G G S T G S T P S S S I S S K S N S E D
 SEQ ID 12 S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
 SEQ ID 13 S R L L E K E N R E L E K I I A E K E E R V S E L R H Q L Q
 SEQ ID 14 T S V T S V N Q A S T S R L E G L Q S E N H R L R M K I T E
 SEQ ID 15 N D R P N G E V K S E L C E S L E T N S K S S V E F P M V K

SEQ ID 11 P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q P L T L P Q
 SEQ ID 12 S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
 SEQ ID 13 S R Q Q L R S R R H P P T P P E P S G G L P R G P P E P P D
 SEQ ID 14 L D K D L E E V T M Q L Q D T P E K T T Y I K Q N H Y Q E L
 SEQ ID 15 S G S T S

SEQ ID 11 Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S F D E P
 SEQ ID 12 R L S C D G S R V H L L Y K
 SEQ ID 13 R L S C D G S R V H L L Y K
 SEQ ID 14 N D I L N L G N F T E S T D G G K A I L K N H L D Q N P Q L
 SEQ ID 15

SEQ ID 11 Q K N A M A H G N S T H Q N S L E A Q K S S D T L T R H Q P
 SEQ ID 12
 SEQ ID 13
 SEQ ID 14 Q W N T T E P S R T C K D P I E D I N S P E H I Q R R L S L
 SEQ ID 15

SEQ ID 11 L L P L Q C G E T D L D L T V Q E T G L Q G P V G G D Q R P
 SEQ ID 12
 SEQ ID 13
 SEQ ID 14 Q L P I L H H A Y L P S I G G V D A S C V S P C V S P T A S
 SEQ ID 15

SEQ ID 11 E V E D P E E L S P A L V V S S S Q S F V I S G G G S T V T
 SEQ ID 12
 SEQ ID 13
 SEQ ID 14 P R H R H V P P S F R V M V S G L
 SEQ ID 15

FIG. 3a.

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SEQ ID 11 E N V V N S
SEQ ID 12
SEQ ID 13
SEQ ID 14
SEQ ID 15

FIG. 3b.

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SEQ. ID. NO. 16 M A R S L T W G C C P W C L T E E E K T A A R I D Q E I N R
SEQ. ID. NO. 17 M A R S L T W R C C P W C L T E D E K A A A R V D Q E I N R

SEQ. ID. NO. 16 I L L E Q K K Q E R E E L K L L L L G P G E S G K S T F I K
SEQ. ID. NO. 17 I L L E Q K K Q D R G E L K L L L L G P G E S G K S T F I K

SEQ. ID. NO. 16 Q M R I I H G V G Y S E E D R R A F R L L I Y Q N I F V S M
SEQ. ID. NO. 17 Q M R I I H G A G Y S E E E R K G F R P L V Y Q N I F V S M

SEQ. ID. NO. 16 Q A M I D A M D R L Q I P F S R P D S K Q H A S L V M T Q D
SEQ. ID. NO. 17 R A M I E A M E R L Q I P F S R P E S K H H A S L V M S Q D

SEQ. ID. NO. 16 P Y K V S T F E K P Y A V A M Q Y L W R D A G I R A C Y E R
SEQ. ID. NO. 17 P Y K V T T F E K R Y A A A M Q W L W R D A G I R A C Y E R

SEQ. ID. NO. 16 R R E F H L L D S A V Y Y L S H L E R I S E D S Y I P T A Q
SEQ. ID. NO. 17 R R E F H L L D S A V Y Y L S H L E R I T E E G Y V P T A Q

SEQ. ID. NO. 16 D V L R S R M P T T G I N E Y C F S V K K T K L R I V D V G
SEQ. ID. NO. 17 D V L R S R M P T T G I N E Y C F S V Q K T N L R I V D V G

SEQ. ID. NO. 16 G Q R S E R R K W I H C F E N V I A L I Y L A S L S E Y D Q
SEQ. ID. NO. 17 G Q K S E R K K W I H C F E N V I A L I Y L A S L S E Y D Q

SEQ. ID. NO. 16 C L E E N D Q E N R M E E S L A L F S T I L E L P W F K S T
SEQ. ID. NO. 17 C L E E N N Q E N R M K E S L A L F G T I L E L P W F K S T

SEQ. ID. NO. 16 S V I L F L N K T D I L E D K I H T S H L A T Y F P S F Q G
SEQ. ID. NO. 17 S V I L F L N K T D I L E E K I P T S H L A T Y F P S F Q G

SEQ. ID. NO. 16 P R R D A E A A K S F I L D M Y A R V Y A S C A E P Q D G G
SEQ. ID. NO. 17 P K Q D A E A A K R F I L D M Y T R M Y T G C V D G P E G S

SEQ. ID. NO. 16 R K G S R A R R F F A H F T C A T D T Q S V R S V F K D V R
SEQ. ID. NO. 17 K K G A R S R R L F S H Y T C A T D T Q N I R K V F K D V R

FIG. 4a.

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SEQ. ID. NO. 16 D S V L A R Y L D E I N L L
SEQ. ID. NO. 17 D S V L A R Y L D E I N L L

FIG. 4b.

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ClustalW Formatted Alignments

SEQ. ID. NO. 18 A T G G C A T T T T A T A G C T G C T G C T G G G
SEQ. ID. NO. 19 A T G T T G C T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 20 A T G G G G C C C G G G G C C C C T T T T G C C C
SEQ. ID. NO. 21 A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 18 T C C T C T T G G C A C T C A C C T G G C A C A C
SEQ. ID. NO. 19 C A C T C T T C C T C C G C C C C C G G G C G C
SEQ. ID. NO. 20 G G G T G G G G T G G C C A C T G C C G C T T C T
SEQ. ID. NO. 21 A G C C C G G G C C G C - G C C G C C G C C G C C

SEQ. ID. NO. 18 C T C T G C C T A C G G G C C A G A C C A G C G A
SEQ. ID. NO. 19 G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 20 G G T T G T G A T G G C G G C A G G G G T G G C T
SEQ. ID. NO. 21 A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 18 G C C C A A A A G A A G G G G G A C A T T A T C C
SEQ. ID. NO. 19 A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 20 C C G G T G T G G G C C T C C C A C T C C C C C C
SEQ. ID. NO. 21 C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 18 T T G G G G G G C T C T T T C C T A T T C A T T T
SEQ. ID. NO. 19 A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 20 A T C T C C C G C G G C C T C A C T C G C G G G T
SEQ. ID. NO. 21 C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 18 T G G A G T A G C A G C T A A A G A T C A A G A T
SEQ. ID. NO. 19 G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 20 C C C C C G C A C C C C T C C T C A G A A C G G
SEQ. ID. NO. 21 G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 18 C T C A A A T C A A G G C C G G A G T C T G T G G
SEQ. ID. NO. 19 G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 20 C G C G C A G T G T A C A T C G G G G C A C T G T
SEQ. ID. NO. 21 C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 18 A A T G T A T C A G G T A T A A T T T C C G T G G
SEQ. ID. NO. 19 T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 20 T T C C C A T G A G C G G G G G C T G G C C A G G
SEQ. ID. NO. 21 T G G G C C T C A T G C C G C T C A C C A A G G A

FIG. 5a.

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SEQ. ID. NO. 18 G T T T C G C T G G T T A C A G G C T A T G A T A
SEQ. ID. NO. 19 C C G G G G G G A G C G C G A G G T G G T G G G G
SEQ. ID. NO. 20 G G G C C A G G C C T G C C A G C C C G C G G T G
SEQ. ID. NO. 21 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 18 T T T G C C A T A G A G G A G A T A A A C A G C A
SEQ. ID. NO. 19 C C C A A G G T C C G C A A G T G C C T G G C C A
SEQ. ID. NO. 20 G A G A T G G C G C T G G A G G A C G T G A A T A
SEQ. ID. NO. 21 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 18 G C C C A G C C C T T C T T C C C A A C T T G A C
SEQ. ID. NO. 19 A C G G C T C C T G G A C A G A T A T G G A C A C
SEQ. ID. NO. 20 G C C G C A G G G A C A T C C T G C C G G A C T A
SEQ. ID. NO. 21 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 18 G C T G G G A T A C A G G A T A T T T G A C A C T
SEQ. ID. NO. 19 A C C C A G C C G C T G T G T C C G A A T C T G C
SEQ. ID. NO. 20 T G A G C T C A A G C T C A T C C A C C A C G A C
SEQ. ID. NO. 21 A C T C C T G C G C C C C T A C T T C C T C G A C

SEQ. ID. NO. 18 T G C A A C A C C G T T T C T A A G G C C T T G G
SEQ. ID. NO. 19 T C C A A G T C T T A T T T G A C C C T G G A A A
SEQ. ID. NO. 20 A G C A A G T G T G A T C C A G G C C A A G C C A
SEQ. ID. NO. 21 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 18 A A G C C A C C C T G A G T T T T G T T G C T C A
SEQ. ID. NO. 19 A T G G G A A G G T T T T C C T G A C G G G T G G
SEQ. ID. NO. 20 C C A A G T A C C T A T A T G A G C T G C T C T A
SEQ. ID. NO. 21 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 18 A A A C A A A A T T G A T T C T T T G A A C C T T
SEQ. ID. NO. 19 G G A C C T C C C A G C T C T G G A C G G A G C C
SEQ. ID. NO. 20 C A A C G A C C C T A T C A A G A T C A T C C T T
SEQ. ID. NO. 21 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 18 G A T G A G T T C T G C A A C T G C T C A G A G C
SEQ. ID. NO. 19 C G G G T G G A T T T C C G G T G T G A C C C C G
SEQ. ID. NO. 20 A T G C C T G G C T G C A G C T C T G T C T C C A
SEQ. ID. NO. 21 A A C C A C T T G A T G G T G T T T G G A G G C G

FIG. 5b.

13/124

SEQ. ID. NO. 18 A C A T T C C C T C T A C G A T T G C T G T G G T
SEQ. ID. NO. 19 A C T T C C A T C T G G T G G G C A G C T C C C G
SEQ. ID. NO. 20 C G C T G G T G G C T G A G G C T G C T A G G A T
SEQ. ID. NO. 21 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 18 G G G A G C A A C T G G C T C A G G C G T C T C C
SEQ. ID. NO. 19 G A G C A T C T G T A G T C A G G G C C A G T G G
SEQ. ID. NO. 20 G T G G A A C C T C A T T G T G C T T T C C T A T
SEQ. ID. NO. 21 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 18 A C G G C A G T G G C A A A T C T G C T G G G G C
SEQ. ID. NO. 19 A G C A C C C C C A A G C C C C A C T G C C A G G
SEQ. ID. NO. 20 G G C T C C A G C T C A C C A G C C C T G T C A A
SEQ. ID. NO. 21 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 18 T C T T C T A C A T T C C C C A G G T C A G T T A
SEQ. ID. NO. 19 T G A A T C G A A C G C C A C A C T C A G A A C G
SEQ. ID. NO. 20 A C C G G C A G C G T T T C C C C A C T T T C T T
SEQ. ID. NO. 21 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 18 T G C C T C C T C C A G C A G A C T C C T C A G C
SEQ. ID. NO. 19 G C G C G C A G T G T A C A T C G G G G C A C T G
SEQ. ID. NO. 20 C C G A A C G C A C C C A T C A G C C A C A C T C
SEQ. ID. NO. 21 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 18 A A C A A G A A T C A A T T C A A G T C T T T C C
SEQ. ID. NO. 19 T T T C C C A T G A G C G G G G G C T G G C C A G
SEQ. ID. NO. 20 C A C A A C C C T A C C C G C G T G A A A C T C T
SEQ. ID. NO. 21 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 18 T C C G A A C C A T C C C C A A T G A T G A G C A
SEQ. ID. NO. 19 G G G G C C A G G C C T G C C A G C C C G C G G T
SEQ. ID. NO. 20 T T G A A A A G T G G G G C T G G A A G A A G A T
SEQ. ID. NO. 21 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 18 C C A G G C C A C T G C C A T G G C A G A C A T C
SEQ. ID. NO. 19 G G A G A T G G C G C T G G A G G A C G T G A A T
SEQ. ID. NO. 20 T G C T A C C A T C C A G C A G A C C A C T G A G
SEQ. ID. NO. 21 C T A C C A G T G G A A G C G C G T G G G C A C G

FIG. 5c.

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SEQ. ID. NO. 18 A T C G A G T A T T T C C G C T G G A A C T G G G
SEQ. ID. NO. 19 A G C C G C A G G G A C A T C C T G C C G G A C T
SEQ. ID. NO. 20 G T C T T C A C T T T C G A C T C T G G A C G A C C
SEQ. ID. NO. 21 C T G A C G C A A G A C G T T C A G A G G T T C T

SEQ. ID. NO. 18 T G G G C A C A A T T G C A G C T G A T G A C G A
SEQ. ID. NO. 19 A T G A G C T C A A G C T C A T C C A C C A C G A
SEQ. ID. NO. 20 T G G A G G A A C G A G T G A A G G A G G C T G G
SEQ. ID. NO. 21 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 18 C T A T G G G C G G C C G G G G A T T G A G A A A
SEQ. ID. NO. 19 C A G C A A G T G T G A T C C A G G C C A A G C C
SEQ. ID. NO. 20 A A T T G A G A T T A C T T T C C G C C A G A G T
SEQ. ID. NO. 21 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 18 T T C C G A G A G G A A G C T G A G G A A A G G G
SEQ. ID. NO. 19 A C C A A G T A C C T A T A T G A G C T G C T C T
SEQ. ID. NO. 20 T T C T T C T C A G A T C C A G C T G T G C C C G
SEQ. ID. NO. 21 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 18 A T A T C T G C A T C G A C T T C A G T G A A C T
SEQ. ID. NO. 19 A C A A C G A C C C T A T C A A G A T C A T C C T
SEQ. ID. NO. 20 T C A A A A A C C T G A A G C G C C A G G A T G C
SEQ. ID. NO. 21 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 18 C A T C T C C C A G T A C T C T G A T G A G G A A
SEQ. ID. NO. 19 T A T G C C T G G C T G C A G C T C T G T C T C C
SEQ. ID. NO. 20 C C G A A T C A T C G T G G G A C T T T T C T A T
SEQ. ID. NO. 21 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 18 G A G A T C C A G C A T G T G G T A G A G G T G A
SEQ. ID. NO. 19 A C G C T G G T G G C T G A G G C T G C T A G G A
SEQ. ID. NO. 20 G A G A C T G A A G C C C G G A A A G T T T T T T
SEQ. ID. NO. 21 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 18 T T C A A A A T T C C A C G G C C A A A G T C A T
SEQ. ID. NO. 19 T G T G G A A C C T C A T T G T G C T T T C C T A
SEQ. ID. NO. 20 G T G A G G T G T A C A A G G A G C G T C T C T T
SEQ. ID. NO. 21 T G G C A G C A A A A G T G T T C T G T T G T G C

FIG. 5d.

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SEQ. ID. NO. 18 C G T G G T T T T C T C C A G T G G C C C A G A T
SEQ. ID. NO. 19 T G G C T C C A G C T C A C C A G C C C T G T C A
SEQ. ID. NO. 20 T G G G A A G A A G T A C G T C T G G T T C C T C
SEQ. ID. NO. 21 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 18 C T T G A G C C C C T C A T C A A G G A G A T T G
SEQ. ID. NO. 19 A A C C G G C A G C G T T T C C C C A C T T T C T
SEQ. ID. NO. 20 A T T G G G T G G T A T G C T G A C A A T T G G T
SEQ. ID. NO. 21 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 18 T C C G G C G C A A T A T C A C G G G C A A G A T
SEQ. ID. NO. 19 T C C G A A C G C A C C C A T C A G C C A C A C T
SEQ. ID. NO. 20 T C A A G A T C T A C G A C C C T T C T A T C A A
SEQ. ID. NO. 21 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 18 C T G G C T G G C C A G C G A G G C C T G G G C C
SEQ. ID. NO. 19 C C A C A A C C C T A C C C G C G T G A A A C T C
SEQ. ID. NO. 20 C T G C A C A G T G G A T G A G A T G A C T G A G
SEQ. ID. NO. 21 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 18 A G C T C C T C C C T G A T C G C C A T G C C T C
SEQ. ID. NO. 19 T T T G A A A A G T G G G G C T G G A A G A A G A
SEQ. ID. NO. 20 G C G G T G G A G G G C C A C A T C A C A A C T G
SEQ. ID. NO. 21 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 18 A G T A C T T C C A C G T G G T T G G C G G C A C
SEQ. ID. NO. 19 T T G C T A C C A T C C A G C A G A C C A C T G A
SEQ. ID. NO. 20 A G A T T G T C A T G C T G A A T C C T G C C A A
SEQ. ID. NO. 21 C T G C C A T G G A G G G C T A C A T T G G C G T

SEQ. ID. NO. 18 C A T T G G A T T C G C T C T G A A G G C T G G G
SEQ. ID. NO. 19 G G T C T T C A C T T C G A C T C T G G A C G A C
SEQ. ID. NO. 20 T A C C C G C A G C A T T T C C A A C A T G A C A
SEQ. ID. NO. 21 G G A T T T C G A G C C C C T G A G C T C C A A G

SEQ. ID. NO. 18 C A G A T C C C A G G C T T C C G G G A A T T C C
SEQ. ID. NO. 19 C T G G A G G A A C G A G T G A A G G A G G C T G
SEQ. ID. NO. 20 T C C C A G G A A T T T G T G G A G A A A C T A A
SEQ. ID. NO. 21 C A G A T C A A G A C C A T C T C A G G A A A G A

FIG. 5e.

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SEQ. ID. NO. 18 T G A A G A A G G T C C A T C C C A G G A A G T C
SEQ. ID. NO. 19 G A A T T G A G A T T A C T T T C C G C C A G A G
SEQ. ID. NO. 20 C C A A G C G A C T G A A A A G A C A C C C T G A
SEQ. ID. NO. 21 C T C C A C A G C A G T A T G A G A G A G A G T A

SEQ. ID. NO. 18 T G T C C A C A A T G G T T T T G C C A A G G A G
SEQ. ID. NO. 19 T T T C T T C T C A G A T C C A G C T G T G C C C
SEQ. ID. NO. 20 G G A G A C A G G A G G C T T C C A G G A G G C A
SEQ. ID. NO. 21 C A A C A A C A A G C G G T C A G G C G T G G G G

SEQ. ID. NO. 18 T T T T G G G A A G A A A C A T T T A A C T G C C
SEQ. ID. NO. 19 G T C A A A A A C C T G A A G C G C C A G G A T G
SEQ. ID. NO. 20 C C G C T G G C C T A T G A T G C C A T C T G G G
SEQ. ID. NO. 21 C C C A G C A A G T T C C A C G G G T A C G C C T

SEQ. ID. NO. 18 A C C T C C A A G A A G G T G C A A A A G G A C C
SEQ. ID. NO. 19 C C C G A A T C A T C G T G G G A C T T T T C T A
SEQ. ID. NO. 20 C C T T G G C A C T G G C C C T G A A C A A G A C
SEQ. ID. NO. 21 A C G A T G G C A T C T G G G T C A T C G C C A A

SEQ. ID. NO. 18 T T T A C C T G T G G A C A C C T T T C T G A G A
SEQ. ID. NO. 19 T G A G A C T G A A G C C C G G A A A G T T T T T
SEQ. ID. NO. 20 A T C T G G A G G A G G C G G C C G T T C T G G T
SEQ. ID. NO. 21 G A C A C T G C A G A G G G C C A T G G A G A C A

SEQ. ID. NO. 18 G G T C A C G A A G A A A G T G G C G A C A G G T
SEQ. ID. NO. 19 T G T G A G G T G T A C A A G G A G C G T C T C T
SEQ. ID. NO. 20 G T G C G C C T G G A G G A C T T C A A C T A C A
SEQ. ID. NO. 21 C T G C A T G C C A G C A G C C G G C A C C A G C

SEQ. ID. NO. 18 T T A G C A A C A G C T C G A C A G C C T T C C G
SEQ. ID. NO. 19 T T G G G A A G A A G T A C G T C T G G T T C C T
SEQ. ID. NO. 20 A C A A C C A G A C C A T T A C C G A C C A A A T
SEQ. ID. NO. 21 G G A T C C A G G A C T T C A A C T A C A C G G A

SEQ. ID. NO. 18 A C C C C T C T G T A C A G G G G A T G A G A A C
SEQ. ID. NO. 19 C A T T G G G T G G T A T G C T G A C A A T T G G
SEQ. ID. NO. 20 C T A C C G G G C A A T G A A C T C T T C G T C C
SEQ. ID. NO. 21 C C A C A C G C T G G G C A G G A T C A T C C T C

FIG. 5f.

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SEQ. ID. NO. 18 A T C A G C A G T G T C G A G A C C C C T T A C A
SEQ. ID. NO. 19 T T C A A G A T C T A C G A C C C T T C T A T C A
SEQ. ID. NO. 20 T T T G A G G G T G T C T C T G G C C A T G T G G
SEQ. ID. NO. 21 A A T G C C A T G A A C G A G A C C A A C T T T C T

SEQ. ID. NO. 18 T A G A T T A C A C G C A T T T A C G G A T A T C
SEQ. ID. NO. 19 A C T G C A C A G T G G A T G A G A T G A C T G A
SEQ. ID. NO. 20 T G T T T G A T G C C A G C G G C T C T C G G A T
SEQ. ID. NO. 21 T C G G G G T C A C G G G T C A A G T T G T A T T

SEQ. ID. NO. 18 C T A C A A T G T G T A C T T A G C A G T C T A C
SEQ. ID. NO. 19 G G C G G T G G A G G G C C A C A T C A C A A C T
SEQ. ID. NO. 20 G G C A T G G A C G C T T A T C G A G C A G C T T
SEQ. ID. NO. 21 C C G G A A T G G G G A G A G A A T G G G G A C C

SEQ. ID. NO. 18 T C C A T T G C C C A C G C C T T G C A A G A T A
SEQ. ID. NO. 19 G A G A T T G T C A T G C T G A A T C C T G C C A
SEQ. ID. NO. 20 C A G G G T G G C A G C T A C A A G A A G A T T G
SEQ. ID. NO. 21 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 18 T A T A T A C C T G C T T A C C T G G G A G A G G
SEQ. ID. NO. 19 A T A C C C G C A G C A T T T C C A A C A T G A C
SEQ. ID. NO. 20 G C T A C T A T G A C A G C A C C A A G G A T G A
SEQ. ID. NO. 21 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 18 G C T C T T C A C C A A T G G C T C C T G T G C A
SEQ. ID. NO. 19 A T C C C A G G A A T T T G T G G A G A A A C T A
SEQ. ID. NO. 20 T C T T T C C T G G T C C A A A A C A G A T A A A
SEQ. ID. NO. 21 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 18 G A C A T C A A G A A A G T T G A G G C G T G G C
SEQ. ID. NO. 19 A C C A A G C G A C T G A A A A G A C A C C C T G
SEQ. ID. NO. 20 T G G A T T G G A G G G T C C C C C C C A G C T G
SEQ. ID. NO. 21 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 18 A G G T C C T G A A G C A C C T A C G G C A T C T
SEQ. ID. NO. 19 A G G A G A C A G G A G G C T T C C A G G A G G C
SEQ. ID. NO. 20 A C C A G A C C C T G G T C A T C A A G A C A T T
SEQ. ID. NO. 21 A A G G A T C C G A A C C A C C A A A A G A C A A

FIG. 5g.

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SEQ. ID. NO. 18 A A A C T T T A C A A A C A A T A T G G G G G A G
SEQ. ID. NO. 19 A C C G C T G G C C T A T G A T G C C A T C T G G
SEQ. ID. NO. 20 C C G C T T C C T G T C A C A G A A A C T C T T T
SEQ. ID. NO. 21 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 18 C A G G T G A C C T T T G A T G A G T G T G G T G
SEQ. ID. NO. 19 G C C T T G G C A C T G G C C C T G A A C A A G A
SEQ. ID. NO. 20 A T C T C C G T C T C A G T T C T C T C C A G C C
SEQ. ID. NO. 21 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 18 A C C T G G T G G G G A A C T A T T C C A T C A T
SEQ. ID. NO. 19 C A T C T G G A G G A G G C G G C C G T T C T G G
SEQ. ID. NO. 20 T G G G C A T T G T C C T A G C T G T T G T C T G
SEQ. ID. NO. 21 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 18 C A A C T G G C A C C T C T C C C C A G A G G A T
SEQ. ID. NO. 19 T G T G C G C C T G G A G G A C T T C A A C T A C
SEQ. ID. NO. 20 T C T G T C C T T T A A C A T C T A C A A C T C A
SEQ. ID. NO. 21 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 18 G G C T C C A T C G T G T T T A A G G A A G T C G
SEQ. ID. NO. 19 A A C A A C C A G A C C A T T A C C G A C C A A A
SEQ. ID. NO. 20 C A T G T C C G T T A T A T C C A G A A C T C A C
SEQ. ID. NO. 21 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 18 G G T A T T A C A A C G T C T A T G C C A A G A A
SEQ. ID. NO. 19 T C T A C C G G G C A A T G A A C T C T T C G T C
SEQ. ID. NO. 20 A G C C C A A C C T G A A C A A C C T G A C T G C
SEQ. ID. NO. 21 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 18 G G G A G A A A G A C T C T T C A T C A A C G A G
SEQ. ID. NO. 19 C T T T G A G G G T G T C T C T G G C C A T G T G
SEQ. ID. NO. 20 T G T G G G C T G C T C A C T G G C T T T A G C T
SEQ. ID. NO. 21 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 18 G A G A A A A T C C T G T G G A G T G G G T T C T
SEQ. ID. NO. 19 G T G T T T G A T G C C A G C G G C T C T C G G A
SEQ. ID. NO. 20 G C T G T C T T C C C C C T G G G G C T C G A T G
SEQ. ID. NO. 21 G G A G G G A T G C T C T C C T A T G C T T C C A

FIG. 5h.

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SEQ. ID. NO. 18 C C A G G G A G G T G C C C T T C T C C A A C T G
SEQ. ID. NO. 19 T G G C A T G G A C G C T T A T C G A G C A G C T
SEQ. ID. NO. 20 G T T A C C A C A T T G G G A G G A A C C A G T T
SEQ. ID. NO. 21 T A T T T C T C T T T G G C C T T G A T G G A T C

SEQ. ID. NO. 18 C A G C C G A G A C T G C C T G G C A G G G A C C
SEQ. ID. NO. 19 T C A G G G T G G C A G C T A C A A G A A G A T T
SEQ. ID. NO. 20 T C C T T T C G T C T G C C A G G C C C G C C T C
SEQ. ID. NO. 21 C T T T G T C T C T G A A A A G A C C T T T G A A

SEQ. ID. NO. 18 A G G A A A G G G A T C A T T G A G G G G G A G C
SEQ. ID. NO. 19 G G C T A C T A T G A C A G C A C C A A G G A T G
SEQ. ID. NO. 20 T G G C T C C T G G G C C T G G G C T T T A G T C
SEQ. ID. NO. 21 A C A C T T T G C A C C G T C A G G A C C T G G A

SEQ. ID. NO. 18 C C A C C T G C T G C T T T G A G T G T G T G G A
SEQ. ID. NO. 19 A T C T T T C C T G G T C C A A A A C A G A T A A
SEQ. ID. NO. 20 T G G G C T A C G G T T C C A T G T T C A C C A A
SEQ. ID. NO. 21 T T C T C A C C G T G G G C T A C A C G A C C G C

SEQ. ID. NO. 18 G T G T C C T G A T G G G G A G T A T A G T G A T
SEQ. ID. NO. 19 A T G G A T T G G A G G G T C C C C C C C A G C T
SEQ. ID. NO. 20 G A T T T G G T G G G T C C A C A C G G T C T T C
SEQ. ID. NO. 21 T T T T G G G G C C A T G T T T G C A A A G A C C

SEQ. ID. NO. 18 G A G A C A G A T G C C A G T G C C T G T A A C A
SEQ. ID. NO. 19 G A C C A G A C C C T G G T C A T C A A G A C A T
SEQ. ID. NO. 20 A C A A A G A A G G A A G A A A A G A A G G A G T
SEQ. ID. NO. 21 T G G A G A G T C C A C G C C A T C T T C A A A A

SEQ. ID. NO. 18 A G T G C C C A G A T G A C T T C T G G T C C A A
SEQ. ID. NO. 19 T C C G C T T C C T G T C A C A G A A A C T C T T
SEQ. ID. NO. 20 G G A G G A A G A C T C T G G A A C C C T G G A A
SEQ. ID. NO. 21 A T G T G A A A A T G A A G A A G A A G A T C A T

SEQ. ID. NO. 18 T G A G A A C C A C A C C T C C T G C A T T G C C
SEQ. ID. NO. 19 T A T C T C C G T C T C A G T T C T C T C C A G C
SEQ. ID. NO. 20 G C T G T A T G C C A C A G T G G G C C T G C T G
SEQ. ID. NO. 21 C A A G G A C C A G A A A C T G C T T G T G A T C

FIG. 5i.

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SEQ. ID. NO. 18 A A G G A G A T C G A G T T T C T G T C G T G G A
SEQ. ID. NO. 19 C T G G G C A T T G T C C T A G C T G T T G T C T
SEQ. ID. NO. 20 G T G G G C A T G G A T G T C C T C A C T C T C G
SEQ. ID. NO. 21 G T G G G G G G C A T G C T G C T G A T C G A C C

SEQ. ID. NO. 18 C G G A G C C C T T T G G G A T C G C A C T C A C
SEQ. ID. NO. 19 G T C T G T C C T T T A A C A T C T A C A A C T C
SEQ. ID. NO. 20 C C A T C T G G C A G A T C G T G G A C C C T C T
SEQ. ID. NO. 21 T G T G T A T C C T G A T C T G C T G G C A G G C

SEQ. ID. NO. 18 C C T C T T T G C C G T G C T G G G C A T T T T C
SEQ. ID. NO. 19 A C A T G T C C G T T A T A T C C A G A A C T C A
SEQ. ID. NO. 20 G C A C C G G A C C A T T G A G A C A T T T G C C
SEQ. ID. NO. 21 T G T G G A C C C C C T G C G A A G G A C A G T G

SEQ. ID. NO. 18 C T G A C A G C C T T T G T G C T G G G T G T G T
SEQ. ID. NO. 19 C A G C C C A A C C T G A A C A A C C T G A C T G
SEQ. ID. NO. 20 A A G G A G G A A C C T A A G G A A G A T A T T G
SEQ. ID. NO. 21 G A G A A G T A C A G C A T G G A G C C G G A C C

SEQ. ID. NO. 18 T T A T C A A G T T C C G C A A C A C A C C C A T
SEQ. ID. NO. 19 C T G T G G G C T G C T C A C T G G C T T T A G C
SEQ. ID. NO. 20 A C G T C T C T A T T C T G C C C C A G C T G G A
SEQ. ID. NO. 21 C A G C A G G A C G G G A T A T C T C C A T C C G

SEQ. ID. NO. 18 T G T C A A G G C C A C C A A C C G A G A G C T C
SEQ. ID. NO. 19 T G C T G T C T T C C C C C T G G G G C T C G A T
SEQ. ID. NO. 20 G C A T T G C A G C T C C A G G A A G A T G A A T
SEQ. ID. NO. 21 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 18 T C C T A C C T C C T C C T C T T C T C C C T G C
SEQ. ID. NO. 19 G G T T A C C A C A T T G G G A G G A A C C A G T
SEQ. ID. NO. 20 A C A T G G C T T G G C A T T T T C T A T G G T T
SEQ. ID. NO. 21 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 18 T C T G C T G C T T C T C C A G C T C C C T G T T
SEQ. ID. NO. 19 T T C C T T T C G T C T G C C A G G C C C G C C T
SEQ. ID. NO. 20 A C A A G G G G C T G C T G C T G C T G G G
SEQ. ID. NO. 21 T C G T C T A T G C C T A C A A G G G A C T T C T

FIG. 5j.

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SEQ. ID. NO. 18 C T T C A T C G G G G A G C C C C A G G A C T G G
SEQ. ID. NO. 19 C T G G C T C C T G G G C C T G G G C T T T A G T
SEQ. ID. NO. 20 A A T C T T C C T T G C T T A T G A G A C C A A G
SEQ. ID. NO. 21 C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 18 A C G T G C C G C C T G C G C C A G C C G G C C T
SEQ. ID. NO. 19 C T G G G C T A C G G T T C C A T G T T C A C C A
SEQ. ID. NO. 20 A G T G T G T C C A C T G A G A A G A T C A A T G
SEQ. ID. NO. 21 T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 18 T T G G C A T C A G C T T C G T G C T C T G C A T
SEQ. ID. NO. 19 A G A T T T G G T G G G T C C A C A C G G T C T T
SEQ. ID. NO. 20 A T C A C C G G G C T G T G G G C A T G G C T A T
SEQ. ID. NO. 21 C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 18 C T C A T G C A T C C T G G T G A A A A C C A A C
SEQ. ID. NO. 19 C A C A A A G A A G G A A G A A A A G A A G G A G
SEQ. ID. NO. 20 C T A C A A T G T G G C A G T C C T G T G C C T C
SEQ. ID. NO. 21 C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 18 C G T G T C C T C C T G G T G T T T G A G G C C A
SEQ. ID. NO. 19 T G G A G G A A G A C T C T G G A A C C C T G G A
SEQ. ID. NO. 20 A T C A C T G C T C C T G T C A C C A T G A T T C
SEQ. ID. NO. 21 A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 18 A G A T C C C C A C C A G C T T C C A C C G C A A
SEQ. ID. NO. 19 A G C T G T A T G C C A C A G T G G G C C T G C T
SEQ. ID. NO. 20 T G T C C A G C C A G C A G G A T G C A G C C T T
SEQ. ID. NO. 21 T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 18 G T G G T G G G G G C T C A A C C T G C A G T T C
SEQ. ID. NO. 19 G G T G G G C A T G G A T G T C C T C A C T C T C
SEQ. ID. NO. 20 T G C C T T T G C C T C T C T T G C C A T A G T T
SEQ. ID. NO. 21 C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 18 C T G C T G G T T T T C C T C T G C A C C T T C A
SEQ. ID. NO. 19 G C C A T C T G G C A G A T C G T G G A C C C T C
SEQ. ID. NO. 20 T T C T C C T C C T A T A T C A C T C T T G T T G
SEQ. ID. NO. 21 C T G G T C A T C A T C T T C T G C A G C A C C A

FIG. 5k.

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SEQ. ID. NO. 18 T G C A G A T T G T C A T C T G T G T G A T C T G
SEQ. ID. NO. 19 T G C A C C G G A C C A T T G A G A C A T T T G C
SEQ. ID. NO. 20 T G C T C T T T G T G C C C A A G A T G C G C A G
SEQ. ID. NO. 21 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 18 G C T C T A C A C C G C G C C C C C C T C A A G C
SEQ. ID. NO. 19 C A A G G A G G A A C C T A A G G A A G A T A T T
SEQ. ID. NO. 20 G C T G A T C A C C C G A G G G G A A T G G C A G
SEQ. ID. NO. 21 G A A G C T C A T C A C C C T G A G A A C A A A C

SEQ. ID. NO. 18 T A C C G C A A C C A G G A G C T G G A G G A T G
SEQ. ID. NO. 19 G A C G T C T C T A T T C T G C C C C A G C T G G
SEQ. ID. NO. 20 T C G G A G G C G C A G G A C A C C A T G A A G A
SEQ. ID. NO. 21 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 18 A G A T C A T C T T C A T C A C G T G C C A C G A
SEQ. ID. NO. 19 A G C A T T G C A G C T C C A G G A A G A T G A A
SEQ. ID. NO. 20 C A G G G T C A T C G A C C A A C A A C A A C G A
SEQ. ID. NO. 21 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 18 G G G C T C C C T C A T G G C C C T G G G C T T C
SEQ. ID. NO. 19 T A C A T G G C T T G G C A T T T T C T A T G G T
SEQ. ID. NO. 20 G G A G G A G A A G T C C C G G C T G T T G G A G
SEQ. ID. NO. 21 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 18 C T G A T C G G C T A C A C C T G C C T G C T G G
SEQ. ID. NO. 19 T A C A A G G G G C T G C T G C T G C T G C T G G
SEQ. ID. NO. 20 A A G G A G A A C C G T G A A C T G G A A A A G A
SEQ. ID. NO. 21 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 18 C T G C C A T C T G C T T C T T C T T T G C C T T
SEQ. ID. NO. 19 G A A T C T T C C T T G C T T A T G A G A C C A A
SEQ. ID. NO. 20 T C A T T G C T G A G A A A G A G G A G C G T G T
SEQ. ID. NO. 21 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 18 C A A G T C C C G G A A G C T G C C G G A G A A C
SEQ. ID. NO. 19 G A G T G T G T C C A C T G A G A A G A T C A A T
SEQ. ID. NO. 20 C T C T G A A C T G C G C C A T C A A C T C C A G
SEQ. ID. NO. 21 G T C A G A A A A C C A T C G C C T G C G A A T G

FIG. 5L.

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SEQ. ID. NO. 18 T T C A A T G A A G C C A A G T T C A T C A C C T
SEQ. ID. NO. 19 G A T C A C C G G G C T G T G G G C A T G G C T A
SEQ. ID. NO. 20 T C T C G G C A G C A G C T C C G C T C C C G G C
SEQ. ID. NO. 21 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 18 T C A G C A T G C T C A T C T T C T T C A T C G T
SEQ. ID. NO. 19 T C T A C A A T G T G G C A G T C C T G T G C C T
SEQ. ID. NO. 20 G C C A C C C A C C G A C A C C C C C A G A A C C
SEQ. ID. NO. 21 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 18 C T G G A T C T C C T T C A T T C C A G C C T A T
SEQ. ID. NO. 19 C A T C A C T G C T C C T G T C A C C A T G A T T
SEQ. ID. NO. 20 C T C T G G G G G C C T G C C C A G G G G A C C C
SEQ. ID. NO. 21 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 18 G C C A G C A C C T A T G G C A A G T T T G T C T
SEQ. ID. NO. 19 C T G T C C A G C C A G C A G G A T G C A G C C T
SEQ. ID. NO. 20 C C T G A G C C C C C C G A C C G G C T T A G C T
SEQ. ID. NO. 21 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 18 C T G C C G T A G A G G T G A T T G C C A T C C T
SEQ. ID. NO. 19 T T G C C T T T G C C T C T C T T G C C A T A G T
SEQ. ID. NO. 20 G T G A T G G G A G T C G A G T G C A T T T G C T
SEQ. ID. NO. 21 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 18 G G C A G C C A G C T T T G G C T T G C T G G C G
SEQ. ID. NO. 19 T T T C T C C T C C T A T A T C A C T C T T G T T
SEQ. ID. NO. 20 T T A T A A G T G A G G G T A G G G T G A G G G A
SEQ. ID. NO. 21 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 18 T G C A T C T T C T T C A A C A A G A T C T A C A
SEQ. ID. NO. 19 G T G C T C T T T G T G C C C A A G A T G C G C A
SEQ. ID. NO. 20 G G A C A G G C C A G T A G G G G G A G G G A A A
SEQ. ID. NO. 21 A A G G C C A T T T T A A A A A A T C A C C T C G

SEQ. ID. NO. 18 T C A T T C T C T T C A A G C C A T C C C G C A A
SEQ. ID. NO. 19 G G C T G A T C A C C C G A G G G G A A T G G C A
SEQ. ID. NO. 20 G G G A G A G G G G A A G G G C A G G G G A C T C
SEQ. ID. NO. 21 A T C A A A A T C C C C A G C T A C A G T G G A A

FIG. 5m.

