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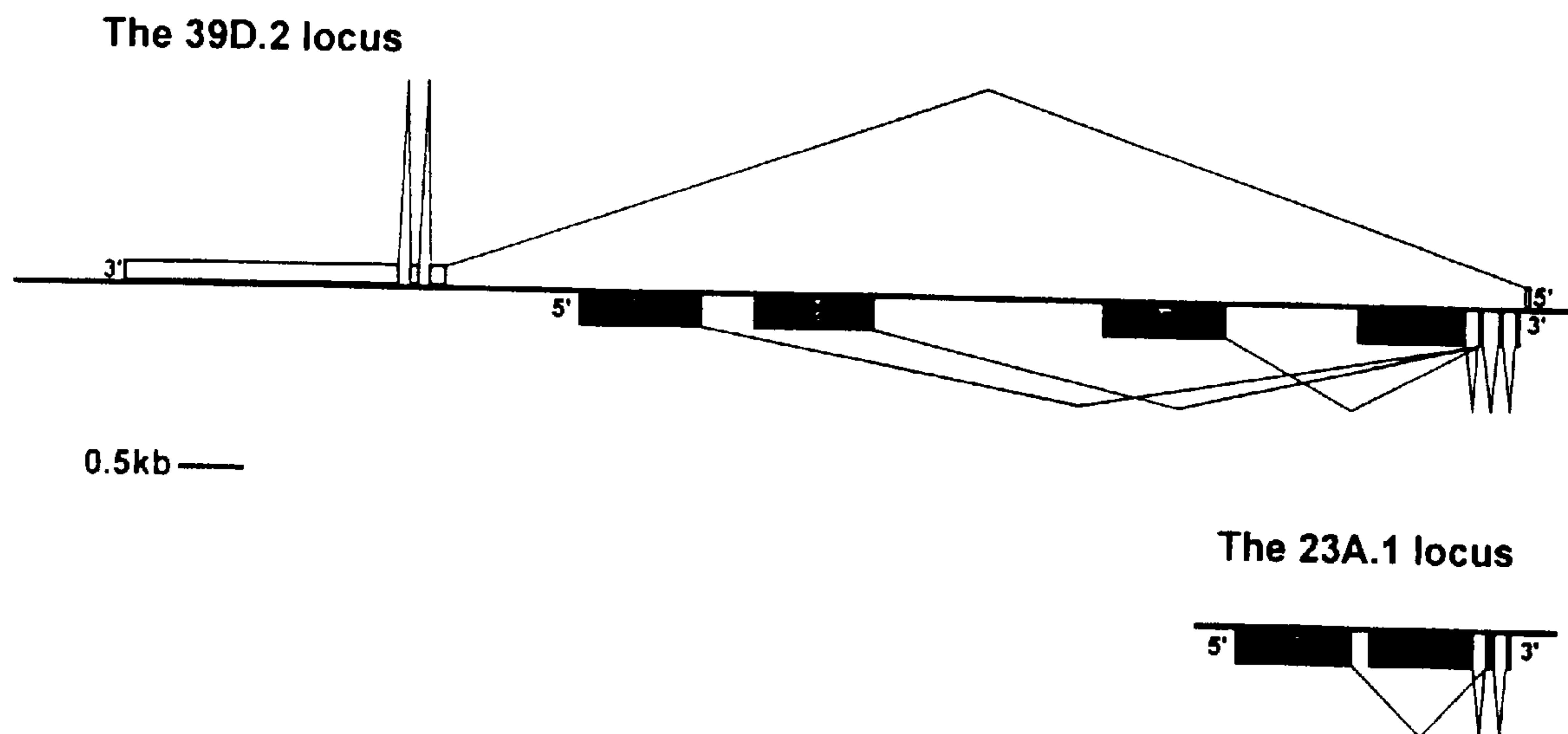
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(54) Titre : NOUVEAUX RECEPTEURS GUSTATIFS DES DROSOPHILES

(54) Title: GUSTATORY RECEPTORS IN DROSOPHILA



(57) **Abrégé/Abstract:**

The present invention provides nucleic acids and amino acids for novel gustatory receptors as well as methods for identifying gustatory receptors. More specifically, the present invention provides nucleic acids and amino acids for novel gustatory receptors in *Drosophila* as well as methods of using the provided nucleic acids and amino acids. In addition, this invention provides methods of identifying ligands which bind to the novel gustatory receptors as well as a variety of methods for using the receptors and ligands so identified.

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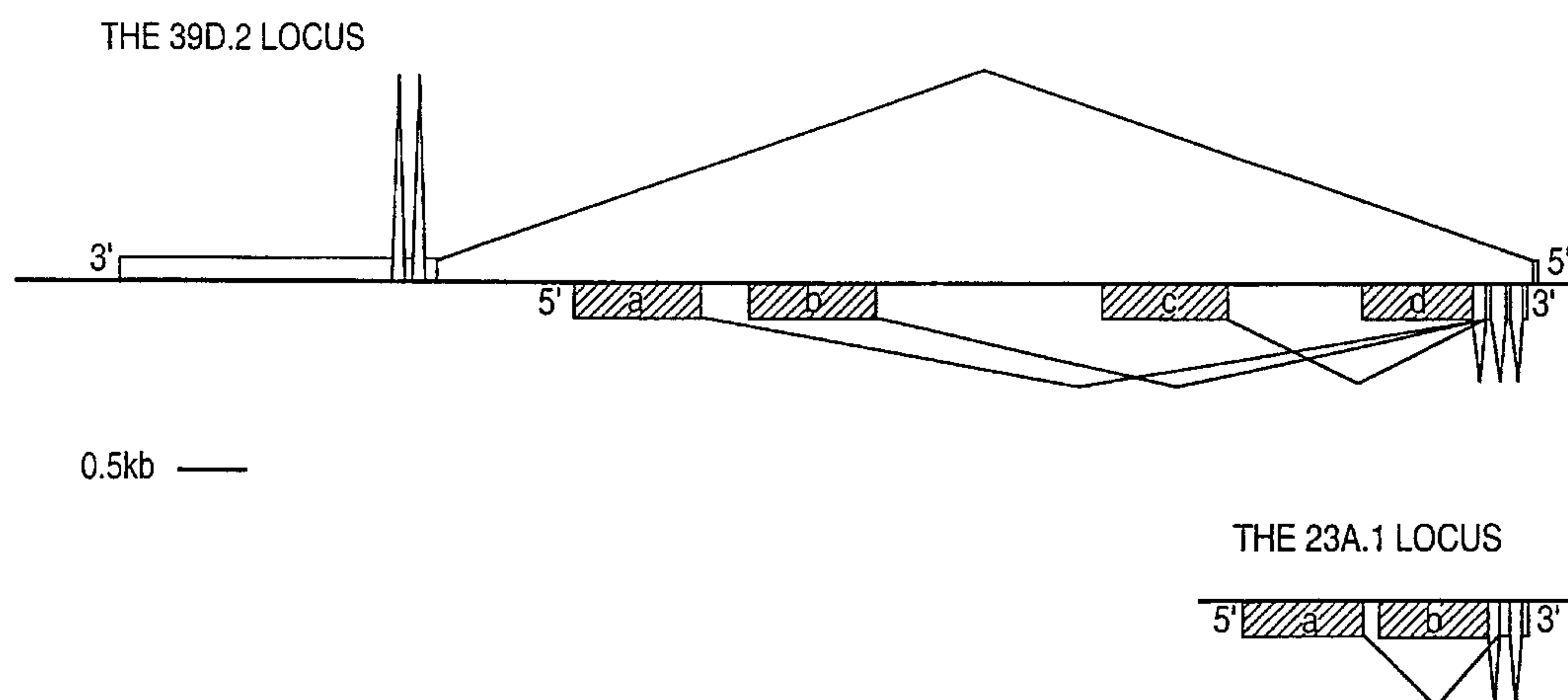
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(54) Title: GUSTATORY RECEPTORS IN DROSOPHILA



(57) Abstract: The present invention provides nucleic acids and amino acids for novel gustatory receptors as well as methods for identifying gustatory receptors. More specifically, the present invention provides nucleic acids and amino acids for novel gustatory receptors in *Drosophila* as well as methods of using the provided nucleic acids and amino acids. In addition, this invention provides methods of identifying ligands which bind to the novel gustatory receptors as well as a variety of methods for using the receptors and ligands so identified.

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NOVEL TASTE RECEPTORS IN DROSOPHILA

INVENTORS: John R. Carlson, Peter J. Clyne, Coral G. Warr

5 RELATED APPLICATIONS

This application claims priority to U.S. provisional patent application No. 60/181,704 filed February 10, 2000 and U.S. provisional patent application No. 60/138,668 filed June 14, 1999 both applications herein incorporated by reference in their entirety.

10

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15 FIELD OF THE INVENTION

This invention pertains to novel taste receptors and to methods of using such receptors. More particularly, this invention pertains to the nucleic acids and amino acids of novel taste receptors in *Drosophila* and to methods of using such nucleic acids and amino acids.

20

BACKGROUND OF THE INVENTION

Studies in insect gustation have a long history in general physiology. Much more emphasis has been placed on the physiological characteristics of the sensory cells than on the central cellular mechanisms of taste processing (Mitchell *et al.*, (1999) Microsc. Res. Tech. 47,401-415). For a survey review of the organization of the olfactory and gustatory systems in *Drosophila*, see Stocker, (1994) Cell Tissue Res. 275, 3-26.

25

Both male and female *Drosophila* flies possess gustatory receptors on their legs, but males possess more of these receptors than females (Possidente *et al.*, (1989) Dev.

Biol. 132, 448-457). The labellar hairs of larger flies are not only sensitive to a variety of simple and compound sugars (Dethier, (1955) Q. Rev. Biol. 30, 348), but also to a wide variety of other molecules, such as amino acids (Shiraishi & Kuwabara, (1970) J. Gen. Physiol. 56, 768).

5 Behavioral studies have shown that *Drosophila* are sensitive to quinine (Tompkins *et al.*, (1979) Proc. Natl. Acad. Sci. USA 76, 884), which is perceived by humans as bitter, and other insects have been shown to be sensitive to an array of structurally diverse bitter compounds. Moreover, an individual insect taste receptor cell can respond to a broad range of structurally heterogeneous alkaloids and other bitter molecules
10 (Glendinning & Hills, (1997) J. Neurophysiol. 78, 734; Chapman *et al.*, (1991) J. Exp. Biol. 158, 241).

Little is known about the molecular mechanisms of taste perception in animals, particularly the initial events of taste signaling. Several genes known to affect the formation of gustatory sensilla or alter the feeding behavior of *Drosophila* have been
15 identified (Singh, (1997) Microsc. Res. Tech. 3, 547-563). For example, a mutation in the malvolio (*mvl*) gene affects taste behavior in *Drosophila melanogaster* (Orgad *et al.*, (1998) J. Exp. Biol. 201, 115-120). Also, scalloped (*sd*) mutants show defects in response to a number of taste stimuli (Inamdar *et al.*, (1993) J. Neurogenet. 9, 123-139). Flies containing different Shaker alleles exhibit a variety of defects in their gustatory
20 response to sucrose, NaCl and KCl (Balakrishnan *et al.*, (1991) J. Exp. Biol. 157, 161-181).

Although two putative mammalian taste receptors have recently been described (Hoon *et al.*, (1999) Cell 96, 541), remarkably little is understood in general about taste receptors across species.

25 In the present invention, a large and diverse family of seven transmembrane domain proteins was identified from the *Drosophila* genome database with a computer algorithm that identifies proteins on the basis of structure. Eighteen of nineteen genes examined were expressed in the *Drosophila* labellum, a gustatory organ of the proboscis.

Expression was not detected in a variety of other tissues. The genes were not expressed in the labellum of a *Drosophila* mutant, *pox-neuro 70*, in which taste neurons are eliminated. Tissue specificity of expression of these genes, along with their structural similarity, supports the possibility that the family encodes a large and divergent family of taste receptors.

SUMMARY OF THE INVENTION

This invention provides isolated nucleic acid molecules including the following:

(a) isolated nucleic acid molecules that encode the amino acid sequences of *Drosophila* Gustatory Receptor proteins; (b) isolated nucleic acid molecules that encode protein fragments of at least six amino acids of a *Drosophila* Gustatory Receptor proteins; and (c) isolated nucleic acid molecules which hybridize to nucleic acid molecules which include nucleotide sequences encoding *Drosophila* Gustatory Receptor proteins under conditions of sufficient stringency to produce a clear signal.

This invention also provides such isolated nucleic acid molecules wherein the nucleic acids include at least one exon-intron boundary located in one of the following positions: (a) the nucleotides encoding the amino acids which include the third extracellular loop of a *Drosophila* Gustatory Receptor protein; and (b) the nucleotides encoding the amino acids which include the seventh transmembrane domain of a *Drosophila* Gustatory Receptor protein.

This invention further provides such isolated nucleic acid molecules which have the nucleic acid sequence of one of the following sequences: SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91.

This invention also provides such isolated nucleic acid molecules operably linked to one or more expression control elements.

This invention further provides vectors which include any of the aforementioned nucleic acid molecules and host cells which include such vectors.

This invention also provides host cells transformed so as to contain any of the aforementioned nucleic acid molecules, wherein such host cells can be either prokaryotic host cells or eukaryotic host cells.

This invention also provides methods for producing proteins or protein fragments wherein the methods include transforming host cells with any of the aforementioned nucleic acids under conditions in which the protein or protein fragment encoded by said nucleic acid molecule is expressed. This invention also provides such methods wherein the host cells are either prokaryotic host cells or eukaryotic host cells. This invention further provides isolated proteins or protein fragments produced by such methods.

This invention provides isolated proteins or protein fragments which include: (a) isolated proteins encoded by one of the following amino acid sequences: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92; (b) isolated protein fragments which include at least six amino acids of any of the following sequences: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92; (c) isolated proteins which include conservative amino acid substitutions of any of the following sequences: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92; and (d) naturally occurring amino acid sequence variants of any of the following sequences: SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92.

The present invention further provides such isolated proteins or protein fragments which include at least one of the following conserved amino acids: Serine in the amino terminal domain; Phenylalanine in the first transmembrane domain; Arginine in the first extracellular loop; Leucine in the fourth transmembrane domain; Leucine in the third transmembrane domain; Glycine in the fifth transmembrane domain; Tyrosine in the fifth

transmembrane domain; Leucine in the third extracellular loop; Phenylalanine in the third extracellular loop; Alanine in the seventh transmembrane domain; Glycine in the seventh transmembrane domain; Leucine in the seventh transmembrane domain; Aspartate in the seventh transmembrane domain; Alanine in the seventh transmembrane domain;

5 Threonine in the seventh transmembrane domain; Tyrosine in the seventh transmembrane domain; Valine in the seventh transmembrane domain; Glutamine in the carboxy terminal domain; and Phenylalanine in the carboxy terminal domain.

The present invention also provides isolated antibodies that bind to any of the aforementioned polypeptides. The present invention also provides such antibodies which
10 are either monoclonal antibodies or polyclonal antibodies.

This invention also provides methods of identifying agents which modulate the expression of any of the aforementioned proteins or protein fragments by: (a) exposing cells which express the proteins or protein fragments to the agents; and (b) determining whether the agent modulates expression of said proteins or protein fragments, thereby
15 identifying agents which modulate the expression of the proteins or protein fragments.

The present invention also provides methods of identifying agents which modulate the activity of any of the aforementioned proteins or protein fragments by: (a) exposing cells which express the proteins or protein fragments to the agents; and (b) determining whether the agents modulate the activity of said proteins or protein fragments, thereby
20 identifying agents which modulate the activity of the proteins or protein fragments.

The present invention also provides such methods where the agent modulates at least one activity of the proteins or protein fragments.

This invention provides methods of identifying agents which modulate the transcription of any of the aforementioned nucleic acid molecules by: (a) exposing cells
25 which transcribe the nucleic acids to the agents; and (b) determining whether the agents modulate transcription of said nucleic acids, thereby identifying agents which modulate the transcription of the nucleic acid.