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SEQ. ID. NO. 18 C A C C A T C G A G G A G G T G C G T T G C A G C
SEQ. ID. NO. 19 G T C G G A G G C G C A G G A C A C C A T G A A G
SEQ. ID. NO. 20 A G G A A G C A G G G G G T C C C C A T C C C C A
SEQ. ID. NO. 21 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 18 A C C G C A G C T C A C G C T T T C A A G G T G G
SEQ. ID. NO. 19 A C A G G G T C A T C G A C C A A C A A C A A C G
SEQ. ID. NO. 20 G C T G G G A A G A A C A T G C T A T C C A A T C
SEQ. ID. NO. 21 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 18 C T G C C C G G G C C A C G C T G C G C C G C A G
SEQ. ID. NO. 19 A G G A G G A G A A G T C C C G G C T G T T G G A
SEQ. ID. NO. 20 T C A T C T C T T G T A A A T A C A T G T C C C C
SEQ. ID. NO. 21 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 18 C A A C G T C T C C C G C A A G C G G T C C A G C
SEQ. ID. NO. 19 G A A G G A G A A C C G T G A A C T G G A A A A G
SEQ. ID. NO. 20 C T G T G A G T T C T G G G C T G A T T T G G G T
SEQ. ID. NO. 21 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 18 A G C C T T G G A G G C T C C A C G G G A T C C A
SEQ. ID. NO. 19 A T C A T T G C T G A G A A A G A G G A G C G T G
SEQ. ID. NO. 20 C T C T C A T A C C T C T G G G A A A C A G A C C
SEQ. ID. NO. 21 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 18 C C C C C T C C T C C T C C A T C A G C A G C A A
SEQ. ID. NO. 19 T C T C T G A A C T G C G C C A T C A G C T C C A
SEQ. ID. NO. 20 T T T T T C T C T C T T A C T G C T T C A T G T A
SEQ. ID. NO. 21 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 18 G A G C A A C A G C G A A G A C C C A T T C C C A
SEQ. ID. NO. 19 G T C T C G G C A G C A G C T C C G C T C C C G G
SEQ. ID. NO. 20 A T T T T G T A T C A C C T C T T C A C A A T T T
SEQ. ID. NO. 21 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 18 C A G C C C G A G A G G C A G A A G C A G C A G C
SEQ. ID. NO. 19 C G C C A C C C A C C G A C A C C C C C A G A A C
SEQ. ID. NO. 20 A G T T C G T A C C T G G C T T G A A G C T G C T
SEQ. ID. NO. 21 C G C C A C A G A C A T G T G C C A C C C T C C T

FIG. 5n.

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SEQ. ID. NO. 18 A G C C G C T G G C C C T A A C C C A G C A A G A
SEQ. ID. NO. 19 C C T C T G G G G G C C T G C C C A G G G G A C C
SEQ. ID. NO. 20 C A C T G C T C A C A C G C T G C C T C C T C A G
SEQ. ID. NO. 21 T C C G A G T C A T G G T C T C G G G C C T G T A

SEQ. ID. NO. 18 G C A G C A G C A G C A G C C C C T G A C C C T C
SEQ. ID. NO. 19 C C C T G A G C C C C C C G A C C G G C T T A G C
SEQ. ID. NO. 20 C A G C C T C A C T G C A T C T T T C T C T T C C
SEQ. ID. NO. 21 A G G G T G G G A G G C C T G G G C C C G G G G C

SEQ. ID. NO. 18 C C A C A G C A G C A A C G A T C T C A G C A G C
SEQ. ID. NO. 19 T G T G A T G G G A G T C G A G T G C A T T T G C
SEQ. ID. NO. 20 C A T G C A A C A C C C T C T T C T A G T T A C C
SEQ. ID. NO. 21 C T C C C C C G T G A C A G A A C C A C A C T G G

SEQ. ID. NO. 18 A G C C C A G A T G C A A G C A G A A G G T C A T
SEQ. ID. NO. 19 T T T A T A A G T G A G G G T A G G G T G A G G G
SEQ. ID. NO. 20 A C G G C A A C C C C T
SEQ. ID. NO. 21 G C A G A G G G G T C T G C T G C A G A A A C A C

SEQ. ID. NO. 18 C T T T G G C A G C G G C A C G G T C A C C T T C
SEQ. ID. NO. 19 A G G A C A G G C C A G T A G G G G G A G G G A A
SEQ. ID. NO. 20
SEQ. ID. NO. 21 T G T C G G C T C T G G C T G C G G A G A A G C T

SEQ. ID. NO. 18 T C A C T G A G C T T T G A T G A G C C T C A G A
SEQ. ID. NO. 19 A G G G A G A G G G G A A G G G C A G G G G A C T
SEQ. ID. NO. 20
SEQ. ID. NO. 21 G G G C A C C A T G G C T G G C C T C T C A G G A

SEQ. ID. NO. 18 A G A A C G C C A T G G C C C A C G G G A A T T C
SEQ. ID. NO. 19 C A G G A A G C A G G G G G T C C C C A T C C C C
SEQ. ID. NO. 20
SEQ. ID. NO. 21 C C A C T C G G A T G G C A C T C A G G T G G A C

SEQ. ID. NO. 18 T A C G C A C C A G A A C T C C C T G G A G G C C
SEQ. ID. NO. 19 A G C T G G G A A G A A C A T G C T A T C C A A T
SEQ. ID. NO. 20
SEQ. ID. NO. 21 A G G A C G G G G C A G G G G G A G A C T T G G C

FIG. 50.

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SEQ. ID. NO. 18 C A G A A A A G C A G C G A T A C G C T G A C C C
SEQ. ID. NO. 19 C T C A T C T C T T G T A A A T A C A T G T C C C
SEQ. ID. NO. 20
SEQ. ID. NO. 21 A C C T G A C C T C G A G C C T T A T T T G T G A

SEQ. ID. NO. 18 G A C A C C A G C C A T T A C T C C C G C T G C A
SEQ. ID. NO. 19 C C T G T G A G T T C T G G G C T G A T T T G G G
SEQ. ID. NO. 20
SEQ. ID. NO. 21 A G T C C T T A T T T C T T C A C A A A G A A G A

SEQ. ID. NO. 18 G T G C G G G G A A A C G G A C T T A G A T C T G
SEQ. ID. NO. 19 T C T C T C A T A C C T C T G G G A A A C A G A C
SEQ. ID. NO. 20
SEQ. ID. NO. 21 G G A A C G G A A A T G G G A C G T C T T C C T T

SEQ. ID. NO. 18 A C C G T C C A G G A A A C A G G T C T G C A A G
SEQ. ID. NO. 19 C T T T T T C T C T C T T A C T G C T T C A T G T
SEQ. ID. NO. 20
SEQ. ID. NO. 21 A A C A T C T G C A A A C A A G G A G G C G C T G

SEQ. ID. NO. 18 G A C C T G T G G G T G G A G A C C A G C G G C C
SEQ. ID. NO. 19 A A T T T T G T A T C A C C T C T T C A C A A T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21 G G A T A T C A A A C T T G C A A A A A A A A A

SEQ. ID. NO. 18 A G A G G T G G A G G A C C C T G A A G A G T T G
SEQ. ID. NO. 19 T A G T T C G T A C C T G G C T T G A A G C T G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21 A A A A A A A A A A A A

SEQ. ID. NO. 18 T C C C C A G C A C T T G T A G T G T C C A G T T
SEQ. ID. NO. 19 T C A C T G C T C A C A C G C T G C C T C C T C A
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18 C A C A G A G C T T T G T C A T C A G T G G T G G
SEQ. ID. NO. 19 G C A G C C T C A C T G C A T C T T T C T C T T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

FIG. 5p.

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SEQ. ID. NO. 18 A G G C A G C A C T G T T A C A G A A A A C G T A
SEQ. ID. NO. 19 C C A T G C A A C A C C C T C T T C T A G T T A C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18 G T G A A T T C A
SEQ. ID. NO. 19 C A C G G C A A C C C C T G C A G C T C C T C T G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C T T T G T G C T C T G T T C C T G T C C A G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A G G G G T C T C C C A A C A A G T G C T C T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A C C C C A A A G G G G C C T C T C C T T T T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T C C A C T G T C A T A A T C T C T T T C C A T
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C T T A C T T G C C C T T C T A T A C T T T C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 A C A T G T G G C T C C C C C T G A A T T T T G C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

FIG. 5q.

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SEQ. ID. NO. 18
SEQ. ID. NO. 19 T T C C T T T G G G G A G C T C A T T C T T T C G
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 C C A A G G T C A C A T G C T C C C T T G C C T C
SEQ. ID. NO. 20
SEQ. ID. NO. 21

SEQ. ID. NO. 18
SEQ. ID. NO. 19 T G G C T C C G T G C A
SEQ. ID. NO. 20
SEQ. ID. NO. 21

FIG. 5r.

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SEQ. ID. NO. 22 A T G C T G C T G C T G C T G C T G G T G C C T C T C T T C
SEQ. ID. NO. 23 A T G G G C C C G G G G G G A C C C T G T A C C C C A G T G

SEQ. ID. NO. 22 C T C C G C C C C C T G G G C G C T G G C G G G G C G C A G
SEQ. ID. NO. 23 G G G T G G C C G C T G C C T C T T C T G C T G G T G A T G

SEQ. ID. NO. 22 A C C C C C A A C G C C A C C T C G G A A G G T T G C C A G
SEQ. ID. NO. 23 G C G G C T G G G G T G G C T C C G G T G T G G G C C T C T

SEQ. ID. NO. 22 A T T A T A C A T C C G C C C T G G G A A G G T G G C A T C
SEQ. ID. NO. 23 C A C T C C C C T C A T C T C C C G C G G C C T C A C C C G

SEQ. ID. NO. 22 A G G T A C C G T G G C T T G A C T C G C G A C C A G G T G
SEQ. ID. NO. 23 A G G G T C C C C C C G C A C C C C T C C T C A G A A C G G

SEQ. ID. NO. 22 A A G G C C A T C A A C T T C C T G C C T G T G G A C T A T
SEQ. ID. NO. 23 C G T G C A G T A T A C A T C G G G G G C G C T G T T T C C C

SEQ. ID. NO. 22 G A G A T C G A A T A T G T G T G C C G A G G G G A G C G C
SEQ. ID. NO. 23 A T G A G C G G G G G C T G G C C G G G G G C C A G G C C

SEQ. ID. NO. 22 G A G G T G G T G G G G C C C A A G G T G C G C A A A T G C
SEQ. ID. NO. 23 T G C C A G C C C G C G G T G G A G A T G G C G C T G G A G

SEQ. ID. NO. 22 C T G G C C A A C G G C T C C T G G A C G G A T A T G G A C
SEQ. ID. NO. 23 G A C G T T A A C A G C C G C A G A G A C A T C C T G C C G

SEQ. ID. NO. 22 A C A C C C A G C C G C T G T G T C C G A A T C T G C T C C
SEQ. ID. NO. 23 G A C T A C G A G C T C A A G C T T A T C C A C C A C G A C

SEQ. ID. NO. 22 A A G T C T T A T T T G A C C C T G G A A A A T G G G A A G
SEQ. ID. NO. 23 A G C A A G T G T G A C C C A G G G C A A G C C A C C A A G

SEQ. ID. NO. 22 G T T T T C C T G A C G G G T G G G G A C C T C C C A G C T
SEQ. ID. NO. 23 T A C T T G T A C G A A C T A C T C T A C A A T G A C C C C

FIG. 6a.

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SEQ. ID. NO. 22 C T G G A T G G A G C C C G G G T G G A G T T C C G A T G T
SEQ. ID. NO. 23 A T C A A G A T C A T T C T C A T G C C T G G C T G T A G T

SEQ. ID. NO. 22 G A C C C C G A C T T C C A T C T G G T G G G C A G C T C C
SEQ. ID. NO. 23 T C T G T C T C C A C A C T T G T A G C T G A G G C T G C C

SEQ. ID. NO. 22 C G G A G C G T C T G T A G T C A G G G C C A G T G G A G C
SEQ. ID. NO. 23 C G G A T G T G G A A C C T T A T T G T G C T C T C A T A T

SEQ. ID. NO. 22 A C C C C C A A G C C C C A C T G C C A G G T G A A T C G A
SEQ. ID. NO. 23 G G C T C C A G T T C A C C A G C C T T G T C A A A C C G A

SEQ. ID. NO. 22 A C G C C A C A C T C A G A A C G G C G T G C A G T A T A C
SEQ. ID. NO. 23 C A G C G G T T T C C C A C G T T C T T C C G G A C G C A T

SEQ. ID. NO. 22 A T C G G G G C G C T G T T T C C C A T G A G C G G G G G C
SEQ. ID. NO. 23 C C A T C C G C C A C A C T C C A C A A T C C C A C C C G G

SEQ. ID. NO. 22 T G G C C G G G G G G C C A G G C C T G C C A G C C C G C G
SEQ. ID. NO. 23 G T G A A A C T C T T C G A A A A G T G G G G C T G G A A G

SEQ. ID. NO. 22 G T G G A G A T G G C G C T G G A G G A C G T T A A C A G C
SEQ. ID. NO. 23 A A G A T C G C T A C C A T C C A A C A G A C C A C C G A G

SEQ. ID. NO. 22 C G C A G A G A C A T C C T G C C G G A C T A C G A G C T C
SEQ. ID. NO. 23 G T C T T C A C C T C A A C G C T G G A T G A C C T G G A G

SEQ. ID. NO. 22 A A G C T T A T C C A C C A C G A C A G C A A G T G T G A C
SEQ. ID. NO. 23 G A G C G A G T G A A A G A G G C T G G G A T C G A G A T C

SEQ. ID. NO. 22 C C A G G G C A A G C C A C C A A G T A C T T G T A C G A A
SEQ. ID. NO. 23 A C T T T C C G A C A G A G T T T C T T C T C G G A T C C A

SEQ. ID. NO. 22 C T A C T C T A C A A T G A C C C C A T C A A G A T C A T T
SEQ. ID. NO. 23 G C T G T G C C T G T T A A A A C C T G A A G C G T C A A

SEQ. ID. NO. 22 C T C A T G C C T G G C T G T A G T T C T G T C T C C A C A
SEQ. ID. NO. 23 G A T G C T C G A A T C A T C G T G G G A C T T T T C T A T

FIG. 6b.

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SEQ. ID. NO. 22 C T T G T A G C T G A G G C T G C C C G G A T G T G G A A C
SEQ. ID. NO. 23 G A G A C G G A A G C C C G G A A A G T T T T T T G T G A G

SEQ. ID. NO. 22 C T T A T T G T G C T C T C A T A T G G C T C C A G T T C A
SEQ. ID. NO. 23 G T C T A T A A G G A A A G G C T C T T T G G G A A G A A G

SEQ. ID. NO. 22 C C A G C C T T G T C A A A C C G A C A G C G G T T T C C C
SEQ. ID. NO. 23 T A C G T C T G G T T C C T C A T C G G G T G G T A T G C T

SEQ. ID. NO. 22 A C G T T C T T C C G G A C G C A T C C A T C C G C C A C A
SEQ. ID. NO. 23 G A C A A C T G G T T C A A G A C C T A T G A C C C G T C A

SEQ. ID. NO. 22 C T C C A C A A T C C C A C C C G G G T G A A A C T C T T C
SEQ. ID. NO. 23 A T C A A T T G T A C A G T G G A A G A A A T G A C C G A G

SEQ. ID. NO. 22 G A A A A G T G G G G C T G G A A G A A G A T C G C T A C C
SEQ. ID. NO. 23 G C G G T G G A G G G C C A C A T C A C C A C G G A G A T T

SEQ. ID. NO. 22 A T C C A A C A G A C C A C C G A G G T C T T C A C C T C A
SEQ. ID. NO. 23 G T C A T G C T G A A C C C T G C C A A C A C C C G A A G C

SEQ. ID. NO. 22 A C G C T G G A T G A C C T G G A G G A G C G A G T G A A A
SEQ. ID. NO. 23 A T T T C C A A C A T G A C G T C A C A G G A A T T T G T G

SEQ. ID. NO. 22 G A G G C T G G G A T C G A G A T C A C T T T C C G A C A G
SEQ. ID. NO. 23 G A G A A A C T A A C C A A G C G G C T G A A A A G A C A C

SEQ. ID. NO. 22 A G T T T C T T C T C G G A T C C A G C T G T G C C T G T T
SEQ. ID. NO. 23 C C C G A G G A G A C T G G A G G C T T C C A G G A G G C A

SEQ. ID. NO. 22 A A A A A C C T G A A G C G T C A A G A T G C T C G A A T C
SEQ. ID. NO. 23 C C A C T G G C C T A T G A T G C T A T C T G G G C C T T G

SEQ. ID. NO. 22 A T C G T G G G A C T T T T C T A T G A G A C G G A A G C C
SEQ. ID. NO. 23 G C T T T G G C C T T G A A C A A G A C G T C T G G A G G A

SEQ. ID. NO. 22 C G G A A A G T T T T T T G T G A G G T C T A T A A G G A A
SEQ. ID. NO. 23 G G T G G T C G T T C C G G C G T G C G C C T G G A G G A C

FIG. 6c.

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SEQ. ID. NO. 22 A G G C T C T T T G G G A A G A A G T A C G T C T G G T T C
SEQ. ID. NO. 23 T T T A A C T A C A A C A A C C A G A C C A T T A C A G A C

SEQ. ID. NO. 22 C T C A T C G G G T G G T A T G C T G A C A A C T G G T T C
SEQ. ID. NO. 23 C A G A T C T A C C G G G C C A T G A A C T C C T C C T C C

SEQ. ID. NO. 22 A A G A C C T A T G A C C C G T C A A T C A A T T G T A C A
SEQ. ID. NO. 23 T T T G A G G G C G T T T C T G G C C A T G T G G T C T T T

SEQ. ID. NO. 22 G T G G A A G A A A T G A C C G A G G C G G T G G A G G G C
SEQ. ID. NO. 23 G A T G C C A G C G G C T C C C G G A T G G C A T G G A C A

SEQ. ID. NO. 22 C A C A T C A C C A C G G A G A T T G T C A T G C T G A A C
SEQ. ID. NO. 23 C T T A T C G A G C A G C T A C A G G G C G G C A G C T A C

SEQ. ID. NO. 22 C C T G C C A A C A C C C G A A G C A T T T T C C A A C A T G
SEQ. ID. NO. 23 A A G A A G A T C G G C T A C T A C G A C A G C A C C A A G

SEQ. ID. NO. 22 A C G T C A C A G G A A T T T G T G G A G A A A C T A A C C
SEQ. ID. NO. 23 G A T G A T C T T T C C T G G T C C A A A A C G G A C A A G

SEQ. ID. NO. 22 A A G C G G C T G A A A A G A C A C C C C G A G G A G A C T
SEQ. ID. NO. 23 T G G A T T G G A G G G T C T C C C C C A G C T G A C C A G

SEQ. ID. NO. 22 G G A G G C T T C C A G G A G G C A C C A C T G G C C T A T
SEQ. ID. NO. 23 A C C T T G G T C A T C A A G A C A T T C C G T T T C C T G

SEQ. ID. NO. 22 G A T G C T A T C T G G G C C T T G G C T T T G G C C T T G
SEQ. ID. NO. 23 T C T C A G A A A C T C T T T A T C T C C G T C T C A G T T

SEQ. ID. NO. 22 A A C A A G A C G T C T G G A G G A G G T G G T C G T T C C
SEQ. ID. NO. 23 C T C T C C A G C C T G G G C A T T G T T C T T G C T G T T

SEQ. ID. NO. 22 G G C G T G C G C C T G G A G G A C T T T A A C T A C A A C
SEQ. ID. NO. 23 G T C T G T C T G T C C T T T A A C A T C T A C A A C T C C

SEQ. ID. NO. 22 A A C C A G A C C A T T A C A G A C C A G A T C T A C C G G
SEQ. ID. NO. 23 C A C G T T C G T T A T A T C C A G A A C T C C C A G C C C

FIG. 6d.

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SEQ. ID. NO. 22 G C C A T G A A C T C C T C C T C C T T T G A G G G C G T T
SEQ. ID. NO. 23 A A C C T G A A C A A T C T G A C T G C T G T G G G C T G C

SEQ. ID. NO. 22 T C T G G C C A T G T G G T C T T T G A T G C C A G C G G C
SEQ. ID. NO. 23 T C A C T G G C A C T G G C T G C T G T C T T C C C T C T C

SEQ. ID. NO. 22 T C C C G G A T G G C A T G G A C A C T T A T C G A G C A G
SEQ. ID. NO. 23 G G G C T G G A T G G T T A C C A C A T A G G G A G A A G C

SEQ. ID. NO. 22 C T A C A G G G C G G C A G C T A C A A G A A G A T C G G C
SEQ. ID. NO. 23 C A G T T C C C G T T T G T C T G C C A G G C C C G C C T T

SEQ. ID. NO. 22 T A C T A C G A C A G C A C C A A G G A T G A T C T T T C C
SEQ. ID. NO. 23 T G G C T C T T G G G C T T G G G C T T T A G T C T G G G C

SEQ. ID. NO. 22 T G G T C C A A A C G G A C A A G T G G A T T G G A G G G
SEQ. ID. NO. 23 T A T G G C T C T A T G T T C A C C A A G A T C T G G T G G

SEQ. ID. NO. 22 T C T C C C C C A G C T G A C C A G A C C T T G G T C A T C
SEQ. ID. NO. 23 G T C C A C A C A G T C T T C A C G A A G A A G G A G G A G

SEQ. ID. NO. 22 A A G A C A T T C C G T T T C C T G T C T C A G A A A C T C
SEQ. ID. NO. 23 A A G A A G G A G T G G A G G A A G A C C C T A G A G C C C

SEQ. ID. NO. 22 T T T A T C T C C G T C T C A G T T C T C T C C A G C C T G
SEQ. ID. NO. 23 T G G A A A C T C T A T G C C A C T G T G G G C C T G C T G

SEQ. ID. NO. 22 G G C A T T G T T C T T G C T G T T G T C T G T C T G T C C
SEQ. ID. NO. 23 G T G G G C A T G G A T G T C C T G A C T C T T G C C A T C

SEQ. ID. NO. 22 T T T A A C A T C T A C A A C T C C C A C G T T C G T T A T
SEQ. ID. NO. 23 T G G C A G A T T G T G G A C C C C T T G C A C C G A A C C

SEQ. ID. NO. 22 A T C C A G A A C T C C C A G C C C A A C C T G A A C A A T
SEQ. ID. NO. 23 A T T G A G A C T T T T G C C A A G G A G G A A C C A A A G

SEQ. ID. NO. 22 C T G A C T G C T G T G G G C T G C T C A C T G G C A C T G
SEQ. ID. NO. 23 G A A G A C A T C G A T G T C T C C A T T C T G C C C C A G

FIG. 6e.

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SEQ. ID. NO. 22 G C T G C T G T C T T C C C T C T C G G G C T G G A T G G T
SEQ. ID. NO. 23 T T G G A G C A C T G C A G C T C C A A G A A G A T G A A T

SEQ. ID. NO. 22 T A C C A C A T A G G G A G A A G C C A G T T C C C G T T T
SEQ. ID. NO. 23 A C G T G G C T T G G C A T T T T C T A T G G T T A C A A G

SEQ. ID. NO. 22 G T C T G C C A G G C C C G C C T T T G G C T C T T G G G C
SEQ. ID. NO. 23 G G G C T G C T G C T G C T G C T G G G A A T C T T T C T T

SEQ. ID. NO. 22 T T G G G C T T T A G T C T G G G C T A T G G C T C T A T G
SEQ. ID. NO. 23 G C T T A C G A A A C C A A G A G C G T G T C C A C T G A A

SEQ. ID. NO. 22 T T C A C C A A G A T C T G G T G G G T C C A C A C A G T C
SEQ. ID. NO. 23 A A G A T C A A T G A C C A C A G G G C C G T G G G C A T G

SEQ. ID. NO. 22 T T C A C G A A G A A G G A G G A G A A G A A G G A G T G G
SEQ. ID. NO. 23 G C T A T C T A C A A T G T C G C G G T C C T G T G T C T C

SEQ. ID. NO. 22 A G G A A G A C C C T A G A G C C C T G G A A A C T C T A T
SEQ. ID. NO. 23 A T C A C T G C T C C T G T G A C C A T G A T C C T T T C C

SEQ. ID. NO. 22 G C C A C T G T G G G C C T G C T G G T G G G C A T G G A T
SEQ. ID. NO. 23 A G T C A G C A G G A C G C A G C C T T T G C C T T T G C C

SEQ. ID. NO. 22 G T C C T G A C T C T T G C C A T C T G G C A G A T T G T G
SEQ. ID. NO. 23 T C T C T G G C C A T C G T G T T C T C T T C C T A C A T C

SEQ. ID. NO. 22 G A C C C C T T G C A C C G A A C C A T T G A G A C T T T T
SEQ. ID. NO. 23 A C T C T G G T T G T G C T C T T T G T G C C C A A G A T G

SEQ. ID. NO. 22 G C C A A G G A G G A A C C A A A G G A A G A C A T C G A T
SEQ. ID. NO. 23 C G C A G G C T G A T C A C C C G A G G G G A A T G G C A G

SEQ. ID. NO. 22 G T C T C C A T T C T G C C C C A G T T G G A G C A C T G C
SEQ. ID. NO. 23 T C T G A A A C G C A G G A C A C C A T G A A A A C A G G A

SEQ. ID. NO. 22 A G C T C C A A G A A G A T G A A T A C G T G G C T T G G C
SEQ. ID. NO. 23 T C A T C C A C C A A C A A C A A C G A G G A A G A G A A G

FIG. 6f

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SEQ. ID. NO. 22 A T T T T C T A T G G T T A C A A G G G G C T G C T G C T G
SEQ. ID. NO. 23 T C C C G A C T G T T G G A G A A G G A A A A C C G A G A A

SEQ. ID. NO. 22 C T G C T G G G A A T C T T T C T T G C T T A C G A A A C C
SEQ. ID. NO. 23 C T G G A A A A G A T C A T C G C T G A G A A A G A G G A G

SEQ. ID. NO. 22 A A G A G C G T G T C C A C T G A A A A G A T C A A T G A C
SEQ. ID. NO. 23 C G C G T C T C T G A A C T G C G C C A T C A G C T C C A G

SEQ. ID. NO. 22 C A C A G G G C C G T G G G C A T G G C T A T C T A C A A T
SEQ. ID. NO. 23 T C T C G G C A G C A A C T C C G C T C A C G G C G C C A C

SEQ. ID. NO. 22 G T C G C G G T C C T G T G T C T C A T C A C T G C T C C T
SEQ. ID. NO. 23 C C C C C A A C A C C C C C A G A T C C C T C T G G G G G C

SEQ. ID. NO. 22 G T G A C C A T G A T C C T T T C C A G T C A G C A G G A C
SEQ. ID. NO. 23 C T T C C C A G G G G A C C C T C T G A G C C C C C T G A C

SEQ. ID. NO. 22 G C A G C C T T T G C C T T T G C C T C T C T G G C C A T C
SEQ. ID. NO. 23 C G G C T T A G C T G T G A T G G G A G T C G A G T A C A T

SEQ. ID. NO. 22 G T G T T C T C T T C C T A C A T C A C T C T G G T T G T G
SEQ. ID. NO. 23 T T G C T T T A C A A G

SEQ. ID. NO. 22 C T C T T T G T G C C C A A G A T G C G C A G G C T G A T C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A C C C G A G G G G A A T G G C A G T C T G A A A C G C A G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A C A C C A T G A A A A C A G G A T C A T C C A C C A A C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 A A C A A C G A G G A A G A G A A G T C C C G A C T G T T G
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A G A A G G A A A A C C G A G A A C T G G A A A A G A T C
SEQ. ID. NO. 23

FIG. 6g.

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SEQ. ID. NO. 22 A T C G C T G A G A A A G A G G A G C G C G T C T C T G A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T G C G C C A T C A G C T C C A G T C T C G G C A G C A A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C T C C G C T C A C G G C G C C A C C C C C C A A C A C C C
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C A G A T C C C T C T G G G G G C C T T C C C A G G G G A
SEQ. ID. NO. 23

SEQ. ID. NO. 22 C C C T C T G A G C C C C C T G A C C G G C T T A G C T G T
SEQ. ID. NO. 23

SEQ. ID. NO. 22 G A T G G G A G T C G A G T A C A T T T G C T T T A C A A G
SEQ. ID. NO. 23

FIG. 6h.

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SEQ. ID. NO. 24 M L L L L L V P L F L R P L G A G G A Q T P N A T S E G C Q
SEQ. ID. NO. 25 M G P G G P C T P V G W P L P L L L V M A A G V A P V W A S

SEQ. ID. NO. 24 I I H P P W E G G I R Y R G L T R D Q V K A I N F L P V D Y
SEQ. ID. NO. 25 H S P H L P R P H P R V P P H P S S E R R A V Y I G A L F P

SEQ. ID. NO. 24 E I E Y V C R G E R E V V G P K V R K C L A N G S W T D M D
SEQ. ID. NO. 25 M S G G W P G G Q A C Q P A V E M A L E D V N S R R D I L P

SEQ. ID. NO. 24 T P S R C V R I C S K S Y L T L E N G K V F L T G G D L P A
SEQ. ID. NO. 25 D Y E L K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P

SEQ. ID. NO. 24 L D G A R V E F R C D P D F H L V G S S R S V C S Q G Q W S
SEQ. ID. NO. 25 I K I I L M P G C S S V S T L V A E A A R M W N L I V L S Y

SEQ. ID. NO. 24 T P K P H C Q V N R T P H S E R R A V Y I G A L F P M S G G
SEQ. ID. NO. 25 G S S S P A L S N R Q R F P T F F R T H P S A T L H N P T R

SEQ. ID. NO. 24 W P G G Q A C Q P A V E M A L E D V N S R R D I L P D Y E L
SEQ. ID. NO. 25 V K L F E K W G W K K I A T I Q Q T T E V F T S T L D D L E

SEQ. ID. NO. 24 K L I H H D S K C D P G Q A T K Y L Y E L L Y N D P I K I I
SEQ. ID. NO. 25 E R V K E A G I E I T F R Q S F F S D P A V P V K N L K R Q

SEQ. ID. NO. 24 L M P G C S S V S T L V A E A A R M W N L I V L S Y G S S S
SEQ. ID. NO. 25 D A R I I V G L F Y E T E A R K V F C E V Y K E R L F G K K

SEQ. ID. NO. 24 P A L S N R Q R F P T F F R T H P S A T L H N P T R V K L F
SEQ. ID. NO. 25 Y V W F L I G W Y A D N W F K T Y D P S I N C T V E E M T E

SEQ. ID. NO. 24 E K W G W K K I A T I Q Q T T E V F T S T L D D L E E R V K
SEQ. ID. NO. 25 A V E G H I T T E I V M L N P A N T R S I S N M T S Q E F V

SEQ. ID. NO. 24 E A G I E I T F R Q S F F S D P A V P V K N L K R Q D A R I
SEQ. ID. NO. 25 E K L T K R L K R H P E E T G G F Q E A P L A Y D A I W A L

FIG. 7a

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SEQ. ID. NO. 24 I V G L F Y E T E A R K V F C E V Y K E R L F G K K Y V W F
SEQ. ID. NO. 25 A L A L N K T S G G G G R S G V R L E D F N Y N N Q T I T D

SEQ. ID. NO. 24 L I G W Y A D N W F K T Y D P S I N C T V E E M T E A V E G
SEQ. ID. NO. 25 Q I Y R A M N S S S F E G V S G H V V F D A S G S R M A W T

SEQ. ID. NO. 24 H I T T E I V M L N P A N T R S I S N M T S Q E F V E K L T
SEQ. ID. NO. 25 L I E Q L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K

SEQ. ID. NO. 24 K R L K R H P E E T G G F Q E A P L A Y D A I W A L A L A L
SEQ. ID. NO. 25 W I G G S P P A D Q I L V I K T F R F L S Q K L F I S V S V

SEQ. ID. NO. 24 N K T S G G G G R S G V R L E D F N Y N N Q T I T D Q I Y R
SEQ. ID. NO. 25 L S S L G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P

SEQ. ID. NO. 24 A M N S S S F E G V S G H V V F D A S G S R M A W T L I E Q
SEQ. ID. NO. 25 N L N N L T A V G C S L A L A A V F P L G L D G Y H I G R S

SEQ. ID. NO. 24 L Q G G S Y K K I G Y Y D S T K D D L S W S K T D K W I G G
SEQ. ID. NO. 25 Q F P F V C Q A R L W L L G L G F S L G Y G S M F T K I W W

SEQ. ID. NO. 24 S P P A D Q I L V I K T F R F L S Q K L F I S V S V L S S L
SEQ. ID. NO. 25 V H T V F T K K E E K K E W R K T L E P W K L Y A T V G L L

SEQ. ID. NO. 24 G I V L A V V C L S F N I Y N S H V R Y I Q N S Q P N L N N
SEQ. ID. NO. 25 V G M D V L T L A I W Q I V D P L H R T I E T F A K E E P K

SEQ. ID. NO. 24 L T A V G C S L A L A A V F P L G L D G Y H I G R S Q F P F
SEQ. ID. NO. 25 E D I D V S I L P Q L E H C S S K K M N T W L G I F Y G Y K

SEQ. ID. NO. 24 V C Q A R L W L L G L G F S L G Y G S M F T K I W W V H T V
SEQ. ID. NO. 25 G L L L L L G I F L A Y E T K S V S T E K I N D H R A V G M

SEQ. ID. NO. 24 F T K K E E K K E W R K T L E P W K L Y A T V G L L V G M D
SEQ. ID. NO. 25 A I Y N V A V L C L I T A P V T M I L S S Q Q D A A F A F A

SEQ. ID. NO. 24 V L T L A I W Q I V D P L H R T I E T F A K E E P K E D I D
SEQ. ID. NO. 25 S L A I V F S S Y I T L V V L F V P K M R R L I T R G E W Q

FIG. 7b.

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SEQ. ID. NO. 24 V S I L P Q L E H C S S K K M N T W L G I F Y G Y K G L L L
SEQ. ID. NO. 25 S E T Q D T M K T G S S T N N N E E E K S R L L E K E N R E

SEQ. ID. NO. 24 L L G I F L A Y E T K S V S T E K I N D H R A V G M A I Y N
SEQ. ID. NO. 25 L E K I I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H

SEQ. ID. NO. 24 V A V L C L I T A P V T M I L S S Q Q D A A F A F A S L A I
SEQ. ID. NO. 25 P P T P P D P S G G L P R G P S E P P D R L S C D G S R V H

SEQ. ID. NO. 24 V F S S Y I T L V V L F V P K M R R L I T R G E W Q S E T Q
SEQ. ID. NO. 25 L L Y K

SEQ. ID. NO. 24 D T M K T G S S T N N N E E E K S R L L E K E N R E L E K I
SEQ. ID. NO. 25

SEQ. ID. NO. 24 I A E K E E R V S E L R H Q L Q S R Q Q L R S R R H P P T P
SEQ. ID. NO. 25

SEQ. ID. NO. 24 P D P S G G L P R G P S E P P D R L S C D G S R V H L L Y K
SEQ. ID. NO. 25

FIG. 7c.

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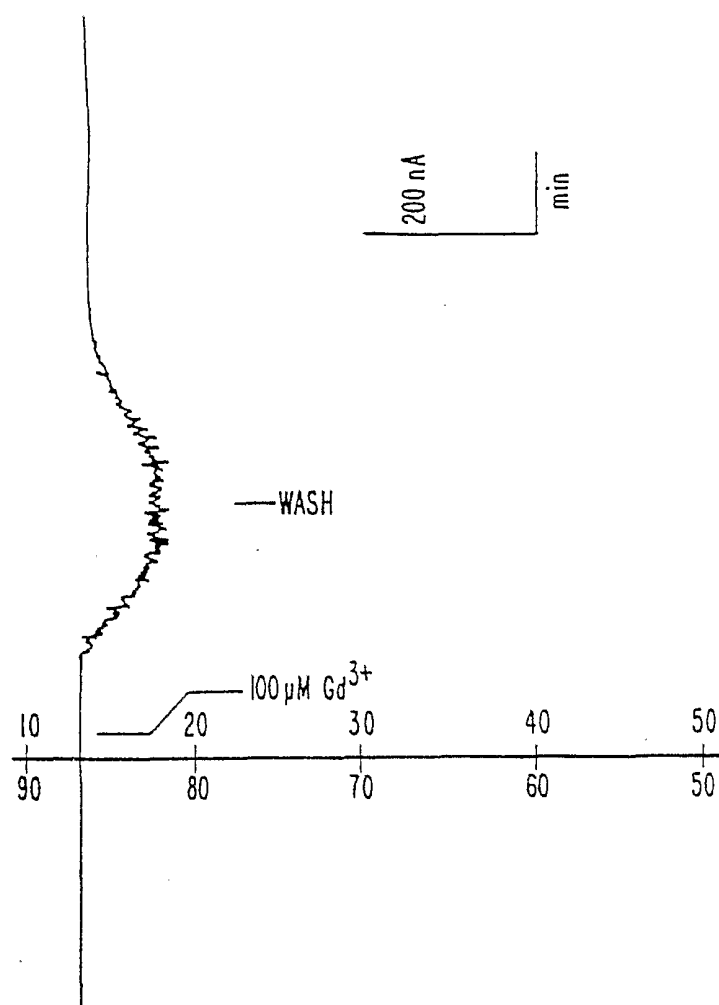


FIG. 8.

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ClustalW Formatted Alignments

SEQ. ID. NO. 38 A T G G T A T G C G A G G G A A A G C G A T C A G
SEQ. ID. NO. 34 A T G G G A T C G C T G C T T G C G C T C C C G G
SEQ. ID. NO. 30 A T G G C A T T T T A T A G C T G C T G C T G G G
SEQ. ID. NO. 26 A T G G G A T C G C T G C T T G C G C T C C T G G

SEQ. ID. NO. 38 C C T C T T G C C C T T G T T T C T T C C T C T T
SEQ. ID. NO. 34 C A C T G C T G C T G C T G T G G G G T G C T G T
SEQ. ID. NO. 30 T C C T C T T G G C A C T C A C C T G G C A C A C
SEQ. ID. NO. 26 C A C T G C T G C C G C T G T G G G G T G C T G T

SEQ. ID. NO. 38 G A C C G C C A A G T T C T A C T G G A T C C T C
SEQ. ID. NO. 34 G G C T G A G G G C C C A G C C A A G A A G G T G
SEQ. ID. NO. 30 C T C T G C C T A C G G G C C A G A C C A G C G A
SEQ. ID. NO. 26 G G C T G A G G G C C C A G C C A A G A A G G T G

SEQ. ID. NO. 38 A C A A T G A T G C A A A G A A C T C A C A G C C
SEQ. ID. NO. 34 C T G A C C C T G G A G G G A G A C T T G G T G C
SEQ. ID. NO. 30 G C C C A A A A G A A G G G G G A C A T T A T C C
SEQ. ID. NO. 26 C T G A C C C T G G A G G G A G A C T T G G T G C

SEQ. ID. NO. 38 A G G A G T A T G C C C A T T C C A T A C G G G T
SEQ. ID. NO. 34 T G G G T G G G C T G T T C C C A G T G C A C C A
SEQ. ID. NO. 30 T T G G G G G G C T C T T T C C T A T T C A T T T
SEQ. ID. NO. 26 T G G G T G G G C T G T T C C C A G T G C A C C A

SEQ. ID. NO. 38 G G A T G G G G A C A T T A T T T T G G G G G G T
SEQ. ID. NO. 34 G A A G G G C G G C C C A G C A G A G G A C T G T
SEQ. ID. NO. 30 T G G A G T A G C A G C T A A A G A T C A A G A T
SEQ. ID. NO. 26 G A A G G G C G G C C C A G C A G A G G A C T G T

SEQ. ID. NO. 38 C T C T T C C C T G T C C A C G C A A A G G G A G
SEQ. ID. NO. 34 G G T C C T G T C A A T G A G C A C C G T G G C A
SEQ. ID. NO. 30 C T C A A A T C A A G G C C G G A G T C T G T G G
SEQ. ID. NO. 26 G G T C C T G T C A A T G A G C A C C G T G G C A

SEQ. ID. NO. 38 A G A G A G G G G T G C C T T G T G G G G A G C T
SEQ. ID. NO. 34 T C C A G C G C C T G G A G G C C A T G C T T T T
SEQ. ID. NO. 30 A A T G T A T C A G G T A T A A T T T C C G T G G
SEQ. ID. NO. 26 T C C A G C G C C T G G A G G C C A T G C T T T T

FIG. 9a.

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SEQ. ID. NO. 38 G A A G A A G G A A A A G G G G A T T C A C A G A
SEQ. ID. NO. 34 T G C A C T G G A C C G C A T C A A C C G T G A C
SEQ. ID. NO. 30 G T T T C G C T G G T T A C A G G C T A T G A T A
SEQ. ID. NO. 26 T G C A C T G G A C C G C A T C A A C C G T G A C

SEQ. ID. NO. 38 C T G G A G G C C A T G C T T T A T G C A A T T G
SEQ. ID. NO. 34 C C G C A C C T G C T G C C T G G C G T G C G C C
SEQ. ID. NO. 30 T T T G C C A T A G A G G A G A T A A A C A G C A
SEQ. ID. NO. 26 C C G C A C C T G C T G C C T G G C G T G C G C C

SEQ. ID. NO. 38 A C C A G A T T A A C A A G G A C C C T G A T C T
SEQ. ID. NO. 34 T G G G T G C A C A C A T C C T C G A C A G T T G
SEQ. ID. NO. 30 G C C C A G C C C T T C T T C C C A A C T T G A C
SEQ. ID. NO. 26 T G G G T G C A C A C A T C C T C G A C A G T T G

SEQ. ID. NO. 38 C C T T T C C A A C A T C A C T C T G G G T G T C
SEQ. ID. NO. 34 C T C C A A G G A C A C A C A T G C G C T G G A G
SEQ. ID. NO. 30 G C T G G G A T A C A G G A T A T T T G A C A C T
SEQ. ID. NO. 26 C T C C A A G G A C A C A C A T G C G C T G G A G

SEQ. ID. NO. 38 C G C A T C C T C G A C A C G T G C T C T A G G G
SEQ. ID. NO. 34 C A G G C A C T G G A C T T T G T G C G T G C C T
SEQ. ID. NO. 30 T G C A A C A C C G T T T C T A A G G C C T T G G
SEQ. ID. NO. 26 C A G G C A C T G G A C T T T G T G C G T G C C T

SEQ. ID. NO. 38 A C A C C T A T G C T T T G G A G C A G T C T C T
SEQ. ID. NO. 34 C A C T C A G C C G T G G T G C T G A T G G C T C
SEQ. ID. NO. 30 A A G C C A C C C T G A G T T T T G T T G C T C A
SEQ. ID. NO. 26 C A C T C A G C C G T G G T G C T G A T G G A T C

SEQ. ID. NO. 38 A A C A T T C G T G C A G G C A T T A A T A G A G
SEQ. ID. NO. 34 A C G C C A C A T C T G C C C C G A C G G C T C T
SEQ. ID. NO. 30 A A A C A A A A T T G A T T C T T T G A A C C T T
SEQ. ID. NO. 26 A C G C C A C A T C T G C C C C G A C G G C T C T

SEQ. ID. NO. 38 A A A G A T G C T T C G G A T G T G A A G T G T G
SEQ. ID. NO. 34 T A T G C G A C C C A T G G T G A T G C T C C C A
SEQ. ID. NO. 30 G A T G A G T T C T G C A A C T G C T C A G A G C
SEQ. ID. NO. 26 T A T G C G A C C C A T G G T G A T G C T C C C A

FIG. 9b

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SEQ. ID. NO. 38 C T A A T G G A G A T C C A C C C A T T T T C A C
SEQ. ID. NO. 34 C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 30 A C A T T C C C T C T A C G A T T G C T G T G G T
SEQ. ID. NO. 26 C T G C C A T C A C T G G T G T T A T T G G C G G

SEQ. ID. NO. 38 C A A G C C C G A C A A G A T T T C T G G C G T C
SEQ. ID. NO. 34 T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 30 G G G A G C A A C T G G C T C A G G C G T C T C C
SEQ. ID. NO. 26 T T C C T A C A G T G A T G T C T C C A T C C A G

SEQ. ID. NO. 38 A T A G G T G C T G C A G C A A G C T C C G T G T
SEQ. ID. NO. 34 G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 30 A C G G C A G T G G C A A A T C T G C T G G G G C
SEQ. ID. NO. 26 G T G G C C A A C C T C T T G A G G C T A T T T C

SEQ. ID. NO. 38 C C A T C A T G G T T G C T A A C A T T T T A A G
SEQ. ID. NO. 34 A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 30 T C T T C T A C A T T C C C C A G G T C A G T T A
SEQ. ID. NO. 26 A G A T C C C A C A G A T T A G C T A C G C C T C

SEQ. ID. NO. 38 A C T T T T T A A G A T A C C T C A A A T C A G C
SEQ. ID. NO. 34 T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 30 T G C C T C C T C C A G C A G A C T C C T C A G C
SEQ. ID. NO. 26 T A C C A G T G C C A A G C T G A G T G A C A A G

SEQ. ID. NO. 38 T A T G C A T C C A C A G C C C C A G A G C T A A
SEQ. ID. NO. 34 T C C C G C T A T G A C T A C T T T G C C C G C A
SEQ. ID. NO. 30 A A C A A G A A T C A A T T C A A G T C T T T C C
SEQ. ID. NO. 26 T C C C G C T A T G A C T A C T T T G C C C G C A

SEQ. ID. NO. 38 G T G A T A A C A C C A G G T A T G A C T T T T T
SEQ. ID. NO. 34 C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 30 T C C G A A C C A T C C C C A A T G A T G A G C A
SEQ. ID. NO. 26 C A G T G C C T C C T G A C T T C T T C C A A G C

SEQ. ID. NO. 38 C T C T C G A G T G G T T C C G C C T G A C T C C
SEQ. ID. NO. 34 C A A G G C C A T G G C T G A G A T T C T C C G C
SEQ. ID. NO. 30 C C A G G C C A C T G C C A T G G C A G A C A T C
SEQ. ID. NO. 26 C A A G G C C A T G G C T G A G A T T C T C C G C

FIG. 9c.

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SEQ. ID. NO. 38 T A C C A A G C C C A A G C C A T G G T G G A C A
SEQ. ID. NO. 34 T T C T T C A A C T G G A C C T A T G T G T C C A
SEQ. ID. NO. 30 A T C G A G T A T T T C C G C T G G A A C T G G G
SEQ. ID. NO. 26 T T C T T C A A C T G G A C C T A T G T G T C C A

SEQ. ID. NO. 38 T C G T G A C A G C A C T G G G A T G G A A T T A
SEQ. ID. NO. 34 C T G T G G C G T C T G A G G G C G A C T A T G G
SEQ. ID. NO. 30 T G G G C A C A A T T G C A G C T G A T G A C G A
SEQ. ID. NO. 26 C T G A G G C C T C T G A G G G C G A C T A T G G

SEQ. ID. NO. 38 T G T T T C G A C A C T G G C T T C T G A G G G G
SEQ. ID. NO. 34 C G A G A C A G G C A T T G A G G C C T T T G A G
SEQ. ID. NO. 30 C T A T G G G C G G C C G G G G A T T G A G A A A
SEQ. ID. NO. 26 C G A G A C A G G C A T T G A G G C C T T T G A G

SEQ. ID. NO. 38 A A C T A T G G T G A G A G C G G T G T G G A G G
SEQ. ID. NO. 34 C T A G A G G C T C G T G C C C G C A A C A T C T
SEQ. ID. NO. 30 T T C C G A G A G G A A G C T G A G G A A A G G G
SEQ. ID. NO. 26 C T A G A G G C T C G T G C C C G C A A C A T C T

SEQ. ID. NO. 38 C C T T C A C C C A G A T C T C G A G G G A G A T
SEQ. ID. NO. 34 G T G T G G C C A C C T C G G A G A A A G T G G G
SEQ. ID. NO. 30 A T A T C T G C A T C G A C T T C A G T G A A C T
SEQ. ID. NO. 26 G T G T G G C C A C C T C G G A G A A A G T G G G

SEQ. ID. NO. 38 T G G T G G T G T T T G C A T T G C T C A G T C A
SEQ. ID. NO. 34 C C G T G C C A T G A G C C G C G C G G C C T T T
SEQ. ID. NO. 30 C A T C T C C C A G T A C T C T G A T G A G G A A
SEQ. ID. NO. 26 C C G T G C C A T G A G C C G C G C G G C C T T T

SEQ. ID. NO. 38 C A G A A A A T C C C A C G T G A A C C A A G A C
SEQ. ID. NO. 34 G A G G G T G T G G T G C G A G C C C T G C T G C
SEQ. ID. NO. 30 G A G A T C C A G C A T G T G G T A G A G G T G A
SEQ. ID. NO. 26 G A G G G T G T G G T G C G A G C C C T G C T G C

SEQ. ID. NO. 38 C T G G A G A A T T T G A A A A A T T A T C A A
SEQ. ID. NO. 34 A G A A G C C C A G T G C C C G C G T G G C T G T
SEQ. ID. NO. 30 T T C A A A A T T C C A C G G C C A A A G T C A T
SEQ. ID. NO. 26 A G A A G C C C A G T G C C C G C G T G G C T G T

FIG. 9d.

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SEQ. ID. NO. 38 A C G C C T G C T A G A A A C A C C T A A T G C T
SEQ. ID. NO. 34 C C T G T T C A C C C G T T C T G A G G A T G C C
SEQ. ID. NO. 30 C G T G G T T T T C T C C A G T G G C C C A G A T
SEQ. ID. NO. 26 C C T G T T C A C C C G T T C T G A G G A T G C C

SEQ. ID. NO. 38 C G A G C A G T G A T T A T G T T T G C C A A T G
SEQ. ID. NO. 34 C G G G A G C T G C T T G C T G C C A G C C A G C
SEQ. ID. NO. 30 C T T G A G C C C C T C A T C A A G G A G A T T G
SEQ. ID. NO. 26 C G G G A G C T G C T T G C T G C C A G C C A G C

SEQ. ID. NO. 38 A G G A T G A C A T C A G G A G G A T A T T G G A
SEQ. ID. NO. 34 G C C T C A A T G C C A G C T T C A C C T G G G T
SEQ. ID. NO. 30 T C C G G C G C A A T A T C A C G G G C A A G A T
SEQ. ID. NO. 26 G C C T C A A T G C C A G C T T C A C C T G G G T

SEQ. ID. NO. 38 A G C A G C A A A A A A A C T A A A C C A A A G T
SEQ. ID. NO. 34 G G C C A G T G A T G G T T G G G G G G C C C T G
SEQ. ID. NO. 30 C T G G C T G G C C A G C G A G G C C T G G G C C
SEQ. ID. NO. 26 G G C C A G T G A T G G T T G G G G G G C C C T G

SEQ. ID. NO. 38 G G G C A T T T T C T C T G G A T T G G C T C A G
SEQ. ID. NO. 34 G A G A G T G T G G T G G C A G G C A G T G A G G
SEQ. ID. NO. 30 A G C T C C T C C C T G A T C G C C A T G C C T C
SEQ. ID. NO. 26 G A G A G T G T G G T G G C A G G C A G T G A G G

SEQ. ID. NO. 38 A T A G T T G G G G A T C C A A A A T A G C A C C
SEQ. ID. NO. 34 G G G C T G C T G A G G G T G C T A T C A C C A T
SEQ. ID. NO. 30 A G T A C T T C C A C G T G G T T G G C G G C A C
SEQ. ID. NO. 26 G G G C T G C T G A G G G T G C T A T C A C C A T

SEQ. ID. NO. 38 T G T C T A T C A G C A A G A G G A G A T T G C A
SEQ. ID. NO. 34 C G A G C T G G C C T C C T A C C C C A T C A G T
SEQ. ID. NO. 30 C A T T G G A T T C G C T C T G A A G G C T G G G
SEQ. ID. NO. 26 C G A G C T G G C C T C C T A C C C C A T C A G T

SEQ. ID. NO. 38 G A A G G G G C T G T G A C A A T T T T G C C C A
SEQ. ID. NO. 34 G A C T T T G C C T C C T A C T T C C A G A G C C
SEQ. ID. NO. 30 C A G A T C C C A G G C T T C C G G G A A T T C C
SEQ. ID. NO. 26 G A C T T T G C C T C C T A C T T C C A G A G C C

FIG. 9e.

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SEQ. ID. NO. 38 A A C G A G C A T C A A T T G A T G G A T T T G A
SEQ. ID. NO. 34 T G G A C C C T T G G A A C A A C A G C C G G A A
SEQ. ID. NO. 30 T G A A G A A G G T C C A T C C C A G G A A G T C
SEQ. ID. NO. 26 T G G A C C C T T G G A A C A A C A G C C G G A A

SEQ. ID. NO. 38 T C G A T A C T T T T A G A A G C C G A A C T C T T
SEQ. ID. NO. 34 C C C C T G G T T C C G T G A A T T C T G G G A G
SEQ. ID. NO. 30 T G T C C A C A A T G G T T T T G C C A A G G A G
SEQ. ID. NO. 26 C C C C T G G T T C C G T G A A T T C T G G G A G

SEQ. ID. NO. 38 G C C A A T A A T C G A A G A A A T G T G T G G T
SEQ. ID. NO. 34 C A G A G G T T C C G C T G C A G C T T C C G G C
SEQ. ID. NO. 30 T T T T G G G A A G A A A C A T T T A A C T G C C
SEQ. ID. NO. 26 C A G A G G T T C C G C T G C A G C T T C C G G C

SEQ. ID. NO. 38 T T G C A G A A T T C T G G G A G G A G A A T T T
SEQ. ID. NO. 34 A G C G A G A C T G C G C A G C C C A C T C T C T
SEQ. ID. NO. 30 A C C T C C A A G A A G G T G C A A A A G G A C C
SEQ. ID. NO. 26 A G C G A G A C T G C G C A G C C C A C T C T C T

SEQ. ID. NO. 38 T G G C T G C A A G T T A G G A T C A C A T G G G
SEQ. ID. NO. 34 C C G G G C T G T G C C C T T T G A G C A G G A G
SEQ. ID. NO. 30 T T T A C C T G T G G A C A C C T T T C T G A G A
SEQ. ID. NO. 26 C C G G G C T G T G C C C T T T G A A C A G G A G

SEQ. ID. NO. 38 A A A A G G A A C A G T C A T A T A A A G A A A T
SEQ. ID. NO. 34 T C C A A G A T C A T G T T T G T G G T C A A T G
SEQ. ID. NO. 30 G G T C A C G A A G A A A G T G G C G A C A G G T
SEQ. ID. NO. 26 T C C A A G A T C A T G T T T G T G G T C A A T G

SEQ. ID. NO. 38 G C A C A G G G C T G G A G C G A A T T G C T C G
SEQ. ID. NO. 34 C A G T G T A C G C C A T G G C C C A T G C G C T
SEQ. ID. NO. 30 T T A G C A A C A G C T C G A C A G C C T T C C G
SEQ. ID. NO. 26 C A G T G T A C G C C A T G G C C C A T G C G C T

SEQ. ID. NO. 38 G G A T T C A T C T T A T G A A C A G G A A G G A
SEQ. ID. NO. 34 C C A C A A C A T G C A C C G T G C C C T C T G C
SEQ. ID. NO. 30 A C C C C T C T G T A C A G G G G A T G A G A A C
SEQ. ID. NO. 26 C C A C A A C A T G C A C C G T G C C C T C T G C

FIG. 9f.

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SEQ. ID. NO. 38 A A G G T C C A A T T T G T A A T T G A T G C T G
SEQ. ID. NO. 34 C C C A A C A C C A C C C G G C T C T G T G A C G
SEQ. ID. NO. 30 A T C A G C A G T G T C G A G A C C C C T T A C A
SEQ. ID. NO. 26 C C C A A C A C C A C C C G G C T C T G T G A C G

SEQ. ID. NO. 38 T A T A T T C C A T G G C T T A C G C C C T G C A
SEQ. ID. NO. 34 C G A T G C G G C C A G T T A A C G G G C G C C G
SEQ. ID. NO. 30 T A G A T T A C A C G C A T T T A C G G A T A T C
SEQ. ID. NO. 26 C G A T G C G G C C A G T T A A C G G G C G C C G

SEQ. ID. NO. 38 C A A T A T G C A C A A A G A T C T C T G C C C T
SEQ. ID. NO. 34 C C T C T A C A A G G A C T T T G T G C T C A A C
SEQ. ID. NO. 30 C T A C A A T G T G T A C T T A G C A G T C T A C
SEQ. ID. NO. 26 C C T C T A C A A G G A C T T T G T G C T C A A C

SEQ. ID. NO. 38 G G A T A C A T T G G C C T T T G T C C A C G A A
SEQ. ID. NO. 34 G T C A A G T T T G A T G C C C C C T T T C G C C
SEQ. ID. NO. 30 T C C A T T G C C C A C G C C T T G C A A G A T A
SEQ. ID. NO. 26 G T C A A G T T T G A T G C C C C C T T T C G C C

SEQ. ID. NO. 38 T G A G T A C C A T T G A T G G G A A A G A G C T
SEQ. ID. NO. 34 C A G C T G A C A C C C A C A A T G A G G T C C G
SEQ. ID. NO. 30 T A T A T A C C T G C T T A C C T G G G A G A G G
SEQ. ID. NO. 26 C A G C T G A C A C C C A C A A T G A G G T C C G

SEQ. ID. NO. 38 A C T T G G T T A T A T T C G G G C T G T A A A T
SEQ. ID. NO. 34 C T T T G A C C G C T T T G G T G A T G G T A T T
SEQ. ID. NO. 30 G C T C T T C A C C A A T G G C T C C T G T G C A
SEQ. ID. NO. 26 C T T T G A C C G C T T T G G T G A T G G T A T T

SEQ. ID. NO. 38 T T T A A T G G C A G T G C T G G C A C T C C T G
SEQ. ID. NO. 34 G G C C G C T A C A A C A T C T T C A C C T A T C
SEQ. ID. NO. 30 G A C A T C A A G A A A G T T G A G G C G T G G C
SEQ. ID. NO. 26 G G C C G C T A C A A C A T C T T C A C C T A T C

SEQ. ID. NO. 38 T C A C T T T T A A T G A A A A C G G A G A T G C
SEQ. ID. NO. 34 T G C G T G C A G G C A G T G G G C G C T A T C G
SEQ. ID. NO. 30 A G G T C C T G A A G C A C C T A C G G C A T C T
SEQ. ID. NO. 26 T G C G T G C A G G C A G T G G G C G C T A T C G

FIG. 9g.

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SEQ. ID. NO. 38 T C C T G G A C G T T A T G A T A T C T T C C A G
SEQ. ID. NO. 34 C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 30 A A A C T T T A C A A A C A A T A T G G G G G A G
SEQ. ID. NO. 26 C T A C C A G A A G G T G G G C T A C T G G G C A

SEQ. ID. NO. 38 T A T C A A A T A A C C A A C A A A A G C A C A G
SEQ. ID. NO. 34 G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 30 C A G G T G A C C T T T G A T G A G T G T G G T G
SEQ. ID. NO. 26 G A A G G C T T G A C T C T G G A C A C C A G C C

SEQ. ID. NO. 38 A G T A C A A A G T C A T C G G C C A C T G G A C
SEQ. ID. NO. 34 T C A T C C C A T G G G C C T C A C C C T C A G C
SEQ. ID. NO. 30 A C C T G G T G G G G A A C T A T T C C A T C A T
SEQ. ID. NO. 26 T C A T C C C A T G G G C C T C A C C G T C A G C

SEQ. ID. NO. 38 C A A T C A G C T T C A T C T A A A A G T G G A A
SEQ. ID. NO. 34 C G G C C C C C T G C C C G C C T C T C G C T G C
SEQ. ID. NO. 30 C A A C T G G C A C C T C T C C C C A G A G G A T
SEQ. ID. NO. 26 C G G C C C C C T G G C C G C C T C T C G C T G C

SEQ. ID. NO. 38 G A C A T G C A G T G G G C T C A T A G A G A A C
SEQ. ID. NO. 34 A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 30 G G C T C C A T C G T G T T T A A G G A A G T C G
SEQ. ID. NO. 26 A G T G A G C C C T G C C T C C A G A A T G A G G

SEQ. ID. NO. 38 A T A C T C A C C C G G C G T C T G T C T G C A G
SEQ. ID. NO. 34 T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 30 G G T A T T A C A A C G T C T A T G C C A A G A A
SEQ. ID. NO. 26 T G A A G A G T G T G C A G C C G G G C G A A G T

SEQ. ID. NO. 38 C C T G C C G T G T A A G C C A G G G G A G A G G
SEQ. ID. NO. 34 C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 30 G G G A G A A A G A C T C T T C A T C A A C G A G
SEQ. ID. NO. 26 C T G C T G C T G G C T C T G C A T T C C G T G C

SEQ. ID. NO. 38 A A G A A A A C G G T G A A A G G G G T C C C T T
SEQ. ID. NO. 34 C A G C C C T A T G A G T A C C G A T T G G A C G
SEQ. ID. NO. 30 G A G A A A A T C C T G T G G A G T G G G T T C T
SEQ. ID. NO. 26 C A G C C C T A T G A G T A C C G A T T G G A C G

FIG. 9h.

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SEQ. ID. NO. 38 G C T G C T G G C A C T G T G A A C G C T G T G A
SEQ. ID. NO. 34 A A T T C A C T T G C G C T G A T T G T G G C C T
SEQ. ID. NO. 30 C C A G G G A G G T G C C C T T C T C C A A C T G
SEQ. ID. NO. 26 A A T T C A C T T G C G C T G A T T G T G G C C T

SEQ. ID. NO. 38 A G G T T A C A A C T A C C A G G T G G A T G A G
SEQ. ID. NO. 34 G G G C T A C T G G C C C A A T G C C A G C C T G
SEQ. ID. NO. 30 C A G C C G A G A C T G C C T G G C A G G G A C C
SEQ. ID. NO. 26 G G G C T A C T G G C C C A A T G C C A G C C T G

SEQ. ID. NO. 38 C T G T C C T G T G A A C T T T G C C C T C T G G
SEQ. ID. NO. 34 A C T G G C T G C T T C G A A C T G C C C C A G G
SEQ. ID. NO. 30 A G G A A A G G G A T C A T T G A G G G G G A G C
SEQ. ID. NO. 26 A C T G G C T G C T T C G A A C T G C C C C A G G

SEQ. ID. NO. 38 A T C A G A G A C C C A A C A T G A A C C G C A C
SEQ. ID. NO. 34 A G T A C A T C C G C T G G G G C G A T G C C T G
SEQ. ID. NO. 30 C C A C C T G C T G C T T T G A G T G T G T G G A
SEQ. ID. NO. 26 A G T A C A T C C G C T G G G G C G A T G C C T G

SEQ. ID. NO. 38 A G G C T G C C A G C T T A T C C C C A T C A T C
SEQ. ID. NO. 34 G G C T G T G G G A C C T G T C A C C A T C G C C
SEQ. ID. NO. 30 G T G T C C T G A T G G G G A G T A T A G T G A T
SEQ. ID. NO. 26 G G C T G T G G G A C C T G T C A C C A T C G C C

SEQ. ID. NO. 38 A A A T T G G A G T G G C A T T C T C C C T G G G
SEQ. ID. NO. 34 T G C C T C G G T G C C C T G G C C A C C C T C T
SEQ. ID. NO. 30 G A G A C A G A T G C C A G T G C C T G T A A C A
SEQ. ID. NO. 26 T G C C T C G G T G C C C T G G C C A C C C T G T

SEQ. ID. NO. 38 C T G T G G T G C C T G T G T T T G T T G C A A T
SEQ. ID. NO. 34 T T G T G C T G G G T G T C T T T G T G C G G C A
SEQ. ID. NO. 30 A G T G C C C A G A T G A C T T C T G G T C C A A
SEQ. ID. NO. 26 T T G T G C T G G G T G T C T T T G T G C G G C A

SEQ. ID. NO. 38 A T T G G G A A T C A T C G C C A C C A C C T T T
SEQ. ID. NO. 34 C A A T G C C A C A C C A G T G G T C A A G G C C
SEQ. ID. NO. 30 T G A G A A C C A C A C C T C C T G C T T C G A A
SEQ. ID. NO. 26 C A A T G C C A C A C C A G T G G T C A A G G C C

FIG. 9i.

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SEQ. ID. NO. 38 G T G A T C G T G A C C T T T G T C C G C T A T A
SEQ. ID. NO. 34 T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 30 C T G C C C C A G G A G T A C A T C C G C T G G G
SEQ. ID. NO. 26 T C A G G T C G G G A G C T C T G C T A C A T C C

SEQ. ID. NO. 38 A T G A C A C A C C T A T C G T G A G G G C T T C
SEQ. ID. NO. 34 T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 30 G C G A T G C C T G G G C T G T G G G A C C T G T
SEQ. ID. NO. 26 T G C T G G G T G G T G T C T T C C T C T G C T A

SEQ. ID. NO. 38 A G G A C G C G A A C T T A G T T A C G T G C T C
SEQ. ID. NO. 34 C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 30 C A C C A T C G C C T G C C T C G G T G C C C T G
SEQ. ID. NO. 26 C T G C A T G A C C T T C A T C T T C A T T G C C

SEQ. ID. NO. 38 C T A A C G G G G A T T T T T C T C T G T T A T T
SEQ. ID. NO. 34 A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 30 G C C A C C C T G T T T G T G C T G G G T G T C T
SEQ. ID. NO. 26 A A G C C A T C C A C G G C A G T G T G T A C C T

SEQ. ID. NO. 38 C A A T C A C G T T T T T A A T G A T T G C A G C
SEQ. ID. NO. 34 T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 30 T T G T G C G G C A C A A T G C C A C A C C A G T
SEQ. ID. NO. 26 T A C G G C G T C T T G G T T T G G G C A C T G C

SEQ. ID. NO. 38 A C C A G A T A C A A T C A T A T G C T C C T T C
SEQ. ID. NO. 34 C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 30 G G T C A A G G C C T C A G G T C G G G A G C T C
SEQ. ID. NO. 26 C T T C T C T G T C T G C T A C T C A G C C C T G

SEQ. ID. NO. 38 C G A C G G G T C T T C C T A G G A C T T G G C A
SEQ. ID. NO. 34 C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 30 T G C T A C A T C C T G C T G G G T G G T G T C T
SEQ. ID. NO. 26 C T C A C C A A G A C C A A C C G C A T T G C A C

SEQ. ID. NO. 38 T G T G T T T C A G C T A T G C A G C C C T T C T
SEQ. ID. NO. 34 G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 30 T C C T C T G C T A C T G C A T G A C C T T C A T
SEQ. ID. NO. 26 G C A T C T T C G G T G G G G C C C G G G A G G G

FIG. 9j.

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SEQ. ID. NO. 38 G A C C A A A A C A A A C C G T A T C C A C C G A
SEQ. ID. NO. 34 T G C C C A G C G G C C A C G C T T C A T C A G T
SEQ. ID. NO. 30 C T T C A T T G C C A A G C C A T C C A C G G C A
SEQ. ID. NO. 26 T G C C C A G C G G C C A C G C T T C A T C A G T

SEQ. ID. NO. 38 A T A T T T G A G C A G G G G A A G A A A T C T G
SEQ. ID. NO. 34 C C T G C C T C A C A G G T G G C C A T C T G C C
SEQ. ID. NO. 30 G T G T G T A C C T T A C G G C G T C T T G G T T
SEQ. ID. NO. 26 C C T G C C T C A C A G G T G G C C A T C T G C C

SEQ. ID. NO. 38 T C A C A G C G C C C A A G T T C A T T A G T C C
SEQ. ID. NO. 34 T G G C A C T T A T C T C G G G C C A G C T G C T
SEQ. ID. NO. 30 T G G G C A C T G C C T T C T C T G T C T G C T A
SEQ. ID. NO. 26 T G G C A C T T A T C T C G G G C C A G C T G C T

SEQ. ID. NO. 38 A G C A T C T C A G C T G G T G A T C A C C T T C
SEQ. ID. NO. 34 C A T C G T G G T C G C C T G G C T G G T G G T G
SEQ. ID. NO. 30 C T C A G C C C T G C T C A C C A A G A C C A A C
SEQ. ID. NO. 26 C A T C G T G G T C G C C T G G C T G G T G G T G

SEQ. ID. NO. 38 A G C C T C A T C T C C G T C C A G C T C C T T G
SEQ. ID. NO. 34 G A G G C A C C G G G C A C A G G C A A G G A G A
SEQ. ID. NO. 30 C G C A T T G C A C G C A T C T T C G G T G G G G
SEQ. ID. NO. 26 G A G G C A C C G G G C A C A G G C A A G G A G A

SEQ. ID. NO. 38 G A G T G T T T G T C T G G T T T G T T G T G G A
SEQ. ID. NO. 34 C A G C C C C C G A A C G G C G G G A G G T G G T
SEQ. ID. NO. 30 C C C G G G A G G G T G C C C A G C G G C C A C G
SEQ. ID. NO. 26 C A G C C C C C G A A C G G C G G G A G G T G G T

SEQ. ID. NO. 38 T C C C C C C A C A T C A T C A T T G A C T A T
SEQ. ID. NO. 34 G A C A C T G C G C T G C A A C C A C C G C G A T
SEQ. ID. NO. 30 C T T C A T C A G T C C T G C C T C A C A G G T G
SEQ. ID. NO. 26 G A C A C T G C G C T G C A A C C A C C G C G A T

SEQ. ID. NO. 38 G G A G A G C A G C G G A C A C T A G A T C C A G
SEQ. ID. NO. 34 G C A A G T A T G T T G G G C T C G C T G G C C T
SEQ. ID. NO. 30 G C C A T C T G C C T G G C A C T T A T C T C G G
SEQ. ID. NO. 26 G C A A G T A T G T T G G G C T C G C T G G C C T

FIG. 9k.

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SEQ. ID. NO. 38 A G A A G G C C A G G G G A G T G C T C A A G T G
SEQ. ID. NO. 34 A C A A T G T G C T C C T C A T C G C G C T C T G
SEQ. ID. NO. 30 G C C A G C T G C T C A T C G T G G T C G C C T G
SEQ. ID. NO. 26 A C A A T G T G C T C C T C A T C G C G C T C T G

SEQ. ID. NO. 38 T G A C A T T T C T G A T C T C T C A C T C A T T
SEQ. ID. NO. 34 C A C G C T T T A T G C C T T C A A G A C T C G C
SEQ. ID. NO. 30 G C T G G T G G T G G A G G C A C C G G G C A C A
SEQ. ID. NO. 26 C A C G C T T T A T G C C T T C A A T A C T C G C

SEQ. ID. NO. 38 T G T T C A C T T G G A T A C A G T A T C C T C T
SEQ. ID. NO. 34 A A G T G C C C C G A A A A C T T C A A C G A G G
SEQ. ID. NO. 30 G G C A A G G A G A C A G C C C C C G A A C G G C
SEQ. ID. NO. 26 A A G T G C C C C G A A A A C T T C A A C G A G G

SEQ. ID. NO. 38 T G A T G G T C A C T T G T A C T G T T T A T G C
SEQ. ID. NO. 34 C C A A G T T C A T T G G C T T C A C C A T G T A
SEQ. ID. NO. 30 G G G A G G T G G T G A C A C T G C G C T G C A A
SEQ. ID. NO. 26 C C A A G T T C A T T G G C T T C A C C A T G T A

SEQ. ID. NO. 38 C A T T A A A A C G A G A G G T G T C C C A G A G
SEQ. ID. NO. 34 C A C C A C C T G C A T C A T C T G G C T G G C A
SEQ. ID. NO. 30 C C A C C G C G A T G C A A G T A T G T T G G G C
SEQ. ID. NO. 26 C A C C A C C T G C A T C A T C T G G C T G G C A

SEQ. ID. NO. 38 A C T T T C A A T G A A G C C A A A C C T A T T G
SEQ. ID. NO. 34 T T C C T G C C C A T C T T C T A T G T C A C C T
SEQ. ID. NO. 30 T C G C T G G C C T A C A A T G T G C T C C T C A
SEQ. ID. NO. 26 T T G T T G C C C A T C T T C T A T G T C A C C T

SEQ. ID. NO. 38 G A T T T A C C A T G T A T A C C A C C T G C A T
SEQ. ID. NO. 34 C C A G T G A C T A C C G G G T A C A G A C C A C
SEQ. ID. NO. 30 T C G C G C T C T G C A C G C T T T A T G C C T T
SEQ. ID. NO. 26 C C A G T G A C T A C C G G G T A C A G A C C A C

SEQ. ID. NO. 38 C A T T T G G T T A G C T T T C A T C C C C A T C
SEQ. ID. NO. 34 C A C C A T G T G C G T G T C A G T C A G C C T C
SEQ. ID. NO. 30 C A A T A C T C G C A A G T G C C C C G A A A A C
SEQ. ID. NO. 26 C A C C A T G T G C G T G T C A G T C A G C C T C

FIG. 9L.

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SEQ. ID. NO. 38 T T T T T T G G T A C A G C C C A G T C A G C A G
SEQ. ID. NO. 34 A G C G G C T C C G T G G T G C T T T G G C T G C C
SEQ. ID. NO. 30 T T C A A C G A G G C C A A G T T C A T T G G C T
SEQ. ID. NO. 26 A G C G G C T C C G T G G T G C T T T G G C T G C C

SEQ. ID. NO. 38 A A A A G A T G T A C A T C C A G A C A A C A A C
SEQ. ID. NO. 34 T C T T T G C G C C C A A G C T G C A C A T C A T
SEQ. ID. NO. 30 T C A C C A T G T A C A C C A C C T G C A T C A T
SEQ. ID. NO. 26 T C T T T G C G C C C A A G C T G C A C A T C A T

SEQ. ID. NO. 38 A C T T A C T G T C T C C A T G A G T T T A A G T
SEQ. ID. NO. 34 C C T C T T C C A G C C G C A G A A G A A C A C C
SEQ. ID. NO. 30 C T G G C T G G C A T T G T T G C C C A T C T T C
SEQ. ID. NO. 26 C C T C T T C C A G C C G C A G A A G A A C G T G

SEQ. ID. NO. 38 G C T T C A G T A T C T C T G G G C A T G C T C T
SEQ. ID. NO. 34 A T C G A G G A G G T G C G T T G C A G C A C C G
SEQ. ID. NO. 30 T A T G T C A C C T C C A G T G A C T A C C G G G
SEQ. ID. NO. 26 G T T A G C C A C C G G G C A C C C A C C A G C C

SEQ. ID. NO. 38 A T A T G C C C A A G G T T T A T A T T A T A A T
SEQ. ID. NO. 34 C A G C T C A C G C T T T C A A G G T G G C T G C
SEQ. ID. NO. 30 T A C A G A C C A C C A C C A T G T G C G T G T C
SEQ. ID. NO. 26 G C T T T G G C A G T G C T G C T G C C A G G G C

SEQ. ID. NO. 38 T T T T C A T C C A G A A C A G A A T A C C A T C
SEQ. ID. NO. 34 C C G G G C C A C G C T G C G C C G C A G C A A C
SEQ. ID. NO. 30 A G T C A G C C T C A G C G G C T C C G T G G T G
SEQ. ID. NO. 26 C A G C T C C A G C C T T G G C C A A G G G T C T

SEQ. ID. NO. 38 G A G G A G G T G C G T T G C A G C A C C G C A G
SEQ. ID. NO. 34 G T C T C C C G C A A G C G G T C C A G C A G C C
SEQ. ID. NO. 30 C T T G G C T G C C T C T T T G C G C C C A A G C
SEQ. ID. NO. 26 G G C T C C C A G T T T G T C C C C A C T G T T T

SEQ. ID. NO. 38 C T C A C G C T T T C A A G G T G G C T G C C C G
SEQ. ID. NO. 34 T T G G A G G C T C C A C G G G A T C C A C C C C
SEQ. ID. NO. 30 T G C A C A T C A T C C T C T T C C A G C C G C A
SEQ. ID. NO. 26 G C A A T G G C C G T G A G G T G G T G G A C T C

FIG. 9m.

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SEQ. ID. NO. 38 G G C C A C G C T G C G C C G C A G C A A C G T C
SEQ. ID. NO. 34 C T C C T C C T C C A T C A G C A G C A A G A G C
SEQ. ID. NO. 30 G A A G A A C G T G G T T A G C C A C C G G G C A
SEQ. ID. NO. 26 G A C A A C G T C A T C G C T T

SEQ. ID. NO. 38 T C C C G C A A G C G G T C C A G C A G C C T T G
SEQ. ID. NO. 34 A A C A G C G A A G A C C C A T T C C C A C A G C
SEQ. ID. NO. 30 C C C A C C A G C C G C T T T G G C A G T G C T G
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G C T C C A C G G G A T C C A C C C C C T C
SEQ. ID. NO. 34 C C G A G A G G C A G A A G C A G C A G C A G C C
SEQ. ID. NO. 30 C T G C C A G G G C C A G C T C C A G C C T T G G
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T C C T C C A T C A G C A G C A A G A G C A A C
SEQ. ID. NO. 34 G C T G G C C C T A A C C C A G C A A G A G C A G
SEQ. ID. NO. 30 C C A A G G G T C T G G C T C C C A G T T T G T C
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G A A G A C C C A T T C C C A C A G C C C G
SEQ. ID. NO. 34 C A G C A G C A G C C C C T G A C C C T C C C A C
SEQ. ID. NO. 30 C C C A C T G T T T G C A A T G G C C G T G A G G
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G A G G C A G A A G C A G C A G C A G C C G C T
SEQ. ID. NO. 34 A G C A G C A A C G A T C T C A G C A G C A G C C
SEQ. ID. NO. 30 T G G T G G A C T C G A C A A C G T C A T C G C T
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G C C C T A A C C C A G C A A G A G C A G C A G
SEQ. ID. NO. 34 C A G A T G C A A G C A G A A G G T C A T C T T T
SEQ. ID. NO. 30 T
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G C A G C C C C T G A C C C T C C C A C A G C
SEQ. ID. NO. 34 G G C A G C G G C A C G G T C A C C T T C T C A C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

FIG. 9n.