This invention further provides methods of identifying binding partners for the

aforementioned proteins or protein fragments by: (a) exposing said proteins or protein fragments to potential binding partners; and (b) determining if the potential binding partners bind to said proteins or protein fragments, thereby identifying binding partners for the proteins or protein fragments.

5 The present invention also provides methods of modulating the expression of nucleic acids encoding the aforementioned proteins or protein fragments by administering an effective amount of agents which modulate the expression of the nucleic acids encoding the proteins or protein fragments.

10 This invention also provides methods of modulating at least one activity of the aforementioned proteins or protein fragments by administering an effective amount of the agents which modulate at least one activity of the proteins or protein fragments.

 This invention provides methods of identifying novel gustatory receptor genes by: (a) selecting candidate gustatory receptor genes by screening nucleic acid databases using an algorithm trained to identify seven transmembrane receptors genes; (b) screening
15 said selected candidate gustatory receptor genes by identifying nucleic acid sequences with conserved amino acid residues and intron-exon boundaries common to gustatory receptors, and having open reading frames of sufficient size so as to encode a seven transmembrane receptor; and (c) identifying the novel gustatory receptor genes and measuring the expression of gustatory receptor genes wherein the detection of expression
20 confirms said candidate gustatory genes as gustatory genes.

 This invention also provides methods of identifying novel gustatory receptor genes by: (a) selecting candidate gustatory receptor genes by screening nucleic acid databases for nucleic acid sequences with sufficient homology to at least one known gustatory receptor gene; (b) screening said selected candidate gustatory receptor genes by
25 identifying nucleic acids with conserved amino acid residues and intron-exon boundaries common to gustatory receptors, and having open reading frames of sufficient size so as to encode a seven transmembrane receptor; and (c) identifying the novel gustatory receptor genes and measuring the expression of gustatory receptor genes wherein the detection of

expression confirms said candidate gustatory genes as gustatory genes.

The present invention also provides transgenic insects modified to contain any of the aforementioned nucleic acid molecules.

5 This invention also provides such transgenic insects, wherein the nucleic acid molecules contain mutations that alter expression of the encoded proteins.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 Amino acid sequence alignment of nineteen GR proteins. Single-letter abbreviations for the amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; 10 F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr. Letters following protein designations identify alternative splicing products of individual genes. Residues conserved in >50% of the predicted proteins are shaded. The approximate locations of the seven predicted transmembrane domains are indicated. Intron-exon boundaries are shown with vertical 15 lines. The sequences shown are the first 19 full-length proteins identified. All DNA sequences are from the Berkeley *Drosophila* Genome Project (BDGP) database. See the Examples for a complete description.

Figure 2 Representative hydropathy plots of GR proteins. Hydrophobic peaks 20 predicted by Kyte-Doolittle analysis appear above the center lines. The approximate positions of the seven putative transmembrane domains are indicated above the first hydropathy plot. Similar plots were obtained for all of the GR proteins.

Figure 3 Genomic organization of the 39D.2 and 23A.1 loci. In the 39D.2 locus, 25 the gray boxes labeled a through d represent four large 5' exons, each of which can be spliced individually to the three 3' exons (indicated in black) to produce alternative transcripts encoding four different proteins. All the exons of the 39D.2 locus are located in an intron of another gene, which is in the opposite orientation and whose exons are

represented by white boxes. This other gene appears to encode a basic helix-loop-helix transcription factor expressed during embryogenesis. In the 23A.1 locus, the gray boxes labeled a and b represent two alternative large 5' exons, either of which can be spliced to the two small 3' exons (indicated in black) to produce transcripts encoding two different proteins.

Figure 4 Tissue specificity of expression of 32D.1 in the labellum. Shown is a gel photograph of an RT-PCR experiment with primers spanning an intron in 32D.1. The size of the predicted PCR product from cDNA is 372 base pairs; any remaining genomic DNA would generate a product of 559 base pairs. A cDNA band is observed in the labellum lane only. In addition, 32D.1 is not expressed in the labellum of the *poxn 70* mutant. Positive controls are described in the Examples.

The amount of each tissue used to prepare cDNA was that determined to give approximately the same signal with a pair of positive control primers, CG-GATCCCTATGTCAAGGTG (SEQ ID NO: 93) and GAAGAGCTTCGTGCTGGTCT (SEQ ID NO: 94), representing the *Drosophila* synaptotagmin gene (Perin *et al.*, (1991) J. Biol. Chem. 266, 615). Specifically, the amount of tissue used in each cDNA preparation was as follows: fifty labella, five heads from which taste organs (the labellum, the LSO, the dorsal cibarial sense organ, and the ventral cibarial sense organ) had been surgically removed, twenty thoraces, twenty abdomens, two-hundred legs, and twenty anterior wing margins (the portion of the wing containing chemosensory sensilla).

Complementary DNA preparation and PCR were performed as in Clyne *et al.*, (1999) Neuron 22, 327-338. For all genes, primer pairs (Available as supplementary material at www.sciencemag.org/feature/data/1046815.shl) that span introns were used to distinguish bands amplified from cDNA from those amplified from any remaining genomic DNA. All negative results were confirmed by testing at least one additional primer pair.

Figure 5 GR gene expression in microdissected labral sense organs (LSOs). The shaded areas show the four major taste organs of the *Drosophila* head: the LSO, the dorsal cibarial sense organ (DCSO), the ventral cibarial sense organ (VCSO), and the labellum. The gel track shows an amplification product from RNA extracted from fifty LSOs, amplified with primers N23A.3J and N23A.2D from two exons of gene 23A.1. Specifically, one primer is from the large exon 23A.1a (Figure 3), and the other is from the First common exon at the 3' end. The amplification product is 430 base pairs, which is the expected length for a cDNA product; any remaining genomic DNA would generate a product of 1598 base pairs. The primer pair did not amplify a product from non-gustatory tissue (see Examples, Table 1). The following transcripts were detected in the LSO: 22B.1, 23A.1a, 23A.1b, 32D.1, 39D.2c, 43C.1, and 58A.2.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

I. Specific Embodiments

A. *Drosophila* Gustatory Receptor Proteins

The present invention provides a family of isolated proteins, allelic variants of the proteins, and conservative amino acid substitutions of the proteins. As used herein, protein or polypeptide refers to any one of the proteins that has the amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92. The invention also includes naturally occurring allelic variants and proteins that have a slightly different amino acid sequence than that specifically recited above. Allelic variants, though possessing a slightly different amino acid sequence than those recited above, will still have the same or similar biological functions associated with any of the amino acid proteins.

As used herein, the family of proteins related to any one of the amino acid sequences depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80,

82, 84, 86, 88, 90 and 92 refers to proteins that have been isolated from organisms in addition to *Drosophila*. The methods used to identify and isolate other members of the family of proteins related to these amino acid proteins are described below.

5 The proteins of the present invention are preferably in isolated form. As used herein, a protein is said to be isolated when physical, mechanical or chemical methods are employed to remove the protein from cellular constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated protein.

10 The proteins of the present invention further include conservative amino acid substitution variants (*i.e.*, conservative) of the proteins herein described. As used herein, a conservative variant refers to at least one alteration in the amino acid sequence that does not adversely affect the biological functions of the protein. A substitution, insertion or deletion is said to adversely affect the protein when the altered sequence prevents or disrupts a biological function associated with the protein. For example, the overall
15 charge, structure or hydrophobic-hydrophilic properties of the protein can be altered without adversely affecting a biological activity. Accordingly, the amino acid sequence can often be altered, for example to render the peptide more hydrophobic or hydrophilic, without adversely affecting the biological activities of the protein.

Ordinarily, the allelic variants, the conservative substitution variants, and the
20 members of the protein family, will have an amino acid sequence having at least 10% amino acid sequence identity with the sequences set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84 or 86 more preferably at least 35%, even more preferably at least 40% and most preferably at least 45%. Identity or homology
25 with respect to such sequences is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the known peptides, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology, and not considering any conservative substitutions as part of the sequence identity.

N-terminal, C-terminal or internal extensions, deletions or insertions into the peptide sequence shall not be construed as affecting homology.

The proteins of the present invention have seven transmembrane domains as defined by hydropathy analysis (Kyte & Doolittle, (1982) J. Mol. Biol. 157, 105-132).

5 Furthermore, the proteins of the present invention have conserved amino acid residues in defined domains of the protein. For example, the proteins of the present invention have at least one of the following conserved amino acids as depicted in Figure 1, including but not limited to, Serine in the amino terminal domain; Phenylalanine in the first transmembrane domain; Arginine in the first extracellular loop; Leucine in the fourth
10 transmembrane domain; Leucine in the third transmembrane domain; Glycine in the fifth transmembrane domain; Tyrosine in the fifth transmembrane domain; Leucine in the third extracellular loop; Phenylalanine in the third extracellular loop; Alanine in the seventh transmembrane domain; Glycine in the seventh transmembrane domain; Leucine in the seventh transmembrane domain; Aspartate in the seventh transmembrane domain;
15 Alanine in the seventh transmembrane domain; Threonine in the seventh transmembrane domain; Tyrosine in the seventh transmembrane domain; Valine in the seventh transmembrane domain; Glutamine in the carboxy terminal domain; and Phenylalanine in the carboxy terminal domain. In addition, the conserved amino acids may be selected from any of the amino acid residues indicated as being conserved among *Drosophila*
20 Gustatory Receptor (DGR) proteins as depicted in Figure 1 (shaded).

Thus, the proteins of the present invention include molecules having the amino acid sequence disclosed in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92; fragments thereof having a consecutive sequence of at
25 least about 3, 4, 5, 6, 10, 15, 20, 25, 30, 35 or more amino acid residues of the proteins, for instance, antigenic fragments such as those found in the extracellular loops of the protein (see Figure 1); amino acid sequence variants wherein an amino acid residue has been inserted N- or C-terminal to, or within, the disclosed sequence; and amino acid

sequence variants of the disclosed sequences, or their fragments as defined above, that have been substituted by another residue. Contemplated variants further include those containing predetermined mutations by, *e.g.*, homologous recombination, site-directed or PCR mutagenesis, and the corresponding proteins of other insect species, including but not limited to the order *Diptera*, *Lepidoptera*, *Homoptera* and *Coleoptera*, within these orders, preferably the genus *Drosophila*, *Anopheles*, *Aedes*, *Ceratitis*, *Muscidae*, *Culicidae*, *Anagasta* and *Popilla* and the alleles or other naturally occurring variants of the family of proteins; and derivatives wherein the protein has been covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid (for example a detectable moiety such as an enzyme or radioisotope).

As described below, members of the family of proteins can be used: 1) to identify agents which modulate at least one activity of the protein; 2) to identify binding partners for the protein, 3) as an antigen to raise polyclonal or monoclonal antibodies, and 4) in methods to modify insect behavior.

B. Nucleic Acid Molecules

The present invention further provides nucleic acid molecules which encode any of the proteins having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92 and the related proteins herein described, preferably in isolated form. As used herein, "nucleic acid" is defined as RNA or DNA that encodes a protein or peptide as defined above, is complementary to a nucleic acid sequence encoding such peptides, hybridizes to such a nucleic acid and remains stably bound to it under appropriate stringency conditions, or encodes a polypeptide sharing at least 75% sequence identity, preferably at least 80%, and more preferably at least 85%, with the peptide sequences in conserved domains. Specifically contemplated are genomic DNA, cDNA, mRNA and antisense molecules, as well as nucleic acids based on alternative

backbones or including alternative bases whether derived from natural sources or synthesized. Such hybridizing or complementary nucleic acids, however, are defined further as being novel and non-obvious over any prior art nucleic acid including that which encodes, hybridizes under appropriate stringency conditions, or is complementary to nucleic acid encoding a protein according to the present invention.

Homology or identity at the amino acid or nucleotide level is determined by **BLAST** (**B**asic **L**ocal **A**lignment **S**earch **T**ool) analysis using the algorithm employed by the programs **blastp**, **blastn**, **blastx**, **tblastn** and **tblastx** (Karlin *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268 and Altschul, (1993) J. Mol. Evol. 36, 290-300, fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the **BLAST** program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases (see Altschul *et al.*, (1994) Nature Genetics 6, 119-129 which is fully incorporated by reference). The search parameters for **histogram**, **descriptions**, **alignments**, **expect** (*i.e.*, the statistical significance threshold for reporting matches against database sequences), **cutoff**, **matrix** and **filter** are at the default settings. The default scoring matrix used by **blastp**, **blastx**, **tblastn**, and **tblastx** is the **BLOSUM62** matrix (Henikoff *et al.*, (1992) Proc. Natl. Acad. Sci. USA 89, 10915-10919, fully incorporated by reference). For **blastn**, the scoring matrix is set by the ratios of **M** (*i.e.*, the reward score for a pair of matching residues) to **N** (*i.e.*, the penalty score for mismatching residues), wherein the default values for **M** and **N** are 5 and -4, respectively.

“Stringent conditions” are those that (1) employ low ionic strength and high temperature for washing, for example, 0.5 M sodium phosphate buffer at pH 7.2, 1 mM EDTA at pH 8.0 in 7% SDS at either 65°C or 55°C, or (2) employ during hybridization a denaturing agent such as formamide, for example, 50% formamide with 0.1% bovine

serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 0.05 M sodium phosphate buffer at pH 6.5 with 0.75 M NaCl, 0.075 M sodium citrate at 42°C. Another example is use of 50% formamide, 5× SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate at pH 6.8, 0.1% sodium pyrophosphate, 5× Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS and 10% dextran sulfate at 55°C, with washes at 55°C in 0.2× SSC and 0.1% SDS. A skilled artisan can readily determine and vary the stringency conditions appropriately to obtain a clear and detectable hybridization signal. Preferred molecules are those that hybridize under the above conditions to the complements of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91, and which encode a functional protein.

As used herein, a nucleic acid molecule is said to be "isolated" when the nucleic acid molecule is substantially separated from contaminant nucleic acid encoding other polypeptides from the source of nucleic acid. For information on how to extract and manipulate nucleic acids from *Drosophila*, see, for example, Roberts, (1998) *Drosophila: A Practical Approach*, IRL Press.

The present invention further provides fragments of any one of the encoding nucleic acids molecules. As used herein, a fragment of an encoding nucleic acid molecule refers to a small portion of the entire protein coding sequence. The size of the fragment will be determined by the intended use. For example, if the fragment is chosen so as to encode an active portion of the protein, the fragment will need to be large enough to encode the functional region(s) of the protein. For instance, fragments of the invention encode antigenic fragments such as the extracellular loops or N-terminal domain of the protein depicted in SEQ ID NO: 9 (21D.1) and as set forth in Figure 1. If the fragment is to be used as a nucleic acid probe or PCR primer, then the fragment length is chosen so as to obtain a relatively small number of false positives during probing and priming.

Fragments of the encoding nucleic acid molecules of the present invention (*i.e.*, synthetic oligonucleotides) that are used as probes or specific primers for the polymerase

chain reaction (PCR), or to synthesize gene sequences encoding proteins of the invention can easily be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci *et al.*, (1981) J. Am. Chem. Soc. 103, 3185-3191) or using automated synthesis methods. In addition, larger DNA segments can readily be prepared by well known methods, such as synthesis of a group of oligonucleotides that define various modular segments of the gene, followed by ligation of oligonucleotides to build the complete modified gene.

The encoding nucleic acid molecules of the present invention may further be modified so as to contain a detectable label for diagnostic and probe purposes. A variety of such labels are known in the art and can readily be employed with the encoding molecules herein described. Suitable labels include, but are not limited to, fluorescent-labeled, biotin-labeled, radio-labeled nucleotides and the like. A skilled artisan can employ any of the art known labels to obtain a labeled encoding nucleic acid molecule.

Modifications to the primary structure itself by deletion, addition, or alteration of the amino acids incorporated into the protein sequence during translation can be made without destroying the activity of the protein. Such substitutions or other alterations result in proteins having an amino acid sequence encoded by a nucleic acid falling within the contemplated scope of the present invention.