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SEQ. ID. NO. 38 A G C A A C G A T C T C A G C A G C A G C C C A G
SEQ. ID. NO. 34 T G A G C T T T G A T G A G C C T C A G A A G A A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A T G C A A G C A G A A G G T C A T C T T T G G C
SEQ. ID. NO. 34 C G C C A T G G C C C A C G G G A A T T C T A C G
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G C G G C A C G G T C A C C T T C T C A C T G A
SEQ. ID. NO. 34 C A C C A G A A C T C C C T G G A G G C C C A G A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C T T T G A T G A G C C T C A G A A G A A C G C
SEQ. ID. NO. 34 A A A G C A G C G A T A C G C T G A C C C G A C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A T G G C C C A C G G G A A T T C T A C G C A C
SEQ. ID. NO. 34 C C A G C C A T T A C T C C C G C T G C A G T G C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A G A A C T C C C T G G A G G C C C A G A A A A
SEQ. ID. NO. 34 G G G G A A A C G G A C T T A G A T C T G A C C G
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C A G C G A T A C G C T G A C C C G A C A C C A
SEQ. ID. NO. 34 T C C A G G A A A C A G G T C T G C A A G G A C C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G C C A T T A C T C C C G C T G C A G T G C G G G
SEQ. ID. NO. 34 T G T G G G T G G A G A C C A G C G G C C A G A G
SEQ. ID. NO. 30
SEQ. ID. NO. 26

FIG. 90.

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SEQ. ID. NO. 38 G A A A C G G A C T T A G A T C T G A C C G T C C
SEQ. ID. NO. 34 G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A G G A A A C A G G T C T G C A A G G A C C T G T
SEQ. ID. NO. 34 C A G C A C T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G G G T G G A G A C C A G C G G C C A G A G G T G
SEQ. ID. NO. 34 G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 G A G G A C C C T G A A G A G T T G T C C C C A G
SEQ. ID. NO. 34 A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A C T T G T A G T G T C C A G T T C A C A G A G
SEQ. ID. NO. 34 A T T C A
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C T T T G T C A T C A G T G G T G G A G G C A G C
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 A C T G T T A C A G A A A A C G T A G T G A A T T
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

SEQ. ID. NO. 38 C A
SEQ. ID. NO. 34
SEQ. ID. NO. 30
SEQ. ID. NO. 26

FIG. 9p.

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ClustalW Formatted Alignments

SEQ. ID. NO. 39 M V C E G K R S A S C P C F F L L T A K F Y W I L
SEQ. ID. NO. 35 M G S L L A L P A L L L L W G A V A E G P A K K V
SEQ. ID. NO. 31 M A F Y S C C W V L L A L T W H T S A Y G P D Q R
SEQ. ID. NO. 27 M G S L L A L L A L L P L W G A V A E G P A K K V

SEQ. ID. NO. 39 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
SEQ. ID. NO. 35 L T L E G D L V L G G L F P V H Q K G G P A E D C
SEQ. ID. NO. 31 A Q K K G D I I L G G L F P I H F G V A A K D Q D
SEQ. ID. NO. 27 L T L E G D L V L G G L F P V H Q K G G P A E D C

SEQ. ID. NO. 39 L F P V H A K G E R G V P C G E L K K E K G I H R
SEQ. ID. NO. 35 G P V N E H R G I Q R L E A M L F A L D R I N R D
SEQ. ID. NO. 31 L K S R P E S V E C I R Y N F R G F R W L Q A M I
SEQ. ID. NO. 27 G P V N E H R G I Q R L E A M L F A L D R I N R D

SEQ. ID. NO. 39 L E A M L Y A I D Q I N K D P D L L S N I T L G V
SEQ. ID. NO. 35 P H L L P G V R L G A H I L D S C S K D T H A L E
SEQ. ID. NO. 31 F A I E E I N S S P A L L P N L T L G Y R I F D T
SEQ. ID. NO. 27 P H L L P G V R L G A H I L D S C S K D T H A L E

SEQ. ID. NO. 39 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
SEQ. ID. NO. 35 Q A L D F V R A S L S R G A D G S R H I C P D G S
SEQ. ID. NO. 31 C N T V S K A L E A T L S F V A Q N K I D S L N L
SEQ. ID. NO. 27 Q A L D F V R A S L S R G A D G S R H I C P D G S

SEQ. ID. NO. 39 K D A S D V K C A N G D P P I F T K P D K I S G V
SEQ. ID. NO. 35 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
SEQ. ID. NO. 31 D E F C N C S E H I P S T I A V V G A T G S G V S
SEQ. ID. NO. 27 Y A T H G D A P T A I T G V I G G S Y S D V S I Q

SEQ. ID. NO. 39 I G A A A S S V S I M V A N I L R L F K I P Q I S
SEQ. ID. NO. 35 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
SEQ. ID. NO. 31 T A V A N L L G L F Y I P Q V S Y A S S S R L L S
SEQ. ID. NO. 27 V A N L L R L F Q I P Q I S Y A S T S A K L S D K

SEQ. ID. NO. 39 Y A S T A P E L S D N T R Y D F F S R V V P P D S
SEQ. ID. NO. 35 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
SEQ. ID. NO. 31 N K N Q F K S F L R T I P N D E H Q A T A M A D I
SEQ. ID. NO. 27 S R Y D Y F A R T V P P D F F Q A K A M A E I L R

FIG. 10a.

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SEQ. ID. NO. 39 Y Q A Q A M V D I V T A L G W N Y V S T L A S E G
 SEQ. ID. NO. 35 F F N W T Y V S T V A S E G D Y G E T G I E A F E
 SEQ. ID. NO. 31 I E Y F R W N W V G T I A A D D D Y G R P G I E K
 SEQ. ID. NO. 27 F F N W T Y V S T E A S E G D Y G E T G I E A F E

SEQ. ID. NO. 39 N Y G E S G V E A F T Q I S R E I G G V C I A Q S
 SEQ. ID. NO. 35 L E A R A R N I C V A T S E K V G R A M S R A A F
 SEQ. ID. NO. 31 F R E E A E E R D I C I D F S E L I S Q Y S D E E
 SEQ. ID. NO. 27 L E A R A R N I C V A T S E K V G R A M S R A A F

SEQ. ID. NO. 39 Q K I P R E P R P G E F E K I I K R L L E T P N A
 SEQ. ID. NO. 35 E G V V R A L L Q K P S A R V A V L F T R S E D A
 SEQ. ID. NO. 31 E I Q H V V E V I Q N S T A K V I V V F S S G P D
 SEQ. ID. NO. 27 E G V V R A L L Q K P S A R V A V L F T R S E D A

SEQ. ID. NO. 39 R A V I M F A N E D D I R R I L E A A K K L N Q S
 SEQ. ID. NO. 35 R E L L A A S Q R L N A S F T W V A S D G W G A L
 SEQ. ID. NO. 31 L E P L I K E I V R R N I T G K I W L A S E A W A
 SEQ. ID. NO. 27 R E L L A A S Q R L N A S F T W V A S D G W G A L

SEQ. ID. NO. 39 G H F L W I G S D S W G S K I A P V Y Q Q E E I A
 SEQ. ID. NO. 35 E S V V A G S E G A A E G A I T I E L A S Y P I S
 SEQ. ID. NO. 31 S S S L I A M P Q Y F H V V G G T I G F A L K A G
 SEQ. ID. NO. 27 E S V V A G S E G A A E G A I T I E L A S Y P I S

SEQ. ID. NO. 39 E G A V T I L P K R A S I D G F D R Y F R S R T L
 SEQ. ID. NO. 35 D F A S Y F Q S L D P W N N S R N P W F R E F W E
 SEQ. ID. NO. 31 Q I P G F R E F L K K V H P R K S V H N G F A K E
 SEQ. ID. NO. 27 D F A S Y F Q S L D P W N N S R N P W F R E F W E

SEQ. ID. NO. 39 A N N R R N V W F A E F W E E N F G C K L G S H G
 SEQ. ID. NO. 35 Q R F R C S F R Q R D C A A H S L R A V P F E Q E
 SEQ. ID. NO. 31 F W E E T F N C H L Q E G A K G P L P V D T F L R
 SEQ. ID. NO. 27 Q R F R C S F R Q R D C A A H S L R A V P F E Q E

SEQ. ID. NO. 39 K R N S H I K K C T G L E R I A R D S S Y E Q E G
 SEQ. ID. NO. 35 S K I M F V V N A V Y A M A H A L H N M H R A L C
 SEQ. ID. NO. 31 G H E E S G D R F S N S S T A F R P L C T G D E N
 SEQ. ID. NO. 27 S K I M F V V N A V Y A M A H A L H N M H R A L C

FIG. 10b.

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SEQ. ID. NO. 39 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
SEQ. ID. NO. 35 P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 31 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y
SEQ. ID. NO. 27 P N T T R L C D A M R P V N G R R L Y K D F V L N

SEQ. ID. NO. 39 G Y I G L C P R M S T I D G K E L L G Y I R A V N
SEQ. ID. NO. 35 V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 31 S I A H A L Q D I Y T C L P G R G L F T N G S C A
SEQ. ID. NO. 27 V K F D A P F R P A D T H N E V R F D R F G D G I

SEQ. ID. NO. 39 F N G S A G T P V T F N E N G D A P G R Y D I F Q
SEQ. ID. NO. 35 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 31 D I K K V E A W Q V L K H L R H L N F T N N M G E
SEQ. ID. NO. 27 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A

SEQ. ID. NO. 39 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
SEQ. ID. NO. 35 E G L T L D T S L I P W A S P S A G P L P A S R C
SEQ. ID. NO. 31 Q V T F D E C G D L V G N Y S I I N W H L S P E D
SEQ. ID. NO. 27 E G L T L D T S L I P W A S P S A G P L A A S R C

SEQ. ID. NO. 39 D M Q W A H R E H T H P A S V C S L P C K P G E R
SEQ. ID. NO. 35 S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 31 G S I V F K E V G Y Y N V Y A K K G E R L F I N E
SEQ. ID. NO. 27 S E P C L Q N E V K S V Q P G E V C C W L C I P C

SEQ. ID. NO. 39 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
SEQ. ID. NO. 35 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 31 E K I L W S G F S R E V P F S N C S R D C L A G T
SEQ. ID. NO. 27 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L

SEQ. ID. NO. 39 L S C E L C P L D Q R P N M N R T G C Q L I P I I
SEQ. ID. NO. 35 T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 31 R K G I I E G E P T C C F E C V E C P D G E Y S D
SEQ. ID. NO. 27 T G C F E L P Q E Y I R W G D A W A V G P V T I A

SEQ. ID. NO. 39 K L E W H S P W A V V P V F V A I L G I I A T T F
SEQ. ID. NO. 35 C L G A L A T L F V L G V F V R H N A T P V V K A
SEQ. ID. NO. 31 E T D A S A C N K C P D D F W S N E N H T S C F E
SEQ. ID. NO. 27 C L G A L A T L F V L G V F V R H N A T P V V K A

FIG. 10c.

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SEQ. ID. NO. 39 V I V T F V R Y N D T P I V R A S G R E L S Y V L
 SEQ. ID. NO. 35 S G R E L C Y I L L G G V F L C Y C M T F I F I A
 SEQ. ID. NO. 31 L P Q E Y I R W G D A W A V G P V T I A C L G A L
 SEQ. ID. NO. 27 S G R E L C Y I L L G G V F L C Y C M T F I F I A

SEQ. ID. NO. 39 L T G I F L C Y S I T F L M I A A P D T I I C S F
 SEQ. ID. NO. 35 K P S T A V C T L R R L G L G T A F S V C Y S A L
 SEQ. ID. NO. 31 A T L F V L G V F V R H N A T P V V K A S G R E L
 SEQ. ID. NO. 27 K P S T A V C T L R R L G L G T A F S V C Y S A L

SEQ. ID. NO. 39 R R V F L G L G M C F S Y A A L L T K T N R I H R
 SEQ. ID. NO. 35 L T K T N R I A R I F G G A R E G A Q R P R F I S
 SEQ. ID. NO. 31 C Y I L L G G V F L C Y C M T F I F I A K P S T A
 SEQ. ID. NO. 27 L T K T N R I A R I F G G A R E G A Q R P R F I S

SEQ. ID. NO. 39 I F E Q G K K S V T A P K F I S P A S Q L V I T F
 SEQ. ID. NO. 35 P A S Q V A I C L A L I S G Q L L I V V A W L V V
 SEQ. ID. NO. 31 V C T L R R L G L G T A F S V C Y S A L L T K T N
 SEQ. ID. NO. 27 P A S Q V A I C L A L I S G Q L L I V V A W L V V

SEQ. ID. NO. 39 S L I S V Q L L G V F V W F V V D P P H I I I D Y
 SEQ. ID. NO. 35 E A P G T G K E T A P E R R E V V T L R C N H R D
 SEQ. ID. NO. 31 R I A R I F G G A R E G A Q R P R F I S P A S Q V
 SEQ. ID. NO. 27 E A P G T G K E T A P E R R E V V T L R C N H R D

SEQ. ID. NO. 39 G E Q R T L D P E K A R G V L K C D I S D L S L I
 SEQ. ID. NO. 35 A S M L G S L A Y N V L L I A L C T L Y A F K T R
 SEQ. ID. NO. 31 A I C L A L I S G Q L L I V V A W L V V E A P G T
 SEQ. ID. NO. 27 A S M L G S L A Y N V L L I A L C T L Y A F N T R

SEQ. ID. NO. 39 C S L G Y S I L L M V T C T V Y A I K T R G V P E
 SEQ. ID. NO. 35 K C P E N F N E A K F I G F T M Y T T C I I W L A
 SEQ. ID. NO. 31 G K E T A P E R R E V V T L R C N H R D A S M L G
 SEQ. ID. NO. 27 K C P E N F N E A K F I G F T M Y T T C I I W L A

SEQ. ID. NO. 39 T F N E A K P I G F T M Y T T C I I W L A F I P I
 SEQ. ID. NO. 35 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
 SEQ. ID. NO. 31 S L A Y N V L L I A L C T L Y A F N T R K C P E N
 SEQ. ID. NO. 27 L L P I F Y V T S S D Y R V Q T T T M C V S V S L

FIG. 10d.

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SEQ. ID. NO. 39 F F G T A Q S A E K M Y I Q T T T L T V S M S L S
SEQ. ID. NO. 35 S G S V V L G C L F A P K L H I I L F Q P Q K N T
SEQ. ID. NO. 31 F N E A K F I G F T M Y T T C I I W L A L L P I F
SEQ. ID. NO. 27 S G S V V L G C L F A P K L H I I L F Q P Q K N

SEQ. ID. NO. 39 A S V S L G M L Y M P K V Y I I I F H P E Q N T I
SEQ. ID. NO. 35 I E E V R C S T A A H A F K V A A R A T L R R S N
SEQ. ID. NO. 31 Y V T S S D Y R V Q T T T M C V S V S L S G S V V
SEQ. ID. NO. 27

SEQ. ID. NO. 39 E E V R C S T A A H A F K V A A R A T L R R S N V
SEQ. ID. NO. 35 V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 31 L G C L F A P K L H I I L F Q P Q K N V V S H R A
SEQ. ID. NO. 27

SEQ. ID. NO. 39 S R K R S S S L G G S T G S T P S S S I S S K S N
SEQ. ID. NO. 35 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
SEQ. ID. NO. 31 P T S R F G S A A A R A S S S L G Q G S G S Q F V
SEQ. ID. NO. 27

SEQ. ID. NO. 39 S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
SEQ. ID. NO. 35 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
SEQ. ID. NO. 31 P T V C N G R E V V D S T T S S L
SEQ. ID. NO. 27

SEQ. ID. NO. 39 Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
SEQ. ID. NO. 35 G S G T V T F S L S F D E P Q K N A M A H G N S T
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 S G T V T F S L S F D E P Q K N A M A H G N S T H
SEQ. ID. NO. 35 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
SEQ. ID. NO. 35 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
SEQ. ID. NO. 31
SEQ. ID. NO. 27

FIG. 10e.

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SEQ. ID. NO. 39 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
SEQ. ID. NO. 35 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 E D P E E L S P A L V V S S S Q S F V I S G G G S
SEQ. ID. NO. 35 S T V T E N V V N S
SEQ. ID. NO. 31
SEQ. ID. NO. 27

SEQ. ID. NO. 39 T V T E N V V N S
SEQ. ID. NO. 35
SEQ. ID. NO. 31
SEQ. ID. NO. 27

FIG. 10f.

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ClustalW Formatted Alignments

SEQ. ID. NO. 40 A T G G T A T G C G A G G G A A A G C G A T C A G
SEQ. ID. NO. 46 A T G G G A T C G C T G C T T G C G C T C C C G G
SEQ. ID. NO. 36 A T G G G A T C G C T G C T T G C G C T C C C G G
SEQ. ID. NO. 32 A T G G C A T T T T A T A G C T G C T G C T G G G

SEQ. ID. NO. 40 C C T C T T G C C C T T G T T T C T T C C T C T T
SEQ. ID. NO. 46 C A C T G C T G C T G C T G T G G G G T G C T G T
SEQ. ID. NO. 36 C A C T G C T G C T G C T G T G G G G T G C T G T
SEQ. ID. NO. 32 T C C T C T T G G C A C T C A C C T G G C A C A C

SEQ. ID. NO. 40 G A C C G C C A A G T T C T A C T G G A T C C T C
SEQ. ID. NO. 46 G G C T G A G G G C C C A G C C A A G A A G G T G
SEQ. ID. NO. 36 G G C T G A G G G C C C A G C C A A G A A G G T G
SEQ. ID. NO. 32 C T C T G C C T A C G G G C C A G A C C A G C G A

SEQ. ID. NO. 40 A C A A T G A T G C A A A G A A C T C A C A G C C
SEQ. ID. NO. 46 C T G A C C C T G G A G G G A G A C T T G G T G C
SEQ. ID. NO. 36 C T G A C C C T G G A G G G A G A C T T G G T G C
SEQ. ID. NO. 32 G C C C A A A A G A A G G G G G A C A T T A T C C

SEQ. ID. NO. 40 A G G A G T A T G C C C A T T C C A T A C G G G T
SEQ. ID. NO. 46 T G G G T G G G C T G T T C C C A G T G C A C C A
SEQ. ID. NO. 36 T G G G T G G G C T G T T C C C A G T G C A C C A
SEQ. ID. NO. 32 T T G G G G G G C T C T T T C C T A T T C A T T T

SEQ. ID. NO. 40 G G A T G G G G A C A T T A T T T T G G G G G G T
SEQ. ID. NO. 46 G A A G G G C G G C C C A G C A G A G G A C T G T
SEQ. ID. NO. 36 G A A G G G C G G C C C A G C A G A G G A C T G T
SEQ. ID. NO. 32 T G G A G T A G C A G C T A A A G A T C A A G A T

SEQ. ID. NO. 40 C T C T T C C C T G T C C A C G C A A A G G G A G
SEQ. ID. NO. 46 G G T C C T G T C A A T G A G C A C C G T G G C A
SEQ. ID. NO. 36 G G T C C T G T C A A T G A G C A C C G T G G C A
SEQ. ID. NO. 32 C T C A A A T C A A G G C C G G A G T C T G T G G

SEQ. ID. NO. 40 A G A G A G G G G T G C C T T G T G G G G A G C T
SEQ. ID. NO. 46 T C C A G C G C C T G G A G G C C A T G C T T T T
SEQ. ID. NO. 36 T C C A G C G C C T G G A G G C C A T G C T T T T
SEQ. ID. NO. 32 A A T G T A T C A G G T A T A A T T T C C G T G G

FIG. 11a.

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SEQ. ID. NO. 40 G A A G A A G G A A A A G G G G A T T C A C A G A
SEQ. ID. NO. 46 T G C A C T G G A C C G C A T C A A C C G T G A C
SEQ. ID. NO. 36 T G C A C T G G A C C G C A T C A A C C G T G A C
SEQ. ID. NO. 32 G T T T C G C T G G T T A C A G G C T A T G A T A

SEQ. ID. NO. 40 C T G G A G G C C A T G C T T T A T G C A A T T G
SEQ. ID. NO. 46 C C G C A C C T G C T G C C T G G C G T G C G C C
SEQ. ID. NO. 36 C C G C A C C T G C T G C C T G G C G T G C G C C
SEQ. ID. NO. 32 T T T G C C A T A G A G G A G A T A A A C A G C A

SEQ. ID. NO. 40 A C C A G A T T A A C A A G G A C C C T G A T C T
SEQ. ID. NO. 46 T G G G T G C A C A C A T C C T C G A C A G T T G
SEQ. ID. NO. 36 T G G G T G C A C A C A T C C T C G A C A G T T G
SEQ. ID. NO. 32 G C C C A G C C C T T C T T C C C A A C T T G A C

SEQ. ID. NO. 40 C C T T T C C A A C A T C A C T C T G G G T G T C
SEQ. ID. NO. 46 C T C C A A G G A C A C A C A T G C G C T G G A G
SEQ. ID. NO. 36 C T C C A A G G A C A C A C A T G C G C T G G A G
SEQ. ID. NO. 32 G C T G G G A T A C A G G A T A T T T G A C A C T

SEQ. ID. NO. 40 C G C A T C C T C G A C A C G T G C T C T A G G G
SEQ. ID. NO. 46 C A G G C A C T G G A C T T T G T G C G T G C C T
SEQ. ID. NO. 36 C A G G C A C T G G A C T T T G T G C G T G C C T
SEQ. ID. NO. 32 T G C A A C A C C G T T T C T A A G G C C T T G G

SEQ. ID. NO. 40 A C A C C T A T G C T T T G G A G C A G T C T C T
SEQ. ID. NO. 46 C A C T C A G C C G T G G T G C T G A T G G C T C
SEQ. ID. NO. 36 C A C T C A G C C G T G G T G C T G A T G G C T C
SEQ. ID. NO. 32 A A G C C A C C C T G A G T T T T G T T G C T C A

SEQ. ID. NO. 40 A A C A T T C G T G C A G G C A T T A A T A G A G
SEQ. ID. NO. 46 A C G C C A C A T C T G C C C C G A C G G C T C T
SEQ. ID. NO. 36 A C G C C A C A T C T G C C C C G A C G G C T C T
SEQ. ID. NO. 32 A A A C A A A A T T G A T T C T T T G A A C C T T

SEQ. ID. NO. 40 A A A G A T G C T T C G G A T G T G A A G T G T G
SEQ. ID. NO. 46 T A T G C G A C C C A T G G T G A T G C T C C C A
SEQ. ID. NO. 36 T A T G C G A C C C A T G G T G A T G C T C C C A
SEQ. ID. NO. 32 G A T G A G T T C T G C A A C T G C T C A G A G C

FIG. 11b.

66/124

SEQ. ID. NO. 40 C T A A T G G A G A T C C A C C C A T T T T C A C
SEQ. ID. NO. 46 C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 36 C T G C C A T C A C T G G T G T T A T T G G C G G
SEQ. ID. NO. 32 A C A T T C C C T C T A C G A T T G C T G T G G T

SEQ. ID. NO. 40 C A A G C C C G A C A A G A T T T C T G G C G T C
SEQ. ID. NO. 46 T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 36 T T C C T A C A G T G A T G T C T C C A T C C A G
SEQ. ID. NO. 32 G G G A G C A A C T G G C T C A G G C G T C T C C

SEQ. ID. NO. 40 A T A G G T G C T G C A G C A A G C T C C G T G T
SEQ. ID. NO. 46 G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 36 G T G G C C A A C C T C T T G A G G C T A T T T C
SEQ. ID. NO. 32 A C G G C A G T G G C A A A T C T G C T G G G G C

SEQ. ID. NO. 40 C C A T C A T G G T T G C T A A C A T T T T A A G
SEQ. ID. NO. 46 A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 36 A G A T C C C A C A G A T T A G C T A C G C C T C
SEQ. ID. NO. 32 T C T T C T A C A T T C C C C A G G T C A G T T A

SEQ. ID. NO. 40 A C T T T T T A A G A T A C C T C A A A T C A G C
SEQ. ID. NO. 46 T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 36 T A C C A G T G C C A A G C T G A G T G A C A A G
SEQ. ID. NO. 32 T G C C T C C T C C A G C A G A C T C C T C A G C

SEQ. ID. NO. 40 T A T G C A T C C A C A G C C C C A G A G C T A A
SEQ. ID. NO. 46 T C C C G C T A T G A C T A C T T T T G C C C G C A
SEQ. ID. NO. 36 T C C C G C T A T G A C T A C T T T T G C C C G C A
SEQ. ID. NO. 32 A A C A A G A A T C A A T T C A A G T C T T T C C

SEQ. ID. NO. 40 G T G A T A A C A C C A G G T A T G A C T T T T T
SEQ. ID. NO. 46 C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 36 C A G T G C C T C C T G A C T T C T T C C A A G C
SEQ. ID. NO. 32 T C C G A A C C A T C C C C A A T G A T G A G C A

SEQ. ID. NO. 40 C T C T C G A G T G G T T C C G C C T G A C T C C
SEQ. ID. NO. 46 C A A G G C C A T G G C T G A G A T T C T C C G C
SEQ. ID. NO. 36 C A A G G C C A T G G C T G A G A T T C T C C G C
SEQ. ID. NO. 32 C C A G G C C A C T G C C A T G G C A G A C A T C

FIG. 11c.

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SEQ. ID. NO. 40 T A C C A A G C C C A A G C C A T G G T G G A C A
SEQ. ID. NO. 46 T T C T T C A A C T G G A C C T A T G T G T C C A
SEQ. ID. NO. 36 T T C T T C A A C T G G A C C T A T G T G T C C A
SEQ. ID. NO. 32 A T C G A G T A T T T C C G C T G G A A C T G G G

SEQ. ID. NO. 40 T C G T G A C A G C A C T G G G A T G G A A T T A
SEQ. ID. NO. 46 C T G T G G C G T C T G A G G G C G A C T A T G G
SEQ. ID. NO. 36 C T G T G G C G T C T G A G G G C G A C T A T G G
SEQ. ID. NO. 32 T G G G C A C A A T T G C A G C T G A T G A C G A

SEQ. ID. NO. 40 T G T T T C G A C A C T G G C T T C T G A G G G G
SEQ. ID. NO. 46 C G A G A C A G G C A T T G A G G C C T T T G A G
SEQ. ID. NO. 36 C G A G A C A G G C A T T G A G G C C T T T G A G
SEQ. ID. NO. 32 C T A T G G G C G G C C G G G G A T T G A G A A A

SEQ. ID. NO. 40 A A C T A T G G T G A G A G C G G T G T G G A G G
SEQ. ID. NO. 46 C T A G A G G C T C G T G C C C G C A A C A T C T
SEQ. ID. NO. 36 C T A G A G G C T C G T G C C C G C A A C A T C T
SEQ. ID. NO. 32 T T C C G A G A G G A A G C T G A G G A A A G G G

SEQ. ID. NO. 40 C C T T C A C C C A G A T C T C G A G G G A G A T
SEQ. ID. NO. 46 G T G T G G C C A C C T C G G A G A A A G T G G G
SEQ. ID. NO. 36 G T G T G G C C A C C T C G G A G A A A G T G G G
SEQ. ID. NO. 32 A T A T C T G C A T C G A C T T C A G T G A A C T

SEQ. ID. NO. 40 T G G T G G T G T T T G C A T T G C T C A G T C A
SEQ. ID. NO. 46 C C G T G C C A T G A G C C G C G C G G C C T T T
SEQ. ID. NO. 36 C C G T G C C A T G A G C C G C G C G G C C T T T
SEQ. ID. NO. 32 C A T C T C C C A G T A C T C T G A T G A G G A A

SEQ. ID. NO. 40 C A G A A A A T C C C A C G T G A A C C A A G A C
SEQ. ID. NO. 46 G A G G G T G T G G T G C G A G C C C T G C T G C
SEQ. ID. NO. 36 G A G G G T G T G G T G C G A G C C C T G C T G C
SEQ. ID. NO. 32 G A G A T C C A G C A T G T G G T A G A G G T G A

SEQ. ID. NO. 40 C T G G A G A A T T T G A A A A A T T A T C A A
SEQ. ID. NO. 46 A G A A G C C C A G T G C C C G C G T G G C T G T
SEQ. ID. NO. 36 A G A A G C C C A G T G C C C G C G T G G C T G T
SEQ. ID. NO. 32 T T C A A A A T T C C A C G G C C A A A G T C A T

FIG. 11d.

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SEQ. ID. NO. 40 A C G C C T G C T A G A A A C A C C T A A T G C T
SEQ. ID. NO. 46 C C T G T T C A C C C G T T C T G A G G A T G C C
SEQ. ID. NO. 36 C C T G T T C A C C C G T T C T G A G G A T G C C
SEQ. ID. NO. 32 C G T G G T T T T C T C C A G T G G C C C A G A T

SEQ. ID. NO. 40 C G A G C A G T G A T T A T G T T T G C C A A T G
SEQ. ID. NO. 46 C G G G A G C T G C T T G C T G C C A G C C A G C
SEQ. ID. NO. 36 C G G G A G C T G C T T G C T G C C A G C C A G C
SEQ. ID. NO. 32 C T T G A G C C C C T C A T C A A G G A G A T T G

SEQ. ID. NO. 40 A G G A T G A C A T C A G G A G G A T A T T G G A
SEQ. ID. NO. 46 G C C T C A A T G C C A G C T T C A C C T G G G T
SEQ. ID. NO. 36 G C C T C A A T G C C A G C T T C A C C T G G G T
SEQ. ID. NO. 32 T C C G G C G C A A T A T C A C G G G C A A G A T

SEQ. ID. NO. 40 A G C A G C A A A A A A A C T A A A C C A A A G T
SEQ. ID. NO. 46 G G C C A G T G A T G G T T G G G G G G C C C T G
SEQ. ID. NO. 36 G G C C A G T G A T G G T T G G G G G G C C C T G
SEQ. ID. NO. 32 C T G G C T G G C C A G C G A G G C C T G G G C C

SEQ. ID. NO. 40 G G G C A T T T T C T C T G G A T T G G C T C A G
SEQ. ID. NO. 46 G A G A G T G T G G T G G C A G G C A G T G A G G
SEQ. ID. NO. 36 G A G A G T G T G G T G G C A G G C A G T G A G G
SEQ. ID. NO. 32 A G C T C C T C C C T G A T C G C C A T G C C T C

SEQ. ID. NO. 40 A T A G T T G G G G A T C C A A A A T A G C A C C
SEQ. ID. NO. 46 G G G C T G C T G A G G G T G C T A T C A C C A T
SEQ. ID. NO. 36 G G G C T G C T G A G G G T G C T A T C A C C A T
SEQ. ID. NO. 32 A G T A C T T C C A C G T G G T T G G C G G C A C

SEQ. ID. NO. 40 T G T C T A T C A G C A A G A G G A G A T T G C A
SEQ. ID. NO. 46 C G A G C T G G C C T C C T A C C C C A T C A G T
SEQ. ID. NO. 36 C G A G C T G G C C T C C T A C C C C A T C A G T
SEQ. ID. NO. 32 C A T T G G A T T C G C T C T G A A G G C T G G G

SEQ. ID. NO. 40 G A A G G G G C T G T G A C A A T T T T G C C C A
SEQ. ID. NO. 46 G A C T T T G C C T C C T A C T T C C A G A G C C
SEQ. ID. NO. 36 G A C T T T G C C T C C T A C T T C C A G A G C C
SEQ. ID. NO. 32 C A G A T C C C A G G C T T C C G G G A A T T C C

FIG. 11e.

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SEQ. ID. NO. 40 A A C G A G C A T C A A T T G A T G G A T T T G A
SEQ. ID. NO. 46 T G G A C C C T T G G A A C A A C A G C C G G A A
SEQ. ID. NO. 36 T G G A C C C T T G G A A C A A C A G C C G G A A
SEQ. ID. NO. 32 T G A A G A A G G T C C A T C C C A G G A A G T C

SEQ. ID. NO. 40 T C G A T A C T T T A G A A G C C G A A C T C T T
SEQ. ID. NO. 46 C C C C T G G T T C C G T G A A T T C T G G G A G
SEQ. ID. NO. 36 C C C C T G G T T C C G T G A A T T C T G G G A G
SEQ. ID. NO. 32 T G T C C A C A A T G G T T T T G C C A A G G A G

SEQ. ID. NO. 40 G C C A A T A A T C G A A G A A A T G T G T G G T
SEQ. ID. NO. 46 C A G A G G T T C C G C T G C A G C T T C C G G C
SEQ. ID. NO. 36 C A G A G G T T C C G C T G C A G C T T C C G G C
SEQ. ID. NO. 32 T T T T G G G A A G A A A C A T T T A A C T G C C

SEQ. ID. NO. 40 T T G C A G A A T T C T G G G A G G A G A A T T T
SEQ. ID. NO. 46 A G C G A G A C T G C G C A G C C C A C T C T C T
SEQ. ID. NO. 36 A G C G A G A C T G C G C A G C C C A C T C T C T
SEQ. ID. NO. 32 A C C T C C A A G A A G G T G C A A A A G G A C C

SEQ. ID. NO. 40 T G G C T G C A A G T T A G G A T C A C A T G G G
SEQ. ID. NO. 46 C C G G G C T G T G C C C T T T G A G C A G G A G
SEQ. ID. NO. 36 C C G G G C T G T G C C C T T T G A G C A G G A G
SEQ. ID. NO. 32 T T T A C C T G T G G A C A C C T T T C T G A G A

SEQ. ID. NO. 40 A A A A G G A A C A G T C A T A T A A A G A A A T
SEQ. ID. NO. 46 T C C A A G A T C A T G T T T G T G G T C A A T G
SEQ. ID. NO. 36 T C C A A G A T C A T G T T T G T G G T C A A T G
SEQ. ID. NO. 32 G G T C A C G A A G A A A G T G G C G A C A G G T

SEQ. ID. NO. 40 G C A C A G G G C T G G A G C G A A T T G C T C G
SEQ. ID. NO. 46 C A G T G T A C G C C A T G G C C C A T G C G C T
SEQ. ID. NO. 36 C A G T G T A C G C C A T G G C C C A T G C G C T
SEQ. ID. NO. 32 T T A G C A A C A G C T C G A C A G C C T T C C G

SEQ. ID. NO. 40 G G A T T C A T C T T A T G A A C A G G A A G G A
SEQ. ID. NO. 46 C C A C A A C A T G C A C C G T G C C C T C T G C
SEQ. ID. NO. 36 C C A C A A C A T G C A C C G T G C C C T C T G C
SEQ. ID. NO. 32 A C C C C T C T G T A C A G G G G A T G A G A A C

FIG. 11f.

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SEQ. ID. NO. 40 A A G G T C C A A T T T G T A A T T G A T G C T G
SEQ. ID. NO. 46 C C C A A C A C C A C C C G G C T C T G T G A C G
SEQ. ID. NO. 36 C C C A A C A C C A C C C G G C T C T G T G A C G
SEQ. ID. NO. 32 A T C A G C A G T G T C G A G A C C C C T T A C A

SEQ. ID. NO. 40 T A T A T T C C A T G G C T T A C G C C C T G C A
SEQ. ID. NO. 46 C G A T G C G G C C A G T T A A C G G G C G C C G
SEQ. ID. NO. 36 C G A T G C G G C C A G T T A A C G G G C G C C G
SEQ. ID. NO. 32 T A G A T T A C A C G C A T T T A C G G A T A T C

SEQ. ID. NO. 40 C A A T A T G C A C A A A G A T C T C T G C C C T
SEQ. ID. NO. 46 C C T C T A C A A G G A C T T T G T G C T C A A C
SEQ. ID. NO. 36 C C T C T A C A A G G A C T T T G T G C T C A A C
SEQ. ID. NO. 32 C T A C A A T G T G T A C T T A G C A G T C T A C

SEQ. ID. NO. 40 G G A T A C A T T G G C C T T T G T C C A C G A A
SEQ. ID. NO. 46 G T C A A G T T T G A T G C C C C C T T T C G C C
SEQ. ID. NO. 36 G T C A A G T T T G A T G C C C C C T T T C G C C
SEQ. ID. NO. 32 T C C A T T G C C C A C G C C T T G C A A G A T A

SEQ. ID. NO. 40 T G A G T A C C A T T G A T G G G A A A G A G C T
SEQ. ID. NO. 46 C A G C T G A C A C C C A C A A T G A G G T C C G
SEQ. ID. NO. 36 C A G C T G A C A C C C A C A A T G A G G T C C G
SEQ. ID. NO. 32 T A T A T A C C T G C T T A C C T G G G A G A G G

SEQ. ID. NO. 40 A C T T G G T T A T A T T C G G G C T G T A A A T
SEQ. ID. NO. 46 C T T T G A C C G C T T T G G T G A T G G T A T T
SEQ. ID. NO. 36 C T T T G A C C G C T T T G G T G A T G G T A T T
SEQ. ID. NO. 32 G C T C T T C A C C A A T G G C T C C T G T G C A

SEQ. ID. NO. 40 T T T A A T G G C A G T G C T G G C A C T C C T G
SEQ. ID. NO. 46 G G C C G C T A C A A C A T C T T C A C C T A T C
SEQ. ID. NO. 36 G G C C G C T A C A A C A T C T T C A C C T A T C
SEQ. ID. NO. 32 G A C A T C A A G A A A G T T G A G G C G T G G C

SEQ. ID. NO. 40 T C A C T T T T A A T G A A A A C G G A G A T G C
SEQ. ID. NO. 46 T G C G T G C A G G C A G T G G G C G C T A T C G
SEQ. ID. NO. 36 T G C G T G C A G G C A G T G G G C G C T A T C G
SEQ. ID. NO. 32 A G G T C C T G A A G C A C C T A C G G C A T C T

FIG. 11a.

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SEQ. ID. NO. 40 T C C T G G A C G T T A T G A T A T C T T C C A G
SEQ. ID. NO. 46 C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 36 C T A C C A G A A G G T G G G C T A C T G G G C A
SEQ. ID. NO. 32 A A A C T T T A C A A A C A A T A T G G G G G A G

SEQ. ID. NO. 40 T A T C A A A T A A C C A A C A A A A G C A C A G
SEQ. ID. NO. 46 G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 36 G A A G G C T T G A C T C T G G A C A C C A G C C
SEQ. ID. NO. 32 C A G G T G A C C T T T G A T G A G T G T G G T G

SEQ. ID. NO. 40 A G T A C A A A G T C A T C G G C C A C T G G A C
SEQ. ID. NO. 46 T C A T C C C A T G G G C C T C A C C C T C A G C
SEQ. ID. NO. 36 T C A T C C C A T G G G C C T C A C C C T C A G C
SEQ. ID. NO. 32 A C C T G G T G G G G A A C T A T T C C A T C A T

SEQ. ID. NO. 40 C A A T C A G C T T C A T C T A A A A G T G G A A
SEQ. ID. NO. 46 C G G C C C C C T G C C C G C C T C T C G C T G C
SEQ. ID. NO. 36 C G G C C C C C T G C C C G C C T C T C G C T G C
SEQ. ID. NO. 32 C A A C T G G C A C C T C T C C C C A G A G G A T

SEQ. ID. NO. 40 G A C A T G C A G T G G G C T C A T A G A G A A C
SEQ. ID. NO. 46 A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 36 A G T G A G C C C T G C C T C C A G A A T G A G G
SEQ. ID. NO. 32 G G C T C C A T C G T G T T T A A G G A A G T C G

SEQ. ID. NO. 40 A T A C T C A C C C G G C G T C T G T C T G C A G
SEQ. ID. NO. 46 T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 36 T G A A G A G T G T G C A G C C G G G C G A A G T
SEQ. ID. NO. 32 G G T A T T A C A A C G T C T A T G C C A A G A A

SEQ. ID. NO. 40 C C T G C C G T G T A A G C C A G G G G A G A G G
SEQ. ID. NO. 46 C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 36 C T G C T G C T G G C T C T G C A T T C C G T G C
SEQ. ID. NO. 32 G G G A G A A A G A C T C T T C A T C A A C G A G

SEQ. ID. NO. 40 A A G A A A A C G G T G A A A G G G G T C C C T T
SEQ. ID. NO. 46 C A G C C C T A T G A G T A C C G A T T G G A C G
SEQ. ID. NO. 36 C A G C C C T A T G A G T A C C G A T T G G A C G
SEQ. ID. NO. 32 G A G A A A A T C C T G T G G A G T G G G T T C T

FIG. 11h.