C. Isolation of Other Related Nucleic Acid Molecules

As described above, the identification and characterization of the nucleic acid molecules having SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91 allows a skilled artisan to isolate nucleic acid molecules that encode other members of the protein family in addition to the sequences herein described. Further, the presently disclosed nucleic acid molecules allow a skilled artisan to isolate nucleic acid molecules that encode other members of the family of proteins in addition to the protein having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and

92.

Essentially, a skilled artisan can readily use any one of the amino acid sequences selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 5 86, 88, 90 and 92, to generate antibody probes to screen expression libraries prepared from appropriate cells. Typically, polyclonal antiserum from mammals such as rabbits immunized with the purified protein (as described below) or monoclonal antibodies can be used to probe a cDNA or genomic expression library to obtain the appropriate coding sequence for other members of the protein family. The cloned cDNA sequence can be 10 expressed as a fusion protein, expressed directly using its own control sequences, or expressed by constructions using control sequences appropriate to the particular host used for expression of the enzyme.

Alternatively, a portion of the coding sequence herein described can be synthesized and used as a probe to retrieve DNA encoding a member of the protein family from any 15 organism. Oligomers containing approximately 18-20 nucleotides (encoding about a six to seven amino acid stretch) are prepared and used to screen genomic DNA or cDNA libraries to obtain hybridization under stringent conditions or conditions of sufficient stringency to eliminate an undue level of false positives.

Additionally, pairs of oligonucleotide primers can be prepared for use in a polymerase 20 chain reaction (PCR) to selectively clone an encoding nucleic acid molecule. A PCR denature/anneal/extend cycle for using such PCR primers is well known in the art and can readily be adapted for use in isolating other encoding nucleic acid molecules. For example, degenerate primers can be used to clone any *Drosophila* Gustatory Receptor (DGR) gene across species. Specifically, based on the sequence information derived from the family of 25 *Drosophila* Gustatory Receptors, degenerate primers can be designed based on conserved sequences among gustatory receptors, which can then be used to clone nucleic acid molecules encoding gustatory receptor proteins from other species of insects.

Applicants have also identified a method for isolating nucleic acid molecules that

encode other members of the protein family in addition to the sequences herein described. Essentially, a two-step strategy is employed to identify gustatory receptor genes from the genomic database. First, a computer algorithm was designed to search genomic sequences for open reading frames (ORFs) from candidate gustatory receptor genes. Second, RT-PCR is
5 used to determine if transcripts from any of these ORFs are expressed in gustatory organs.

The algorithm is used to identify G protein-coupled receptors (GPCR) genes using statistical characterization of amino acid physico-chemical profiles in combination with a non-parametric discriminant function. The algorithm is trained on a set of putative sequences from a database. In the first step, three sets of descriptors are used to summarize the
10 physico-chemical profiles of the sequences. These are GES scale of hydropathy (Engelman *et al.*, (1986) *Annu. Rev. Biophys. Biophys. Chem.* 15, 321-353), polarity (Brown, (1991) *Molecular Biology Labfax*, Academic Press), and amino acid usage frequency. For the first two of these measurements, a computed sliding window profile is employed (White, (1994) *Membrane Protein Structure*, Oxford University Press) using a kernel of a certain number of
15 amino acids as a constant function convoluted with a certain number of amino acids as a Gaussian function. These profiles are then summarized with three statistics; the periodicity, average derivative and the variance of the derivative.

Each sequence is then characterized by multiple variables using a non-parametric linear discriminant function that is optimized to separate the known family proteins from
20 random proteins in the training set. The same linear discriminant function with the scores derived from the training set is used to screen any nucleic acid database for candidate genes. The candidate sequences are given significance values by an odds ratio of the proteins and non-family proteins, computed using the observed empirical distribution of the training set. Those sequences with a sufficiently high odds ratio are considered for further analysis. The
25 algorithm can also be used to identify any protein family by altering the training set of sequences.

The method of identification further includes steps for identifying novel gustatory receptor genes comprising selecting candidate gustatory receptor genes by screening a nucleic

acid database using an algorithm trained to identify seven transmembrane receptors genes; screening said selected candidate gustatory receptor genes by identifying nucleic acid sequences with conserved amino acid residues and intron-exon boundaries common to gustatory receptors, and open reading frames of sufficient size as to encode a seven
5 transmembrane receptor. As an additional step, the expression of gustatory receptor genes is measured to confirm candidate gustatory gene as an gustatory gene. The exon-intron boundaries and conserved amino acid residues may be selected from any of the positions depicted in Figure 3. Alternatively, selecting candidate gustatory receptor genes by screening a nucleic acid database for nucleic acid sequences with sufficient homology to at least one
10 known gustatory receptor gene is also encompassed in the invention. In a preferred embodiment, the nucleic acid database is a genomic database, an EST database or even an gustatory receptor database as previously described (Skoufos *et al.*, (1999) Nucleic Acids Research 27, 343-345).

In one example of the invention, the training set could consist of known gustatory
15 receptors from *Drosophila* and could be used to search genomic sequences for new gustatory receptors in other species. In a similar example, the training set could consist of known sequences coding for receptors from a particular family and could be used to identify homologs across species. Specifically, gustatory receptors of one species could be used as a training set to identify gustatory receptors in another species.

20 **D. rDNA molecules containing a DNA molecule**

The present invention further provides recombinant DNA molecules (rDNAs) that contain a coding sequence. As used herein, a rDNA molecule is a DNA molecule that has been subjected to molecular manipulation *in vitro*. Methods for generating rDNA molecules
25 are well known in the art, for example, see Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press. In the preferred rDNA molecules, a coding DNA sequence is operably linked to expression control sequences or vector sequences.

The choice of vector and expression control sequences to which one of the protein family encoding sequences of the present invention is operably linked depends directly, as is well known in the art, on the functional properties desired, *e.g.*, protein expression, and the host cell to be transformed. A vector contemplated by the present invention is at least capable of directing the replication or insertion into the host chromosome, and preferably also
5 expression, of the structural gene included in the rDNA molecule.

Expression control elements that are used for regulating the expression of an operably linked protein encoding sequence are known in the art and include, but are not limited to, inducible promoters, constitutive promoters, secretion signals, and other regulatory elements.
10 Preferably, the inducible promoter is readily controlled, such as being responsive to a nutrient in the host cell's medium.

In one embodiment, the vector containing a coding nucleic acid molecule will include a prokaryotic replicon, *i.e.*, a DNA sequence having the ability to direct autonomous replication and maintenance of the recombinant DNA molecule extra-chromosomally in a prokaryotic host cell, such as a bacterial host cell, transformed therewith. Such replicons are
15 well known in the art. In addition, vectors that include a prokaryotic replicon may also include a gene whose expression confers a detectable marker such as a drug resistance. Typical bacterial drug resistance genes are those that confer resistance to ampicillin or tetracycline.

Vectors that include a prokaryotic replicon can further include a prokaryotic or bacteriophage promoter capable of directing the expression (transcription and translation) of the coding gene sequences in a bacterial host cell, such as *E. coli*. A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and transcription to occur. Promoter sequences compatible with bacterial hosts
20 are typically provided in plasmid vectors containing convenient restriction sites for insertion of a DNA segment of the present invention. Typical of such vector plasmids are pUC8, pUC9, pBR322 and pBR329 available from BioRad Laboratories, pPL and pKK223 available from Pharmacia.

Expression vectors compatible with eukaryotic cells, preferably those compatible with invertebrate cells such as insect cells, can also be used to form a rDNA molecules that contains a coding sequence. Eukaryotic cell expression vectors are well known in the art and are available from several commercial sources. Typically, such vectors are provided
5 containing convenient restriction sites for insertion of the desired DNA segment. Typical of such vectors are pSVL and pKSV-10 (Pharmacia), pBPV-1/pML2d (International Biotechnologies, Inc.), pTDT1 (ATCC, #31255), the vector pCDM8 described herein, and the like eukaryotic expression vectors. Vectors may be modified to include insect cell specific promoters if needed.

10 Eukaryotic cell expression vectors used to construct the rDNA molecules of the present invention may further include a selectable marker that is effective in an eukaryotic cell, preferably a drug resistance selection marker. A preferred drug resistance marker is the gene whose expression results in neomycin resistance, *i.e.*, the neomycin phosphotransferase (*neo*) gene (Southern *et al.*, (1982) J. Mol. Appl. Genet. 1, 327-341). Alternatively, the
15 selectable marker can be present on a separate plasmid, and the two vectors are introduced by co-transfection of the host cell, and selected by culturing in the appropriate drug for the selectable marker.

E. Host Cells Containing an Exogenously Supplied Coding Nucleic Acid

20 The present invention further provides host cells transformed with a nucleic acid molecule that encodes a protein of the present invention. The host cell can be either prokaryotic or eukaryotic. Eukaryotic cells useful for expression of a protein of the invention are not limited, so long as the cell line is compatible with cell culture methods and compatible with the propagation of the expression vector and expression of the gene product. Preferred
25 eukaryotic host cells include, but are not limited to, yeast, insect and mammalian cells, preferably insect cells such as those from a *Drosophila* cell line. Preferred *Drosophila* host cells include *Drosophila* Schneider line 2, and the like insect tissue culture cell lines. Any prokaryotic host can be used to express a rDNA molecule encoding a protein of the

invention. The preferred prokaryotic host is *E. coli*.

Transformation of appropriate cell hosts with a rDNA molecule of the present invention is accomplished by well known methods that typically depend on the type of vector used and host system employed. With regard to transformation of prokaryotic host cells, 5 electroporation and salt treatment methods are typically employed, see, for example, Cohen *et al.*, (1972) Proc. Natl. Acad. Sci. USA 69, 2110-2114; and Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press. With regard to transformation of vertebrate cells with vectors containing rDNAs, electroporation, cationic lipid or salt treatment methods are typically employed, see, for example, Graham *et al.*, (1973) 10 Virology 52, 456-467; Wigler *et al.*, (1979) Proc. Natl. Acad. Sci. USA 76, 1373-1376.

Successfully transformed cells, *i.e.*, cells that contain a rDNA molecule of the present invention, can be identified by well known techniques including the selection for a selectable marker. For example, cells resulting from the introduction of an rDNA of the present invention can be cloned to produce single colonies. Cells from those colonies can be 15 harvested, lysed and their DNA content examined for the presence of the rDNA using a method such as that described by Southern, (1975) J. Mol. Biol. 98, 503-517; or Berent *et al.*, (1985) Biotech. Histochem. 3, 208; or the proteins produced from the cell assayed via an immunological method.

20 F. Production of Recombinant Proteins using a rDNA Molecule

The present invention further provides methods for producing a protein of the invention using nucleic acid molecules herein described. In general terms, the production of a recombinant form of a protein typically involves the following steps: First, a nucleic acid molecule is obtained that encodes a protein of the invention, such as any of the nucleic acid 25 molecule depicted in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91. The nucleic acid molecule is then preferably placed in operable linkage with suitable control sequences, as described above, to form an expression unit containing the

protein open reading frame. The expression unit is used to transform a suitable host and the transformed host is cultured under conditions that allow the production of the recombinant protein. Optionally the recombinant protein is isolated from the medium or from the cells; recovery and purification of the protein may not be necessary in some instances where some
5 impurities may be tolerated.

Each of the foregoing steps can be done in a variety of ways. For example, the desired coding sequences may be obtained from genomic fragments and used directly in appropriate hosts. The construction of expression vectors that are operable in a variety of hosts is accomplished using appropriate replicons and control sequences, as set forth above. The
10 control sequences, expression vectors, and transformation methods are dependent on the type of host cell used to express the gene and were discussed in detail earlier. Suitable restriction sites can, if not normally available, be added to the ends of the coding sequence so as to provide an excisable gene to insert into these vectors. A skilled artisan can readily adapt any host-expression system known in the art for use with the nucleic acid molecules of the
15 invention to produce recombinant protein.

G. Methods to Identify Binding Partners

Another embodiment of the present invention provides methods for use in isolating and identifying binding partners of any of the DGR proteins of the invention. In detail, a
20 protein of the invention is mixed with a potential binding partner or an extract or fraction of a cell under conditions that allow the association of potential binding partners with the protein of the invention. After mixing, peptides, polypeptides, proteins or other molecules that have become associated with a protein of the invention are separated from the mixture. The binding partner that bound to the protein of the invention can then be removed and further
25 analyzed. To identify and isolate a binding partner, the entire protein, for instance a protein comprising the entire amino acid sequence of any of the proteins depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92 can be used.

Alternatively, a fragment of any of the proteins can be used.

As used herein, a cellular extract refers to a preparation or fraction which is made from a lysed or disrupted cell. The preferred source of cellular extracts will be cells derived from *Drosophila*, for instance, labellar cellular extract.

5 A variety of methods can be used to obtain an extract of a cell. Cells can be disrupted using either physical or chemical disruption methods. Examples of physical disruption methods include, but are not limited to, sonication and mechanical shearing. Examples of chemical lysis methods include, but are not limited to, detergent lysis and enzyme lysis. A skilled artisan can readily adapt methods for preparing cellular extracts in order to obtain
10 extracts for use in the present methods.

Once an extract of a cell is prepared, the extract is mixed with any of the proteins of the invention under conditions in which association of the protein with the binding partner can occur. A variety of conditions can be used, the most preferred being conditions that closely resemble conditions found in the cytoplasm of a *Drosophila* cell. Features such as osmolarity,
15 pH, temperature and the concentration of cellular extract used, can be varied to optimize the association of the protein with the binding partner.

As used herein, the term "binding partner" refers to any molecule that binds to a DGR protein of the invention. Binding partners to any one of the Gustatory receptors of the invention include, but are not limited to, small molecules, peptides, polypeptides and proteins.
20 In one embodiment, the binding partner is a co-receptor that forms a dimer complex with the Gustatory receptor, such complexes being necessary for efficient signal transduction. In another embodiment, the binding partner can be a G protein or a subunit of a G protein as the Gustatory receptors of the invention are assumed to be G protein-linked because of their seven transmembrane domains.

25 After mixing under appropriate conditions, the bound complex is separated from the mixture. A variety of techniques can be utilized to separate the mixture. For example, antibodies specific to a protein of the invention can be used to immunoprecipitate the binding partner complex. Alternatively, standard chemical separation techniques such as

chromatography and density-sediment centrifugation can be used.

After removal of non-associated cellular constituents found in the extract, the binding partner can be dissociated from the complex using conventional methods. For example, dissociation can be accomplished by altering the salt concentration or pH of the mixture.

5 To aid in separating associated binding partner pairs from the mixed extract, the protein of the invention can be immobilized on a solid support. For example, the protein can be attached to a nitrocellulose matrix or acrylic beads. Attachment of the protein to a solid support aids in separating peptide-binding partner pairs from other constituents found in the extract. The identified binding partners can be either a single protein or a complex made up of
10 two or more proteins. Alternatively, binding partners may be identified using a Far-Western assay according to the procedures of Takayama *et al.*, (1997) *Methods Mol. Biol.* 69, 171-184 or identified through the use of epitope tagged proteins or GST fusion proteins.

Alternatively, the nucleic acid molecules of the invention can be used in a yeast two-hybrid system. The yeast two-hybrid system has been used to identify other protein partner
15 pairs (Alifragis *et al.*, (1997) *Proc. Natl. Acad. Sci. USA* 94, 13099-13104; Dong *et al.*, (1999) *Gene* 237, 421-428) and can readily be adapted to employ the nucleic acid molecules herein described.

In another embodiment, binding partners may be identified in insects using single unit recordings as previously described (Kaissling, (1995) *Single unit recordings in insect gustatory organs*, in: Spielman & Brand, (1995) *Experimental Cell Biology of Taste and Olfaction*, CRC Press). Using single unit recordings *in vivo*, response profiles are established for potential ligands, these profiles are then categorized into distinct functional classes indicative of distinct receptor-ligand interactions (see, *e.g.*, U.S. Patent No. 5,993,778). Single
20 unit recordings in transgenic insects which contain transgenes resulting in over- or under-
25 expression of a gene are also useful for identifying and characterizing ligands which bind to multiple gustatory receptors as well as identifying and characterizing new gustatory receptors.

The nucleic acids of the invention and their corresponding proteins can be used on an array or microarray for high-throughput screening for agents which interact with either the

nucleic acids of the invention or their corresponding proteins.

An “array” or “microarray” generally refers to a grid system which has each position or probe cell occupied by a defined nucleic acid fragments also known as oligonucleotides. The arrays themselves are sometimes referred to as “chips” or “biochips”. High-density
5 nucleic acid and protein microarrays often have thousands of probe cells in a variety of grid styles. For DNA microarray protocols particularly suited to studying *Drosophila*, see, for example, Sullivan *et al.*, (2000) *Drosophila* Protocols, Cold Spring Harbor Laboratory Press.

A typical molecular detection chip includes a substrate on which an array of recognition sites, binding sites or hybridization sites are arranged. Each site has a respective
10 molecular receptor which binds or hybridizes with a molecule having a predetermined structure. The solid support substrates which can be used to form surface of the array or chip include organic and inorganic substrates, such as glass, polystyrenes, polyimides, silicon dioxide and silicon nitride. For direct attachment of probes to the electrodes, the electrode surface must be fabricated with materials capable of forming conjugates with the probes.

15 Once the array is fabricated, a sample solution is applied to the molecular detection chip and molecules in the sample bind or hybridize at one or more sites. The sites at which binding occurs are detected, and one or more molecular structures within the sample are subsequently deduced. Detection of labeled batches is a traditional detection strategy and includes radioisotope, fluorescent and biotin labels, but other options are available, including
20 electronic signal transduction.

Polymer arrays of nucleic acid probes can be used to extract information from, for example, nucleic acid samples. These samples are exposed to the probes under conditions that permit binding. The arrays are then scanned to determine to which probes the sample molecules have interacted with the nucleic acids of the polymer array. One can obtain
25 information by careful probe selection and using algorithms to compare patterns of interactions. For example, the method is useful in screening for novel gustatory receptors in multiple organisms. For example, *Drosophila* degenerate gustatory receptor oligonucleotide arrays can be used to examine a nucleic acid sample from another insect species in order to

identify novel gustatory receptors in that species.

In typical applications, a complex solution containing one or more substances to be characterized contacts a polymer array comprising nucleic acids. For example, the array is comprised of nucleic acid probes. The probes of the array can be either DNA or RNA, which
5 may be either single-stranded or double-stranded. In a preferred embodiment of the invention, the probes are arranged (either by immobilization, typically by covalent attachment, of a pre-synthesized probe or by synthesis of the probe on the substrate) on the substrate or chips in lanes stretching across the chip and separated, and these lanes are in turned arranged in blocks of preferably five lanes, although blocks of other sizes will have
10 useful application. The present invention provides individual probes, sets of probes, and arrays of probe sets on chips, in specific patterns which are used to characterize the substances in a complex mixture by producing a distinct image which is representative of the binding interactions between the probes on the chip and the substances in the complex mixture. The pattern of hybridization to the chip allows inferences to be drawn about the
15 substances present in the complex mixture.

The substances in the complex solution will bind to the nucleic acids on the array. The substances of the complex mixture which bind to the nucleic acids of the array may include, but are not limited to, complementary nucleic acids, non-complementary nucleic acids, proteins, antibodies, oligosaccharides, etc. The types of binding may include, but are
20 not limited to, specific and non-specific, competitive and non-competitive, allosteric, cooperative, non-cooperative, complementary and non-complementary, etc. For example, the nucleic acids of the array can bind to complementary nucleic acids in the complex mixture but can also bind in a tertiary manner, independent of base pairing, to non-complementary nucleic acids.

25 The nucleic acids of the array or the substances of the complex mixture may be tagged with a detectable label. The detectable label can be, for example, a luminescent label, a light scattering label or a radioactive label. Accordingly, locations at which substances interact can be identified by either determining if the signal of the label has been quenched by binding or

identifying locations where the signal of the label is present in cases where the substances of the complex mixture have been labeled. Based on the locations where binding is detected, information regarding the complex mixture can be obtained.

5 The methods of this invention will find particular use wherever high through-put of samples is required. In particular, this invention is useful in ligand screening settings and for determining the composition of complex mixtures.

10 Polypeptides are an exemplary system for exploring the relationship between structure and function in biology. When the twenty naturally occurring amino acids are condensed into a polymeric molecule they form a wide variety of three-dimensional configurations, each resulting from a particular amino acid sequence and solvent condition. For example, the number of possible polypeptide configurations using the twenty naturally occurring amino acids for a polymer five amino acids long is over three million. Typical proteins are more than one-hundred amino acids in length.

15 In typical applications, a complex solution containing one or more substances to be characterized contacts a polymer array comprising polypeptides. The polypeptides of the invention can be prepared by classical methods known in the art, for example, by using standard solid phase techniques. The standard methods include exclusive solid phase synthesis, partial solid phase synthesis methods, fragment condensation, classical solution synthesis and recombinant DNA technology (see Merrifield, (1963) Am. Chem. Soc. 85, 20 2149-2152). On solid phase, the synthesis is typically commenced from the C-terminal end of the peptide using an alpha-amino protected resin. A suitable starting material can be prepared, for instance, by attaching the required alpha-amino acid to a chloromethylated resin, a hydroxy-methyl resin or a benzhydrylamine resin.

25 The alpha-amino protecting groups are those known to be useful in the art of stepwise synthesis of peptides. Included are acyl type protecting groups, aromatic urethane type protecting groups, aliphatic urethane protecting groups and alkyl type protecting groups. The side chain protecting group remains intact during coupling and is not split off during the deprotection of the amino-terminus protecting group or during coupling. The side chain

protecting group must be removable upon the completion of the synthesis of the final peptide and under reaction conditions that will not alter the target peptide.

After removal of the alpha-amino protecting group, the remaining protected amino acids are coupled stepwise in the desired order. An excess of each protected amino acid is
5 generally used with an appropriate carboxyl group activator such as dicyclohexylcarbodiimide (DCC) in solution, for example, in methylene chloride, dimethyl formamide (DMF) mixtures.

In a preferred embodiment, the polypeptides or proteins of the array can bind to other co-receptors to form a heteroduplex on the array. In yet another embodiment, the
10 polypeptides or proteins of the array can bind to peptides or small molecules.

These procedures can also be used to synthesize peptides in which amino acids other than the twenty naturally occurring, genetically encoded amino acids are substituted at one, two, or more positions of any of the compounds of the invention. For instance, naphthylalanine can be substituted for tryptophan, facilitating synthesis. Other synthetic amino
15 acids that can be substituted into the peptides of the present invention include L-hydroxypropyl, L-3, 4-dihydroxyphenylalanyl, d-amino acids such as L-d-hydroxylysyl and D-d-methylalanyl, L- α -methylalanyl and β -amino acids non-naturally occurring synthetic amino acids can also be incorporated into the peptides of the present invention (see Roberts *et al.*, (1983) Peptide Synthesis 5, 341-449).

20 One can replace the naturally occurring side chains of the twenty genetically encoded amino acids (or D amino acids) with other side chains, for instance with groups such as alkyl, lower alkyl, cyclic four, five, six, to seven-membered alkyl, amide, amide lower alkyl, amide di(lower alkyl), lower alkoxy, hydroxy, carboxy and the lower ester derivatives thereof, and with four, five, six, to seven-membered heterocyclic. In particular, proline analogs in which
25 the ring size of the proline residue is changed from five members to four, six or seven members can be employed. Cyclic groups can be saturated or unsaturated, and if unsaturated, can be aromatic or non-aromatic. Heterocyclic groups preferably contain one or more nitrogen, oxygen, and/or sulphur heteroatoms. Examples of such groups include the

furazanyl, furyl, imidazolidinyl, imidazolyl, imidazoliny, isothiazolyl, isoxazolyl, morpholinyl, oxazolyl, piperazinyl, piperidyl, pyranyl, pyrazinyl, pyrazolidinyl, pyrazolinyl, pyrazolyl, pyridazinyl, pyridyl, pyrimidinyl, pyrrolidinyl, pyrrolinyl, pyrrolyl, thiadiazolyl, thiazolyl, thienyl, thiomorpholinyl and triazolyl. These heterocyclic groups can be substituted
5 or unsubstituted. Where a group is substituted, the substituent can be alkyl, alkoxy, halogen, oxygen, or substituted or unsubstituted phenyl.

One can also readily modify the peptides of the instant invention by phosphorylation (see Bannwarth *et al.*, (1996) *Biorg. Med. Chem. Let.* 6, 2141-2146) and other methods for making peptide derivatives of the compounds of the present invention are described in Hruby
10 *et al.*, (1990) *Biochem. J.* 268, 249-262). Thus, the peptide compounds of the invention also serve as a basis to prepare peptide mimetics with similar biological activity. The array can also comprise peptide mimetics with the same or similar desired biological activity as the corresponding peptide compound but with more favorable activity than the peptide with respect to solubility, stability, and susceptibility to hydrolysis and proteolysis (see Morgan *et al.*, (1989) *Ann. Rep. Med. Chem.* 24, 243-252).
15

Peptides suitable for use in this embodiment generally include those peptides, for example, ligands, that bind to a receptor, such as seven transmembrane proteins. Such peptides typically comprise about 150 amino acid residues or less and, more preferably, about 100 amino acid residues or less. Polypeptides or proteins suitable for use in this embodiment
20 generally include those polypeptides or proteins that interact with a receptor, such as a co-receptor or G protein. Such polypeptides or proteins typically comprise about 150 amino acid residues or more and, more preferably, about 400 amino acids or more.

The peptides of the present invention may exist in a cyclized form with an intramolecular disulfide bond between the thiol groups of the cysteines. Alternatively, an
25 intermolecular disulfide bond between the thiol groups of the cysteines can be produced to yield a dimeric (or higher oligomeric) compound. One or more of the cysteine residues may also be substituted with a homocysteine. Other embodiments of this invention provide for analogs of these disulfide derivatives in which one of the sulfurs has been replaced by a CH₂

group or other isostere for sulfur. These analogs can be made via an intramolecular or intermolecular displacement, using methods known in the art.

H. Methods to Identify Agents that Modulate Expression of DGRs.

5 Another embodiment of the present invention provides methods for identifying agents that modulate the expression of a nucleic acid encoding any one of the DGRproteins of the invention such as any protein having the amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92. Such assays may
10 utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention, for instance a nucleic acid encoding any one of the proteins having the amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92, if it is capable of up- or down-regulating expression of the
15 nucleic acid in a cell.

In one assay format, cell lines that contain reporter gene fusions between the open reading frame of any one of the nucleotides depicted in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91, and any assay fusion partner may be
20 prepared. Numerous assay fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, (1990) Anal. Biochem. 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential
25 expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of a nucleic acid encoding at least one of the proteins having the sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74,

76, 78, 80, 82, 84, 86, 88, 90 and 92.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a nucleic acid encoding at least one protein of the invention selected from the group of proteins having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92. For instance, mRNA expression may be monitored directly by hybridization to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press.

Probes to detect differences in RNA expression levels between cells exposed to the agent and control cells may be prepared from the nucleic acids of the invention. It is preferable, but not necessary, to design probes which hybridize only with target nucleic acids under conditions of high stringency. Only highly complementary nucleic acid hybrids form under conditions of high stringency. Accordingly, the stringency of the assay conditions determines the amount of complementary nucleotides which should exist between two nucleic acid strands in order to form a hybrid. Stringency should be chosen to maximize the difference in stability between the probe:target hybrid and potential probe:non-target hybrids.

Probes may be designed from the nucleic acids of the invention through methods known in the art. For instance, the G+C content of the probe and the probe length can affect probe binding to its target sequence. Methods to optimize probe specificity are commonly available in Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press; or Ausubel *et al.*, (1995) Current Protocols in Molecular Biology, Greene Publishing Company.

Hybridization conditions are modified using known methods, such as those described by Sambrook *et al.*, (1989) and Ausubel *et al.*, (1995) as required for each probe. Hybridization of total cellular RNA or RNA enriched for polyA⁺ RNA can be accomplished in any available format. For instance, total cellular RNA or RNA enriched for polyA RNA

can be affixed to a solid support and the solid support exposed to at least one probe comprising at least one, or part of one of the sequences of the invention under conditions in which the probe will specifically hybridize. Alternatively, nucleic acid fragments comprising at least one, or part of one of the sequences of the invention can be affixed to a solid support, such as a porous glass wafer. The glass wafer can then be exposed to total cellular RNA or polyA RNA from a sample under conditions in which the affixed sequences will specifically hybridize. Such glass wafers and hybridization methods are widely available, for example, those disclosed by Beattie, 1995 (WO 9511755). By examining for the ability of a given probe to specifically hybridize to an RNA sample from an untreated cell population and from a cell population exposed to the agent, agents which up- or down-regulate the expression of a nucleic acid encoding at least one protein having the amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92 are identified.

Hybridization for qualitative and quantitative analysis of mRNA may also be carried out by using a RNase Protection Assay (*i.e.*, RPA, see Ma *et al.*, (1996) Methods 10, 273-238). Briefly, an expression vehicle comprising cDNA encoding the gene product and a phage specific DNA dependent RNA polymerase promoter (*e.g.*, T7, T3 or SP6 RNA polymerase) is linearized at the 3' end of the cDNA molecule, downstream from the phage promoter, wherein such a linearized molecule is subsequently used as a template for synthesis of a labeled antisense transcript of the cDNA by *in vitro* transcription. The labeled transcript is then hybridized to a mixture of isolated RNA (*i.e.*, total or fractionated mRNA) by incubation at 45°C overnight in a buffer comprising 80% formamide, 40 mM Pipes (pH 6.4), 0.4 M NaCl and 1 mM EDTA. The resulting hybrids are then digested in a buffer comprising 40 µg/ml ribonuclease A and 2 µg/ml ribonuclease. After deactivation and extraction of extraneous proteins, the samples are loaded onto urea-polyacrylamide gels for analysis.

In another assay format, agents which effect the expression of the instant gene products, cells or cell lines would first be identified which express said gene products

physiologically. Cells and cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and the cytosolic cascades. Further, such cells or cell lines would be
5 transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5'-promoter containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be
10 distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag. Such a process is well known in the art (see Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Cells or cell lines transduced or transfected as outlined above would then be contacted with agents under appropriate conditions; for example, the agent comprises an acceptable
15 excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be
20 disrupted and the polypeptides from disrupted cells are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent contacted" sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal
25 from the "agent contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

I. Methods to Identify Agents that Modulate Activity of DGRs

Another embodiment of the present invention provides methods for identifying agents that modulate at least one activity of a protein of the invention such as any one of the proteins having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26,
5 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92. Such methods or assays may utilize any means of monitoring or detecting the desired activity including, but not limited to, behavioral and electrophysiological studies.

10 In one format, the relative amounts of a protein of the invention are expressed in a cell population that has been exposed to the agent to be tested and is compared to an un-exposed control cell population. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control,
15 unexposed cell line or population. The cellular lysates are then analyzed with the probe.

Antibody probes are prepared by immunizing suitable mammalian hosts in appropriate immunization protocols using the peptides, polypeptides or proteins of the invention if they are of sufficient length, or if desired, required to enhance immunogenicity, conjugated to suitable carriers. Methods for preparing immunogenic conjugates with carriers
20 such as BSA, KLH, or other carrier proteins are well known in the art. In some circumstances, direct conjugation using, for example, carbodiimide reagents may be effective; in other instances linking reagents such as those supplied by Pierce Chemical Co., may be desirable to provide accessibility to the hapten. The hapten peptides can be extended at either the amino or carboxy terminus with a cysteine residue or interspersed with cysteine residues,
25 for example, to facilitate linking to a carrier. Administration of the immunogens is conducted generally by injection over a suitable time period and with use of suitable adjuvants, as is generally understood in the art. During the immunization schedule, titers of antibodies are taken to determine adequacy of antibody formation.