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SEQ. ID. NO. 40 G C T G C T G G C A C T G T G A A C G C T G T G A
SEQ. ID. NO. 46 A A T T C A C T T G C G C T G A T T G T G G C C T
SEQ. ID. NO. 36 A A T T C A C T T G C G C T G A T T G T G G C C T
SEQ. ID. NO. 32 C C A G G G A G G T G C C C T T C T C C A A C T G

SEQ. ID. NO. 40 A G G T T A C A A C T A C C A G G T G G A T G A G
SEQ. ID. NO. 46 G G G C T A C T G G C C C A A T G C C A G C C T G
SEQ. ID. NO. 36 G G G C T A C T G G C C C A A T G C C A G C C T G
SEQ. ID. NO. 32 C A G C C G A G A C T G C C T G G C A G G G A C C

SEQ. ID. NO. 40 C T G T C C T G T G A A C T T T G C C C T C T G G
SEQ. ID. NO. 46 A C T G G C T G C T T C G A A C T G C C C C A G G
SEQ. ID. NO. 36 A C T G G C T G C T T C G A A C T G C C C C A G G
SEQ. ID. NO. 32 A G G A A A G G G A T C A T T G A G G G G G A G C

SEQ. ID. NO. 40 A T C A G A G A C C C A A C A T G A A C C G C A C
SEQ. ID. NO. 46 A G T A C A T C C G C T G G G G C G A T G C C T G
SEQ. ID. NO. 36 A G T A C A T C C G C T G G G G C G A T G C C T G
SEQ. ID. NO. 32 C C A C C T G C T G C T T T G A G T G T G T G G A

SEQ. ID. NO. 40 A G G C T G C C A G C T T A T C C C C A T C A T C
SEQ. ID. NO. 46 G G C T G T G G G A C C T G T C A C C A T C G C C
SEQ. ID. NO. 36 G G C T G T G G G A C C T G T C A C C A T C G C C
SEQ. ID. NO. 32 G T G T C C T G A T G G G G A G T A T A G T G A T

SEQ. ID. NO. 40 A A A T T G G A G T G G C A T T C T C C C T G G G
SEQ. ID. NO. 46 T G C C T C G G T G C C C T G G C C A C C C T C T
SEQ. ID. NO. 36 T G C C T C G G T G C C C T G G C C A C C C T C T
SEQ. ID. NO. 32 G A G A C A G A T G C C A G T G C C T G T A A C A

SEQ. ID. NO. 40 C T G T G G T G C C T G T G T T T G T T G C A A T
SEQ. ID. NO. 46 T T G T G C T G G G T G T C T T T G T G C G G C A
SEQ. ID. NO. 36 T T G T G C T G G G T G T C T T T G T G C G G C A
SEQ. ID. NO. 32 A G T G C C C A G A T G A C T T C T G G T C C A A

SEQ. ID. NO. 40 A T T G G G A A T C A T C G C C A C C A C C T T T
SEQ. ID. NO. 46 C A A T G C C A C A C C A G T G G T C A A G G C C
SEQ. ID. NO. 36 C A A T G C C A C A C C A G T G G T C A A G G C C
SEQ. ID. NO. 32 T G A G A A C C A C A C C T C C T G C T T C G A A

FIG. 11i.

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SEQ. ID. NO. 40 G T G A T C G T G A C C T T T G T C C G C T A T A
SEQ. ID. NO. 46 T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 36 T C A G G T C G G G A G C T C T G C T A C A T C C
SEQ. ID. NO. 32 C T G C C C C A G G A G T A C A T C C G C T G G G

SEQ. ID. NO. 40 A T G A C A C A C C T A T C G T G A G G G C T T C
SEQ. ID. NO. 46 T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 36 T G C T G G G T G G T G T C T T C C T C T G C T A
SEQ. ID. NO. 32 G C G A T G C C T G G G C T G T G G G A C C T G T

SEQ. ID. NO. 40 A G G A C G C G A A C T T A G T T A C G T G C T C
SEQ. ID. NO. 46 C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 36 C T G C A T G A C C T T C A T C T T C A T T G C C
SEQ. ID. NO. 32 C A C C A T C G C C T G C C T C G G T G C C C T G

SEQ. ID. NO. 40 C T A A C G G G G A T T T T T C T C T G T T A T T
SEQ. ID. NO. 46 A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 36 A A G C C A T C C A C G G C A G T G T G T A C C T
SEQ. ID. NO. 32 G C C A C C C T G T T T G T G C T G G G T G T C T

SEQ. ID. NO. 40 C A A T C A C G T T T T T A A T G A T T G C A G C
SEQ. ID. NO. 46 T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 36 T A C G G C G T C T T G G T T T G G G C A C T G C
SEQ. ID. NO. 32 T T G T G C G G C A C A A T G C C A C A C C A G T

SEQ. ID. NO. 40 A C C A G A T A C A A T C A T A T G C T C C T T C
SEQ. ID. NO. 46 C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 36 C T T C T C T G T C T G C T A C T C A G C C C T G
SEQ. ID. NO. 32 G G T C A A G G C C T C A G G T C G G G A G C T C

SEQ. ID. NO. 40 C G A C G G G T C T T C C T A G G A C T T G G C A
SEQ. ID. NO. 46 C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 36 C T C A C C A A G A C C A A C C G C A T T G C A C
SEQ. ID. NO. 32 T G C T A C A T C C T G C T G G G T G G T G T C T

SEQ. ID. NO. 40 T G T G T T T C A G C T A T G C A G C C C T T C T
SEQ. ID. NO. 46 G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 36 G C A T C T T C G G T G G G G C C C G G G A G G G
SEQ. ID. NO. 32 T C C T C T G C T A C T G C A T G A C C T T C A T

FIG. 11j.

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SEQ. ID. NO. 40 G A C C A A A A C A A A C C G T A T C C A C C G A
SEQ. ID. NO. 46 T G C C C A G C G G C C A C G C T T C A T C A G T
SEQ. ID. NO. 36 T G C C C A G C G G C C A C G C T T C A T C A G T
SEQ. ID. NO. 32 C T T C A T T G C C A A G C C A T C C A C G G C A

SEQ. ID. NO. 40 A T A T T T G A G C A G G G G A A G A A A T C T G
SEQ. ID. NO. 46 C C T G C C T C A C A G G T G G C C A T C T G C C
SEQ. ID. NO. 36 C C T G C C T C A C A G G T G G C C A T C T G C C
SEQ. ID. NO. 32 G T G T G T A C C T T A C G G C G T C T T G G T T

SEQ. ID. NO. 40 T C A C A G C G C C C A A G T T C A T T A G T C C
SEQ. ID. NO. 46 T G G C A C T T A T C T C G G G C C A G C T G C T
SEQ. ID. NO. 36 T G G C A C T T A T C T C G G G C C A G C T G C T
SEQ. ID. NO. 32 T G G G C A C T G C C T T C T C T G T C T G C T A

SEQ. ID. NO. 40 A G C A T C T C A G C T G G T G A T C A C C T T C
SEQ. ID. NO. 46 C A T C G T G G T C G C C T G G C T G G T G G T G
SEQ. ID. NO. 36 C A T C G T G G T C G C C T G G C T G G T G G T G
SEQ. ID. NO. 32 C T C A G C C C T G C T C A C C A A G A C C A A C

SEQ. ID. NO. 40 A G C C T C A T C T C C G T C C A G C T C C T T G
SEQ. ID. NO. 46 G A G G C A C C G G G C A C A G G C A A G G A G A
SEQ. ID. NO. 36 G A G G C A C C G G G C A C A G G C A A G G A G A
SEQ. ID. NO. 32 C G C A T T G C A C G C A T C T T C G G T G G G G

SEQ. ID. NO. 40 G A G T G T T T G T C T G G T T T G T T G T G G A
SEQ. ID. NO. 46 C A G C C C C C G A A C G G C G G G A G G T G G T
SEQ. ID. NO. 36 C A G C C C C C G A A C G G C G G G A G G T G G T
SEQ. ID. NO. 32 C C C G G G A G G G T G C C C A G C G G C C A C G

SEQ. ID. NO. 40 T C C C C C C C A C A T C A T C A T T G A C T A T
SEQ. ID. NO. 46 G A C A C T G C G C T G C A A C C A C C G C G A T
SEQ. ID. NO. 36 G A C A C T G C G C T G C A A C C A C C G C G A T
SEQ. ID. NO. 32 C T T C A T C A G T C C T G C C T C A C A G G T G

SEQ. ID. NO. 40 G G A G A G C A G C G G A C A C T A G A T C C A G
SEQ. ID. NO. 46 G C A A G T A T G T T G G G C T C G C T G G C C T
SEQ. ID. NO. 36 G C A A G T A T G T T G G G C T C G C T G G C C T
SEQ. ID. NO. 32 G C C A T C T G C C T G G C A C T T A T C T C G G

FIG. 11k.

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SEQ. ID. NO. 40 A G A A G G C C A G G G G A G T G C T C A A G T G
SEQ. ID. NO. 46 A C A A T G T G C T C C T C A T C G C G C T C T G
SEQ. ID. NO. 36 A C A A T G T G C T C C T C A T C G C G C T C T G
SEQ. ID. NO. 32 G C C A G C T G C T C A T C G T G G T C G C C T G

SEQ. ID. NO. 40 T G A C A T T T C T G A T C T C T C A C T C A T T
SEQ. ID. NO. 46 C A C G C T T T A T G C C T T C A A G A C T C G C
SEQ. ID. NO. 36 C A C G C T T T A T G C C T T C A A G A C T C G C
SEQ. ID. NO. 32 G C T G G T G G T G G A G G C A C C G G G C A C A

SEQ. ID. NO. 40 T G T T C A C T T G G A T A C A G T A T C C T C T
SEQ. ID. NO. 46 A A G T G C C C C G A A A A C T T C A A C G A G G
SEQ. ID. NO. 36 A A G T G C C C C G A A A A C T T C A A C G A G G
SEQ. ID. NO. 32 G G C A A G G A G A C A G C C C C C G A A C G G C

SEQ. ID. NO. 40 T G A T G G T C A C T T G T A C T G T T T A T G C
SEQ. ID. NO. 46 C C A A G T T C A T T G G C T T C A C C A T G T A
SEQ. ID. NO. 36 C C A A G T T C A T T G G C T T C A C C A T G T A
SEQ. ID. NO. 32 G G G A G G T G G T G A C A C T G C G C T G C A A

SEQ. ID. NO. 40 C A T T A A A A C G A G A G G T G T C C C A G A G
SEQ. ID. NO. 46 C A C C A C C T G C A T C A T C T G G C T G G C A
SEQ. ID. NO. 36 C A C C A C C T G C A T C A T C T G G C T G G C A
SEQ. ID. NO. 32 C C A C C G C G A T G C A A G T A T G T T G G G C

SEQ. ID. NO. 40 A C T T T C A A T G A A G C C A A A C C T A T T G
SEQ. ID. NO. 46 T T C C T G C C C A T C T T C T A T G T C A C C T
SEQ. ID. NO. 36 T T C C T G C C C A T C T T C T A T G T C A C C T
SEQ. ID. NO. 32 T C G C T G G C C T A C A A T G T G C T C C T C A

SEQ. ID. NO. 40 G A T T T A C C A T G T A T A C C A C C T G C A T
SEQ. ID. NO. 46 C C A G T G A C T A C C G G G T A C A G A C C A C
SEQ. ID. NO. 36 C C A G T G A C T A C C G G G T A C A G A C C A C
SEQ. ID. NO. 32 T C G C G C T C T G C A C G C T T T A T G C C T T

SEQ. ID. NO. 40 C A T T T G G T T A G C T T T C A T C C C C A T C
SEQ. ID. NO. 46 C A C C A T G T G C G T G T C A G T C A G C C T C
SEQ. ID. NO. 36 C A C C A T G T G C G T G T C A G T C A G C C T C
SEQ. ID. NO. 32 C A A T A C T C G C A A G T G C C C C G A A A A C

FIG. 11L

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SEQ. ID. NO. 40 T T T T T T G G T A C A G C C C A G T C A G C A G
SEQ. ID. NO. 46 A G C G G C T C C G T G G T G C T T G G C T G C C
SEQ. ID. NO. 36 A G C G G C T C C G T G G T G C T T G G C T G C C
SEQ. ID. NO. 32 T T C A A C G A G G C C A A G T T C A T T G G C T

SEQ. ID. NO. 40 A A A A G A T G T A C A T C C A G A C A A C A A C
SEQ. ID. NO. 46 T C T T T G C G C C C A A G C T G C A C A T C A T
SEQ. ID. NO. 36 T C T T T G C G C C C A A G C T G C A C A T C A T
SEQ. ID. NO. 32 T C A C C A T G T A C A C C A C C T G C A T C A T

SEQ. ID. NO. 40 A C T T A C T G T C T C C A T G A G T T T A A G T
SEQ. ID. NO. 46 C C T C T T C C A G C C G C A G A A G A A C A C C
SEQ. ID. NO. 36 C C T C T T C C A G C C G C A G A A G A A C A C C
SEQ. ID. NO. 32 C T G G C T G G C A T T G T T G C C C A T C T T C

SEQ. ID. NO. 40 G C T T C A G T A T C T C T G G G C A T G C T C T
SEQ. ID. NO. 46 A T C G A G G A G G T G C G T T G C A G C A C C G
SEQ. ID. NO. 36 A T C G A G G A G G T G C G T T G C A G C A C C G
SEQ. ID. NO. 32 T A T G T C A C C T C C A G T G A C T A C C G G G

SEQ. ID. NO. 40 A T A T G C C C A A G G T T T A T A T T A T A A T
SEQ. ID. NO. 46 C A G C T C A C G C T T T C A A G G T G G C T G C
SEQ. ID. NO. 36 C A G C T C A C G C T T T C A A G G T G G C T G C
SEQ. ID. NO. 32 T A C A G A C C A C C A C C A T G T G C G T G T C

SEQ. ID. NO. 40 T T T T C A T C C A G A A C A G A A T A C C A T C
SEQ. ID. NO. 46 C C G G G C C A C G C T G C G C C G C A G C A A C
SEQ. ID. NO. 36 C C G G G C C A C G C T G C G C C G C A G C A A C
SEQ. ID. NO. 32 A G T C A G C C T C A G C G G C T C C G T G G T G

SEQ. ID. NO. 40 G A G G A G G T G C G T T G C A G C A C C G C A G
SEQ. ID. NO. 46 G T C T C C C G C A A G C G G T C C A G C A G C C
SEQ. ID. NO. 36 G T C T C C C G C A A G C G G T C C A G C A G C C
SEQ. ID. NO. 32 C T T G G C T G C C T C T T T G C G C C C A A G C

SEQ. ID. NO. 40 C T C A C G C T T T C A A G G T G G C T G C C C G
SEQ. ID. NO. 46 T T G G A G G C T C C A C G G G A T C C A C C C C
SEQ. ID. NO. 36 T T G G A G G C T C C A C G G G A T C C A C C C C
SEQ. ID. NO. 32 T G C A C A T C A T C C T C T T C C A G C C G C A

FIG. 1 Im.

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SEQ. ID. NO. 40 G G C C A C G C T G C G C C G C A G C A A C G T C
SEQ. ID. NO. 46 C T C C T C C T C C A T C A G C A G C A A G A G C
SEQ. ID. NO. 36 C T C C T C C T C C A T C A G C A G C A A G A G C
SEQ. ID. NO. 32 G A A G A A C G T G G T T A G C C A C C G G G C A

SEQ. ID. NO. 40 T C C C G C A A G C G G T C C A G C A G C C T T G
SEQ. ID. NO. 46 A A C A G C G A A G A C C C A T T C C C A C A G C
SEQ. ID. NO. 36 A A C A G C G A A G A C C C A T T C C C A C A G C
SEQ. ID. NO. 32 C C C A C C A G C C G C T T T G G C A G T G C T G

SEQ. ID. NO. 40 G A G G C T C C A C G G G A T C C A C C C C C T C
SEQ. ID. NO. 46 C C G A G A G G C A G A A G C A G C A G C A G C C
SEQ. ID. NO. 36 C C G A G A G G C A G A A G C A G C A G C A G C C
SEQ. ID. NO. 32 C T G C C A G G G C C A G C T C C A G C C T T G G

SEQ. ID. NO. 40 C T C C T C C A T C A G C A G C A A G A G C A A C
SEQ. ID. NO. 46 G C T G G C C C T A A C C C A G C A A G A G C A G
SEQ. ID. NO. 36 G C T G G C C C T A A C C C A G C A A G A G C A G
SEQ. ID. NO. 32 C C A A G G G T C T G G C T C C C A G T T T G T C

SEQ. ID. NO. 40 A G C G A A G A C C C A T T C C C A C A G C C C G
SEQ. ID. NO. 46 C A G C A G C A G C C C C T G A C C C T C C C A C
SEQ. ID. NO. 36 C A G C A G C A G C C C C T G A C C C T C C C A C
SEQ. ID. NO. 32 C C C A C T G T T T T G C A A T G G C C G T G A G G

SEQ. ID. NO. 40 A G A G G C A G A A G C A G C A G C A G C C G C T
SEQ. ID. NO. 46 A G C A G C A A C G A T C T C A G C A G C A G C C
SEQ. ID. NO. 36 A G C A G C A A C G A T C T C A G C A G C A G C C
SEQ. ID. NO. 32 T G G T G G A C T C G A C A A C G T C A T C G C T

SEQ. ID. NO. 40 G G C C C T A A C C C A G C A A G A G C A G C A G
SEQ. ID. NO. 46 C A G A T G C A A G C A G A A G G T C A T C T T T
SEQ. ID. NO. 36 C A G A T G C A A G C A G A A G G T C A T C T T T
SEQ. ID. NO. 32 T A T G A C T C T G G A G T C C A T C A T G G C G

SEQ. ID. NO. 40 C A G C A G C C C C T G A C C C T C C C A C A G C
SEQ. ID. NO. 46 G G C A G C G G C A C G G T C A C C T T C T C A C
SEQ. ID. NO. 36 G G C A G C G G C A C G G T C A C C T T C T C A C
SEQ. ID. NO. 32 T G C T G C C T G A G C G A G G A G G C C A A G G

FIG. 1In.

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SEQ. ID. NO. 40 A G C A A C G A T C T C A G C A G C A G C C C A G
SEQ. ID. NO. 46 T G A G C T T T G A T G A G C C T C A G A A G A A
SEQ. ID. NO. 36 T G A G C T T T G A T G A G C C T C A G A A G A A
SEQ. ID. NO. 32 A A G C C C G G C G G A T C A A C G A C G A G A T

SEQ. ID. NO. 40 A T G C A A G C A G A A G G T C A T C T T T G G C
SEQ. ID. NO. 46 C G C C A T G G C C C A C G G G A A T T C T A C G
SEQ. ID. NO. 36 C G C C A T G G C C C A C G G G A A T T C T A C G
SEQ. ID. NO. 32 C G A G C G G C A G C T C C G C A G G G A C A A G

SEQ. ID. NO. 40 A G C G G C A C G G T C A C C T T C T C A C T G A
SEQ. ID. NO. 46 C A C C A G A A C T C C C T G G A G G C C C A G A
SEQ. ID. NO. 36 C A C C A G A A C T C C C T G G A G G C C C A G A
SEQ. ID. NO. 32 C G G G A C G C C C G C C G G G A G C T C A A G C

SEQ. ID. NO. 40 G C T T T G A T G A G C C T C A G A A G A A C G C
SEQ. ID. NO. 46 A A A G C A G C G A T A C G C T G A C C C G A C A
SEQ. ID. NO. 36 A A A G C A G C G A T A C G C T G A C C C G A C A
SEQ. ID. NO. 32 T G C T G C T G C T C G G G A C A G G A G A G A G

SEQ. ID. NO. 40 C A T G G C C C A C G G G A A T T C T A C G C A C
SEQ. ID. NO. 46 C C A G C C A T T A C T C C C G C T G C A G T G C
SEQ. ID. NO. 36 C C A G C C A T T A C T C C C G C T G C A G T G C
SEQ. ID. NO. 32 T G G C A A G A G T A C G T T T A T C A A G C A G

SEQ. ID. NO. 40 C A G A A C T C C C T G G A G G C C C A G A A A A
SEQ. ID. NO. 46 G G G G A A A C G G A C T T A G A T C T G A C C G
SEQ. ID. NO. 36 G G G G A A A C G G A C T T A G A T C T G A C C G
SEQ. ID. NO. 32 A T G A G A A T C A T C C A T G G G T C A G G A T

SEQ. ID. NO. 40 G C A G C G A T A C G C T G A C C C G A C A C C A
SEQ. ID. NO. 46 T C C A G G A A A C A G G T C T G C A A G G A C C
SEQ. ID. NO. 36 T C C A G G A A A C A G G T C T G C A A G G A C C
SEQ. ID. NO. 32 A C T C T G A T G A A G A T A A A A G G G G C T T

SEQ. ID. NO. 40 G C C A T T A C T C C C G C T G C A G T G C G G G
SEQ. ID. NO. 46 T G T G G G T G G A G A C C A G C G G C C A G A G
SEQ. ID. NO. 36 T G T G G G T G G A G A C C A G C G G C C A G A G
SEQ. ID. NO. 32 C A C C A A G C T G G T G T A T C A G A A C A T C

FIG. 11a.

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SEQ. ID. NO. 40 G A A A C G G A C T T A G A T C T G A C C G T C C
SEQ. ID. NO. 46 G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 36 G T G G A G G A C C C T G A A G A G T T G T C C C
SEQ. ID. NO. 32 T T C A C G G C C A T G C A G G C C A T G A T C A

SEQ. ID. NO. 40 A G G A A A C A G G T C T G C A A G G A C C T G T
SEQ. ID. NO. 46 C A G C A C T T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 36 C A G C A C T T T G T A G T G T C C A G T T C A C A
SEQ. ID. NO. 32 G A G C C A T G G A C A C A C T C A A G A T C C C

SEQ. ID. NO. 40 G G G T G G A G A C C A G C G G C C A G A G G T G
SEQ. ID. NO. 46 G A G C T T T G T C A T C A G T G G T G G A G G C
SEQ. ID. NO. 36 G A G C T T T G T C A T C A G T G G T G G A C G C
SEQ. ID. NO. 32 A T A C A A G T A T G A G C A C A A T A A G G C T

SEQ. ID. NO. 40 G A G G A C C C T G A A G A G T T G T C C C C A G
SEQ. ID. NO. 46 A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 36 A G C A C T G T T A C A G A A A A C G T A G T G A
SEQ. ID. NO. 32 C A T G C A C A A T T A G T T C G A G A A G T T G

SEQ. ID. NO. 40 C A C T T G T A G T G T C C A G T T C A C A G A G
SEQ. ID. NO. 46 A T T C A G C G G C C G C C A T G A C T C T G G A
SEQ. ID. NO. 36 A T T C A A T G A C T C T G G A G T C C A T C A T
SEQ. ID. NO. 32 A T G T G G A G A A G G T G T C T G C T T T T G A

SEQ. ID. NO. 40 C T T T G T C A T C A G T G G T G G A G G C A G C
SEQ. ID. NO. 46 G T C C A T C A T G G C G T G C T G C C T G A G C
SEQ. ID. NO. 36 G G C G T G C T G C C T G A G C G A G G A G G C C
SEQ. ID. NO. 32 G A A T C C A T A T G T A G A T G C A A T A A A G

SEQ. ID. NO. 40 A C T G T T A C A G A A A A C G T A G T G A A T T
SEQ. ID. NO. 46 G A G G A G G C C A A G G A A G C C C G G C G G A
SEQ. ID. NO. 36 A A G G A A G C C C G G C G G A T C A A C G A C G
SEQ. ID. NO. 32 A G T T T A T G G A A T G A T C C T G G A A T C C

SEQ. ID. NO. 40 C A - - - - -
SEQ. ID. NO. 46 T C A A C G A C G A G A T C G A G C G G C A G C T
SEQ. ID. NO. 36 A G A T C G A G C G G C A G C T C C G C A G G G A
SEQ. ID. NO. 32 A G G A A T G C T A T G A T A G A C G A C G A G A

FIG. 11p.

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SEQ. ID. NO. 40 - - - - -
SEQ. ID. NO. 46 C C G C A G G G A C A A G C G G G A C G C C C G C
SEQ. ID. NO. 36 C A A G C G G G A C G C C C G C C G G G A G C T C
SEQ. ID. NO. 32 A T A T C A A T T A T C T G A C T C T A C C A A A

SEQ. ID. NO. 40 - - - - - A T G A C T C T G G
SEQ. ID. NO. 46 C G G G A G C T C A A G C T G C T G C T G C T C G
SEQ. ID. NO. 36 A A G C T G C T G C T G C T C G G G A C A G G A G
SEQ. ID. NO. 32 T A C T A T C T T A A T G A C T T G G A C C G C G

SEQ. ID. NO. 40 A G T C C A T C A T G G C G T G C T G C C T G A G
SEQ. ID. NO. 46 G G A C A G G A G A G A G T G G C A A G A G T A C
SEQ. ID. NO. 36 A G A G T G G C A A G A G T A C G T T T A T C A A
SEQ. ID. NO. 32 T A G C T G A C C C T G C C T A C C T G C C T A C

SEQ. ID. NO. 40 C G A G G A G G C C A A G G A A G C C C G G C G G
SEQ. ID. NO. 46 G T T T A T C A A G C A G A T G A G A A T C A T C
SEQ. ID. NO. 36 G C A G A T G A G A A T C A T C C A T G G G T C A
SEQ. ID. NO. 32 G C A A C A A G A T G T G C T T A G A G T T C G A

SEQ. ID. NO. 40 A T C A A C G A C G A G A T C G A G C G G C A G C
SEQ. ID. NO. 46 C A T G G G T C A G G A T A C T C T G A T G A A G
SEQ. ID. NO. 36 G G A T A C T C T G A T G A A G A T A A A A G G G
SEQ. ID. NO. 32 G T C C C C A C C A C A G G G A T C A T C G A A T

SEQ. ID. NO. 40 T C C G C A G G G A C A A G C G G G A C G C C C G
SEQ. ID. NO. 46 A T A A A A G G G G C T T C A C C A A G C T G G T
SEQ. ID. NO. 36 G C T T C A C C A A G C T G G T G T A T C A G A A
SEQ. ID. NO. 32 A C C C C T T T G A C T T A C A A A G T G T C A T

SEQ. ID. NO. 40 C C G G G A G C T C A A G C T G C T G C T G C T C
SEQ. ID. NO. 46 G T A T C A G A A C A T C T T C A C G G C C A T G
SEQ. ID. NO. 36 C A T C T T C A C G G C C A T G C A G G C C A T G
SEQ. ID. NO. 32 T T T C A G A A T G G T C G A T G T A G G G G G C

SEQ. ID. NO. 40 G G G A C A G G A G A G A G T G G C A A G A G T A
SEQ. ID. NO. 46 C A G G C C A T G A T C A G A G C C A T G G A C A
SEQ. ID. NO. 36 A T C A G A G C C A T G G A C A C A C T C A A G A
SEQ. ID. NO. 32 C A A A G G T C A G A G A G A A G A A A A T G G A

FIG. 11q.

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SEQ. ID. NO. 40 C G T T T A T C A A G C A G A T G A G A A T C A T
SEQ. ID. NO. 46 C A C T C A A G A T C C C A T A C A A G T A T G A
SEQ. ID. NO. 36 T C C C A T A C A A G T A T G A G C A C A A T A A
SEQ. ID. NO. 32 T A C A C T G C T T T G A A A A T G T C A C C T C

SEQ. ID. NO. 40 C C A T G G G T C A G G A T A C T C T G A T G A A
SEQ. ID. NO. 46 G C A C A A T A A G G C T C A T G C A C A A T T A
SEQ. ID. NO. 36 G G C T C A T G C A C A A T T A G T T C G A G A A
SEQ. ID. NO. 32 T A T C A T G T T T C T A G T A G C G C T T A G T

SEQ. ID. NO. 40 G A T A A A A G G G G C T T C A C C A A G C T G G
SEQ. ID. NO. 46 G T T C G A G A A G T T G A T G T G G A G A A G G
SEQ. ID. NO. 36 G T T G A T G T G G A G A A G G T G T C T G C T T
SEQ. ID. NO. 32 G A A T A T G A T C A A G T T C T C G T G G A G T

SEQ. ID. NO. 40 T G T A T C A G A A C A T C T T C A C G G C C A T
SEQ. ID. NO. 46 T G T C T G C T T T T G A G A A T C C A T A T G T
SEQ. ID. NO. 36 T T G A G A A T C C A T A T G T A G A T G C A A T
SEQ. ID. NO. 32 C A G A C A A T G A G A A C C G A A T G G A G G A

SEQ. ID. NO. 40 G C A G G C C A T G A T C A G A G C C A T G G A C
SEQ. ID. NO. 46 A G A T G C A A T A A A G A G T T T A T G G A A T
SEQ. ID. NO. 36 A A A G A G T T T A T G G A A T G A T C C T G G A
SEQ. ID. NO. 32 A A G C A A G G C T C T C T T T A G A A C A A T T

SEQ. ID. NO. 40 A C A C T C A A G A T C C C A T A C A A G T A T G
SEQ. ID. NO. 46 G A T C C T G G A A T C C A G G A A T G C T A T G
SEQ. ID. NO. 36 A T C C A G G A A T G C T A T G A T A G A C G A C
SEQ. ID. NO. 32 A T C A C A T A C C C C T G G T T C C A G A A C T

SEQ. ID. NO. 40 A G C A C A A T A A G G C T C A T G C A C A A T T
SEQ. ID. NO. 46 A T A G A C G A C G A G A A T A T C A A T T A T C
SEQ. ID. NO. 36 G A G A A T A T C A A T T A T C T G A C T C T A C
SEQ. ID. NO. 32 C C T C G G T T A T T C T G T T C T T A A A C A A

SEQ. ID. NO. 40 A G T T C G A G A A G T T G A T G T G G A G A A G
SEQ. ID. NO. 46 T G A C T C T A C C A A A T A C T A T C T T A A T
SEQ. ID. NO. 36 C A A A T A C T A T C T T A A T G A C T T G G A C
SEQ. ID. NO. 32 G A A A G A T C T T T C T A G A G G A G A A A A T C

FIG. 11r.

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SEQ. ID. NO. 40 G T G T C T G C T T T T G A G A A T C C A T A T G
SEQ. ID. NO. 46 G A C T T G G A C C G C G T A G C T G A C C C T G
SEQ. ID. NO. 36 C G C G T A G C T G A C C C T G C C T A C C T G C
SEQ. ID. NO. 32 A T G T A T T C C C A T C T A G T C G A C T A C T

SEQ. ID. NO. 40 T A G A T G C A A T A A A G A G T T T A T G G A A
SEQ. ID. NO. 46 C C T A C C T G C C T A C G C A A C A A G A T G T
SEQ. ID. NO. 36 C T A C G C A A C A A G A T G T G C T T A G A G T
SEQ. ID. NO. 32 T C C C A G A A T A T G A T G G A C C C C A G A G

SEQ. ID. NO. 40 T G A T C C T G G A A T C C A G G A A T G C T A T
SEQ. ID. NO. 46 G C T T A G A G T T C G A G T C C C C A C C A C A
SEQ. ID. NO. 36 T C G A G T C C C C A C C A C A G G G A T C A T C
SEQ. ID. NO. 32 A G A T G C C C A G G C A G C C C G A G A A T T C

SEQ. ID. NO. 40 G A T A G A C G A C G A G A A T A T C A A T T A T
SEQ. ID. NO. 46 G G G A T C A T C G A A T A C C C C T T T G A C T
SEQ. ID. NO. 36 G A A T A C C C C T T T G A C T T A C A A A G T G
SEQ. ID. NO. 32 A T T C T G A A G A T G T T C G T G G A C C T G A

SEQ. ID. NO. 40 C T G A C T C T A C C A A A T A C T A T C T T A A
SEQ. ID. NO. 46 T A C A A A G T G T C A T T T T C A G A A T G G T
SEQ. ID. NO. 36 T C A T T T T C A G A A T G G T C G A T G T A G G
SEQ. ID. NO. 32 A C C C A G A C A G T G A C A A A A T T A T C T A

SEQ. ID. NO. 40 T G A C T T G G A C C G C G T A G C T G A C C C T
SEQ. ID. NO. 46 C G A T G T A G G G G G C C A A A G G T C A G A G
SEQ. ID. NO. 36 G G G C C A A A G G T C A G A G A G A A G A A A A
SEQ. ID. NO. 32 C T C C C A C T T C A C G T G C G C C A C A G A C

SEQ. ID. NO. 40 G C C T A C C T G C C T A C G C A A C A A G A T G
SEQ. ID. NO. 46 A G A A G A A A A T G G A T A C A C T G C T T T G
SEQ. ID. NO. 36 T G G A T A C A C T G C T T T G A A A A T G T C A
SEQ. ID. NO. 32 A C C G A G A A T A T C C G C T T T G T C T T T G

SEQ. ID. NO. 40 T G C T T A G A G T T C G A G T C C C C A C C A C
SEQ. ID. NO. 46 A A A A T G T C A C C T C T A T C A T G T T T C T
SEQ. ID. NO. 36 C C T C T A T C A T G T T T C T A G T A G C G C T
SEQ. ID. NO. 32 C T G C C G T C A A G G A C A C C A T C C T C C A

FIG. 1/5.

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SEQ. ID. NO. 40 A G G G A T C A T C G A A T A C C C C T T T G A C
SEQ. ID. NO. 46 A G T A G C G C T T A G T G A A T A T G A T C A A
SEQ. ID. NO. 36 T A G T G A A T A T G A T C A A G T T C T C G T G
SEQ. ID. NO. 32 G T T G A A C C T G A A G G A C T G C G G T C T G

SEQ. ID. NO. 40 T T A C A A A G T G T C A T T T T C A G A A T G G
SEQ. ID. NO. 46 G T T C T C G T G G A G T C A G A C A A T G A G A
SEQ. ID. NO. 36 G A G T C A G A C A A T G A G A A C C G A A T G G
SEQ. ID. NO. 32 T T C T A A

SEQ. ID. NO. 40 T C G A T G T A G G G G G C C A A A G G T C A G A
SEQ. ID. NO. 46 A C C G A A T G G A G G A A A G C A A G G C T C T
SEQ. ID. NO. 36 A G G A A A G C A A G G C T C T C T T T A G A A C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A G A A G A A A A T G G A T A C A C T G C T T T
SEQ. ID. NO. 46 C T T T A G A A C A A T T A T C A C A T A C C C C
SEQ. ID. NO. 36 A A T T A T C A C A T A C C C C T G G T T C C A G
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A A A A T G T C A C C T C T A T C A T G T T T C
SEQ. ID. NO. 46 T G G T T C C A G A A C T C C T C G G T T A T T C
SEQ. ID. NO. 36 A A C T C C T C G G T T A T T C T G T T C T T A A
SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G T A G C G C T T A G T G A A T A T G A T C A
SEQ. ID. NO. 46 T G T T C T T A A A C A A G A A A G A T C T T C T
SEQ. ID. NO. 36 A C A A G A A A G A T C T T C T A G A G G A G A A
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G T T C T C G T G G A G T C A G A C A A T G A G
SEQ. ID. NO. 46 A G A G G A G A A A A T C A T G T A T T C C C A T
SEQ. ID. NO. 36 A A T C A T G T A T T C C C A T C T A G T C G A C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A A C C G A A T G G A G G A A A G C A A G G C T C
SEQ. ID. NO. 46 C T A G T C G A C T A C T T C C C A G A A T A T G
SEQ. ID. NO. 36 T A C T T C C C A G A A T A T G A T G G A C C C C
SEQ. ID. NO. 32

FIG. 11f.

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SEQ. ID. NO. 40 T C T T T A G A A C A A T T A T C A C A T A C C C
SEQ. ID. NO. 46 A T G G A C C C C A G A G A G A T G C C C A G G C
SEQ. ID. NO. 36 A G A G A G A T G C C C A G G C A G C C C G A G A
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C T G G T T C C A G A A C T C C T C G G T T A T T
SEQ. ID. NO. 46 A G C C C G A G A A T T C A T T C T G A A G A T G
SEQ. ID. NO. 36 A T T C A T T C T G A A G A T G T T C G T G G A C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C T G T T C T T A A A C A A G A A A G A T C T T C
SEQ. ID. NO. 46 T T C G T G G A C C T G A A C C C A G A C A G T G
SEQ. ID. NO. 36 C T G A A C C C A G A C A G T G A C A A A A T T A
SEQ. ID. NO. 32

SEQ. ID. NO. 40 T A G A G G A G A A A A T C A T G T A T T C C C A
SEQ. ID. NO. 46 A C A A A A T T A T C T A C T C C C A C T T C A C
SEQ. ID. NO. 36 T C T A C T C C C A C T T C A C G T G C G C C A C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 T C T A G T C G A C T A C T T C C C A G A A T A T
SEQ. ID. NO. 46 G T G C G C C A C A G A C A C C G A G A A T A T C
SEQ. ID. NO. 36 A G A C A C C G A G A A T A T C C G C T T T G T C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A T G G A C C C C A G A G A G A T G C C C A G G
SEQ. ID. NO. 46 C G C T T T G T C T T T G C T G C C G T C A A G G
SEQ. ID. NO. 36 T T T G C T G C C G T C A A G G A C A C C A T C C
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C A G C C C G A G A A T T C A T T C T G A A G A T
SEQ. ID. NO. 46 A C A C C A T C C T C C A G T T G A A C C T G A A
SEQ. ID. NO. 36 T C C A G T T G A A C C T G A A G G A C T G C G G
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G T T C G T G G A C C T G A A C C C A G A C A G T
SEQ. ID. NO. 46 G G A C T G C G G T C T G T T C T A A T T G T G C
SEQ. ID. NO. 36 T C T G T T C T A A
SEQ. ID. NO. 32

FIG. 11u.

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SEQ. ID. NO. 40 G A C A A A A T T A T C T A C T C C C A C T T C A
SEQ. ID. NO. 46 C T C C T A G A C A C C C G C C C T G C C C T T C
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C G T G C G C C A C A G A C A C C G A G A A T A T
SEQ. ID. NO. 46 C C T G G T
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 C C G C T T T G T C T T T G C T G C C G T C A A G
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 G A C A C C A T C C T C C A G T T G A A C C T G A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

SEQ. ID. NO. 40 A G G A C T G C G G T C T G T T C T A A
SEQ. ID. NO. 46
SEQ. ID. NO. 36
SEQ. ID. NO. 32

FIG. 1/iv.

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ClustalW Formatted Alignments

SEQ. ID. NO. 41 M V C E G K R S A S C P C F F L L T A K F Y W I L
SEQ. ID. NO. 47 M G S L L A L P A L L L L W G A V A E G P A K K V
SEQ. ID. NO. 37 M G S L L A L P A L L L L W G A V A E G P A K K V
SEQ. ID. NO. 33 M A F Y S C C W V L L A L T W H T S A Y G P D Q R

SEQ. ID. NO. 41 T M M Q R T H S Q E Y A H S I R V D G D I I L G G
SEQ. ID. NO. 47 L T L E G D L V L G G L F P V H Q K G G P A E D C
SEQ. ID. NO. 37 L T L E G D L V L G G L F P V H Q K G G P A E D C
SEQ. ID. NO. 33 A Q K K G D I I L G G L F P I H F G V A A K D Q D

SEQ. ID. NO. 41 L F P V H A K G E R G V P C G E L K K E K G I H R
SEQ. ID. NO. 47 G P V N E H R G I Q R L E A M L F A L D R I N R D
SEQ. ID. NO. 37 G P V N E H R G I Q R L E A M L F A L D R I N R D
SEQ. ID. NO. 33 L K S R P E S V E C I R Y N F R G F R W L Q A M I

SEQ. ID. NO. 41 L E A M L Y A I D Q I N K D P D L L S N I T L G V
SEQ. ID. NO. 47 P H L L P G V R L G A H I L D S C S K D T H A L E
SEQ. ID. NO. 37 P H L L P G V R L G A H I L D S C S K D T H A L E
SEQ. ID. NO. 33 F A I E E I N S S P A L L P N L T L G Y R I F D T

SEQ. ID. NO. 41 R I L D T C S R D T Y A L E Q S L T F V Q A L I E
SEQ. ID. NO. 47 Q A L D F V R A S L S R G A D G S R H I C P D G S
SEQ. ID. NO. 37 Q A L D F V R A S L S R G A D G S R H I C P D G S
SEQ. ID. NO. 33 C N T V S K A L E A T L S F V A Q N K I D S L N L

SEQ. ID. NO. 41 K D A S D V K C A N G D P P I F T K P D K I S G V
SEQ. ID. NO. 47 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
SEQ. ID. NO. 37 Y A T H G D A P T A I T G V I G G S Y S D V S I Q
SEQ. ID. NO. 33 D E F C N C S E H I P S T I A V V G A T G S G V S

SEQ. ID. NO. 41 I G A A A S S V S I M V A N I L R L F K I P Q I S
SEQ. ID. NO. 47 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
SEQ. ID. NO. 37 V A N L L R L F Q I P Q I S Y A S T S A K L S D K
SEQ. ID. NO. 33 T A V A N L L G L F Y I P Q V S Y A S S S R L L S

SEQ. ID. NO. 41 Y A S T A P E L S D N T R Y D F F S R V V P P D S
SEQ. ID. NO. 47 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
SEQ. ID. NO. 37 S R Y D Y F A R T V P P D F F Q A K A M A E I L R
SEQ. ID. NO. 33 N K N Q F K S F L R T I P N D E H Q A T A M A D I

FIG. 12a.

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SEQ. ID. NO. 41 Y Q A Q A M V D I V T A L G W N Y V S T L A S E G
SEQ. ID. NO. 47 F F N W T Y V S T V A S E G D Y G E T G I E A F E
SEQ. ID. NO. 37 F F N W T Y V S T V A S E G D Y G E T G I E A F E
SEQ. ID. NO. 33 I E Y F R W N W V G T I A A D D D Y G R P G I E K

SEQ. ID. NO. 41 N Y G E S G V E A F T Q I S R E I G G V C I A Q S
SEQ. ID. NO. 47 L E A R A R N I C V A T S E K V G R A M S R A A F
SEQ. ID. NO. 37 L E A R A R N I C V A T S E K V G R A M S R A A F
SEQ. ID. NO. 33 F R E E A E E R D I C I D F S E L I S Q Y S D E E

SEQ. ID. NO. 41 Q K I P R E P R P G E F E K I I K R L L E T P N A
SEQ. ID. NO. 47 E G V V R A L L Q K P S A R V A V L F T R S E D A
SEQ. ID. NO. 37 E G V V R A L L Q K P S A R V A V L F T R S E D A
SEQ. ID. NO. 33 E I Q H V V E V I Q N S T A K V I V V F S S G P D

SEQ. ID. NO. 41 R A V I M F A N E D D I R R I L E A A K K L N Q S
SEQ. ID. NO. 47 R E L L A A S Q R L N A S F T W V A S D G W G A L
SEQ. ID. NO. 37 R E L L A A S Q R L N A S F T W V A S D G W G A L
SEQ. ID. NO. 33 L E P L I K E I V R R N I T G K I W L A S E A W A

SEQ. ID. NO. 41 G H F L W I G S D S W G S K I A P V Y Q Q E E I A
SEQ. ID. NO. 47 E S V V A G S E G A A E G A I T I E L A S Y P I S
SEQ. ID. NO. 37 E S V V A G S E G A A E G A I T I E L A S Y P I S
SEQ. ID. NO. 33 S S S L I A M P Q Y F H V V G G T I G F A L K A G

SEQ. ID. NO. 41 E G A V T I L P K R A S I D G F D R Y F R S R T L
SEQ. ID. NO. 47 D F A S Y F Q S L D P W N N S R N P W F R E F W E
SEQ. ID. NO. 37 D F A S Y F Q S L D P W N N S R N P W F R E F W E
SEQ. ID. NO. 33 Q I P G F R E F L K K V H P R K S V H N G F A K E

SEQ. ID. NO. 41 A N N R R N V W F A E F W E E N F G C K L G S H G
SEQ. ID. NO. 47 Q R F R C S F R Q R D C A A H S L R A V P F E Q E
SEQ. ID. NO. 37 Q R F R C S F R Q R D C A A H S L R A V P F E Q E
SEQ. ID. NO. 33 F W E E T F N C H L Q E G A K G P L P V D T F L R

SEQ. ID. NO. 41 K R N S H I K K C T G L E R I A R D S S Y E Q E G
SEQ. ID. NO. 47 S K I M F V V N A V Y A M A H A L H N M H R A L C
SEQ. ID. NO. 37 S K I M F V V N A V Y A M A H A L H N M H R A L C
SEQ. ID. NO. 33 G H E E S G D R F S N S S T A F R P L C T G D E N

FIG. 12b.

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SEQ. ID. NO. 41 K V Q F V I D A V Y S M A Y A L H N M H K D L C P
SEQ. ID. NO. 47 P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 37 P N T T R L C D A M R P V N G R R L Y K D F V L N
SEQ. ID. NO. 33 I S S V E T P Y I D Y T H L R I S Y N V Y L A V Y

SEQ. ID. NO. 41 G Y I G L C P R M S T I D G K E L L G Y I R A V N
SEQ. ID. NO. 47 V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 37 V K F D A P F R P A D T H N E V R F D R F G D G I
SEQ. ID. NO. 33 S I A H A L Q D I Y T C L P G R G L F T N G S C A

SEQ. ID. NO. 41 F N G S A G T P V T F N E N G D A P G R Y D I F Q
SEQ. ID. NO. 47 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 37 G R Y N I F T Y L R A G S G R Y R Y Q K V G Y W A
SEQ. ID. NO. 33 D I K K V E A W Q V L K H L R H L N F T N N M G E

SEQ. ID. NO. 41 Y Q I T N K S T E Y K V I G H W T N Q L H L K V E
SEQ. ID. NO. 47 E G L T L D T S L I P W A S P S A G P L P A S R C
SEQ. ID. NO. 37 E G L T L D T S L I P W A S P S A G P L P A S R C
SEQ. ID. NO. 33 Q V T F D E C G D L V G N Y S I I N W H L S P E D

SEQ. ID. NO. 41 D M Q W A H R E H T H P A S V C S L P C K P G E R
SEQ. ID. NO. 47 S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 37 S E P C L Q N E V K S V Q P G E V C C W L C I P C
SEQ. ID. NO. 33 G S I V F K E V G Y Y N V Y A K K G E R L F I N E

SEQ. ID. NO. 41 K K T V K G V P C C W H C E R C E G Y N Y Q V D E
SEQ. ID. NO. 47 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 37 Q P Y E Y R L D E F T C A D C G L G Y W P N A S L
SEQ. ID. NO. 33 E K I L W S G F S R E V P F S N C S R D C L A G T

SEQ. ID. NO. 41 L S C E L C P L D Q R P N M N R T G C Q L I P I I
SEQ. ID. NO. 47 T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 37 T G C F E L P Q E Y I R W G D A W A V G P V T I A
SEQ. ID. NO. 33 R K G I I E G E P T C C F E C V E C P D G E Y S D

SEQ. ID. NO. 41 K L E W H S P W A V V P V F V A I L G I I A T T F
SEQ. ID. NO. 47 C L G A L A T L F V L G V F V R H N A T P V V K A
SEQ. ID. NO. 37 C L G A L A T L F V L G V F V R H N A T P V V K A
SEQ. ID. NO. 33 E T D A S A C N K C P D D F W S N E N H T S C F E

FIG. 12c.

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SEQ. ID. NO. 41 V I V T F V R Y N D T P I V R A S G R E L S Y V L
SEQ. ID. NO. 47 S G R E L C Y I L L G G V F L C Y C M T F I F I A
SEQ. ID. NO. 37 S G R E L C Y I L L G G V F L C Y C M T F I F I A
SEQ. ID. NO. 33 L P Q E Y I R W G D A W A V G P V T I A C L G A L

SEQ. ID. NO. 41 L T G I F L C Y S I T F L M I A A P D T I I C S F
SEQ. ID. NO. 47 K P S T A V C T L R R L G L G T A F S V C Y S A L
SEQ. ID. NO. 37 K P S T A V C T L R R L G L G T A F S V C Y S A L
SEQ. ID. NO. 33 A T L F V L G V F V R H N A T P V V K A S G R E L

SEQ. ID. NO. 41 R R V F L G L G M C F S Y A A L L T K T N R I H R
SEQ. ID. NO. 47 L T K T N R I A R I F G G A R E G A Q R P R F I S
SEQ. ID. NO. 37 L T K T N R I A R I F G G A R E G A Q R P R F I S
SEQ. ID. NO. 33 C Y I L L G G V F L C Y C M T F I F I A K P S T A

SEQ. ID. NO. 41 I F E Q G K K S V T A P K F I S P A S Q L V I T F
SEQ. ID. NO. 47 P A S Q V A I C L A L I S G Q L L I V V A W L V V
SEQ. ID. NO. 37 P A S Q V A I C L A L I S G Q L L I V V A W L V V
SEQ. ID. NO. 33 V C T L R R L G L G T A F S V C Y S A L L T K T N

SEQ. ID. NO. 41 S L I S V Q L L G V F V W F V V D P P H I I I D Y
SEQ. ID. NO. 47 E A P G T G K E T A P E R R E V V T L R C N H R D
SEQ. ID. NO. 37 E A P G T G K E T A P E R R E V V T L R C N H R D
SEQ. ID. NO. 33 R I A R I F G G A R E G A Q R P R F I S P A S Q V

SEQ. ID. NO. 41 G E Q R T L D P E K A R G V L K C D I S D L S L I
SEQ. ID. NO. 47 A S M L G S L A Y N V L L I A L C T L Y A F K T R
SEQ. ID. NO. 37 A S M L G S L A Y N V L L I A L C T L Y A F K T R
SEQ. ID. NO. 33 A I C L A L I S G Q L L I V V A W L V V E A P G T

SEQ. ID. NO. 41 C S L G Y S I L L M V T C T V Y A I K T R G V P E
SEQ. ID. NO. 47 K C P E N F N E A K F I G F T M Y T T C I I W L A
SEQ. ID. NO. 37 K C P E N F N E A K F I G F T M Y T T C I I W L A
SEQ. ID. NO. 33 G K E T A P E R R E V V T L R C N H R D A S M L G

SEQ. ID. NO. 41 T F N E A K P I G F T M Y T T C I I W L A F I P I
SEQ. ID. NO. 47 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
SEQ. ID. NO. 37 F L P I F Y V T S S D Y R V Q T T T M C V S V S L
SEQ. ID. NO. 33 S L A Y N V L L I A L C T L Y A F N T R K C P E N

FIG. 12d.

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SEQ. ID. NO. 41 F F G T A Q S A E K M Y I Q T T T L T V S M S L S
 SEQ. ID. NO. 47 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 37 S G S V V L G C L F A P K L H I I L F Q P Q K N T
 SEQ. ID. NO. 33 F N E A K F I G F T M Y T T C I I W L A L L P I F

SEQ. ID. NO. 41 A S V S L G M L Y M P K V Y I I I F H P E Q N T I
 SEQ. ID. NO. 47 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 37 I E E V R C S T A A H A F K V A A R A T L R R S N
 SEQ. ID. NO. 33 Y V T S S D Y R V Q T T T M C V S V S L S G S V V

SEQ. ID. NO. 41 E E V R C S T A A H A F K V A A R A T L R R S N V
 SEQ. ID. NO. 47 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 37 V S R K R S S S L G G S T G S T P S S S I S S K S
 SEQ. ID. NO. 33 L G C L F A P K L H I I L F Q P Q K N V V S H R A

SEQ. ID. NO. 41 S R K R S S S L G G S T G S T P S S S I S S K S N
 SEQ. ID. NO. 47 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 37 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q
 SEQ. ID. NO. 33 P T S R F G S A A A R A S S S L G Q G S G S Q F V

SEQ. ID. NO. 41 S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q
 SEQ. ID. NO. 47 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 37 Q Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F
 SEQ. ID. NO. 33 P T V C N G R E V V D S T T S S L M T L E S I M A

SEQ. ID. NO. 41 Q Q P L T L P Q Q Q R S Q Q Q P R C K Q K V I F G
 SEQ. ID. NO. 47 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 37 G S G T V T F S L S F D E P Q K N A M A H G N S T
 SEQ. ID. NO. 33 C C L S E E A K E A R R I N D E I E R Q L R R D K

SEQ. ID. NO. 41 S G T V T F S L S F D E P Q K N A M A H G N S T H
 SEQ. ID. NO. 47 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 37 H Q N S L E A Q K S S D T L T R H Q P L L P L Q C
 SEQ. ID. NO. 33 R D A R R E L K L L L L G T G E S G K S T F I K Q

SEQ. ID. NO. 41 Q N S L E A Q K S S D T L T R H Q P L L P L Q C G
 SEQ. ID. NO. 47 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 37 G E T D L D L T V Q E T G L Q G P V G G D Q R P E
 SEQ. ID. NO. 33 M R I I H G S G Y S D E D K R G F T K L V Y Q N I

FIG. 12e.

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SEQ. ID. NO. 41 E T D L D L T V Q E T G L Q G P V G G D Q R P E V
SEQ. ID. NO. 47 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 37 V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 33 F T A M Q A M I R A M D T L K I P Y K Y E H N K A

SEQ. ID. NO. 41 E D P E E L S P A L V V S S S Q S F V I S G G G S
SEQ. ID. NO. 47 S T V T E N V V N S A A A M T L E S I M A C C L S
SEQ. ID. NO. 37 S T V T E N V V N S M T L E S I M A C C L S E E A
SEQ. ID. NO. 33 H A Q L V R E V D V E K V S A F E N P Y V D A I K

SEQ. ID. NO. 41 T V T E N V V N S M T L E S I M A C C L S E E A K
SEQ. ID. NO. 47 E E A K E A R R I N D E I E R Q L R R D K R D A R
SEQ. ID. NO. 37 K E A R R I N D E I E R Q L R R D K R D A R R E L
SEQ. ID. NO. 33 S L W N D P G I Q E C Y D R R R E Y Q L S D S T K

SEQ. ID. NO. 41 E A R R I N D E I E R Q L R R D K R D A R R E L K
SEQ. ID. NO. 47 R E L K L L L L G T G E S G K S T F I K Q M R I I
SEQ. ID. NO. 37 K L L L L G T G E S G K S T F I K Q M R I I H G S
SEQ. ID. NO. 33 Y Y L N D L D R V A D P A Y L P T Q Q D V L R V R

SEQ. ID. NO. 41 L L L L G T G E S G K S T F I K Q M R I I H G S G
SEQ. ID. NO. 47 H G S G Y S D E D K R G F T K L V Y Q N I F T A M
SEQ. ID. NO. 37 G Y S D E D K R G F T K L V Y Q N I F T A M Q A M
SEQ. ID. NO. 33 V P T T G I I E Y P F D L Q S V I F R M V D V G G

SEQ. ID. NO. 41 Y S D E D K R G F T K L V Y Q N I F T A M Q A M I
SEQ. ID. NO. 47 Q A M I R A M D T L K I P Y K Y E H N K A H A Q L
SEQ. ID. NO. 37 I R A M D T L K I P Y K Y E H N K A H A Q L V R E
SEQ. ID. NO. 33 Q R S E R R K W I H C F E N V T S I M F L V A L S

SEQ. ID. NO. 41 R A M D T L K I P Y K Y E H N K A H A Q L V R E V
SEQ. ID. NO. 47 V R E V D V E K V S A F E N P Y V D A I K S L W N
SEQ. ID. NO. 37 V D V E K V S A F E N P Y V D A I K S L W N D P G
SEQ. ID. NO. 33 E Y D Q V L V E S D N E N R M E E S K A L F R T I

SEQ. ID. NO. 41 D V E K V S A F E N P Y V D A I K S L W N D P G I
SEQ. ID. NO. 47 D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N
SEQ. ID. NO. 37 I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D
SEQ. ID. NO. 33 I T Y P W F Q N S S V I L F L N K K D L L E E K I

FIG. 12f.

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SEQ. ID. NO. 41 Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R
SEQ. ID. NO. 47 D L D R V A D P A Y L P T Q Q D V L R V R V P T T
SEQ. ID. NO. 37 R V A D P A Y L P T Q Q D V L R V R V P T T G I I
SEQ. ID. NO. 33 M Y S H L V D Y F P E Y D G P Q R D A Q A A R E F

SEQ. ID. NO. 41 V A D P A Y L P T Q Q D V L R V R V P T T G I I E
SEQ. ID. NO. 47 G I I E Y P F D L Q S V I F R M V D V G G Q R S E
SEQ. ID. NO. 37 E Y P F D L Q S V I F R M V D V G G Q R S E R R K
SEQ. ID. NO. 33 I L K M F V D L N P D S D K I I Y S H F T C A T D

SEQ. ID. NO. 41 Y P F D L Q S V I F R M V D V G G Q R S E R R K W
SEQ. ID. NO. 47 R R K W I H C F E N V T S I M F L V A L S E Y D Q
SEQ. ID. NO. 37 W I H C F E N V T S I M F L V A L S E Y D Q V L V
SEQ. ID. NO. 33 T E N I R F V F A A V K D T I L Q L N L K D C G L

SEQ. ID. NO. 41 I H C F E N V T S I M F L V A L S E Y D Q V L V E
SEQ. ID. NO. 47 V L V E S D N E N R M E E S K A L F R T I I T Y P
SEQ. ID. NO. 37 E S D N E N R M E E S K A L F R T I I T Y P W F Q
SEQ. ID. NO. 33 F

SEQ. ID. NO. 41 S D N E N R M E E S K A L F R T I I T Y P W F Q N
SEQ. ID. NO. 47 W F Q N S S V I L F L N K K D L L E E K I M Y S H
SEQ. ID. NO. 37 N S S V I L F L N K K D L L E E K I M Y S H L V D
SEQ. ID. NO. 33

SEQ. ID. NO. 41 S S V I L F L N K K D L L E E K I M Y S H L V D Y
SEQ. ID. NO. 47 L V D Y F P E Y D G P Q R D A Q A A R E F I L K M
SEQ. ID. NO. 37 Y F P E Y D G P Q R D A Q A A R E F I L K M F V D
SEQ. ID. NO. 33

SEQ. ID. NO. 41 F P E Y D G P Q R D A Q A A R E F I L K M F V D L
SEQ. ID. NO. 47 F V D L N P D S D K I I Y S H F T C A T D T E N I
SEQ. ID. NO. 37 L N P D S D K I I Y S H F T C A T D T E N I R F V
SEQ. ID. NO. 33

SEQ. ID. NO. 41 N P D S D K I I Y S H F T C A T D T E N I R F V F
SEQ. ID. NO. 47 R F V F A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 37 F A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 33

FIG. 12g.

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SEQ. ID. NO. 41 A A V K D T I L Q L N L K D C G L F
SEQ. ID. NO. 47
SEQ. ID. NO. 37
SEQ. ID. NO. 33

FIG. 12h.

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ClustalW Formatted Alignments

SEQ. ID. NO. 44 A T G T T G C T G C T G C T G C T A C T G G C G C
SEQ. ID. NO. 42 A T G G C T T C C C C G C G G A G C T C C G G G C

SEQ. ID. NO. 44 C A C T C T T C C T C C G C C C C C G G G C G C
SEQ. ID. NO. 42 A G C C C G G G C C G C C G C C G C C G C C G C C

SEQ. ID. NO. 44 G G G C G G G G C G C A G A C C C C C A A C G C C
SEQ. ID. NO. 42 A C C G C C G C C C G C G C G C C T G C T A C T G

SEQ. ID. NO. 44 A C C T C A G A A G G T T G C C A G A T C A T A C
SEQ. ID. NO. 42 C T A C T G C T G C T G C C G C T G C T G C T G C

SEQ. ID. NO. 44 A C C C G C C C T G G G A A G G G G G C A T C A G
SEQ. ID. NO. 42 C T C T G G C G C C C G G G G C C T G G G G C T G

SEQ. ID. NO. 44 G T A C C G G G G C C T G A C T C G G G A C C A G
SEQ. ID. NO. 42 G G C G C G G G G C G C C C C C C G G C C G C C G

SEQ. ID. NO. 44 G T G A A G G C T A T C A A C T T C C T G C C A G
SEQ. ID. NO. 42 C C C A G C A G C C C G C C G C T C T C C A T C A

SEQ. ID. NO. 44 T G G A C T A T G A G A T T G A G T A T G T G T G
SEQ. ID. NO. 42 T G G G C C T C A T G C C G C T C A C C A A G G A

SEQ. ID. NO. 44 C C G G G G G G A G C G C G A G G T G G T G G G G
SEQ. ID. NO. 42 G G T G G C C A A G G G C A G C A T C G G G C G C

SEQ. ID. NO. 44 C C C A A G G T C C G C A A G T G C C T G G C C A
SEQ. ID. NO. 42 G G T G T G C T C C C C G C C G T G G A A C T G G

SEQ. ID. NO. 44 A C G G C T C C T G G A C A G A T A T G G A C A C
SEQ. ID. NO. 42 C C A T C G A G C A G A T C C G C A A C G A G T C

SEQ. ID. NO. 44 A C C C A G C C G C T G T G T C C G A A T C T G C
SEQ. ID. NO. 42 A C T C C T G C G C C C T T A C T T C C T C G A C

FIG. 13a.

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SEQ. ID. NO. 44 T C C A A G T C T T A T T T G A C C C T G G A A A
SEQ. ID. NO. 42 C T G C G G C T C T A T G A C A C G G A G T G C G

SEQ. ID. NO. 44 A T G G G A A G G T T T T C C T G A C G G G T G G
SEQ. ID. NO. 42 A C A A C G C A A A A G G G T T G A A A G C C T T

SEQ. ID. NO. 44 G G A C C T C C C A G C T C T G G A C G G A G C C
SEQ. ID. NO. 42 C T A C G A T G C A A T A A A A T A C G G G C C G

SEQ. ID. NO. 44 C G G G T G G A T T T C C G G T G T G A C C C C G
SEQ. ID. NO. 42 A A C C A C T T G A T G G T G T T T G G A G G C G

SEQ. ID. NO. 44 A C T T C C A T C T G G T G G G C A G C T C C C G
SEQ. ID. NO. 42 T C T G T C C A T C C G T C A C A T C C A T C A T

SEQ. ID. NO. 44 G A G C A T C T G T A G T C A G G G C C A G T G G
SEQ. ID. NO. 42 T G C A G A G T C C C T C C A A G G C T G G A A T

SEQ. ID. NO. 44 A G C A C C C C C A A G C C C C A C T G C C A G G
SEQ. ID. NO. 42 C T G G T G C A G C T T T C T T T T G C T G C A A

SEQ. ID. NO. 44 T G A A T C G A A C G C C A C A C T C A G A A C G
SEQ. ID. NO. 42 C C A C G C C T G T T C T A G C C G A T A A G A A

SEQ. ID. NO. 44 G C G C G C A G T G T A C A T C G G G G C A C T G
SEQ. ID. NO. 42 A A A A T A C C C T T A T T T C T T T C G G A C C

SEQ. ID. NO. 44 T T T C C C A T G A G C G G G G G C T G G C C A G
SEQ. ID. NO. 42 G T C C C A T C A G A C A A T G C G G T G A A T C

SEQ. ID. NO. 44 G G G G C C A G G C C T G C C A G C C C G C G G T
SEQ. ID. NO. 42 C A G C C A T T C T G A A G T T G C T C A A G C A

SEQ. ID. NO. 44 G G A G A T G G C G C T G G A G G A C G T G A A T
SEQ. ID. NO. 42 C T A C C A G T G G A A G C G C G T G G G C A C G

SEQ. ID. NO. 44 A G C C G C A G G G A C A T C C T G C C G G A C T
SEQ. ID. NO. 42 C T G A C G C A A G A C G T T C A G A G G T T C T

FIG. 13b.

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SEQ. ID. NO. 44 A T G A G C T C A A G C T C A T C C A C C A C G A
SEQ. ID. NO. 42 C T G A G G T G C G G A A T G A C C T G A C T G G

SEQ. ID. NO. 44 C A G C A A G T G T G A T C C A G G C C A A G C C
SEQ. ID. NO. 42 A G T T C T G T A T G G C G A G G A C A T T G A G

SEQ. ID. NO. 44 A C C A A G T A C C T A T A T G A G C T G C T C T
SEQ. ID. NO. 42 A T T T C A G A C A C C G A G A G C T T C T C C A

SEQ. ID. NO. 44 A C A A C G A C C C T A T C A A G A T C A T C C T
SEQ. ID. NO. 42 A C G A T C C C T G T A C C A G T G T C A A A A A

SEQ. ID. NO. 44 T A T G C C T G G C T G C A G C T C T G T C T C C
SEQ. ID. NO. 42 G C T G A A G G G G A A T G A T G T G C G G A T C

SEQ. ID. NO. 44 A C G C T G G T G G C T G A G G C T G C T A G G A
SEQ. ID. NO. 42 A T C C T T G G C C A G T T T G A C C A G A A T A

SEQ. ID. NO. 44 T G T G G A A C C T C A T T G T G C T T T C C T A
SEQ. ID. NO. 42 T G G C A G C A A A A G T G T T C T G T T G T G C

SEQ. ID. NO. 44 T G G C T C C A G C T C A C C A G C C C T G T C A
SEQ. ID. NO. 42 A T A C G A G G A G A A C A T G T A T G G T A G T

SEQ. ID. NO. 44 A A C C G G C A G C G T T T C C C C A C T T T C T
SEQ. ID. NO. 42 A A A T A T C A G T G G A T C A T T C C G G G C T

SEQ. ID. NO. 44 T C C G A A C G C A C C C A T C A G C C A C A C T
SEQ. ID. NO. 42 G G T A C G A G C C T T C T T G G T G G G A G C A

SEQ. ID. NO. 44 C C A C A A C C C T A C C C G C G T G A A A C T C
SEQ. ID. NO. 42 G G T G C A C A C G G A A G C C A A C T C A T C C

SEQ. ID. NO. 44 T T T G A A A A G T G G G G C T G G A A G A A G A
SEQ. ID. NO. 42 C G C T G C C T C C G G A A G A A T C T G C T T G

SEQ. ID. NO. 44 T T G C T A C C A T C C A G C A G A C C A C T G A
SEQ. ID. NO. 42 C T G C C A T G G A G G G C T A C A T T G G C G T

FIG. 13c.

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SEQ. ID. NO. 44 G G T C T T C A C T T C G A C T C T G G A C G A C
SEQ. ID. NO. 42 G G A T T T C G A G C C C C T G A G C T C C A A G

SEQ. ID. NO. 44 C T G G A G G A A C G A G T G A A G G A G G C T G
SEQ. ID. NO. 42 C A G A T C A A G A C C A T C T C A G G A A A G A

SEQ. ID. NO. 44 G A A T T G A G A T T A C T T T C C G C C A G A G
SEQ. ID. NO. 42 C T C C A C A G C A G T A T G A G A G A G A G T A

SEQ. ID. NO. 44 T T T C T T C T C A G A T C C A G C T G T G C C C
SEQ. ID. NO. 42 C A A C A A C A A G C G G T C A G G C G T G G G G

SEQ. ID. NO. 44 G T C A A A A A C C T G A A G C G C C A G G A T G
SEQ. ID. NO. 42 C C C A G C A A G T T C C A C G G G T A C G C C T

SEQ. ID. NO. 44 C C C G A A T C A T C G T G G G A C T T T T C T A
SEQ. ID. NO. 42 A C G A T G G C A T C T G G G T C A T C G C C A A

SEQ. ID. NO. 44 T G A G A C T G A A G C C C G G A A A G T T T T T
SEQ. ID. NO. 42 G A C A C T G C A G A G G G C C A T G G A G A C A

SEQ. ID. NO. 44 T G T G A G G T G T A C A A G G A G C G T C T C T
SEQ. ID. NO. 42 C T G C A T G C C A G C A G C C G G C A C C A G C

SEQ. ID. NO. 44 T T G G G A A G A A G T A C G T C T G G T T C C T
SEQ. ID. NO. 42 G G A T C C A G G A C T T C A A C T A C A C G G A

SEQ. ID. NO. 44 C A T T G G G T G G T A T G C T G A C A A T T G G
SEQ. ID. NO. 42 C C A C A C G C T G G G C A G G A T C A T C C T C

SEQ. ID. NO. 44 T T C A A G A T C T A C G A C C C T T C T A T C A
SEQ. ID. NO. 42 A A T G C C A T G A A C G A G A C C A A C T T C T

SEQ. ID. NO. 44 A C T G C A C A G T G G A T G A G A T G A C T G A
SEQ. ID. NO. 42 T C G G G G T C A C G G G T C A A G T T G T A T T

SEQ. ID. NO. 44 G G C G G T G G A G G G C C A C A T C A C A A C T
SEQ. ID. NO. 42 C C G G A A T G G G G A G A G A A T G G G G A C C

FIG. 13d.

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SEQ. ID. NO. 44 G A G A T T G T C A T G C T G A A T C C T G C C A
SEQ. ID. NO. 42 A T T A A A T T T A C T C A A T T T C A A G A C A

SEQ. ID. NO. 44 A T A C C C G C A G C A T T T C C A A C A T G A C
SEQ. ID. NO. 42 G C A G G G A G G T G A A G G T G G G A G A G T A

SEQ. ID. NO. 44 A T C C C A G G A A T T T G T G G A G A A A C T A
SEQ. ID. NO. 42 C A A C G C T G T G G C C G A C A C A C T G G A G

SEQ. ID. NO. 44 A C C A A G C G A C T G A A A A G A C A C C C T G
SEQ. ID. NO. 42 A T C A T C A A T G A C A C C A T C A G G T T C C

SEQ. ID. NO. 44 A G G A G A C A G G A G G C T T C C A G G A G G C
SEQ. ID. NO. 42 A A G G A T C C G A A C C A C C A A A A G A C A A

SEQ. ID. NO. 44 A C C G C T G G C C T A T G A T G C C A T C T G G
SEQ. ID. NO. 42 G A C C A T C A T C C T G G A G C A G C T G C G G

SEQ. ID. NO. 44 G C C T T G G C A C T G G C C C T G A A C A A G A
SEQ. ID. NO. 42 A A G A T C T C C C T A C C T C T C T A C A G C A

SEQ. ID. NO. 44 C A T C T G G A G G A G G C G G C C G T T C T G G
SEQ. ID. NO. 42 T C C T C T C T G C C C T C A C C A T C C T C G G

SEQ. ID. NO. 44 T G T G C G C C T G G A G G A C T T C A A C T A C
SEQ. ID. NO. 42 G A T G A T C A T G G C C A G T G C T T T T C T C

SEQ. ID. NO. 44 A A C A A C C A G A C C A T T A C C G A C C A A A
SEQ. ID. NO. 42 T T C T T C A A C A T C A A G A A C C G G A A T C

SEQ. ID. NO. 44 T C T A C C G G G C A A T G A A C T C T T C G T C
SEQ. ID. NO. 42 A G A A G C T C A T A A A G A T G T C G A G T C C

SEQ. ID. NO. 44 C T T T G A G G G T G T C T C T G G C C A T G T G
SEQ. ID. NO. 42 A T A C A T G A A C A A C C T T A T C A T C C T T

SEQ. ID. NO. 44 G T G T T T G A T G C C A G C G G C T C T C G G A
SEQ. ID. NO. 42 G G A G G G A T G C T C T C C T A T G C T T C C A

FIG. 13e.

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SEQ. ID. NO. 44 TGGCATGGACGCTTATCGAGCAGCT
SEQ. ID. NO. 42 TATTTCTCTTTTGGCCTTGATGGATC

SEQ. ID. NO. 44 TCAGGGTGGCAGCTACAAGAAAGATT
SEQ. ID. NO. 42 CTTTGCTCTCTGAAAAGACCTTTGAA

SEQ. ID. NO. 44 GGCTACTATGACAGCACCAAGGATG
SEQ. ID. NO. 42 ACACTTTTGCACCGTCAGGACCTTGA

SEQ. ID. NO. 44 ATCTTTTCCTGGTCCAAAACAGATAA
SEQ. ID. NO. 42 TTCTCACCGTGGGCTACACGACCGC

SEQ. ID. NO. 44 ATGGATTGGAGGGTCCCCCCCAGCT
SEQ. ID. NO. 42 TTTTGGGGGCCATGTTTGC AAAAGACC

SEQ. ID. NO. 44 GACCAGACCCTGGTTCATCAAGACAT
SEQ. ID. NO. 42 TGGAGAGTCCACGCCATCTTCAAAA

SEQ. ID. NO. 44 TCCGCTTCCTGTCACAGAAACTCTTT
SEQ. ID. NO. 42 ATGTGAAAAATGAAGAAGAAAGATCAT

SEQ. ID. NO. 44 TATCTCCGTCTCAGTTCTCTCCAGC
SEQ. ID. NO. 42 CAAGGACCAGAAACTGCTTGTTGATC

SEQ. ID. NO. 44 CTGGGCAATTGTCCTAGCTGTTGTCT
SEQ. ID. NO. 42 GTGGGGGGGCATGCTGCTGATCGACC

SEQ. ID. NO. 44 GTCTGTCCTTTTAACATCTACAACCTC
SEQ. ID. NO. 42 TGTGTATCCTGATCTGCTGGCAGGC

SEQ. ID. NO. 44 ACATGTCCGTTATATCCAGAACTCA
SEQ. ID. NO. 42 TGTGGACCCCTGCGAAGGACAGTG

SEQ. ID. NO. 44 CAGCCCAACCTGAACAACCTGACTG
SEQ. ID. NO. 42 GAGAAGTACAGCATGGAGCCGGACC

SEQ. ID. NO. 44 CTGTGGGCTGCTCACTGGCTTTAGC
SEQ. ID. NO. 42 CAGCAGGACGGGATATCTCCATCCG

FIG. 13f.

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SEQ. ID. NO. 44 T G C T G T C T T C C C C C T G G G G C T C G A T
SEQ. ID. NO. 42 C C C T C T C C T G G A G C A C T G T G A G A A C

SEQ. ID. NO. 44 G G T T A C C A C A T T G G G A G G A A C C A G T
SEQ. ID. NO. 42 A C C C A T A T G A C C A T C T G G C T T G G C A

SEQ. ID. NO. 44 T T C C T T T C G T C T G C C A G G C C C G C C T
SEQ. ID. NO. 42 T C G T C T A T G C C T A C A A G G G A C T T C T

SEQ. ID. NO. 44 C T G G C T C C T G G G C C T G G G C T T T A G T
SEQ. ID. NO. 42 C A T G T T G T T C G G T T G T T T C T T A G C T

SEQ. ID. NO. 44 C T G G G C T A C G G T T C C A T G T T C A C C A
SEQ. ID. NO. 42 T G G G A G A C C C G C A A C G T C A G C A T C C

SEQ. ID. NO. 44 A G A T T T G G T G G G T C C A C A C G G T C T T
SEQ. ID. NO. 42 C C G C A C T C A A C G A C A G C A A G T A C A T

SEQ. ID. NO. 44 C A C A A A G A A G G A A G A A A A G A A G G A G
SEQ. ID. NO. 42 C G G G A T G A G T G T C T A C A A C G T G G G G

SEQ. ID. NO. 44 T G G A G G A A G A C T C T G G A A C C C T G G A
SEQ. ID. NO. 42 A T C A T G T G C A T C A T C G G G G C C G C T G

SEQ. ID. NO. 44 A G C T G T A T G C C A C A G T G G G C C T G C T
SEQ. ID. NO. 42 T C T C C T T C C T G A C C C G G G A C C A G C C

SEQ. ID. NO. 44 G G T G G G C A T G G A T G T C C T C A C T C T C
SEQ. ID. NO. 42 C A A T G T G C A G T T C T G C A T C G T G G C T

SEQ. ID. NO. 44 G C C A T C T G G C A G A T C G T G G A C C C T C
SEQ. ID. NO. 42 C T G G T C A T C A T C T T C T G C A G C A C C A

SEQ. ID. NO. 44 T G C A C C G G A C C A T T G A G A C A T T T G C
SEQ. ID. NO. 42 T C A C C C T C T G C C T G G T A T T C G T G C C

SEQ. ID. NO. 44 C A A G G A G G A A C C T A A G G A A G A T A T T
SEQ. ID. NO. 42 G A A G C T C A T C A C C C T G A G A A C A A A C

FIG. 13g.