While the polyclonal antisera produced in this way may be satisfactory for some applications, for some applications, use of monoclonal preparations is preferred.

Immortalized cell lines which secrete the desired monoclonal antibodies may be prepared using the standard method of Kohler & Milstein, (1975) Nature 256, 495-497 or modifications which effect immortalization of lymphocytes or spleen cells, as is generally known. The immortalized cell lines secreting the desired antibodies are screened by immunoassay in which the antigen is the peptide hapten, polypeptide or protein. When the appropriate immortalized cell culture secreting the desired antibody is identified, the cells can be cultured either *in vitro* or by production in ascites fluid.

The desired monoclonal antibodies are then recovered from the culture supernatant or from the ascites supernatant. Fragments of the monoclonal or polyclonal antisera which contain the immunologically significant portion can be used as antagonists, as well as the intact antibodies. Use of immunologically reactive fragments, such as the Fab, Fab' of F(ab')₂ fragments is often preferable, as these fragments are generally less immunogenic than the whole immunoglobulin.

The antibodies or fragments may also be produced, using current technology, by recombinant means. Antibody regions that bind specifically to the desired regions of the protein can also be produced in the context of chimeras with multiple species origin, particularly humanized antibodies.

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a non-random basis which takes into account the sequence of the target site and its conformation in connection with the agent's action. Agents can be rationally selected or

rationally designed by utilizing the peptide sequences to identify proposed binding motifs, glycosylation and phosphorylation sites on the protein.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention. Dominant-negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be contacted with cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to the parent peptide (see Meyers, (1995) Molecular Biology & Biotechnology, VCH Publishers).

The peptide agents of the invention can be prepared using standard solid phase (or solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production using solid phase peptide synthesis is necessitated if non-gene-encoded amino acids are to be included.

Another class of agents of the present invention are antibodies immunoreactive with critical positions of proteins of the invention. Antibody agents are obtained by immunization of suitable mammalian subjects with peptides, containing as antigenic regions, those portions of the protein intended to be targeted by the antibodies.

J. Transgenic Organisms

Transgenic insects containing mutant, knock-out or modified genes corresponding to any one of the cDNA sequences depicted in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91 are also included in the invention. Transgenic insects are genetically modified insects into which recombinant, exogenous or cloned genetic

material has been experimentally transferred. Such genetic material is often referred to as a “transgene”. The nucleic acid sequence of the transgene, in this case a form of any one of the sequences depicted in SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91, may be integrated either at a locus of a genome where that particular nucleic acid sequence is not otherwise normally found or at the normal locus for the transgene. The transgene may consist of nucleic acid sequences derived from the genome of the same species or of a different species than the species of the target insect.

The term “germ cell line transgenic insect” refers to a transgenic insect in which the genetic alteration or genetic information was introduced into a germ line cell, thereby conferring the ability of the transgenic insect to transfer the genetic information to offspring. If such offspring in fact possess some or all of that alteration or genetic information, then they too are transgenic insects.

The alteration or genetic information may be foreign to the species of insect to which the recipient belongs, foreign only to the particular individual recipient, or may be genetic information already possessed by the recipient. In the last case, the altered or introduced gene may be expressed (*i.e.*, over-expression and knock-out) differently than the native gene.

Transgenic insects can be produced by a variety of different methods including P element-mediated transformation by microinjection (see, *e.g.*, Rubin & Spradling, (1982) Science 218, 348-353; Orr & Sohal, (1993) Arch. Biochem. Biophys. 301, 34-40), transformation by microinjection followed by transgene mobilization (Mockett *et al.*, (1999) Arch. Biochem. Biophys. 371, 260-269), electroporation (Huynh & Zieler, (1999) J. Mol. Biol. 288, 13-20) and through the use of baculovirus (Yamao *et al.*, (1999) Genes Dev. 13, 511-516. Furthermore, the use of adenoviral vectors to direct expression of a foreign gene to gustatory neuronal cells can also be used to generate transgenic insects (see, *e.g.*, Holtmaat *et al.*, (1996) Brain. Res. Mol. Brain Res. 41, 148-156).

A number of recombinant or transgenic insects have been produced, including those which over-express superoxide dismutase (Mockett *et al.*, (1999) Arch. Biochem. Biophys.

371, 260-269); express Syrian hamster prion protein (Raeber *et al.*, (1995) Mech. Dev. 51, 317-327); express cell-cycle inhibitory peptide aptamers (Kolonin & Finley (1998) Proc. Natl. Acad. Sci. USA 95, 14266-14271); and those which lack expression of the putative ribosomal protein S3A gene (Reynaud *et al.*, (1997) Mol. Gen. Genet. 256, 462-467).

- 5 While insects remain the preferred choice for most transgenic experimentation, in some instances it is preferable or even necessary to use alternative animal species. Transgenic procedures have been successfully utilized in a variety of animals, including mice, rats, sheep, goats, pigs, dogs, cats, monkeys, chimpanzees, hamsters, rabbits, cows and guinea pigs (see, *e.g.*, Kim *et al.*, (1997) Mol. Reprod. Dev. 46, 515-526; Houdebine, (1995) 10 Reprod. Nutr. Dev. 35, 609-617; Petters, (1994) Reprod. Fertil. Dev. 6, 643-645; Schnieke *et al.*, (1997) Science 278, 2130-2133; and Amoah, (1997) J. Anim. Sci. 75, 578-585).

- The method of introduction of nucleic acid fragments into insect cells can be by any method which favors co-transformation of multiple nucleic acid molecules. For instance, *Drosophila* embryonic Schneider line 2 (S2) cells can be stably transfected as previously 15 described (Schneider, (1972) J. Embryol. Exp. Morphol. 27, 353-365). Detailed procedures for producing transgenic insects are readily available to one skilled in the art (see Rubin & Spradling, (1982) Science 218, 348-353; Orr & Sohal, (1993) Arch. Biochem. Biophys. 301, 34-40, herein incorporated by reference in their entirety).

20 **K. Uses for Agents that Modulate at Least One Activity of DGRs**

1. Introduction.

- Organisms, including insects, are continually exposed to a great number of gustatory stimuli released by other organisms as well as by other aspects of their environment. The gustatory receptor genes of the present invention play an important role in the detection and 25 processing of these chemical stimuli, some of which have been implicated in initiating and modulating host-seeking and other behaviors, such as mating behaviors (see, for example, Roth, (1951) Ann. Entomol. Soc. Am. 44, 59-74; Jones *et al.*, (1976) Ent. Exp. Appn. 19, 19-22; Gillies, (1980) Bull. Ent. Res. 70, 525-532; Kline *et al.*, (1991) J. Med. Entomol. 28, 254-

258).

Most importantly, the DGR genes of the present invention may be used to track down gustatory receptor genes in insects that damage crops or transmit diseases. The present invention provides the tools and methodologies for finding specific compounds that interfere
5 with the insects' ability to detect tastes.

Of course, the present invention has important implications for improved methods of using pheromones and other semiochemicals for pest control. In addition, recent advancements in many other fields have greatly increased the variety of additional technologies for which the present invention also has significant applications. Examples of
10 such advancements include, but are not limited to the following: (a) the development and application of new techniques of chemical identification and synthesis; (b) new chemical release techniques; (c) more sophisticated application technologies; and (d) more detailed information about the behavior of specific organisms.

While not wishing to be bound by the specific embodiments discussed herein, the
15 following sections provide an overview of the wide variety of applications for which the present invention may be employed.

2. Definitions.

As used herein, the term "allomones" refers to any chemical substance produced or acquired by an organism that, when it contacts an individual of another species, evokes in the
20 receiver a behavioral or developmental reaction adaptively favorable to the transmitter.

As used herein, the term "host" refers to any organism on which another organism depends for some life function. Examples of hosts include, but are not limited to, humans which may serve as a host for the feeding of certain species of mosquito and the leaves of soybeans (*Glycine max* (L.)) which may act as hosts for the oviposit of the green cloverworm
25 (*Plathypena scabra* (F.)).

As used herein, the term "kairomones" refers to any of a heterogeneous group of chemical messengers that are emitted by organisms of one species but benefit members of another species. Examples include, but are not limited to, attractants, phagostimulants, and

other substances that mediate the positive responses of, for example, predators to their prey, herbivores to their food plants, and parasites to their hosts. Kairomones suitable for the purposes of the invention and methods of obtaining them are described, for example, Hedin, (1985) Bioregulators for Pest Control, American Chemical Society.

5 As used herein, the term “pheromone” refers to a substance, or characteristic mixture of substances, that is secreted and released by an organism and detected by a second organism of the same or a closely related species, in which it causes a specific reaction, such as a definite behavioral reaction or a developmental process. Examples include, but are not limited to, the mating pheromones of fungi and insects. More than a thousand moth sex pheromones
10 (Toth *et al.*, (1992) J. Chem. Ecol. 18, 13-25; Arn *et al.*, (1998) Appl. Entomol. Zoo. 33, 507-511) and hundreds of other pheromones have now been identified, including aggregation pheromones from beetles and other groups of insects. Various compositions, including resins and composite polymer dispensers, have been developed for the controlled release of pheromones have been developed (see, *e.g.*, U.S. Patent No. 5,750,129 & 5,504,142).

15 As used herein, the term “semiochemical” refers to any chemical substance that delivers a message or signal from one organism to another. Examples of such chemicals include, but are not limited to, pheromones, kairomones, oviposition deterrents, or stimulants, and a wide range of other classes of chemicals (see, for example, Nordlund *et al.*, (1981) Semiochemicals: Their Role in Pest Control, John Wiley; Howse *et al.*, (1998) Insect
20 Pheromones and Their Use in Pest Management, Chapman & Hall).

As used herein, the term “synomones” refers to any chemical substance which benefits both the emitter and receiver. Examples include, but are not limited to, compounds involved in floral attraction of pollinators and species-isolating mechanisms, such as sex pheromones of related species, where an inhibitor often functions to prevent mating among sympatric species.

25 As used herein, the term “volatile” refers to a chemical which evaporates readily at those temperatures and pressures which are considered the relevant temperatures and pressures for the reference organism of interest.

3. As Tools for Further Scientific Research.

Identification of Gustatory Receptor Genes in Other Organisms. The algorithms of the present invention may be used directly to search for gustatory receptor genes in other organisms, as explained elsewhere herein.

5 Alternatively, nucleic acid probes or primers may be designed based on the DGR genes of the present invention. Such probes or primers may be used to identify and isolate gustatory receptor genes in other organisms. Methods of creating and using the necessary nucleic acid probes and primers are discussed elsewhere herein.

10 The highest probability of success in locating gustatory genes in other organisms using the DGR genes of the present invention will most likely occur by using a boot-strapping or leap-frogging method. Such methods involve first probing organisms most related to fruit flies and successively progressing to more unrelated organisms, using the most newly identified gustatory receptor genes to identify similar genes in the next, more unrelated, insect of interest. Thus, the first organisms to probe with the DGR genes of the present invention
15 most preferably may be other flies from the order *Diptera* (*i.e.*, the two-winged or true flies). Examples of suitable flies include, but are not limited to, the tsetse fly, horse fly, house fly, bluebottle fly, hover fly and mosquito. *Dipterans* which transmit diseases causing serious health problems are of particular interest (*e.g.*, horse fly, tsetse fly, mosquito).

20 After the identification of gustatory receptor genes in various *Diptera* insects, the next organisms to probe most preferably may be from orders within the same subclass as *Diptera*. Finally, the next insects to use would be those from orders not within the same subclass as *Diptera*.

25 The insects which cause substantial health risks, crop damage, or other significant damage (*e.g.*, to housing structure or cotton clothing) may be the most desirable targets for such studies. Examples of such insects include, but are not limited to, green cloverworm, Mexican bean beetle, potato leafhopper, corn earworm, green stink bug, northern corn rootworm, western corn rootworm, cutworms, wireworms, thrips, fleas, aphids (*e.g.*, pea aphid, spotted alfalfa aphid), European corn borer, fall armyworm, southwestern corn borer,

grasshoppers, Japanese beetle, termites, leafhoppers (*e.g.*, potato leafhopper, three-cornered alfalfa hopper), stink bugs, crickets, Hessian fly, greenbugs and weevils (*e.g.*, alfalfa weevil, bollweevil).

5 Gustatory receptor genes identified by this process may then be used to screen non-Insecta organisms for gustatory receptor genes. Organisms of interest may include, but are not limited to, mites, ticks, spiders, nematodes, centipedes, mice, rats, salmon, pigeons, dogs, horses and humans. In a preferred embodiment, the gustatory receptor genes identified by this process would be used to identify gustatory receptor genes in humans.

10 Genetic Manipulations. The tools and methodologies of the present invention may be used by neurobiologists to probe more complex workings of an organism's response system, including those of a mammal's brain.

15 Knock-outs. By systematically knocking out and analyzing the expression patterns of the gustatory receptor genes of the present invention and observing the effects on taste sensitivity and behavior, researchers will be able to piece together a wiring diagram of the gustatory system of the fruit fly.

The term "knock-out" generally refers to mutant organisms which contain a null allele of a specific gene. Methods of making knock-out or disruption transgenic animals, especially mice, are generally known by those skilled in the art and are discussed herein and elsewhere (see, for example, the section herein entitled Transgenic Organisms and the following:
20 Manipulating the Mouse Embryo, (1986) Cold Spring Harbor Laboratory Press; Capecchi, (1989) Science 244, 1288-1292; Li *et al.*, (1995) Cell 80, 401-411; U.S. Patent No. 5,981,830 & 5,789,654, each of which is incorporated herein by reference.

25 Parallel studies may be conducted in other organisms by using the gustatory receptor genes and the methods of the present invention to identify the gustatory receptor genes of other organisms and then creating knock-outs for the gustatory receptor genes of those organisms.

Disabling Genes. Using the gustatory receptor genes of the present invention, it is now possible to selectively disable specific DGR genes and look for changes in taste response

and behavior. Parallel studies may be conducted in other organisms by using the gustatory receptor genes and the methods of the present invention to identify the gustatory receptor genes of other organisms and then disabling gustatory receptor genes of those organisms.

Methods of disabling genes are generally known by those skilled in the art. An
5 example of an effective disabling modification would be a single nucleotide deletion occurring at the beginning of a gustatory receptor gene that would produce a translational reading frameshift. Such a frameshift would disable the gene, resulting in non-expressible gene product and thereby disrupting functional protein production by that gene.

In addition to disabling genes by deleting nucleotides, causing a transitional reading
10 frameshift, disabling modifications would also be possible by other techniques including insertions, substitutions, inversions or transversions of nucleotides within the gene's DNA that would effectively prevent the formation of the protein coded for by the DNA.

It is also within the capabilities of one skilled in the art to disable genes by the use of less specific methods. Examples of less specific methods would be the use of chemical
15 mutagens such as hydroxylamine or nitrosoguanidine or the use of radiation mutagens such as gamma radiation or ultraviolet radiation to randomly mutate genes, such as the DGR genes of the present invention. Such mutated strains could, by chance, contain disabled gustatory receptor genes such that the genes are no longer capable of producing functional proteins for any one or more of the domains. The presence of the desired disabled genes could be detected
20 by routine screening techniques. For further guidance, see U.S. Patent No. 5,759,538.

Over-expression. Using the gustatory receptor genes of the present invention, it is now possible to selectively over-express specific DGR genes and look for changes in taste response and behavior. Parallel studies may be conducted in other organisms by using the gustatory receptor genes and the methods of the present invention to identify the gustatory
25 receptor genes of other organisms and then overexpress the gustatory receptor genes of those organisms.

Methods of overexpressing genes are generally known by those skilled in the art. For examples of producing cells which overexpress specific genes, see, for example, U.S. Patent

No. 5,905,146; 5,849,999; 5,859,311; 5,602,309; 5,952,169 & 5,772,997 (HER2 receptor).