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SEQ. ID. NO. 44 G A C G T C T C T A T T C T G C C C C A G C T G G
SEQ. ID. NO. 42 C C A G A T G C A G C A A C G C A G A A C A G G C

SEQ. ID. NO. 44 A G C A T T G C A G C T C C A G G A A G A T G A A
SEQ. ID. NO. 42 G A T T C C A G T T C A C T C A G A A T C A G A A

SEQ. ID. NO. 44 T A C A T G G C T T G G C A T T T T C T A T G G T
SEQ. ID. NO. 42 G A A A G A A G A T T C T A A A A C G T C C A C C

SEQ. ID. NO. 44 T A C A A G G G G C T G C T G C T G C T G C T G G
SEQ. ID. NO. 42 T C G G T C A C C A G T G T G A A C C A A G C C A

SEQ. ID. NO. 44 G A A T C T T C C T T G C T T A T G A G A C C A A
SEQ. ID. NO. 42 G C A C A T C C C G C C T G G A G G G C C T A C A

SEQ. ID. NO. 44 G A G T G T G T C C A C T G A G A A G A T C A A T
SEQ. ID. NO. 42 G T C A G A A A A C C A T C G C C T G C G A A T G

SEQ. ID. NO. 44 G A T C A C C G G G C T G T G G G C A T G G C T A
SEQ. ID. NO. 42 A A G A T C A C A G A G C T G G A T A A A G A C T

SEQ. ID. NO. 44 T C T A C A A T G T G G C A G T C C T G T G C C T
SEQ. ID. NO. 42 T G G A A G A G G T C A C C A T G C A G C T G C A

SEQ. ID. NO. 44 C A T C A C T G C T C C T G T C A C C A T G A T T
SEQ. ID. NO. 42 G G A C A C A C C A G A A A A G A C C A C C T A C

SEQ. ID. NO. 44 C T G T C C A G C C A G C A G G A T G C A G C C T
SEQ. ID. NO. 42 A T T A A A C A G A A C C A C T A C C A A G A G C

SEQ. ID. NO. 44 T T G C C T T T G C C T C T C T T G C C A T A G T
SEQ. ID. NO. 42 T C A A T G A C A T C C T C A A C C T G G G A A A

SEQ. ID. NO. 44 T T T C T C C T C C T A T A T C A C T C T T G T T
SEQ. ID. NO. 42 C T T C A C T G A G A G C A C A G A T G G A G G A

SEQ. ID. NO. 44 G T G C T C T T T G T G C C C A A G A T G C G C A
SEQ. ID. NO. 42 A A G G C C A T T T T A A A A A A T C A C C T C G

FIG. 13h.

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SEQ. ID. NO. 44 G G C T G A T C A C C C G A G G G G A A T G G C A
SEQ. ID. NO. 42 A T C A A A A T C C C C A G C T A C A G T G G A A

SEQ. ID. NO. 44 G T C G G A G G C G C A G G A C A C C A T G A A G
SEQ. ID. NO. 42 C A C A A C A G A G C C C T C T C G A A C A T G C

SEQ. ID. NO. 44 A C A G G G T C A T C G A C C A A C A A C A A C G
SEQ. ID. NO. 42 A A A G A T C C T A T A G A A G A T A T A A A C T

SEQ. ID. NO. 44 A G G A G G A G A A G T C C C G G C T G T T G G A
SEQ. ID. NO. 42 C T C C A G A A C A C A T C C A G C G T C G G C T

SEQ. ID. NO. 44 G A A G G A G A A C C G T G A A C T G G A A A A G
SEQ. ID. NO. 42 G T C C C T C C A G C T C C C C A T C C T C C A C

SEQ. ID. NO. 44 A T C A T T G C T G A G A A A G A G G A G C G T G
SEQ. ID. NO. 42 C A C G C C T A C C T C C C A T C C A T C G G A G

SEQ. ID. NO. 44 T C T C T G A A C T G C G C C A T C A A C T C C A
SEQ. ID. NO. 42 G C G T G G A C G C C A G C T G T G T C A G C C C

SEQ. ID. NO. 44 G T C T C G G C A G C A G C T C C G C T C C C G G
SEQ. ID. NO. 42 C T G C G T C A G C C C C A C C G C C A G C C C C

SEQ. ID. NO. 44 C G C C A C C C A C C G A C A C C C C C A G A A C
SEQ. ID. NO. 42 C G C C A C A G A C A T G T G C C A C C C T C C T

SEQ. ID. NO. 44 C C T C T G G G G G C C T G C C C A G G G G A C C
SEQ. ID. NO. 42 T C C G A G T C A T G G T C T C G G G C C T G G C

SEQ. ID. NO. 44 C C C T G A G C C C C C C G A C C G G C T T A G C
SEQ. ID. NO. 42 G G C C G C C A T G A C T C T G G A G T C C A T C

SEQ. ID. NO. 44 T G T G A T G G G A G T C G A G T G C A T T T G C
SEQ. ID. NO. 42 A T G G C G T G C T G C C T G A G C G A G G A G G

SEQ. ID. NO. 44 T T T A T A A G G C G G C C G C C A T G A C T C T
SEQ. ID. NO. 42 C C A A G G A A G C C C G G C G G A T C A A C G A

FIG. 13i.

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SEQ. ID. NO. 44 G G A G T C C A T C A T G G C G T G C T G C C T G
SEQ. ID. NO. 42 C G A G A T C G A G C G G C A G C T C C G C A G G

SEQ. ID. NO. 44 A G C G A G G A G G C C A A G G A A G C C C G G C
SEQ. ID. NO. 42 G A C A A G C G G G A C G C C C G C C G G G A G C

SEQ. ID. NO. 44 G G A T C A A C G A C G A G A T C G A G C G G C A
SEQ. ID. NO. 42 T C A A G C T G C T G C T G C T C G G G A C A G G

SEQ. ID. NO. 44 G C T C C G C A G G G A C A A G C G G G A C G C C
SEQ. ID. NO. 42 A G A G A G T G G C A A G A G T A C G T T T A T C

SEQ. ID. NO. 44 C G C C G G G A G C T C A A G C T G C T G C T G C
SEQ. ID. NO. 42 A A G C A G A T G A G A A T C A T C C A T G G G T

SEQ. ID. NO. 44 T C G G G A C A G G A G A G A G T G G C A A G A G
SEQ. ID. NO. 42 C A G G A T A C T C T G A T G A A G A T A A A A G

SEQ. ID. NO. 44 T A C G T T T A T C A A G C A G A T G A G A A T C
SEQ. ID. NO. 42 G G G C T T C A C C A A G C T G G T G T A T C A G

SEQ. ID. NO. 44 A T C C A T G G G T C A G G A T A C T C T G A T G
SEQ. ID. NO. 42 A A C A T C T T C A C G G C C A T G C A G G C C A

SEQ. ID. NO. 44 A A G A T A A A A G G G G C T T C A C C A A G C T
SEQ. ID. NO. 42 T G A T C A G A G C C A T G G A C A C A C T C A A

SEQ. ID. NO. 44 G G T G T A T C A G A A C A T C T T C A C G G C C
SEQ. ID. NO. 42 G A T C C C A T A C A A G T A T G A G C A C A A T

SEQ. ID. NO. 44 A T G C A G G C C A T G A T C A G A G C C A T G G
SEQ. ID. NO. 42 A A G G C T C A T G C A C A A T T A G T T C G A G

SEQ. ID. NO. 44 A C A C A C T C A A G A T C C C A T A C A A G T A
SEQ. ID. NO. 42 A A G T T G A T G T G G A G A A G G T G T C T G C

SEQ. ID. NO. 44 T G A G C A C A A T A A G G C T C A T G C A C A A
SEQ. ID. NO. 42 T T T T G A G A A T C C A T A T G T A G A T G C A

FIG. 13j.

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SEQ. ID. NO. 44 T T A G T T C G A G A A G T T G A T G T G G A G A
SEQ. ID. NO. 42 A T A A A G A G T T T A T G G A A T G A T C C T G

SEQ. ID. NO. 44 A G G T G T C T G C T T T T G A G A A T C C A T A
SEQ. ID. NO. 42 G A A T C C A G G A A T G C T A T G A T A G A C G

SEQ. ID. NO. 44 T G T A G A T G C A A T A A A G A G T T T A T G G
SEQ. ID. NO. 42 A C G A G A A T A T C A A T T A T C T G A C T C T

SEQ. ID. NO. 44 A A T G A T C C T G G A A T C C A G G A A T G C T
SEQ. ID. NO. 42 A C C A A A T A C T A T C T T A A T G A C T T G G

SEQ. ID. NO. 44 A T G A T A G A C G A C G A G A A T A T C A A T T
SEQ. ID. NO. 42 A C C G C G T A G C T G A C C C T G C C T A C C T

SEQ. ID. NO. 44 A T C T G A C T C T A C C A A A T A C T A T C T T
SEQ. ID. NO. 42 G C C T A C G C A A C A A G A T G T G C T T A G A

SEQ. ID. NO. 44 A A T G A C T T G G A C C G C G T A G C T G A C C
SEQ. ID. NO. 42 G T T C G A G T C C C C A C C A C A G G G A T C A

SEQ. ID. NO. 44 C T G C C T A C C T G C C T A C G C A A C A A G A
SEQ. ID. NO. 42 T C G A A T A C C C C T T T G A C T T A C A A A G

SEQ. ID. NO. 44 T G T G C T T A G A G T T C G A G T C C C C A C C
SEQ. ID. NO. 42 T G T C A T T T T C A G A A T G G T C G A T G T A

SEQ. ID. NO. 44 A C A G G G A T C A T C G A A T A C C C C T T T G
SEQ. ID. NO. 42 G G G G G C C A A A G G T C A G A G A G A A G A A

SEQ. ID. NO. 44 A C T T A C A A A G T G T C A T T T T C A G A A T
SEQ. ID. NO. 42 A A T G G A T A C A C T G C T T T G A A A A T G T

SEQ. ID. NO. 44 G G T C G A T G T A G G G G G C C A A A G G T C A
SEQ. ID. NO. 42 C A C C T C T A T C A T G T T T C T A G T A G C G

SEQ. ID. NO. 44 G A G A G A A G A A A A T G G A T A C A C T G C T
SEQ. ID. NO. 42 C T T A G T G A A T A T G A T C A A G T T C T G G

FIG. 13k.

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SEQ. ID. NO. 44 TTGAAAATGTCACCTCTATCATGTT
SEQ. ID. NO. 42 TGGAGTCAGACAATGAGAACCGAAT

SEQ. ID. NO. 44 TCTAGTAGCGCTTAGTGAAATATGAT
SEQ. ID. NO. 42 GGAGGAAAGCAAGGCTCTCTTTAGAA

SEQ. ID. NO. 44 CAAGTTCTCTGTGGAGTCAGACAATG
SEQ. ID. NO. 42 ACAATTATCACATACCCCTGGTTCC

SEQ. ID. NO. 44 AGAACCGAATGGAGGAAAGCAAGGC
SEQ. ID. NO. 42 AGAACTCCTCTGGTTATTCTGTTCCTT

SEQ. ID. NO. 44 TCTCTTTAGAACAAATTATCACATAC
SEQ. ID. NO. 42 AAACAAGAAAGATCTTCTAGAGGAG

SEQ. ID. NO. 44 CCTGGTTTCCAGAACTCCTCTGGTTTA
SEQ. ID. NO. 42 AAAATCATGTATTCCCATCTAGTCG

SEQ. ID. NO. 44 TTCTGTTCCTTAAACAAGAAAGATCTT
SEQ. ID. NO. 42 ACTACTTCCAGAAATATGATGGACC

SEQ. ID. NO. 44 TCTAGAGGAGAAAATCATGTATTCC
SEQ. ID. NO. 42 CCAGAGAGATGCCCAGGCAGCCCCGA

SEQ. ID. NO. 44 CATCTAGTCGACTACTTCCCAGAAAT
SEQ. ID. NO. 42 GAATTTCATTCTGAAGATGTTCTGTGG

SEQ. ID. NO. 44 ATGATGGACCCAGAGAGATGCCCA
SEQ. ID. NO. 42 ACCTGAACCCAGACAGTGACAAAAAT

SEQ. ID. NO. 44 GGCAGCCCGAGAAATTCATTCTGAAG
SEQ. ID. NO. 42 TAACTACTCCCACTTCACTGTGCGCC

SEQ. ID. NO. 44 ATGTTCTGTGGACCTGAACCCAGACA
SEQ. ID. NO. 42 ACAGACACCAGAAATATCCGCTTTG

SEQ. ID. NO. 44 GTGACAAAATTATCTACTCCCACTT
SEQ. ID. NO. 42 TCTTTTGCTGCCGTCAAGGACACCAAT

FIG. 13L.

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SEQ. ID. NO. 44 C A C G T G C G C C A C A G A C A C C G A G A A T
SEQ. ID. NO. 42 C C T C C A G T T G A A C C T G A A G G G C T G C

SEQ. ID. NO. 44 A T C C G C T T T G T C T T T G C T G C C G T C A
SEQ. ID. NO. 42 G G T C T G T A C

SEQ. ID. NO. 44 A G G A C A C C A T C C T C C A G T T G A A C C T
SEQ. ID. NO. 42

SEQ. ID. NO. 44 G A A G G G C T G C G G T C T G T A C
SEQ. ID. NO. 42

FIG. 13m.

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ClustalW Formatted Alignments

SEQ. ID. NO. 45 M L L L L L L A P L F L R P P G A G G A Q T P N A
SEQ. ID. NO. 43 M A S P R S S G Q P G P P P P P P P P A R L L L

SEQ. ID. NO. 45 T S E G C Q I I H P P W E G G I R Y R G L T R D Q
SEQ. ID. NO. 43 L L L L P L L L P L A P G A W G W A R G A P R P P

SEQ. ID. NO. 45 V K A I N F L P V D Y E I E Y V C R G E R E V V G
SEQ. ID. NO. 43 P S S P P L S I M G L M P L T K E V A K G S I G R

SEQ. ID. NO. 45 P K V R K C L A N G S W T D M D T P S R C V R I C
SEQ. ID. NO. 43 G V L P A V E L A I E Q I R N E S L L R P Y F L D

SEQ. ID. NO. 45 S K S Y L T L E N G K V F L T G G D L P A L D G A
SEQ. ID. NO. 43 L R L Y D T E C D N A K G L K A F Y D A I K Y G P

SEQ. ID. NO. 45 R V D F R C D P D F H L V G S S R S I C S Q G Q W
SEQ. ID. NO. 43 N H L M V F G G V C P S V T S I I A E S L Q G W N

SEQ. ID. NO. 45 S T P K P H C Q V N R T P H S E R R A V Y I G A L
SEQ. ID. NO. 43 L V Q L S F A A T T P V L A D K K K Y P Y F F R T

SEQ. ID. NO. 45 F P M S G G W P G G Q A C Q P A V E M A L E D V N
SEQ. ID. NO. 43 V P S D N A V N P A I L K L L K H Y Q W K R V G T

SEQ. ID. NO. 45 S R R D I L P D Y E L K L I H H D S K C D P G Q A
SEQ. ID. NO. 43 L T Q D V Q R F S E V R N D L T G V L Y G E D I E

SEQ. ID. NO. 45 T K Y L Y E L L Y N D P I K I I L M P G C S S V S
SEQ. ID. NO. 43 I S D T E S F S N D P C T S V K K L K G N D V R I

SEQ. ID. NO. 45 T L V A E A A R M W N L I V L S Y G S S S P A L S
SEQ. ID. NO. 43 I L G Q F D Q N M A A K V F C C A Y E E N M Y G S

SEQ. ID. NO. 45 N R Q R F P T F F R T H P S A T L H N P T R V K L
SEQ. ID. NO. 43 K Y Q W I I P G W Y E P S W W E Q V H T E A N S S

FIG. 14a.

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SEQ. ID. NO. 45 F E K W G W K K I A T I Q Q T T E V F T S T L D D
SEQ. ID. NO. 43 R C L R K N L L A A M E G Y I G V D F E P L S S K

SEQ. ID. NO. 45 L E E R V K E A G I E I T F R Q S F F S D P A V P
SEQ. ID. NO. 43 Q I K T I S G K T P Q Q Y E R E Y N N K R S G V G

SEQ. ID. NO. 45 V K N L K R Q D A R I I V G L F Y E T E A R K V F
SEQ. ID. NO. 43 P S K F H G Y A Y D G I W V I A K T L Q R A M E T

SEQ. ID. NO. 45 C E V Y K E R L F G K K Y V W F L I G W Y A D N W
SEQ. ID. NO. 43 L H A S S R H Q R I Q D F N Y T D H T L G R I I L

SEQ. ID. NO. 45 F K I Y D P S I N C T V D E M T E A V E G H I T T
SEQ. ID. NO. 43 N A M N E T N F F G V T G Q V V F R N G E R M G T

SEQ. ID. NO. 45 E I V M L N P A N T R S I S N M T S Q E F V E K L
SEQ. ID. NO. 43 I K F T Q F Q D S R E V K V G E Y N A V A D T L E

SEQ. ID. NO. 45 T K R L K R H P E E T G G - F Q E A P L A Y D A I
SEQ. ID. NO. 43 I I N D T I R F Q G S E P P K D K T I I L E Q L R

SEQ. ID. NO. 45 W A L A L A L N K T S G G G G R S G V R L E D F N
SEQ. ID. NO. 43 K I S L P L Y S I L S A L T I L G M I M A S A F L

SEQ. ID. NO. 45 Y N N Q T I T D Q I Y R A M N S S S F E G V S G H
SEQ. ID. NO. 43 F F N I K N R N Q K L I K M S S P Y M N N L I I L

SEQ. ID. NO. 45 V V F D A S G S R M A W T L I E Q L Q G G S Y K K
SEQ. ID. NO. 43 G G M L S Y A S I F L F G L D G S F V S E K T F E

SEQ. ID. NO. 45 I G Y Y D S T K D D L S W S K T D K W I G G S P P
SEQ. ID. NO. 43 T L C T V R T W I L T V G Y T T A F G A M F A K T

SEQ. ID. NO. 45 A D Q T L V I K T F R F L S Q K L F I S V S V L S
SEQ. ID. NO. 43 W R V H A I F K N V K M K K K I I K D Q K L L V I

SEQ. ID. NO. 45 S L G I V L A V V C L S F N I Y N S H V R Y I Q N
SEQ. ID. NO. 43 V G G M L L I D L C I L I C W Q A V D P L R R T V

FIG. 14b.

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SEQ. ID. NO. 45 S Q P N L N N L T A V G C S L A L A A V F P L G L
SEQ. ID. NO. 43 E K Y S M E P D P A G R D I S I R P L L E H C E N

SEQ. ID. NO. 45 D G Y H I G R N Q F P F V C Q A R L W L L G L G F
SEQ. ID. NO. 43 T H M T I W L G I V Y A Y K G L L M L F G C F L A

SEQ. ID. NO. 45 S L G Y G S M F T K I W W V H T V F T K K E E K K
SEQ. ID. NO. 43 W E T R N V S I P A L N D S K Y I G M S V Y N V G

SEQ. ID. NO. 45 E W R K T L E P W K L Y A T V G L L V G M D V L T
SEQ. ID. NO. 43 I M C I I G A A V S F L T R D Q P N V Q F C I V A

SEQ. ID. NO. 45 L A I W Q I V D P L H R T I E T F A K E E P K E D
SEQ. ID. NO. 43 L V I I F C S T I T L C L V F V P K L I T L R T N

SEQ. ID. NO. 45 I D V S I L P Q L E H C S S R K M N T W L G I F Y
SEQ. ID. NO. 43 P D A A T Q N R R F Q F T Q N Q K K E D S K T S T

SEQ. ID. NO. 45 G Y K G L L L L L G I F L A Y E T K S V S T E K I
SEQ. ID. NO. 43 S V T S V N Q A S T S R L E G L Q S E N H R L R M

SEQ. ID. NO. 45 N D H R A V G M A I Y N V A V L C L I T A P V T M
SEQ. ID. NO. 43 K I T E L D K D L E E V T M Q L Q D T P E K T T Y

SEQ. ID. NO. 45 I L S S Q Q D A A F A F A S L A I V F S S Y I T L
SEQ. ID. NO. 43 I K Q N H Y Q E L N D I L N L G N F T E S T D G G

SEQ. ID. NO. 45 V V L F V P K M R R L I T R G E W Q S E A Q D T M
SEQ. ID. NO. 43 K A I L K N H L D Q N P Q L Q W N T T E P S R T C

SEQ. ID. NO. 45 K T G S S T N N N E E E K S R L L E K E N R E L E
SEQ. ID. NO. 43 K D P I E D I N S P E H I Q R R L S L Q L P I L H

SEQ. ID. NO. 45 K I I A E K E E R V S E L R H Q L Q S R Q Q L R S
SEQ. ID. NO. 43 H A Y L P S I G G V D A S C V S P C V S P T A S P

SEQ. ID. NO. 45 R R H P P T P P E P S G G L P R G P P E P P D R L
SEQ. ID. NO. 43 R H R H V P P S F R V M V S G L A A A M T L E S I

FIG. 14c.

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SEQ. ID. NO. 45 S C D G S R V H L L Y K A A A M T L E S I M A C C
SEQ. ID. NO. 43 M A C C L S E E A K E A R R I N D E I E R Q L R R

SEQ. ID. NO. 45 L S E E A K E A R R I N D E I E R Q L R R D K R D
SEQ. ID. NO. 43 D K R D A R R E L K L L L L G T G E S G K S T F I

SEQ. ID. NO. 45 A R R E L K L L L L G T G E S G K S T F I K Q M R
SEQ. ID. NO. 43 K Q M R I I H G S G Y S D E D K R G F T K L V Y Q

SEQ. ID. NO. 45 I I H G S G Y S D E D K R G F T K L V Y Q N I F T
SEQ. ID. NO. 43 N I F T A M Q A M I R A M D T L K I P Y K Y E H N

SEQ. ID. NO. 45 A M Q A M I R A M D T L K I P Y K Y E H N K A H A
SEQ. ID. NO. 43 K A H A Q L V R E V D V E K V S A F E N P Y V D A

SEQ. ID. NO. 45 Q L V R E V D V E K V S A F E N P Y V D A I K S L
SEQ. ID. NO. 43 I K S L W N D P G I Q E C Y D R R R E Y Q L S D S

SEQ. ID. NO. 45 W N D P G I Q E C Y D R R R E Y Q L S D S T K Y Y
SEQ. ID. NO. 43 T K Y Y L N D L D R V A D P A Y L P T Q Q D V L R

SEQ. ID. NO. 45 L N D L D R V A D P A Y L P T Q Q D V L R V R V P
SEQ. ID. NO. 43 V R V P T T G I I E Y P F D L Q S V I F R M V D V

SEQ. ID. NO. 45 T T G I I E Y P F D L Q S V I F R M V D V G G Q R
SEQ. ID. NO. 43 G G Q R S E R R K W I H C F E N V T S I M F L V A

SEQ. ID. NO. 45 S E R R K W I H C F E N V T S I M F L V A L S E Y
SEQ. ID. NO. 43 L S E Y D Q V L V E S D N E N R M E E S K A L F R

SEQ. ID. NO. 45 D Q V L V E S D N E N R M E E S K A L F R T I I T
SEQ. ID. NO. 43 T I I T Y P W F Q N S S V I L F L N K K D L L E E

SEQ. ID. NO. 45 Y P W F Q N S S V I L F L N K K D L L E E K I M Y
SEQ. ID. NO. 43 K I M Y S H L V D Y F P E Y D G P Q R D A Q A A R

SEQ. ID. NO. 45 S H L V D Y F P E Y D G P Q R D A Q A A R E F I L
SEQ. ID. NO. 43 E F I L K M F V D L N P D S D K I N Y S H F T C A

FIG. 14d.

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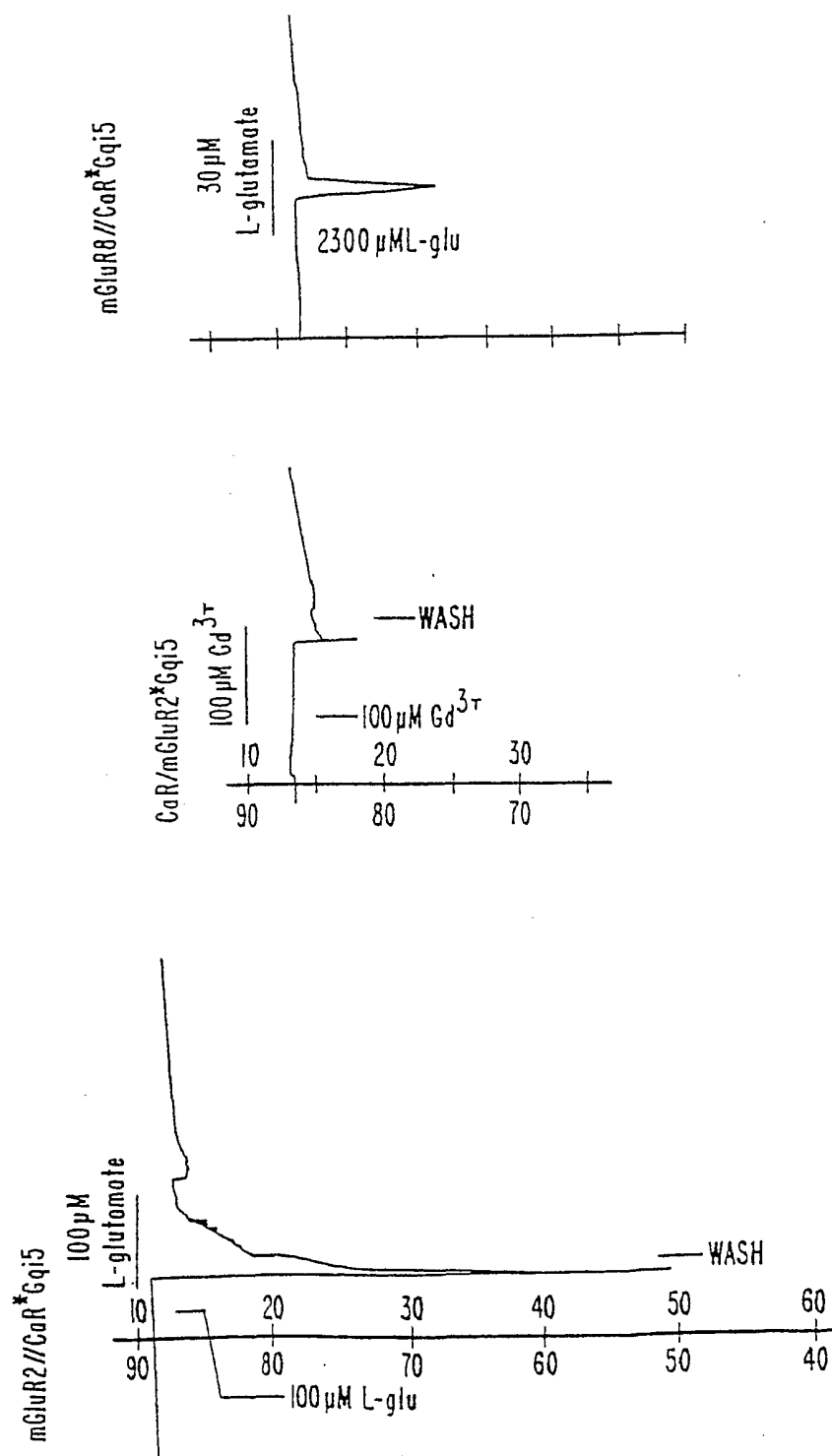
SEQ. ID. NO. 45 K M F V D L N P D S D K I I Y S H F T C A T D T E
SEQ. ID. NO. 43 T D T E N I R F V F A A V K D T I L Q L N L K G C

SEQ. ID. NO. 45 N I R F V F A A V K D T I L Q L N L K G C G L Y
SEQ. ID. NO. 43 G L Y

FIG. 14e.

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FIG. 15.



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SEQ. ID. NO. 48 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
 SEQ. ID. NO. 49 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R
 SEQ. ID. NO. 50 M V C E G K R S A S C P C F F L L T A K F Y W I L T M M Q R

SEQ. ID. NO. 48 T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
 SEQ. ID. NO. 49 T H S Q E Y A H S I R I D G D I T L G G L F P V H G R G S E
 SEQ. ID. NO. 50 T H S Q E Y A H S I R V D G D I I L G G L F P V H A K G E R

SEQ. ID. NO. 48 G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
 SEQ. ID. NO. 49 G K P C G E L K K E K G I H R L E A M L F A L D R I N N D P
 SEQ. ID. NO. 50 G V P C G E L K K E K G I H R L E A M L Y A I D Q I N K D P

SEQ. ID. NO. 48 D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
 SEQ. ID. NO. 49 D L L P N I T L G A R I L D T C S R D T H A L E Q S L T F V
 SEQ. ID. NO. 50 D L L S N I T L G V R I L D T C S R D T Y A L E Q S L T F V

SEQ. ID. NO. 48 Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
 SEQ. ID. NO. 49 Q A L I E K D G T E V R C G S G G P P I I T K P E R V V G V
 SEQ. ID. NO. 50 Q A L I E K D A S D V K C A N G D P P I F T K P D K I S G V

SEQ. ID. NO. 48 I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
 SEQ. ID. NO. 49 I G A S G S S V S I M V A N I L R L F K I P Q I S Y A S T A
 SEQ. ID. NO. 50 I G A A A S S V S I M V A N I L R L F K I P Q I S Y A S T A

SEQ. ID. NO. 48 P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
 SEQ. ID. NO. 49 P D L S D N S R Y D F F S R V V P S D T Y Q A Q A M V D I V
 SEQ. ID. NO. 50 P E L S D N T R Y D F F S R V V P P D S Y Q A Q A M V D I V

SEQ. ID. NO. 48 R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
 SEQ. ID. NO. 49 R A L K W N Y V S T V A S E G S Y G E S G V E A F I Q K S R
 SEQ. ID. NO. 50 T A L G W N Y V S T L A S E G N Y G E S G V E A F T Q I S R

SEQ. ID. NO. 48 E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
 SEQ. ID. NO. 49 E D G G V C I A Q S V K I P R E P K A G E F D K I I R R L L
 SEQ. ID. NO. 50 E I G G V C I A Q S Q K I P R E P R P G E F E K I I K R L L

FIG. 16a.

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SEQ. ID. NO. 48 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
 SEQ. ID. NO. 49 E T S N A R A V I I F A N E D D I R R V L E A A R R A N Q T
 SEQ. ID. NO. 50 E T P N A R A V I M F A N E D D I R R I L E A A K K L N Q S

SEQ. ID. NO. 48 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
 SEQ. ID. NO. 49 G H F F W M G S D S W G S K I A P V L H L E E V A E G A V T
 SEQ. ID. NO. 50 G H F L W I G S D S W G S K I A P V Y Q Q E E I A E G A V T

SEQ. ID. NO. 48 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
 SEQ. ID. NO. 49 I L P K R M S V R G F D R Y F S S R T L D N N R R N I W F A
 SEQ. ID. NO. 50 I L P K R A S I D G F D R Y F R S R T L A N N R R N V W F A

SEQ. ID. NO. 48 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
 SEQ. ID. NO. 49 E F W E D N F H C K L S R H A L K K G S H V K K C T N R E R
 SEQ. ID. NO. 50 E F W E E N F G C K L G S H G K R N - S H I K K C T G L E R

SEQ. ID. NO. 48 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
 SEQ. ID. NO. 49 I G Q D S A Y E Q E G K V Q F V I D A V Y A M G H A L H A M
 SEQ. ID. NO. 50 I A R D S S Y E Q E G K V Q F V I D A V Y S M A Y A L H N M

SEQ. ID. NO. 48 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
 SEQ. ID. NO. 49 H R D L C P G R V G L C P R M D P V D G T Q L L K Y I R N V
 SEQ. ID. NO. 50 H K D L C P G Y I G L C P R M S T I D G K E L L G Y I R A V

SEQ. ID. NO. 48 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
 SEQ. ID. NO. 49 N F S G I A G N P V T F N E N G D A P G R Y D I Y Q Y Q L R
 SEQ. ID. NO. 50 N F N G S A G T P V T F N E N G D A P G R Y D I F Q Y Q I T

SEQ. ID. NO. 48 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
 SEQ. ID. NO. 49 N D S A E Y K V I G S W T D H L H L R I E R M H W P G S G Q
 SEQ. ID. NO. 50 N K S T E Y K V I G H W T N Q L H L K V E D M Q W A H R E H

SEQ. ID. NO. 48 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
 SEQ. ID. NO. 49 Q L P R S I C S L P C Q P G E R K K T V K G M P C C W H C E
 SEQ. ID. NO. 50 T H P A S V C S L P C K P G E R K K T V K G V P C C W H C E

SEQ. ID. NO. 48 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
 SEQ. ID. NO. 49 P C T G Y Q Y Q V D R Y T C K T C P Y D M R P T E N R T G C
 SEQ. ID. NO. 50 R C E G Y N Y Q V D E L S C E L C P L D Q R P N M N R T G C

FIG. 16b.

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SEQ. ID. NO. 48 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
 SEQ. ID. NO. 49 R P I P I I K L E W G S P W A V L P L F L A V V G I A A T L
 SEQ. ID. NO. 50 Q L I P I I K L E W H S P W A V V P V F V A I L G I I A T T

SEQ. ID. NO. 48 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
 SEQ. ID. NO. 49 F V V I T F V R Y N D T P I V K A S G R E L S Y V L L A G I
 SEQ. ID. NO. 50 F V I V T F V R Y N D T P I V R A S G R E L S Y V L L T G I

SEQ. ID. NO. 48 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
 SEQ. ID. NO. 49 F L C Y A T T F L M I A E P D L G T C S L R R I F L G L G M
 SEQ. ID. NO. 50 F L C Y S I T F L M I A A P D T I I C S F R R V F L G L G M

SEQ. ID. NO. 48 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
 SEQ. ID. NO. 49 S I S Y A A L L T K T N R I Y R I F E Q G K R S V S A P R F
 SEQ. ID. NO. 50 C F S Y A A L L T K T N R I H R I F E Q G K K S V T A P K F

SEQ. ID. NO. 48 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
 SEQ. ID. NO. 49 I S P A S Q L A I T F S L I S L Q L L G I C V W F V V D P S
 SEQ. ID. NO. 50 I S P A S Q L V I T F S L I S V Q L L G V F V W F V V D P P

SEQ. ID. NO. 48 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
 SEQ. ID. NO. 49 H S V V D F Q D Q R T L D P R F A R G V L K C D I S D L S L
 SEQ. ID. NO. 50 H I I I D Y G E Q R T L D P E K A R G V L K C D I S D L S L

SEQ. ID. NO. 48 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
 SEQ. ID. NO. 49 I C L L G Y S M L L M V T C T V Y A I K T R G V P E T F N E
 SEQ. ID. NO. 50 I C S L G Y S I L L M V T C T V Y A I K T R G V P E T F N E

SEQ. ID. NO. 48 A K P I G F T M Y T T C I V W L A F I P I F F G T S Q S A D
 SEQ. ID. NO. 49 A K P I G F T M Y T T C I V W L A F I P I F F G T S Q S A D
 SEQ. ID. NO. 50 A K P I G F T M Y T T C I I W L A F I P I F F G T A Q S A E

SEQ. ID. NO. 48 K L Y I Q T T T L T V S V S L S A S V S L G M L Y M P K V Y
 SEQ. ID. NO. 49 K L Y I Q T T T L T V S V S L S A S V S L G M L Y M P K V Y
 SEQ. ID. NO. 50 K M Y I Q T T T L T V S M S L S A S V S L G M L Y M P K V Y

SEQ. ID. NO. 48 I I L F H P E Q N V P K R K R S L K A V V T A A T M S N K F
 SEQ. ID. NO. 49 I I L F H P E Q N T I E E V R C S T A A H A F K V A A R A T
 SEQ. ID. NO. 50 I I I F H P E Q N T I E E V R C S T A A H A F K V A A R A T

FIG. 16c.

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SEQ. ID. NO. 48 T Q K G N F R P N G E A K S E L C E N L E A P A L A T K Q T
SEQ. ID. NO. 49 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S
SEQ. ID. NO. 50 L R R S N V S R K R S S S L G G S T G S T P S S S I S S K S

SEQ. ID. NO. 48 Y V T Y T N H A I
SEQ. ID. NO. 49 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L
SEQ. ID. NO. 50 N S E D P F P Q P E R Q K Q Q Q P L A L T Q Q E Q Q Q Q P L

SEQ. ID. NO. 48
SEQ. ID. NO. 49 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S
SEQ. ID. NO. 50 T L P Q Q Q R S Q Q Q P R C K Q K V I F G S G T V T F S L S

SEQ. ID. NO. 48
SEQ. ID. NO. 49 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T
SEQ. ID. NO. 50 F D E P Q K N A M A H G N S T H Q N S L E A Q K S S D T L T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G
SEQ. ID. NO. 50 R H Q P L L P L Q C G E T D L D L T V Q E T G L Q G P V G G

SEQ. ID. NO. 48
SEQ. ID. NO. 49 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G
SEQ. ID. NO. 50 D Q R P E V E D P E E L S P A L V V S S S Q S F V I S G G G

SEQ. ID. NO. 48
SEQ. ID. NO. 49 S T V T E N V V N S A A A M T L E S I M A C C L S E E A K E
SEQ. ID. NO. 50 S T V T E N V V N S A A A M T L E S I M A C C L S E E A K E

SEQ. ID. NO. 48
SEQ. ID. NO. 49 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T
SEQ. ID. NO. 50 A R R I N D E I E R Q L R R D K R D A R R E L K L L L L G T

SEQ. ID. NO. 48
SEQ. ID. NO. 49 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K
SEQ. ID. NO. 50 G E S G K S T F I K Q M R I I H G S G Y S D E D K R G F T K

SEQ. ID. NO. 48
SEQ. ID. NO. 49 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K
SEQ. ID. NO. 50 L V Y Q N I F T A M Q A M I R A M D T L K I P Y K Y E H N K

FIG. 16d.

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SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

A H A Q L V R E V D V E K V S A F E N P Y V D A I K S L W N
A H A Q L V R E V D V E K V S A F E N P Y V D A I K S L W N

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V
D P G I Q E C Y D R R R E Y Q L S D S T K Y Y L N D L D R V

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q
A D P A Y L P T Q Q D V L R V R V P T T G I I E Y P F D L Q

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M
S V I F R M V D V G G Q R S E R R K W I H C F E N V T S I M

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T
F L V A L S E Y D Q V L V E S D N E N R M E E S K A L F R T

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H
I I T Y P W F Q N S S V I L F L N K K D L L E E K I M Y S H

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N
L V D Y F P E Y D G P Q R D A Q A A R E F I L K M F V D L N

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

P D S D K I I Y S H F T C A T D T E N I R F V F A A V K D T
P D S D K I I Y S H F T C A T D T E N I R F V F A A V K D T

SEQ. ID. NO. 48

SEQ. ID. NO. 49

SEQ. ID. NO. 50

I L Q L N L K D C G L F
I L Q L N L K D C G L F

FIG. 16e.

ph2SpmGluR3 nucleic acid sequence (SEQ ID NO. 51) with encoded amino acid sequence (SEQ ID NO. 52)

	Met	Gly	Ser	Leu	Leu	Ala	Leu	Pro	Ala	Leu	Leu	Leu	Leu	Trp	Gly
1	ATG	GGA	TCG	CTG	CTT	GCG	CTC	CCG	GCA	CTG	CTG	CTG	CTG	TGG	GGT
	Ala	Val	Ala	Leu	Gly	Asp	His	Asn	Phe	Leu	Arg	Arg	Glu	Ile	Lys
46	GCT	GTG	GCT	TTA	GGG	GAC	CAT	AAC	TTT	CTA	AGG	AGA	GAG	ATT	AAA
	Ile	Glu	Gly	Asp	Leu	Val	Leu	Gly	Gly	Leu	Phe	Pro	Ile	Asn	Glu
91	ATA	GAA	GGT	GAC	CTT	GTT	TTA	GGG	GGC	CTG	TTT	CCT	ATT	AAC	GAA
	Lys	Gly	Thr	Gly	Thr	Glu	Glu	Cys	Gly	Arg	Ile	Asn	Glu	Asp	Arg
136	AAA	GGC	ACT	GGA	ACT	GAA	GAA	TGT	GGG	CGA	ATC	AAT	GAA	GAC	CGA
	Gly	Ile	Gln	Arg	Leu	Glu	Ala	Met	Leu	Phe	Ala	Ile	Asp	Glu	Ile
181	GGG	ATT	CAA	CGC	CTG	GAA	GCC	ATG	TTG	TTT	GCT	ATT	GAT	GAA	ATC
	Asn	Lys	Asp	Asp	Tyr	Leu	Leu	Pro	Gly	Val	Lys	Leu	Gly	Val	His
226	AAC	AAA	GAT	GAT	TAC	TTG	CTA	CCA	GGA	GTG	AAG	TTG	GGT	GTT	CAC
	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala	Leu	Glu	Gln	Ser
271	ATT	TTG	GAT	ACA	TGT	TCA	AGG	GAT	ACC	TAT	GCA	TTG	GAG	CAA	TCA
	Leu	Glu	Phe	Val	Arg	Ala	Ser	Leu	Thr	Lys	Val	Asp	Glu	Ala	Glu
316	CTG	GAG	TTT	GTC	AGG	GCA	TCT	TTG	ACA	AAA	GTG	GAT	GAA	GCT	GAG
	Tyr	Met	Cys	Pro	Asp	Gly	Ser	Tyr	Ala	Ile	Gln	Glu	Asn	Ile	Pro
361	TAT	ATG	TGT	CCT	GAT	GGA	TCC	TAT	GCC	ATT	CAA	GAA	AAC	ATC	CCA
	Leu	Leu	Ile	Ala	Gly	Val	Ile	Gly	Gly	Ser	Tyr	Ser	Ser	Val	Ser
406	CTT	CTC	ATT	GCA	GGG	GTC	ATT	GGT	GGC	TCT	TAT	AGC	AGT	GTT	TCC
	Ile	Gln	Val	Ala	Asn	Leu	Leu	Arg	Leu	Phe	Gln	Ile	Pro	Gln	Ile
451	ATA	CAG	GTG	GCA	AAC	CTG	CTG	CGG	CTC	TTC	CAG	ATC	CCT	CAG	ATC
	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser	Arg	Tyr
496	AGC	TAC	GCA	TCC	ACC	AGC	GCC	AAA	CTC	AGT	GAT	AAG	TCG	CGC	TAT
	Asp	Tyr	Phe	Ala	Arg	Thr	Val	Pro	Pro	Asp	Phe	Tyr	Gln	Ala	Lys
541	GAT	TAC	TTT	GCC	AGG	ACC	GTG	CCC	CCC	GAC	TTC	TAC	CAG	GCC	AAA
	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	Asn	Trp	Thr	Tyr	Val	Ser
586	GCC	ATG	GCT	GAG	ATC	TTG	CGC	TTC	TTC	AAC	TGG	ACC	TAC	GTG	TCC
	Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	Thr	Gly	Ile	Glu	Ala
631	ACA	GTA	GCC	TCC	GAG	GGT	GAT	TAC	GGG	GAG	ACA	GGG	ATC	GAG	GCC
	Phe	Glu	Gln	Glu	Ala	Arg	Leu	Arg	Asn	Ile	Cys	Ile	Ala	Thr	Ala
676	TTC	GAG	CAG	GAA	GCC	CGC	CTG	CGC	AAC	ATC	TGC	ATC	GCT	ACG	GCG
	Glu	Lys	Val	Gly	Arg	Ser	Asn	Ile	Arg	Lys	Ser	Tyr	Asp	Ser	Val
721	GAG	AAG	GTG	GGC	CGC	TCC	AAC	ATC	CGC	AAG	TCC	TAC	GAC	AGC	GTG
	Ile	Arg	Glu	Leu	Leu	Gln	Lys	Pro	Asn	Ala	Arg	Val	Val	Val	Leu
766	ATC	CGA	GAA	CTG	TTG	CAG	AAG	CCC	AAC	GCG	CGC	GTC	GTG	GTC	CTC
	Phe	Met	Arg	Ser	Asp	Asp	Ser	Arg	Glu	Leu	Ile	Ala	Ala	Ala	Ser
811	TTC	ATG	CGC	AGC	GAC	GAC	TCG	CGG	GAG	CTC	ATT	GCA	GCC	GCC	AGC
	Arg	Ala	Asn	Ala	Ser	Phe	Thr	Trp	Val	Ala	Ser	Asp	Gly	Trp	Gly
856	CGC	GCC	AAT	GCC	TCC	TTC	ACC	TGG	GTG	GCC	AGC	GAC	GGC	TGG	GGC
	Ala	Gln	Glu	Ser	Ile	Ile	Lys	Gly	Ser	Glu	His	Val	Ala	Tyr	Gly
901	GCG	CAG	GAG	AGC	ATC	ATC	AAG	GGC	AGC	GAG	CAT	GTG	GCC	TAC	GGC
	Ala	Ile	Thr	Leu	Glu	Leu	Ala	Ser	Gln	Pro	Val	Arg	Gln	Phe	Asp
946	GCC	ATC	ACC	CTG	GAG	CTG	GCC	TCC	CAG	CCT	GTC	CGC	CAG	TTC	GAC
	Arg	Tyr	Phe	Gln	Ser	Leu	Asn	Pro	Tyr	Asn	Asn	His	Arg	Asn	Pro
991	CGC	TAC	TTC	CAG	AGC	CTC	AAC	CCC	TAC	AAC	AAC	CAC	CGC	AAC	CCC
	Trp	Phe	Arg	Asp	Phe	Trp	Glu	Gln	Lys	Phe	Gln	Cys	Ser	Leu	Gln
1036	TGG	TTC	CGG	GAC	TTC	TGG	GAG	CAA	AAG	TTT	CAG	TGC	AGC	CTC	CAG
	Asn	Lys	Arg	Asn	His	Arg	Arg	Val	Cys	Asp	Lys	His	Leu	Ala	Ile
1081	AAC	AAA	CGC	AAC	CAC	AGG	CGC	GTC	TGC	GAC	AAG	CAC	CTG	GCC	ATC
	Asp	Ser	Ser	Asn	Tyr	Glu	Gln	Glu	Ser	Lys	Ile	Met	Phe	Val	Val
1126	GAC	AGC	AGC	AAC	TAC	GAG	CAA	GAG	TCC	AAG	ATC	ATG	TTT	GTG	GTG

FIG. 17a.

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	Asn	Ala	Val	Tyr	Ala	Met	Ala	His	Ala	Leu	His	Lys	Met	Gln	Arg
1171	AAC	GCG	GTG	TAT	GCC	ATG	GCC	CAC	GCT	TTG	CAC	AAA	ATG	CAG	CGC
	Thr	Leu	Cys	Pro	Asn	Thr	Thr	Lys	Leu	Cys	Asp	Ala	Met	Lys	Ile
1216	ACC	CTC	TGT	CCC	AAC	ACT	ACC	AAG	CTT	TGT	GAT	GCT	ATG	AAG	ATC
	Leu	Asp	Gly	Lys	Lys	Leu	Tyr	Lys	Asp	Tyr	Leu	Leu	Lys	Ile	Asn
1261	CTG	GAT	GGG	AAG	AAG	TTG	TAC	AAG	GAT	TAC	TTG	CTG	AAA	ATC	AAC
	Phe	Thr	Ala	Pro	Phe	Asn	Pro	Asn	Lys	Asp	Ala	Asp	Ser	Ile	Val
1306	TTC	ACG	GCT	CCA	TTC	AAC	CCA	AAT	AAA	GAT	GCA	GAT	AGC	ATA	GTC
	Lys	Phe	Asp	Thr	Phe	Gly	Asp	Gly	Met	Gly	Arg	Tyr	Asn	Val	Phe
1351	AAG	TTT	GAC	ACT	TTT	GGA	GAT	GGA	ATG	GGG	CGA	TAC	AAC	GTG	TTC
	Asn	Phe	Gln	Asn	Val	Gly	Gly	Lys	Tyr	Ser	Tyr	Leu	Lys	Val	Gly
1396	AAT	TTC	CAA	AAT	GTA	GGT	GGA	AAG	TAT	TCC	TAC	TTG	AAA	GTT	GGT
	His	Trp	Ala	Glu	Thr	Leu	Ser	Leu	Asp	Val	Asn	Ser	Ile	His	Trp
1441	CAC	TGG	GCA	GAA	ACC	TTA	TCG	CTA	GAT	GTC	AAC	TCT	ATC	CAC	TGG
	Ser	Arg	Asn	Ser	Val	Pro	Thr	Ser	Gln	Cys	Ser	Asp	Pro	Cys	Ala
1486	TCC	CGG	AAC	TCA	GTC	CCC	ACT	TCC	CAG	TGC	AGC	GAC	CCC	TGT	GCC
	Pro	Asn	Glu	Met	Lys	Asn	Met	Gln	Pro	Gly	Asp	Val	Cys	Cys	Trp
1531	CCC	AAT	GAA	ATG	AAG	AAT	ATG	CAA	CCA	GGG	GAT	GTC	TGC	TGC	TGG
	Ile	Cys	Ile	Pro	Cys	Glu	Pro	Tyr	Glu	Tyr	Leu	Ala	Asp	Glu	Phe
1576	ATT	TGC	ATC	CCC	TGT	GAA	CCC	TAC	GAA	TAC	CTG	GCT	GAT	GAG	TTT
	Thr	Cys	Met	Asp	Cys	Gly	Ser	Gly	Gln	Trp	Pro	Thr	Ala	Asp	Leu
1621	ACC	TGT	ATG	GAT	TGT	GGG	TCT	GGA	CAG	TGG	CCC	ACT	GCA	GAC	CTA
	Thr	Gly	Cys	Tyr	Asp	Leu	Pro	Glu	Asp	Tyr	Ile	Arg	Trp	Glu	Asp
1666	ACT	GGA	TGC	TAT	GAC	CTT	CCT	GAG	GAC	TAC	ATC	AGG	TGG	GAA	GAC
	Ala	Trp	Ala	Ile	Gly	Pro	Val	Thr	Ile	Ala	Cys	Leu	Gly	Phe	Met
1711	GCC	TGG	GCC	ATT	GGC	CCA	GTC	ACC	ATT	GCC	TGT	CTG	GGT	TTT	ATG
	Cys	Thr	Cys	Met	Val	Val	Thr	Val	Phe	Ile	Lys	His	Asn	Asn	Thr
1756	TGT	ACA	TGC	ATG	GTT	GTA	ACT	GTT	TTT	ATC	AAG	CAC	AAC	AAC	ACA
	Pro	Leu	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Cys	Tyr	Ile	Leu	Leu
1801	CCC	TTG	GTC	AAA	GCA	TCG	GGC	CGA	GAA	CTC	TGC	TAC	ATC	TTA	TTG
	Phe	Gly	Val	Gly	Leu	Ser	Tyr	Cys	Met	Thr	Phe	Phe	Phe	Ile	Ala
1846	TTT	GGG	GTT	GGC	CTG	TCA	TAC	TGC	ATG	ACA	TTC	TTC	TTC	ATT	GCC
	Lys	Pro	Ser	Pro	Val	Ile	Cys	Ala	Leu	Arg	Arg	Leu	Gly	Leu	Gly
1891	AAG	CCA	TCA	CCA	GTC	ATC	TGT	GCA	TTG	CGC	CGA	CTC	GGG	CTG	GGG
	Ser	Ser	Phe	Ala	Ile	Cys	Tyr	Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn
1936	AGT	TCC	TTC	GCT	ATC	TGT	TAC	TCA	GCC	CTG	CTG	ACC	AAG	ACA	AAC
	Cys	Ile	Ala	Arg	Ile	Phe	Asp	Gly	Val	Lys	Asn	Gly	Ala	Gln	Arg
1981	TGC	ATT	GCC	CGC	ATC	TTC	GAT	GGG	GTC	AAG	AAT	GGC	GCT	CAG	AGG
	Pro	Lys	Phe	Ile	Ser	Pro	Ser	Ser	Gln	Val	Phe	Ile	Cys	Leu	Gly
2026	CCA	AAA	TTC	ATC	AGC	CCC	AGT	TCT	CAG	GTT	TTC	ATC	TGC	CTG	GGT
	Leu	Ile	Leu	Val	Gln	Ile	Val	Met	Val	Ser	Val	Trp	Leu	Ile	Leu
2071	CTG	ATC	CTG	GTG	CAA	ATT	GTG	ATG	GTG	TCT	GTG	TGG	CTC	ATC	CTG
	Glu	Ala	Pro	Gly	Thr	Arg	Arg	Tyr	Thr	Leu	Ala	Glu	Lys	Arg	Glu
2116	GAG	GCC	CCA	GGC	ACC	AGG	AGG	TAT	ACC	CTT	GCA	GAG	AAG	CGG	GAA
	Thr	Val	Ile	Leu	Lys	Cys	Asn	Val	Lys	Asp	Ser	Ser	Met	Leu	Ile
2161	ACA	GTC	ATC	CTA	AAA	TGC	AAT	GTC	AAA	GAT	TCC	AGC	ATG	TTG	ATC
	Ser	Leu	Thr	Tyr	Asp	Val	Ile	Leu	Val	Ile	Leu	Cys	Thr	Val	Tyr
2206	TCT	CTT	ACC	TAC	GAT	GTG	ATC	CTG	GTG	ATC	TTA	TGC	ACT	GTG	TAC
	Ala	Phe	Lys	Thr	Arg	Lys	Cys	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys
2251	GCC	TTC	AAA	ACG	CGG	AAG	TGC	CCA	GAA	AAT	TTC	AAC	GAA	GCT	AAG
	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala
2296	TTC	ATA	GGT	TTT	ACC	ATG	TAC	ACC	ACG	TGC	ATC	ATC	TGG	TTG	GCC
	Phe	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser	Ser	Asp	Tyr	Arg	Val	Gln
2341	TTC	CTC	CCT	ATA	TTT	TAT	GTG	ACA	TCA	AGT	GAC	TAC	AGA	GTG	CAG
	Thr	Thr	Thr	Met	Cys	Ile	Ser	Val	Ser	Leu	Ser	Gly	Phe	Val	Val
2386	ACG	ACA	ACC	ATG	TGC	ATC	TCT	GTC	AGC	CTG	AGT	GGC	TTT	GTG	GTC

FIG. 17b.

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	Leu	Gly	Cys	Leu	Phe	Ala	Pro	Lys	Val	His	Ile	Ile	Leu	Phe	Gln
2431	TTG	GGC	TGT	TTG	TTT	GCA	CCC	AAG	GTT	CAC	ATC	ATC	CTG	TTT	CAA
	Pro	Gln	Lys	Asn	Val	Val	Thr	His	Arg	Leu	His	Leu	Asn	Arg	Phe
2476	CCC	CAG	AAG	AAT	GTT	GTC	ACA	CAC	AGA	CTG	CAC	CTC	AAC	AGG	TTC
	Ser	Val	Ser	Gly	Thr	Gly	Thr	Thr	Tyr	Ser	Gln	Ser	Ser	Ala	Ser
2521	AGT	GTC	AGT	GGA	ACT	GGG	ACC	ACA	TAC	TCT	CAG	TCC	TCT	GCA	AGC
	Thr	Tyr	Val	Pro	Thr	Val	Cys	Asn	Gly	Arg	Glu	Val	Leu	Asp	Ser
2566	ACG	TAT	GTG	CCA	ACG	GTG	TGC	AAT	GGG	CGG	GAA	GTC	CTC	GAC	TCC
	Thr	Thr	Ser	Ser	Leu	***									
2611	ACC	ACC	TCA	TCT	CTG	TGA									

FIG. 17c.

ph2SPmGluR3//CaR*AAA*Gqi5 nucleic acid (SEQ ID NO. 53) with encoded amino acid sequence (SEQ ID NO. 54)

	Met	Gly	Ser	Leu	Leu	Ala	Leu	Pro	Ala	Leu	Leu	Leu	Leu	Trp	Gly
1	ATG	GGA	TCG	CTG	CTT	GCG	CTC	CCG	GCA	CTG	CTG	CTG	CTG	TGG	GGT
	Ala	Val	Ala	Leu	Gly	Asp	His	Asn	Phe	Leu	Arg	Arg	Glu	Ile	Lys
46	GCT	GTG	GCT	TTA	GGG	GAC	CAT	AAC	TTT	CTA	AGG	AGA	GAG	ATT	AAA
	Ile	Glu	Gly	Asp	Leu	Val	Leu	Gly	Gly	Leu	Phe	Pro	Ile	Asn	Glu
91	ATA	GAA	GGT	GAC	CTT	GTT	TTA	GGG	GGC	CTG	TTT	CCT	ATT	AAC	GAA
	Lys	Gly	Thr	Gly	Thr	Glu	Glu	Cys	Gly	Arg	Ile	Asn	Glu	Asp	Arg
136	AAA	GGC	ACT	GGA	ACT	GAA	GAA	TGT	GGG	CGA	ATC	AAT	GAA	GAC	CGA
	Gly	Ile	Gln	Arg	Leu	Glu	Ala	Met	Leu	Phe	Ala	Ile	Asp	Glu	Ile
181	GGG	ATT	CAA	CGC	CTG	GAA	GCC	ATG	TTG	TTT	GCT	ATT	GAT	GAA	ATC
	Asn	Lys	Asp	Asp	Tyr	Leu	Leu	Pro	Gly	Val	Lys	Leu	Gly	Val	His
226	AAC	AAA	GAT	GAT	TAC	TTG	CTA	CCA	GGA	GTG	AAG	TTG	GGT	GTT	CAC
	Ile	Leu	Asp	Thr	Cys	Ser	Arg	Asp	Thr	Tyr	Ala	Leu	Glu	Gln	Ser
271	ATT	TTG	GAT	ACA	TGT	TCA	AGG	GAT	ACC	TAT	GCA	TTG	GAG	CAA	TCA
	Leu	Glu	Phe	Val	Arg	Ala	Ser	Leu	Thr	Lys	Val	Asp	Glu	Ala	Glu
316	CTG	GAG	TTT	GTC	AGG	GCA	TCT	TTG	ACA	AAA	GTG	GAT	GAA	GCT	GAG
	Tyr	Met	Cys	Pro	Asp	Gly	Ser	Tyr	Ala	Ile	Gln	Glu	Asn	Ile	Pro
361	TAT	ATG	TGT	CCT	GAT	GGA	TCC	TAT	GCC	ATT	CAA	GAA	AAC	ATC	CCA
	Leu	Leu	Ile	Ala	Gly	Val	Ile	Gly	Gly	Ser	Tyr	Ser	Ser	Val	Ser
406	CTT	CTC	ATT	GCA	GGG	GTC	ATT	GGT	GGC	TCT	TAT	AGC	AGT	GTT	TCC
	Ile	Gln	Val	Ala	Asn	Leu	Leu	Arg	Leu	Phe	Gln	Ile	Pro	Gln	Ile
451	ATA	CAG	GTG	GCA	AAC	CTG	CTG	CGG	CTC	TTC	CAG	ATC	CCT	CAG	ATC
	Ser	Tyr	Ala	Ser	Thr	Ser	Ala	Lys	Leu	Ser	Asp	Lys	Ser	Arg	Tyr
496	AGC	TAC	GCA	TCC	ACC	AGC	GCC	AAA	CTC	AGT	GAT	AAG	TCG	CGC	TAT
	Asp	Tyr	Phe	Ala	Arg	Thr	Val	Pro	Pro	Asp	Phe	Tyr	Gln	Ala	Lys
541	GAT	TAC	TTT	GCC	AGG	ACC	GTG	CCC	CCC	GAC	TTC	TAC	CAG	GCC	AAA
	Ala	Met	Ala	Glu	Ile	Leu	Arg	Phe	Phe	Asn	Trp	Thr	Tyr	Val	Ser
586	GCC	ATG	GCT	GAG	ATC	TTG	CGC	TTC	TTC	AAC	TGG	ACC	TAC	GTG	TCC
	Thr	Val	Ala	Ser	Glu	Gly	Asp	Tyr	Gly	Glu	Thr	Gly	Ile	Glu	Ala
631	ACA	GTA	GCC	TCC	GAG	GGT	GAT	TAC	GGG	GAG	ACA	GGG	ATC	GAG	GCC
	Phe	Glu	Gln	Glu	Ala	Arg	Leu	Arg	Asn	Ile	Cys	Ile	Ala	Thr	Ala
676	TTC	GAG	CAG	GAA	GCC	CGC	CTG	CGC	AAC	ATC	TGC	ATC	GCT	ACG	GCG
	Glu	Lys	Val	Gly	Arg	Ser	Asn	Ile	Arg	Lys	Ser	Tyr	Asp	Ser	Val
721	GAG	AAG	GTG	GGC	CGC	TCC	AAC	ATC	CGC	AAG	TCC	TAC	GAC	AGC	GTG
	Ile	Arg	Glu	Leu	Leu	Gln	Lys	Pro	Asn	Ala	Arg	Val	Val	Val	Leu
766	ATC	CGA	GAA	CTG	TTG	CAG	AAG	CCC	AAC	GCG	CGC	GTC	GTG	GTC	CTC
	Phe	Met	Arg	Ser	Asp	Asp	Ser	Arg	Glu	Leu	Ile	Ala	Ala	Ala	Ser
811	TTC	ATG	CGC	AGC	GAC	GAC	TCG	CGG	GAG	CTC	ATT	GCA	GCC	GCC	AGC
	Arg	Ala	Asn	Ala	Ser	Phe	Thr	Trp	Val	Ala	Ser	Asp	Gly	Trp	Gly
856	CGC	GCC	AAT	GCC	TCC	TTC	ACC	TGG	GTG	GCC	AGC	GAC	GGC	TGG	GGC
	Ala	Gln	Glu	Ser	Ile	Ile	Lys	Gly	Ser	Glu	His	Val	Ala	Tyr	Gly
901	GCG	CAG	GAG	AGC	ATC	ATC	AAG	GGC	AGC	GAG	CAT	GTG	GCC	TAC	GGC
	Ala	Ile	Thr	Leu	Glu	Leu	Ala	Ser	Gln	Pro	Val	Arg	Gln	Phe	Asp
946	GCC	ATC	ACC	CTG	GAG	CTG	GCC	TCC	CAG	CCT	GTC	CGC	CAG	TTC	GAC
	Arg	Tyr	Phe	Gln	Ser	Leu	Asn	Pro	Tyr	Asn	Asn	His	Arg	Asn	Pro
991	CGC	TAC	TTC	CAG	AGC	CTC	AAC	CCC	TAC	AAC	AAC	CAC	CGC	AAC	CCC
	Trp	Phe	Arg	Asp	Phe	Trp	Glu	Gln	Lys	Phe	Gln	Cys	Ser	Leu	Gln
1036	TGG	TTC	CGG	GAC	TTC	TGG	GAG	CAA	AAG	TTT	CAG	TGC	AGC	CTC	CAG
	Asn	Lys	Arg	Asn	His	Arg	Arg	Val	Cys	Asp	Lys	His	Leu	Ala	Ile
1081	AAC	AAA	CGC	AAC	CAC	AGG	CGC	GTC	TGC	GAC	AAG	CAC	CTG	GCC	ATC
	Asp	Ser	Ser	Asn	Tyr	Glu	Gln	Glu	Ser	Lys	Ile	Met	Phe	Val	Val
1126	GAC	AGC	AGC	AAC	TAC	GAG	CAA	GAG	TCC	AAG	ATC	ATG	TTT	GTG	GTG

FIG. 18a.

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	Asn	Ala	Val	Tyr	Ala	Met	Ala	His	Ala	Leu	His	Lys	Met	Gln	Arg
1171	AAC	GCG	GTG	TAT	GCC	ATG	GCC	CAC	GCT	TTG	CAC	AAA	ATG	CAG	CGC
	Thr	Leu	Cys	Pro	Asn	Thr	Thr	Lys	Leu	Cys	Asp	Ala	Met	Lys	Ile
1216	ACC	CTC	TGT	CCC	AAC	ACT	ACC	AAG	CTT	TGT	GAT	GCT	ATG	AAG	ATC
	Leu	Asp	Gly	Lys	Lys	Leu	Tyr	Lys	Asp	Tyr	Leu	Leu	Lys	Ile	Asn
1261	CTG	GAT	GGG	AAG	AAG	TTG	TAC	AAG	GAT	TAC	TTG	CTG	AAA	ATC	AAC
	Phe	Thr	Ala	Pro	Phe	Asn	Pro	Asn	Lys	Asp	Ala	Asp	Ser	Ile	Val
1306	TTC	ACG	GCT	CCA	TTC	AAC	CCA	AAT	AAA	GAT	GCA	GAT	AGC	ATA	GTC
	Lys	Phe	Asp	Thr	Phe	Gly	Asp	Gly	Met	Gly	Arg	Tyr	Asn	Val	Phe
1351	AAG	TTT	GAC	ACT	TTT	GGA	GAT	GGA	ATG	GGG	CGA	TAC	AAC	GTG	TTC
	Asn	Phe	Gln	Asn	Val	Gly	Gly	Lys	Tyr	Ser	Tyr	Leu	Lys	Val	Gly
1396	AAT	TTC	CAA	AAT	GTA	GGT	GGA	AAG	TAT	TCC	TAC	TTG	AAA	GTT	GGT
	His	Trp	Ala	Glu	Thr	Leu	Ser	Leu	Asp	Val	Asn	Ser	Ile	His	Trp
1441	CAC	TGG	GCA	GAA	ACC	TTA	TCG	CTA	GAT	GTC	AAC	TCT	ATC	CAC	TGG
	Ser	Arg	Asn	Ser	Val	Pro	Thr	Ser	Gln	Cys	Ser	Asp	Pro	Cys	Ala
1486	TCC	CGG	AAC	TCA	GTC	CCC	ACT	TCC	CAG	TGC	AGC	GAC	CCC	TGT	GCC
	Pro	Asn	Glu	Met	Lys	Asn	Met	Gln	Pro	Gly	Asp	Val	Cys	Cys	Trp
1531	CCC	AAT	GAA	ATG	AAG	AAT	ATG	CAA	CCA	GGG	GAT	GTC	TGC	TGC	TGG
	Ile	Cys	Ile	Pro	Cys	Glu	Pro	Tyr	Glu	Tyr	Leu	Ala	Asp	Glu	Phe
1576	ATT	TGC	ATC	CCC	TGT	GAA	CCC	TAC	GAA	TAC	CTG	GCT	GAT	GAG	TTT
	Thr	Cys	Met	Asp	Cys	Gly	Ser	Gly	Gln	Trp	Pro	Thr	Ala	Asp	Leu
1621	ACC	TGT	ATG	GAT	TGT	GGG	TCT	GGA	CAG	TGG	CCC	ACT	GCA	GAC	CTA
	Thr	Gly	Cys	Tyr	Asp	Leu	Pro	Glu	Asp	Tyr	Ile	Arg	Trp	Glu	Asp
1666	ACT	GGA	TGC	TAT	GAC	CTT	CCT	GAG	GAC	TAC	ATC	AGG	TGG	GAA	GAC
	Ala	Trp	Ala	Ile	Gly	Pro	Val	Thr	Ile	Ala	Cys	Leu	Gly	Phe	Met
1711	GCC	TGG	GCC	ATT	GGC	CCA	GTC	ACC	ATT	GCC	TGT	CTG	GGT	TTT	ATG
	Cys	Thr	Cys	Met	Val	Val	Thr	Val	Phe	Ile	Lys	His	Asn	Asn	Thr
1756	TGT	ACA	TGC	ATG	GTT	GTA	ACT	GTT	TTT	ATC	AAG	CAC	AAC	AAC	ACA
	Pro	Leu	Val	Lys	Ala	Ser	Gly	Arg	Glu	Leu	Cys	Tyr	Ile	Leu	Leu
1801	CCC	TTG	GTC	AAA	GCA	TCG	GGC	CGA	GAA	CTC	TGC	TAC	ATC	TTA	TTG
	Phe	Gly	Val	Gly	Leu	Ser	Tyr	Cys	Met	Thr	Phe	Phe	Phe	Ile	Ala
1846	TTT	GGG	GTT	GGC	CTG	TCA	TAC	TGC	ATG	ACA	TTC	TTC	TTC	ATT	GCC
	Lys	Pro	Ser	Pro	Val	Ile	Cys	Ala	Leu	Arg	Arg	Leu	Gly	Leu	Gly
1891	AAG	CCA	TCA	CCA	GTC	ATC	TGT	GCA	TTG	CGC	CGA	CTC	GGG	CTG	GGG
	Ser	Ser	Phe	Ala	Ile	Cys	Tyr	Ser	Ala	Leu	Leu	Thr	Lys	Thr	Asn
1936	AGT	TCC	TTC	GCT	ATC	TGT	TAC	TCA	GCC	CTG	CTG	ACC	AAG	ACA	AAC
	Cys	Ile	Ala	Arg	Ile	Phe	Asp	Gly	Val	Lys	Asn	Gly	Ala	Gln	Arg
1981	TGC	ATT	GCC	CGC	ATC	TTC	GAT	GGG	GTC	AAG	AAT	GGC	GCT	CAG	AGG
	Pro	Lys	Phe	Ile	Ser	Pro	Ser	Ser	Gln	Val	Phe	Ile	Cys	Leu	Gly
2026	CCA	AAA	TTC	ATC	AGC	CCC	AGT	TCT	CAG	GTT	TTC	ATC	TGC	CTG	GGT
	Leu	Ile	Leu	Val	Gln	Ile	Val	Met	Val	Ser	Val	Trp	Leu	Ile	Leu
2071	CTG	ATC	CTG	GTG	CAA	ATT	GTG	ATG	GTG	TCT	GTG	TGG	CTC	ATC	CTG
	Glu	Ala	Pro	Gly	Thr	Arg	Arg	Tyr	Thr	Leu	Ala	Glu	Lys	Arg	Glu
2116	GAG	GCC	CCA	GGC	ACC	AGG	AGG	TAT	ACC	CTT	GCA	GAG	AAG	CGG	GAA
	Thr	Val	Ile	Leu	Lys	Cys	Asn	Val	Lys	Asp	Ser	Ser	Met	Leu	Ile
2161	ACA	GTC	ATC	CTA	AAA	TGC	AAT	GTC	AAA	GAT	TCC	AGC	ATG	TTG	ATC
	Ser	Leu	Thr	Tyr	Asp	Val	Ile	Leu	Val	Ile	Leu	Cys	Thr	Val	Tyr
2206	TCT	CTT	ACC	TAC	GAT	GTG	ATC	CTG	GTG	ATC	TTA	TGC	ACT	GTG	TAC
	Ala	Phe	Lys	Thr	Arg	Lys	Cys	Pro	Glu	Asn	Phe	Asn	Glu	Ala	Lys
2251	GCC	TTC	AAA	ACG	CGG	AAG	TGC	CCA	GAA	AAT	TTC	AAC	GAA	GCT	AAG
	Phe	Ile	Gly	Phe	Thr	Met	Tyr	Thr	Thr	Cys	Ile	Ile	Trp	Leu	Ala
2296	TTC	ATA	GGT	TTT	ACC	ATG	TAC	ACC	ACG	TGC	ATC	ATC	TGG	TTG	GCC
	Phe	Leu	Pro	Ile	Phe	Tyr	Val	Thr	Ser	Ser	Asp	Tyr	Arg	Val	Gln
2341	TTC	CTC	CCT	ATA	TTT	TAT	GTG	ACA	TCA	AGT	GAC	TAC	AGA	GTG	CAG
	Thr	Thr	Thr	Met	Cys	Ile	Ser	Val	Ser	Leu	Ser	Gly	Phe	Val	Val
2386	ACG	ACA	ACC	ATG	TGC	ATC	TCT	GTC	AGC	CTG	AGT	GGC	TTT	GTG	GTC

FIG. 18b.

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2431 Leu Gly Cys Leu Phe Ala Pro Lys Val His Ile Ile Leu Phe Gln
 TTG GGC TGT TTG TTT GCA CCC AAG GTT CAC ATC ATC CTG TTT CAA
 Pro Gln Lys Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala
 2476 CCC CAG AAG AAT ACC ATC GAG GAG GTG CGT TGC AGC ACC GCA GCT
 His Ala Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn
 2521 CAC GCT TTC AAG GTG GCT GCC CGT GCC ACG CTG CGC AGC AAC
 Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser
 2566 GTC TCC CGC AAG CGG TCC AGC AGC CTT GGA GGC TCC ACG GGA TCC
 Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro
 2611 ACC CCC TCC TCC TCC ATC AGC AGC AAG AGC AAC AGC GAA GAC CCA
 Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu
 2656 TTC CCA CAG CCC GAG AGG CAG AAG CAG CAG CAG CCG CTG GCC CTA
 Thr Gln Gln Glu Gln Gln Gln Gln Pro Leu Thr Leu Pro Gln Gln
 2701 ACC CAG CAA GAG CAG CAG CAG CAG CAG CCC CTG ACC CTC CCA CAG CAG
 Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe
 2746 CAA CGA TCT CAG CAG CAG CCC AGA TGC AAG CAG AAG GTC ATC TTT
 Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln
 2791 GGC AGC GGC ACG GTC ACC TTC TCA CTG AGC TTT GAT GAG CCT CAG
 Lys Asn Ala Met Ala His Gly Asn Ser Thr His Gln Asn Ser Leu
 2836 AAG AAC GCC ATG GCC CAC GGG AAT TCT ACG CAC CAG AAC TCC CTG
 Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu
 2881 GAG GCC CAG AAA AGC AGC GAT ACG CTG ACC CGA CAC CAG CCA TTA
 Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln
 2926 CTC CCG CTG CAG TGC GGG GAA ACG GAC TTA GAT CTG ACC GTC CAG
 Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu
 2971 GAA ACA GGT CTG CAA GGA CCT GTG GGT GGA GAC CAG CGG CCA GAG
 Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val Ser Ser
 3016 GTG GAG GAC CCT GAA GAG TTG TCC CCA GCA CTT GTA GTG TCC AGT
 Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr Glu
 3061 TCA CAG AGC TTT GTC ATC AGT GGT GGA GGC AGC ACT GTT ACA GAA
 Asn Val Val Asn Ser Ala Ala Ala Met Thr Leu Glu Ser Ile Met
 3106 AAC GTA GTG AAT TCA GCG GCC GCC ATG ACT CTG GAG TCC ATC ATG
 Ala Cys Cys Leu Ser Glu Glu Ala Lys Glu Ala Arg Arg Ile Asn
 3151 GCG TGC TGC CTG AGC GAG GAG GCC AAG GAA GCC CGG CGG ATC AAC
 Asp Glu Ile Glu Arg Gln Leu Arg Arg Asp Lys Arg Asp Ala Arg
 3196 GAC GAG ATC GAG CGG CAG CTC CGC AGG GAC AAG CGG GAC GCC CGC
 Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys
 3241 CGG GAG CTC AAG CTG CTG CTG CTC GGG ACA GGA GAG AGT GGC AAG
 Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr
 3286 AGT ACG TTT ATC AAG CAG ATG AGA ATC ATC CAT GGG TCA GGA TAC
 Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr Gln Asn
 3331 TCT GAT GAA GAT AAA AGG GGC TTC ACC AAG CTG GTG TAT CAG AAC
 Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu
 3376 ATC TTC ACG GCC ATG CAG GCC ATG ATC AGA GCC ATG GAC ACA CTC
 Lys Ile Pro Tyr Lys Tyr Glu His Asn Lys Ala His Ala Gln Leu
 3421 AAG ATC CCA TAC AAG TAT GAG CAC AAT AAG GCT CAT GCA CAA TTA
 Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro
 3466 GTT CGA GAA GTT GAT GTG GAG AAG GTG TCT GCT TTT GAG AAT CCA
 Tyr Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln
 3511 TAT GTA GAT GCA ATA AAG AGT TTA TGG AAT GAT CCT GGA ATC CAG
 Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr
 3556 GAA TGC TAT GAT AGA CGA CGA GAA TAT CAA TTA TCT GAC TCT ACC
 Lys Tyr Tyr Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr
 3601 AAA TAC TAT CTT AAT GAC TTG GAC CGC GTA GCT GAC CCT GCC TAC
 Leu Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr
 3646 CTG CCT ACG CAA CAA GAT GTG CTT AGA GTT CGA GTC CCC ACC ACA

FIG. 18c.

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	Gly	Ile	Ile	Glu	Tyr	Pro	Phe	Asp	Leu	Gln	Ser	Val	Ile	Phe	Arg
3691	GGG	ATC	ATC	GAA	TAC	CCC	TTT	GAC	TTA	CAA	AGT	GTC	ATT	TTC	AGA
	Met	Val	Asp	Val	Gly	Gly	Gln	Arg	Ser	Glu	Arg	Arg	Lys	Trp	Ile
3736	ATG	GTC	GAT	GTA	GGG	GGC	CAA	AGG	TCA	GAG	AGA	AGA	AAA	TGG	ATA
	His	Cys	Phe	Glu	Asn	Val	Thr	Ser	Ile	Met	Phe	Leu	Val	Ala	Leu
3781	CAC	TGC	TTT	GAA	AAT	GTC	ACC	TCT	ATC	ATG	TTT	CTA	GTA	GCG	CTT
	Ser	Glu	Tyr	Asp	Gln	Val	Leu	Val	Glu	Ser	Asp	Asn	Glu	Asn	Arg
3826	AGT	GAA	TAT	GAT	CAA	GTT	CTC	GTG	GAG	TCA	GAC	AAT	GAG	AAC	CGA
	Met	Glu	Glu	Ser	Lys	Ala	Leu	Phe	Arg	Thr	Ile	Ile	Thr	Tyr	Pro
3871	ATG	GAG	GAA	AGC	AAG	GCT	CTC	TTT	AGA	ACA	ATT	ATC	ACA	TAC	CCC
	Trp	Phe	Gln	Asn	Ser	Ser	Val	Ile	Leu	Phe	Leu	Asn	Lys	Lys	Asp
3916	TGG	TTC	CAG	AAC	TCC	TCG	GTT	ATT	CTG	TTC	TTA	AAC	AAG	AAA	GAT
	Leu	Leu	Glu	Glu	Lys	Ile	Met	Tyr	Ser	His	Leu	Val	Asp	Tyr	Phe
3961	CTT	CTA	GAG	GAG	AAA	ATC	ATG	TAT	TCC	CAT	CTA	GTC	GAC	TAC	TTC
	Pro	Glu	Tyr	Asp	Gly	Pro	Gln	Arg	Asp	Ala	Gln	Ala	Ala	Arg	Glu
4006	CCA	GAA	TAT	GAT	GGA	CCC	CAG	AGA	GAT	GCC	CAG	GCA	GCC	CGA	GAA
	Phe	Ile	Leu	Lys	Met	Phe	Val	Asp	Leu	Asn	Pro	Asp	Ser	Asp	Lys
4051	TTC	ATT	CTG	AAG	ATG	TTC	GTG	GAC	CTG	AAC	CCA	GAC	AGT	GAC	AAA
	Ile	Ile	Tyr	Ser	His	Phe	Thr	Cys	Ala	Thr	Asp	Thr	Glu	Asn	Ile
4096	ATT	ATC	TAC	TCC	CAC	TTC	ACG	TGC	GCC	ACA	GAC	ACC	GAG	AAT	ATC
	Arg	Phe	Val	Phe	Ala	Ala	Val	Lys	Asp	Thr	Ile	Leu	Gln	Leu	Asn
4141	CGC	TTT	GTC	TTT	GCT	GCC	GTC	AAG	GAC	ACC	ATC	CTC	CAG	TTG	AAC
	Leu	Lys	Asp	Cys	Gly	Leu	Phe	***							
4186	CTG	AAG	GAC	TGC	GGT	CTG	TTC	TAA							

FIG. 18d.