Modulating or Inhibiting Expression. Using the gustatory receptor genes of the present invention, it is now possible to selectively modulate or inhibit specific DGR genes using antisense oligomers which specifically hybridize with the DNA or RNA encoding the DGR genes. One skilled in the art could so modulate or inhibit the expression of the DGR genes and detect for changes in taste response and behavior. Parallel studies may be conducted in other organisms by using the gustatory receptor genes and the methods of the present invention to identify the gustatory receptor genes in other organisms and then use antisense oligers to the gustatory receptor genes of those organisms. Methods for inhibiting expression of genes, especially genes coding for receptors, using antisense constructs, including generation of antisense sequences *in situ* are described, for example, in U.S. Patent No. 5,856,099; 5,556,956; 5,716,846; 5,135,917 & 6,004,814.

Other methods that can be used to inhibit expression of an endogenous gene are applicable to the present invention. For example, formation of a triple helix at an essential region of a duplex gene serves this purpose. The triplex code, permitting design of the proper single stranded participant is also known in the art. (See Moser *et al.*, (1987) Science 238, 645-650 and Cooney *et al.*, (1988) Science 241, 456-459). Regions in the control sequences containing stretches of purine bases are particularly attractive targets. Triple helix formation along with photo-crosslinking is described, *e.g.*, in Praseuth *et al.*, (1988) Proc. Natl Acad. Sci. USA 85, 1349-1353.

Studying Behavior. Behavioral studies may help organize the gustatory systems in various organisms and may help explain the behavior of various organisms.

The tools and methodologies of the present invention may be used to study the influence of environmental conditions on eating behavior. For example, newly identified gustatory receptor genes may be used to study the effects of different preferences for a particular food source.

In one embodiment, modulation of gustatory receptor activity can be measured by the probosis extension response assay. When gustatory sensilla on either the labellum or the leg

are stimulated with a sugar solution, the fly extends its mouthparts, in a behavior known as the proboscis extension response (PER). A variety of stimuli, including bitter compounds and high concentrations of salts, inhibit the PER when added to the sugar solution. The PER depends on the dose of the sugar solution, and the inhibition by other compounds is dose-dependent as well. The PER is simple to measure, and can be quantitated precisely. It has been characterized in great detail, initially in the classic experiments of Dethier on large flies such as the blowfly *Phormia regina* (Dethier (1955) *Quart. Rev. Biol.* 30, 348-371; Dethier, (1976) *The Hungry Fly*, Harvard Press).

In *Drosophila*, a PER has been shown to be elicited by sugar, and inhibited when NaCl is added to the sugar (Arora, (1987) *Nature* 330, 62-63; Rodrigues & Siddiqi (1978) *Proc. Ind. Acad. Sci.* 87B, 147-160; Tompkins *et al.*, (1979) *Proc. Natl. Acad. Sci. USA* 76, 884-887).

In yet another embodiment, gustatory receptor activation assays may be based on the fact that flies demonstrate strong preferences when presented with two taste stimuli. Using a countercurrent behavioral paradigm in which flies make a series of binary choices between a sucrose medium either with or without quinine sulfate, it has been shown that flies preferentially distribute onto the medium without quinine (Tompkins *et al.*, (1979) *Proc. Natl. Acad. Sci. USA* 76, 884-887), which tastes bitter to humans. Flies manifest preferences for different sugar solutions, as shown in an elegant paradigm in which animals are allowed to feed from the wells of a microtiter dish (Tanimura *et al.*, (1982) *J. Comp. Physiol.* 147, 433-437). Wells of the dish contain agar, with alternate wells containing one of two sugars. Wells containing one sugar are marked with red dye; those containing the other sugar are marked with blue dye. After feeding in the dark, flies are classified according to the color of their abdomen (red, blue, or mixed), which provides a quantitative indication of their feeding preferences, which can be used as a measure for the activity of any particular gustatory receptor.

4. For Organism Detection, Monitoring and Control.

General Pest Management. The gustatory receptor genes identified herein and

identified using the methods of the present invention may be used to identify compounds which may be used for pest management. It is especially desirable to utilize various aspects of the present invention for pest management related to crop protection.

5 The application of pheromones is now firmly established as a key component of pest management and control, especially within the framework of integrated pest management (IPM). An object of organism control is to modulate an organism's behavior or activity so as to reduce the irritation, sickness, or death of the host (*e.g.*, a plant host), or to decrease the general health and proliferation of the organism.

10 For example, the propagation of a mouse population in a given area of actual or potential mice infestation may be prevented or inhibited by a bait containing an effective amount of a first compound which the mice prefer to eat, wherein such compounds could be combined with a second compound, such as a pheromone, which would attract the mice to the bait and would also be combined with a third compound which would have lethal effects on the mice. Thus, in a preferred embodiment, the mice would be attracted to the area by the
15 odor of the second compound, enticed to eat a large amount of the bait because of the taste of the first compound and would die as a result of the presence of the third compound in the bait.

Compositions for attracting insects generally require some physical and/or chemical means for attracting the insects to a bait. In addition, the bait needs to be fully attractive to the taste of the insect so as to induce the attracted insect to ingest the bait. Finally, the bait must
20 be taken in by the insect at a sufficient lethal dose before disgusting the insect in some way or producing a toxic reaction in the insect (see, for example, U.S. Patent No. 4,855,133).

Insect Repellents and Insecticides. The present invention provides the tools and methodologies useful for identifying compounds which modulate insect behavior by exploiting the sensory capabilities of the target insect. For example, attempts have been made
25 to describe and synthesize the complex interactions which underlie host-seeking behavior in mosquitoes. Using the methods and gustatory receptor genes of the present invention, it is possible to design specific compounds which target mosquito gustatory receptor genes. Thus, the present invention provides the ability to alter or to eliminate the orientation and feeding

behaviors of mosquitoes and thereby have a positive impact on world health by controlling mosquito-borne diseases, such as malaria.

Mosquito gustatory receptor genes may be identified and/or targeted using various aspects of the present invention. For example, the gustatory receptor genes of the present invention may be used to design probes as discussed elsewhere herein for the identification and characterization of mosquito gustatory receptor genes. Alternatively, the algorithm of the present invention may be used to identify mosquito gustatory receptor genes in the genetic databases for mosquitoes. Once the mosquito gustatory receptor genes are identified, then various screening methods described elsewhere herein, such as the high throughput assays discussed elsewhere herein, may be used to identify synthetic and natural compounds which may modulate the behavior of the insect.

For general information on insect repellents, see, for example, U.S. Patent No. 4,663,346.

Mating Enhancement and Disruption. The gustatory receptor genes identified herein and identified using the methods of the present invention may be used to identify compounds which interfere with the orientation and mating of a wide range of organisms, including insects. Thus, the present invention enables the identification of compositions which disrupt insect mating by selective inhibition of specific receptor genes involved in mating attraction (see, *e.g.*, U.S. Patent No. 5,064,820).

Animal Repellants. The gustatory receptor genes identified herein and identified using the methods of the present invention may be used to identify compounds which may be used as animal repellants. Such compositions may be used to repel both predatory and non-predatory animals (see, *e.g.*, U.S. Patent No. 4,668,455).

5. Organism Attraction.

Insect Attractants. The gustatory receptor genes identified herein and identified using the methods of the present invention may be used to identify compounds which attract specific insects to a particular location (see, *e.g.*, U.S. Patent No. 4,880,624 & 4,851,218).

For example, aspects of the present invention may be used in various methods which

reduce or eliminate the levels of particular insect pests by selective attraction of a particular insect or pest, such as mosquitoes and tsetse flies. As a particular example, insect traps can be created wherein the taste of a compound selectively attracts a particular insect, like the tsetse fly, and the insect so attracted dies in the trap. Once in the trap, the attraction is maintained by stimulation of a particular gustatory receptor of the invention. In this way, the population of tsetse flies may be reduced or eliminated in a particular area.

The identified compositions which selectively attract and maintain the attraction by stimulation of gustatory receptors may also be combined with an insecticide, for example as an insect bait in microencapsulated form. Alternatively, or in addition, the insect attractant composition may be placed inside an insect trap, or in the vicinity of the entrance to an insect trap.

In addition to killing insects, the trapping of insects is often very important for estimating or calculating how many insects of a particular type are feeding within a specific area. Such estimates are used to determine where and when insecticide spraying should be commenced and terminated.

Insect traps which may be used are, for example, those as described in U.S. Patent No. 5,713,153. Specific examples of insect traps include, but are not limited to, the Gypsy Moth Delta Trap®, Boll Weevil Scout Trap®, Jackson trap, Japanese beetle trap, McPhail trap, Pherocon 1C trap, Pherocon II trap, Pherocon AM trap and Troglo trap.

Kairomones may be used as an attractancy for the enhancement of the pollination of selected plant species.

Attractant compositions which demonstrate biological activity toward one sex which is greater than toward the opposite sex may be useful in trapping one sex of a specific organism over another. For example, a composition may be a highly effective attractant for male apple ermine moths (*Yponomeuta malinellus* (Zeller)) and not so effective an attractant for female apple ermine moths. By attracting and maintaining the attraction of adult males to field traps, the composition provides a means for detecting, monitoring, and controlling this agricultural pest (see, e.g., U.S. Patent No. 5,380,524).

Attracting Predators and Parasitoids. The gustatory receptor genes of the present invention and the gustatory receptor genes identified using the methods of the present invention may also be used to identify chemicals which attract and maintain the attraction of various predators and parasitoids. Attracting the predators and parasitoids which attack
5 certain pests offers an alternative method of pest management.

Animal Attractants. The gustatory receptor genes identified herein and those identified by the methods of the present invention may be used to identify chemicals which attract household domesticated animals. For example, a pheromone-containing litter preparation may attract the animals and absorb liquids and liquid-containing waste released by
10 the attracted animal (see, *e.g.*, U.S. Patent No. 5,415,131).

6. Industrial Applications. The gustatory receptor genes identified by the methods of the present invention may be used for a number of different industrial applications including, but not limited to the following:

(a) Identification of appetite suppressant compounds and using same to suppress
15 and/or control appetite.

(b) As Biosensors.

(1) Explosive and drug detectors. The detectors may be synthetic, such as biologically-inspired robotic sensors, or biological sensors, such as insects which are especially sensitive to certain tastes.

20 (2) Population of gustatory receptor genes expressed in cell culture.
Gustatory receptor genes can be introduced into a cell line and the transformed cells maintained in culture through multiple generations. By creating specific cell lines which express multiple gustatory genes at once, it would be possible to use such cell cultures to investigate how compounds interact with taste receptor genes. Thus, the present invention
25 provides methods for identifying taste fingerprints, wherein such methods include contacting a series of cells containing and expressing known gustatory receptor genes with a desired sample, and determining the type and quantity of the gustatory receptor ligands present in the sample (see, *e.g.*, U.S. Patent No. 5,993,778). As discussed elsewhere herein, the interaction

of substances with the receptors can be identified using appropriate labels, such as those provided by luciferase, the jellyfish green fluorescent protein (GFP) or β -galactosidase.

(3) Biochip Arrays. As discussed elsewhere herein, biochip arrays of gustatory receptor genes can be generated. The arrays may be used to detect gustatory receptor ligands via an appropriate marker or via a chemical or electrical signal. Arrays may be designed for specific purposes, such as, but not limited to, detecting perfumes, explosives, drugs, pollutants, and toxins.

(c) Training organisms to conduct certain tasks. Examples include, but are not limited to, orienting or reorienting the behavior of worker bees of a rearing colony by incorporating a composition which includes one or more pheromones which elicits particular bee behavior towards the larvae. Thus, the beekeeper may orient or reorient the bees towards a particular activity such as, but not limited to, inducing improved acceptance of the larvae at the beginning of rearing, to increase the production of royal jelly, regulate the feeding of the larvae as to favor the development of queen bees, etc. (see, *e.g.*, U.S. Patent No. 5,695,383).

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1 Identification of candidate taste receptor genes.

With approximately 100% of the *Drosophila* genome sequenced, the *Drosophila* gustatory receptor genes have been sequenced. A multi-step strategy was developed to identify taste receptor genes from the genomic database. First, a computer algorithm was designed to search the *Drosophila* genomic sequence for open reading frames (ORFs) from candidate taste receptor genes. Second, RT-PCR was used to determine if transcripts from

any of these ORFs identified through this approach were expressed in specific tissues and organs, including taste tissue deficient in chemosensory neurons.

Example 2 Algorithm for identification of G protein-coupled receptors (GPCR) genes.

5 A computer algorithm that seeks proteins with particular structural properties, as opposed to proteins with particular sequences, identified a large family of candidate gustatory receptors from the *Drosophila* genomic database (Clyne *et al.*, (1999) Neuron 22, 327-338 incorporated herein in its entirety). The algorithm examines the physicochemical properties of the amino acids in an open reading frame (ORF) and then uses a non-parametric discriminant
10 function to identify ORFs likely to encode multitransmembrane domain proteins.

 The algorithm used to identify G protein-coupled receptors (GPCR) genes used statistical characterization of amino acid physico-chemical profiles in combination with a non-parametric discriminant function. The key approach is to use the information in the interplay between the local structure (transmembrane alpha helix) and the global structure
15 (repeated multiple domains) and characterize this information with concise statistical variables.

 The algorithm was trained on a set of one-hundred putative GPCR sequences from the GPCR database (GPCRDB) at <http://swift.embl-heidelberg.de/7tm> and a set of one-hundred random proteins selected from the SWISSPROT database (this training set was later
20 expanded, but that version was not used for the genes reported in this paper). In the first step, three sets of descriptors were used to summarize the physico-chemical profiles of the sequences. These were GES scale of hydropathy (Engelman *et al.*, (1986) Annu. Rev. Biophys. Biophys. Chem. 15, 321-353), polarity (Brown, (1991) Molecular Biology Labfax, Academic Press), and amino acid usage frequency. For the first two of these measurements, a
25 sliding window profile was employed (White, (1994) Membrane Protein Structure, Oxford University Press) using a kernel of 15 amino acid constant function convoluted with a 16 amino acid Gaussian function.

 These profiles were then summarized with three statistics; the periodicity

(characterizing the quasi-periodic presence of the transmembrane domain), average derivative (characterizing the abrupt change between the transmembrane domain and non-transmembrane domain), and the variance of the derivative (also characterizing the abrupt change). GES periodicity, variance of polarity derivative, polarity periodicity and amino acid frequency were used as the four variables and each sequence was therefore characterized by four variables. These four variables were used in a non-parametric linear discriminant function that was then optimized to separate the known GPCRs from random proteins in the training set. The same linear discriminant function with the scores derived from the training set was then used to screen the genomic database for candidate genes.

The candidate sequences were given significance values by an odds ratio of the GPCRs and non-GPCRs computed using the observed empirical distribution of the training set. More detailed information about the algorithm is available at <http://www.neuron.org/cgi/content/full/22/2/327/dc1>.

The computational screens used the genomic sequence data obtained by FTP from the Berkeley *Drosophila* Genome Project (BDGP, <http://www.fruitfly.org>, version 6/98). First, the ORFs of 300 bases or longer in all six frames were identified. Next, a program written to identify GPCRs statistically by their physico-chemical profile was used to screen for candidate ORFs as described above. The number of possible candidates was reduced by comparing them to *Drosophila* codon usage tables (<http://flybase.bio.indiana.edu>, version 10). Candidate ORFs whose codon usage differed at a significance level of 0.0005 by the chi-square statistic were discarded from the candidate set. Using these screening steps, thirty-four candidate ORFs were obtained.

Example 3 Further analysis of genes identified by the algorithm.

Further analysis of genes identified by this algorithm revealed one gene that led to the definition of a distinct large DGR family of membrane proteins. Forty-three members of this family have been identified in the complete *Drosophila* genome. If the sequenced part of the genome is representative, then extrapolation suggests that the entire genome would encode on

the order of 75 DGR proteins, a figure comparable to previous estimates of 100 candidate *Drosophila* odorant receptors (DOR), as described in Clyne *et al.*, (1999) Neuron 22, 327-338).

This previously unidentified family of proteins shows no sequence similarities to odorant receptors or to other known proteins. This family of proteins has been designated the gustatory receptor (GR) family, with each individual gene named according to its cytogenetic location in the genome. Thus, the GR59D.1 and GR59D.2 genes, which was abbreviated here as 59D.1 and 59D.2, refer to two family members located in cytogenetic region 59D on the second chromosome. This designation of location, however, does not reflect additions to the *Drosophila* genome subsequent to the discovery of the gustatory receptor genes.

The first exon of 23A.1b (Figure 1) was identified by the computer algorithm described in Clyne *et al.*, (1999) Neuron 22, 327-338, as described in Example 2, above.

Examination of the genomic DNA surrounding the first exon of 23A.1b identified other exons, and the genomic structure of this gene was determined with RT-PCR.

Using the sequence of this gene, an extensive series of tBLASTn searches of the Berkeley *Drosophila* Genome Project (BDGP) sequence database (available at <http://www.fruitfly.org>) was performed, which identified ORFs of thirty-eight other genes of the GR family. The full sequences of these genes were identified by an analysis of the genomic DNA flanking these ORFs as described in Clyne *et al.*, (1999) Neuron 22, 327-338 using the *Drosophila* intron-exon consensus splice sequences and RT-PCR analysis. The thirty-nine genes encode a total of forty-three proteins.

The National Center for Biotechnology Information (NCBI) accession number of the BDGP genomic clone on which each transcript is found and the sequence range in the genomic clone for the predicted coding region are given as follows for each GR transcript shown in Figure 1 (NCBI and BDGP data are as of 16 October 1999): transcript GR21D.1, accession number AC004420, range 34784 - 33509; GR22B.1, AC003945, 31740 - 30551; GR23A.1a, AC005558, 108490 - 106118; GR23A.1b, AC005558, 107351 - 106118; GR32D.1, AC005115, 19779 - 21141; GR39D.1, AC007208, 62553 - 64348; GR39D.2a,

AC005130, 9170 - 16119; GR39D.2b, AC005130, 10410 - 16119; GR39D.2c, AC005130, 12989 - 16119; GR39D.2d, AC005130, 14750 - 16119; GR43C.1, AC005452, 50105 - 51583; GR47A.1, AC007352, 114644 - 115920; GR58A.1, AC004368, 62323 - 61087; GR58A.2, AC004368, 62511 - 63791; GR58A.3, AC004368, 65521 - 64229; GR59D.1, 5 AC006245, 68825 - 70050; GR59D.2, AC006245, 70261 - 71505; GR59E.1, AC005639, 30167D31539; and GR59E.2, AC005639, 30036 - 28714.

Accession numbers for the other genes are as follows (data are as of 5 January 2000) (complete sequences are available for the first four and only partial sequences are available for the remaining genes; LU, location unknown): transcript GR1F.1, accession number 10 AL035632, range 7301 - 8711; GR47F.1, AC005653, 42838 - 44204; GR68D.1, AC006492, 46040 - 44916; GR77E.1, AC006490, 104929 - 103117; GR28A.1, AC008354, 66711 - 66973; GR57B.1, AC007837, 102661 - 103185; GR65C.1, AC004251, 23136 - 24215; GR93F.1, AC012873, 35043 - 35228; GR93F.2, AC012892, 2781 - 2650; GR93F.3, AC012892, 4271 - 4143; GR93F.4, AC012892, 6482 - 5559; GR94E.1, AC008200, 72472 - 15 72308; GR97D.1, AC007984, 121300 - 121977; GR98B.1, AC007817, 45506 - 46916; GR98B.2, AC007817, 10695 - 10784; GR98B.3, AC007817, 45189 - 45284; GR98B.4, AC007817, 39658 - 39765; GRLU.1, AC017438, 22141 - 21398; GRLU.2, AC017138, 10997 - 11122; GRLU.3, AC015395, 43210 - 43612; GRLU.4, BACR28P1-T7, 28 - 129; GRLU.5, BACR28P1-T7, 388 - 734; GRLU.6, BACR06I03-T7, 1028 - 48; and GRLU.7, 20 AC012799, 8212 - 8123.

Example 4 Sequence analysis of DGR genes.

The amino acid sequences of nineteen members of the GR family indicate the high degree of sequence divergence (Figure 1). Sequence alignment revealed only one residue 25 conserved among all members of the family shown and only 24 residues conserved among more than half of the genes shown. Fifteen of these conserved residues lie in the vicinity of the COOH-terminus. Amino acid identity between individual genes ranged from a maximum of 34% to less than 10%. By contrast, other features of the gene family show

substantial conservation. The positions of a number of introns are conserved (Figure 1), suggesting that the family originated from a common ancestral gene. Overall sequence length, ~380 amino acids, is another common feature. All of the genes encode approximately seven predicted transmembrane domains, a feature characteristic of G protein-coupled receptors (GPCRs) (Figure 2).

The GR proteins were identified as GPCRs when the algorithm was modified to distinguish previously described GPCRs from ion channels. The algorithm was set to positively identify 95% of previously described GPCRs, with 4.3% false positives. Most ion channels have six transmembrane domains.

The genes are widely dispersed in the genome, but at the same time, many are found in clusters. The two largest clusters each contain four genes; there are also several clusters of two or three genes. Genes within these clusters are closely spaced, with intergenic distances ranging from 150 to 450 base pairs (bp) in all cases for which the data were available. There is no rule specifying the orientation of genes within clusters, unlike the case of the *Drosophila* odorant receptors, in which genes within a cluster are in the same orientation in all clusters examined (Clyne *et al.*, (1999) Neuron 22, 327-338).

An unusual form of alternative splicing occurs in at least two chromosomal locations. Four large exons in cytogenetic region 39D each contain sequences specifying six predicted transmembrane domains, followed by three small exons that together specify a putative seventh transmembrane domain and the COOH-terminus (Figure 3). Reverse transcription-polymerase chain reaction (RT-PCR) analysis revealed that each of the four large exons is spliced to the smaller exons, thereby generating four predicted seven transmembrane domain proteins. These four proteins are thus distinct through the first six transmembrane domains and identical in the seventh and in the COOH-terminal sequences. Likewise, in cytogenetic region 23A, there are two large exons, each of which specifies six transmembrane domains and is spliced to two small exons that together encode a seventh transmembrane domain and the COOH-terminus (Figure 3). Thus, the gene in region 23A encodes two related proteins. This pattern of splicing, in which alternative large 5' exons encoding most of the protein are

joined to common short 3' exons encoding only a small portion of the protein, is unusual among genes encoding GPCRs and proteins in general. This pattern of splicing provides a mechanism at a single locus for generating products that exhibit a pattern observed for this family in general: extreme diversity among all sequences of the proteins except in a small region in the vicinity of the COOH-terminus.

Example 5 Identification of gustatory receptor genes using RT-PCR.

To assess the tissue specificity of expression, RT-PCR with primers that span introns in the coding regions was performed. Of the 19 transcripts tested, 18 were expressed in the labellum (Figure 4 and Table 1), the major gustatory organ of the fly (Falk *et al.*, (1976) J. Morphol. 150, 327; Dethier, (1976) The Hungry Fly, Harvard University Press; Stocker, (1994) Cell Tissue Res. 275, 3; Nayak & Singh, (1983) Int. J. Insect Morphol. Embryol. 12, 273. Moreover, for most of these genes, expression was labellum-specific in that only 1 of the 19 yielded amplification products from heads depleted of taste organs and only 2 showed expression in the thorax, which contains the thoracic nervous system but no characterized taste sensilla. Likewise, expression in several other tissues, including the abdomen, wings, and legs, was limited to a small fraction of genes (Table 1).

For preparation of RNA, individual flies were frozen in liquid nitrogen, and labella were dissected. On average, 50 labella were used for RNA preparation. Total RNA was prepared as described elsewhere (McKenna *et al.*, (1994) J. Biol. Chem. 269, 16340-16347). The RNA was treated with DNaseI (Gibco-BRL) for thirty minutes at 37°C, phenol/chloroform extracted, and precipitated. The entire RNA preparation was used for oligo dT-primed cDNA synthesis using Superscript II Reverse Transcriptase (Gibco-BRL) according to the manufacturer's directions. PCR was performed using Taq polymerase (Sigma) under standard cycling conditions, with an annealing temperature of 60°C, gene-specific primer concentration of 1 pM, and magnesium concentration of 2.5 mM. For all genes, primer pairs which span introns were used in order to distinguish PCR bands amplified from cDNA from those amplified from any remaining genomic DNA.

Example 6 Tissue specificity of GR gene expression

To further analyze the tissue specificity of GR expression, a microdissection experiment was performed in which the labral sense organ (LSO) (Stocker, (1994) Cell Tissue Res. 275, 3; Nayak & Singh, (1983) Int. J. Insect Morphol. Embryol. 12, 273), a small taste organ that lines the pharynx, was surgically excised from each of fifty animals. The LSO consists of a very limited number of cells and is highly enriched in taste neurons; it does not, for example, contain muscle cells. By RT-PCR amplification, the expression of seven GR transcripts in this taste organ was detected (Figure 5). These results indicate that expression of the GR family extends to include at least one additional taste organ besides the labellum. The data are also fully consistent with the notion that the GR genes are expressed in taste neurons.

To confirm the gene expression in taste receptor neurons, a *Drosophila* mutant, *pox-neuro 70* (*poxn 70*) was used, in which chemosensory bristles are transformed into mechanosensory bristles (Awasaki & Kimura, (1997) J. Neurobiol. 32, 707; Dambly-Chaudiere *et al.*, (1992) Cell 69, 159; Nottebohm *et al.*, (1994) Neuron 12, 25; Nottebohm *et al.*, (1992) Nature 359, 829).

Specifically, in *poxn 70*, which behaves as a null mutation with respect to adult chemosensory organs, chemosensory bristles are transformed into mechanosensory bristles with respect to various morphological and developmental criteria. In particular, most chemosensory bristles in wild-type *Drosophila* are innervated by five neurons: four chemosensory neurons and one mechanosensory neuron. In contrast, wild-type mechanosensory bristles contain a single mechanosensory neuron.

In chemosensory bristles transformed to mechanosensory bristles by *poxn 70* (Awasaki & Kimura, (1997) J. Neurobiol. 32, 707), the number of neurons is reduced from five to one. We predicted that if the GR family is in fact expressed in the chemosensory neurons of taste sensilla, their expression would likely be eliminated in the *poxn 70* mutant. Consistent with this prediction, eighteen of nineteen GR transcripts examined were not

expressed in the labellum of the *poxn 70* mutant (Table 1 and Figure 4). RT-PCR was performed from RNA extracted from the indicated tissues (see description for Figure 4). All primer pairs spanned introns. Positive controls are described in Figure 4. These results indicate that the GR gene family is expressed in labellar chemosensory neurons.

5

Table 1. Tissue-specific expression of GR genes.

	Gene	Labellum	<i>poxn</i> Labellum	Head minus taste organs	Thorax	Abdomen	Leg	Wing
5	21D.1	+	-	-	-	-	-	-
	22B.1	+	-	-	-	+	+	+
	23A.1a	+	-	-	-	-	-	-
	23A.1b	+	-	-	-	-	-	-
	32D.1	+	-	-	-	-	-	-
10	39D.1	+	-	-	-	-	-	-
	39D.2a	+	-	-	-	-	-	-
	39D.2b	+	-	-	-	-	-	-
	39D.2c	+	+	-	+	+	-	-
	39D.2d	+	-	-	+	-	-	+
15	43C.1	+	-	+	-	+	+	+
	47A.1	+	-	-	-	-	-	-
	58A.1	+	-	-	-	-	-	-
	58A.2	+	-	-	+	-	-	-
	58A.3	+	-	-	-	-	-	-
20	59D.1	+	-	-	-	-	-	-
	59D.2	+	-	-	-	-	-	-
	59E.1	-	-	-	-	+	-	+
	59E.2	+	-	-	-	-	-	-

Example 7 Receptor diversity.

25 The large size of this protein family likely reflects the diversity of compounds that flies can detect. The extreme diversity of these receptors may not only reflect diversity among

the ligands that they bind, but also diversity in the signal transduction components with which they interact. For example, the lack of conserved intracellular regions suggests the possibility that, during the evolution of this sensory modality, multiple G proteins arose, each interacting with a different subset of receptors. Finally, it seems likely that the *Drosophila* genome encodes taste receptors in addition to those of the GR family.

Although applicants have detected expression in the labellum and the LSO, few if any family members are expressed in the leg or wing chemosensory hairs (Table 1), some of which are morphologically similar to labellar taste hairs (Stocker, (1994) Cell Tissue Res. 275, 3). The *Drosophila* olfactory system also contains more than one organ, the antenna and maxillary palp, which respond to all, or nearly all, of the same odorants and which derive from the same imaginal discs (Carlson, (1996) Trends Genet. 12, 175). However, most individual members of the DOR gene family are expressed in one or the other but not in both olfactory organs (Clyne, (1999) Neuron. 22, 327; Vosshall *et al.*, (1999) Cell 96, 725). Perhaps the distinction among taste receptor genes is even more extreme in the gustatory system, whose organs derive from different imaginal discs. For example, the legs may express a completely distinct family of genes or a subfamily whose similarities to the present family are sufficiently tenuous as to place it slightly beyond the boundaries that define the GR family.

Example 8 Transgenic *Drosophila*

P element mediated germline transformation of *Drosophila* can be carried out as previously described (Rubin & Spradling, (1982) Science 218, 348-353). *Drosophila* embryos are isolated and microinjected with P element expression constructs as previously described (Karess & Rubin, (1984) Cell 38, 135-146) containing a particular DGR nucleotide sequence, at 0.5 mg/ml together with a helper plasmid at 0.1 mg/ml.

Non-transformed (Generation 0 or G₀) injected adults are individually back crossed to the recipient strain and the G₁ progeny screened for the w⁺ transformation marker (Klemenz *et al.*, (1987) Nucleic Acids Res. 10, 3947-3959). Transformed lines homozygous for the transgene are established from orange eyed G₁ flies as previously described (Klemenz *et al.*,

(1987) Nucleic Acids Res. 10, 3947-3959).

A line of *Drosophila* in which the 39D.2c gene can be over-expressed is constructed as described above. The 39D.2c coding sequences are joined to an upstream activating sequence (UAS) and introduced by P element-mediated germline transformation into
5 *Drosophila*. A yeast GAL4 transcription factor gene, coupled to a heat shock promoter, is then crossed into the transgenic line. As expected, heat shock of this line results in induction of 39D.2c expression. The heat shock-induced expression of GAL4, also results in binding of GAL4 to the UAS, and subsequent induction of 39D.2c expression. This transgenic line of
10 *Drosophila*, and three other transgenic lines containing other DGR genes, can be tested for elevated responses to any of fifty different tastes. Elevated response to any particular taste is indicative of an ligand which binds and activates the over-expressed receptor (see, *e.g.*, Zhao & Firestein, (1998) Science 279, 237-242).

Although the present invention has been described in detail with reference to
15 examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents and publications referred to in this application are herein incorporated by reference in their entirety. The results of the experiments disclosed herein have been published in the journal Science (2000) 287, 1830-1834, this article herein
20 incorporated by reference in its entirety.

SEQUENCE LISTING

<110> Carlson, John R.
 Clyne, Peter J.
 Warr, Coral G.
 Yale University

<120> Novel Taste Receptors in Drosophila

<130> 44574-5072

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<151> 1999-06-14

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ggt	tgg	acc	gtg	ctg	ata	gcg	gcc	acc	tcc	ttc	acc	gtg	tac	ggc	ctc	192
Gly	Trp	Thr	Val	Leu	Ile	Ala	Ala	Thr	Ser	Phe	Thr	Val	Tyr	Gly	Leu	
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ttc	cag	gag	agc	agc	gta	gaa	gag	aaa	cag	gac	tcg	gag	tcc	acc	atc	240
Phe	Gln	Glu	Ser	Ser	Val	Glu	Glu	Lys	Gln	Asp	Ser	Glu	Ser	Thr	Ile	
65					70				75						80	

tcg	agc	ata	ggt	cac	acg	gtt	gac	ttc	att	cag	ctg	gtg	ggc	atg	cgg	288
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Val	Ala	His	Leu	Ala	Ala	Leu	Leu	Glu	Ala	Leu	Trp	Gln	Arg	Gln	Ala	
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Gln	Arg	Gly	Phe	Phe	Ala	Glu	Leu	Gly	Glu	Ile	Asp	Arg	Leu	Leu	Ser	
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Lys	Ala	Leu	Arg	Val	Asp	Val	Glu	Ala	Met	Arg	Ile	Asn	Met	Arg	Arg	
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caa	ctc	ctt	atc	ctg	ggc	gcc	aag	ctg	ctc	tcc	cgc	gga	gac	aga	ttc	528
Gln	Leu	Leu	Ile	Leu	Gly	Ala	Lys	Leu	Leu	Ser	Arg	Gly	Asp	Arg	Phe	
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ccg	atc	tac	tgg	atc	agc	tac	ttg	ctg	cca	ctg	ctt	gtg	tgc	gga	ttg	576
Pro	Ile	Tyr	Trp	Ile	Ser	Tyr	Leu	Leu	Pro	Leu	Leu	Val	Cys	Gly	Leu	
			180					185					190			
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cag	gtg	ggc	aac	gac	ttc	ctg	gct	atc	acc	tcc	aac	tgc	tac	tgg	atg	864
Gln	Val	Gly	Asn	Asp	Phe	Leu	Ala	Ile	Thr	Ser	Asn	Cys	Tyr	Trp	Met	
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ttc	ctc	aac	ttc	cgc	cag	tcg	gcg	gcc	tcg	ccc	ttc	gac	atc	ctg	caa	912
Phe	Leu	Asn	Phe	Arg	Gln	Ser	Ala	Ala	Ser	Pro	Phe	Asp	Ile	Leu	Gln	
	290					295					300					
atc	gtg	gcc	agt	ggc	gta	tgg	tct	gcc	ccc	cac	ttg	ggt	aac	gtg	ctc	960

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Ile Val Ala Ser Gly Val Trp Ser Ala Pro His Leu Gly Asn Val Leu
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gtc ctc tca ctg ctt tgc gac cga acg gcc cag tgc gcg tct cgt ctt 1008
 Val Leu Ser Leu Leu Cys Asp Arg Thr Ala Gln Cys Ala Ser Arg Leu
 325 330 335

gcc ctg tgc ctg cac cag gta agc gtg gat tta agg aat gag agc cac 1056
 Ala Leu Cys Leu His Gln Val Ser Val Asp Leu Arg Asn Glu Ser His
 340 345 350

aat gct ctg ata acc cag ttc tcg ctg cag cta ctc cac cag cgg ctc 1104
 Asn Ala Leu Ile Thr Gln Phe Ser Leu Gln Leu Leu His Gln Arg Leu
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cac ttc agc gcc gct ggc ttc ttc aac gtg gac tgc acc ctt ctc tat 1152
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Gly Trp Thr Val Leu Ile Ala Ala Thr Ser Phe Thr Val Tyr Gly Leu
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Phe Gln Glu Ser Ser Val Glu Glu Lys Gln Asp Ser Glu Ser Thr Ile
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Ser Ser Ile Gly His Thr Val Asp Phe Ile Gln Leu Val Gly Met Arg
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Val Ala His Leu Ala Ala Leu Leu Glu Ala Leu Trp Gln Arg Gln Ala
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Gln Arg Gly Phe Phe Ala Glu Leu Gly Glu Ile Asp Arg Leu Leu Ser

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Asn	Ala	Leu	Ile	Thr	Gln	Phe	Ser	Leu	Gln	Leu	Leu	His	Gln	Arg	Leu	
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His	Phe	Ser	Ala	Ala	Gly	Phe	Phe	Asn	Val	Asp	Cys	Thr	Leu	Leu	Tyr	
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Thr	Ile	Val	Gly	Ala	Thr	Thr	Thr	Tyr	Leu	Ile	Ile	Leu	Ile	Gln	Phe	
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 20 25 30
 gaa caa att cga gaa agc cag gtg cgg gga acg cga aag aac ttc cta 144
 Glu Gln Ile Arg Glu Ser Gln Val Arg Gly Thr Arg Lys Asn Phe Leu
 35 40 45
 cac gat ggc tcc ttc cat gag gca gtt gct cca gtt ctg gcg gtg gcc 192
 His Asp Gly Ser Phe His Glu Ala Val Ala Pro Val Leu Ala Val Ala
 50 55 60
 cag tgc ttt tgc cta atg ccc gtg tgt gga atc agt gct cca acg tac 240
 Gln Cys Phe Cys Leu Met Pro Val Cys Gly Ile Ser Ala Pro Thr Tyr
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 Arg Gly Leu Ser Phe Asn Arg Arg Ser Trp Arg Phe Trp Tyr Ser Ser
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 Leu Tyr Leu Cys Ser Thr Ser Val Asp Leu Ala Phe Ser Ile Arg Arg
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 gtg gcc cac agt gtg ctg gat gtg cgc agt gtg gag ccc atc gtt ttt 384
 Val Ala His Ser Val Leu Asp Val Arg Ser Val Glu Pro Ile Val Phe
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 His Val Ser Ile Leu Ile Ala Ser Trp Gln Phe Leu Asn Leu Ala Gln
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 Pro Gly Tyr Thr Cys Cys Leu Gln Arg Ala Arg Pro Ala Arg Arg Leu
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Ile Cys Leu Gln Leu Leu Lys Ser Ile Asn Thr Met Pro Ser Ser Ala	
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Thr Ala Val Leu Leu Phe Val Ser Ala Ile Asn Asp Gln Ala Arg Glu	
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cca ctg cgt ctg ctg cgc ctt gtc ccg ctc aaa gga tat cat ccg gag	1152
Pro Leu Arg Leu Leu Arg Leu Val Pro Leu Lys Gly Tyr His Pro Glu	
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His Asp Gly Ser Phe His Glu Ala Val Ala Pro Val Leu Ala Val Ala
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Gln Cys Phe Cys Leu Met Pro Val Cys Gly Ile Ser Ala Pro Thr Tyr
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Arg Gly Leu Ser Phe Asn Arg Arg Ser Trp Arg Phe Trp Tyr Ser Ser
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Leu Tyr Leu Cys Ser Thr Ser Val Asp Leu Ala Phe Ser Ile Arg Arg
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Val Ala His Ser Val Leu Asp Val Arg Ser Val Glu Pro Ile Val Phe
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Leu Trp Pro Gly Leu Met Arg His Trp Ala Ala Val Glu Arg Arg Leu
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Pro Gly Tyr Thr Cys Cys Leu Gln Arg Ala Arg Pro Ala Arg Arg Leu
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Lys Leu Val Ala Phe Val Leu Leu Val Val Ser Leu Met Glu His Leu
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Leu Ser Ile Ile Ser Val Val Tyr Tyr Asp Phe Cys Pro Arg Arg Ser

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Thr	Ala	Val	Leu	Leu	Phe	Val	Ser	Ala	Ile	Asn	Asp	Gln	Ala	Arg	Glu	
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Gln Val Leu Gly Phe His Gly Leu Pro Leu Pro Gly Asp Gly Asn Pro	
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35 40 45	
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ctc tat cgc ggc gac atg ttc ggc tgt gcc aat gat gcc ctt aaa tac	240
Leu Tyr Arg Gly Asp Met Phe Gly Cys Ala Asn Asp Ala Leu Lys Tyr	
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115 120 125	
tgt cgc tat ctg ata ttc ctg tac gcc atg atg gcc gcc gaa gtg gcg	432
Cys Arg Tyr Leu Ile Phe Leu Tyr Ala Met Met Ala Ala Glu Val Ala	
130 135 140	
atc cat ttg gga ttg tgg cag ttc caa gcg ctc acc caa cat atg ttg	480
Ile His Leu Gly Leu Trp Gln Phe Gln Ala Leu Thr Gln His Met Leu	
145 150 155 160	
ctc ttt tgg agc acc tat gag ccg ctc gtg tgg ctg acg tat ctg cgc	528
Leu Phe Trp Ser Thr Tyr Glu Pro Leu Val Trp Leu Thr Tyr Leu Arg	
165 170 175	
aat ctg cag ttc gta ctg cac ttg gag ctg ctc agg gag cag ctg acc	576
Asn Leu Gln Phe Val Leu His Leu Glu Leu Leu Arg Glu Gln Leu Thr	
180 185 190	
ggc ttg gaa cgc gaa atg ggt ctg ctg gcg gag tac tcg cga ttt gct	624
Gly Leu Glu Arg Glu Met Gly Leu Leu Ala Glu Tyr Ser Arg Phe Ala	
195 200 205	

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agc gaa acg ggt cgg agt ttt cct gga ttc gaa agt ttc ctg cgc cga 672
Ser Glu Thr Gly Arg Ser Phe Pro Gly Phe Glu Ser Phe Leu Arg Arg
    210                215                220

cga cta gtg cag aag cag cgc atc tat agc cat gtg tat gac atg ctc 720
Arg Leu Val Gln Lys Gln Arg Ile Tyr Ser His Val Tyr Asp Met Leu
225                230                235                240

aaa tgt ttc cag ggt gcc ttc aac ttc tcc att ctc gcc gtc ctg ctg 768
Lys Cys Phe Gln Gly Ala Phe Asn Phe Ser Ile Leu Ala Val Leu Leu
                245                250                255

acc atc aac ata cgc atc gcc gtg gac tgc tac ttc atg tac tac agc 816
Thr Ile Asn Ile Arg Ile Ala Val Asp Cys Tyr Phe Met Tyr Tyr Ser
                260                265                270

atc tac aac aat gtg att aac aac gat tac tac cta atc gtt ccc gcc 864
Ile Tyr Asn Asn Val Ile Asn Asn Asp Tyr Tyr Leu Ile Val Pro Ala
                275                280                285

ttg ctc gag att ccc gcc ttc ata tac gct tcg cag agc tgc atg gtc 912
Leu Leu Glu Ile Pro Ala Phe Ile Tyr Ala Ser Gln Ser Cys Met Val
    290                295                300

gtg gtg ccc agg atc gcc cac cag ctg cat aat ata gtc acc gat tcc 960
Val Val Pro Arg Ile Ala His Gln Leu His Asn Ile Val Thr Asp Ser
305                310                315                320

ggt tgc tgc agc tgt ccc gat ctc tcc ctg cag att cag aac ttt tca 1008
Gly Cys Cys Ser Cys Pro Asp Leu Ser Leu Gln Ile Gln Asn Phe Ser
                325                330                335

ctg caa ctc ctg cat cag ccg ata cga atc gat tgc ctc ggc ctg acc 1056
Leu Gln Leu Leu His Gln Pro Ile Arg Ile Asp Cys Leu Gly Leu Thr
                340                345                350

atc ctg gat tgc agt ctt cta act cgg atg gcc tgt tcc gtg ggc acc 1104
Ile Leu Asp Cys Ser Leu Leu Thr Arg Met Ala Cys Ser Val Gly Thr
                355                360                365

tac atg atc tat agc atc cag ttt ata cca aag ttc agc aat acc tat 1152
Tyr Met Ile Tyr Ser Ile Gln Phe Ile Pro Lys Phe Ser Asn Thr Tyr
    370                375                380

atg tag 1158
Met
385

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<210> 6

<211> 385

<212> PRT

<213> Drosophila melanogaster

<400> 6

Met Ser Gly His Leu Gly Arg Val Leu Gln Phe His Leu Arg Leu Tyr

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Gln Val Leu Gly Phe His Gly Leu Pro Leu Pro Gly Asp Gly Asn Pro	20	25	30
Ala Arg Thr Arg Arg Arg Leu Met Ala Trp Ser Leu Phe Leu Leu Ile	35	40	45
Ser Leu Ser Ala Leu Val Leu Ala Cys Leu Phe Ser Gly Glu Glu Phe	50	55	60
Leu Tyr Arg Gly Asp Met Phe Gly Cys Ala Asn Asp Ala Leu Lys Tyr	65	70	75
Val Phe Ala Glu Leu Gly Val Leu Ala Ile Tyr Leu Glu Thr Leu Ser	85	90	95
Ser Gln Arg His Leu Ala Asn Phe Trp Trp Leu His Phe Lys Leu Gly	100	105	110
Gly Gln Lys Thr Gly Leu Val Ser Leu Arg Ser Glu Phe Gln Gln Phe	115	120	125
Cys Arg Tyr Leu Ile Phe Leu Tyr Ala Met Met Ala Ala Glu Val Ala	130	135	140
Ile His Leu Gly Leu Trp Gln Phe Gln Ala Leu Thr Gln His Met Leu	145	150	155
Leu Phe Trp Ser Thr Tyr Glu Pro Leu Val Trp Leu Thr Tyr Leu Arg	165	170	175
Asn Leu Gln Phe Val Leu His Leu Glu Leu Leu Arg Glu Gln Leu Thr	180	185	190
Gly Leu Glu Arg Glu Met Gly Leu Leu Ala Glu Tyr Ser Arg Phe Ala	195	200	205
Ser Glu Thr Gly Arg Ser Phe Pro Gly Phe Glu Ser Phe Leu Arg Arg	210	215	220
Arg Leu Val Gln Lys Gln Arg Ile Tyr Ser His Val Tyr Asp Met Leu	225	230	235
Lys Cys Phe Gln Gly Ala Phe Asn Phe Ser Ile Leu Ala Val Leu Leu	245	250	255
Thr Ile Asn Ile Arg Ile Ala Val Asp Cys Tyr Phe Met Tyr Tyr Ser	260	265	270
Ile Tyr Asn Asn Val Ile Asn Asn Asp Tyr Tyr Leu Ile Val Pro Ala	275	280	285
Leu Leu Glu Ile Pro Ala Phe Ile Tyr Ala Ser Gln Ser Cys Met Val	290	295	300

Val Val Pro Arg Ile Ala His Gln Leu His Asn Ile Val Thr Asp Ser
 305 310 315 320

Gly Cys Cys Ser Cys Pro Asp Leu Ser Leu Gln Ile Gln Asn Phe Ser
 325 330 335

Leu Gln Leu Leu His Gln Pro Ile Arg Ile Asp Cys Leu Gly Leu Thr
 340 345 350

Ile Leu Asp Cys Ser Leu Leu Thr Arg Met Ala Cys Ser Val Gly Thr
 355 360 365

Tyr Met Ile Tyr Ser Ile Gln Phe Ile Pro Lys Phe Ser Asn Thr Tyr
 370 375 380

Met
 385

<210> 7
 <211> 1119
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1119)
 <223> Coding region GR10B.1

<400> 7

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Met Arg Val Gly Lys Leu Cys Arg Leu Ala Leu Arg Phe Trp Met Gly	
1 5 10 15	
ttg att ctg gtc ctg ggt ttc tcc agc cac tac tac aat ccc act cgg	96
Leu Ile Leu Val Leu Gly Phe Ser Ser His Tyr Tyr Asn Pro Thr Arg	
20 25 30	
cgg cgt ttg gtt tac tcg aga att ttg cag aca tac gac tgg ctg tta	144
Arg Arg Leu Val Tyr Ser Arg Ile Leu Gln Thr Tyr Asp Trp Leu Leu	
35 40 45	
atg gtc atc aac ttg ggt gct ttt tac ctc tac tat aga tac gcc atg	192
Met Val Ile Asn Leu Gly Ala Phe Tyr Leu Tyr Tyr Arg Tyr Ala Met	
50 55 60	
acg tat ttt ctg gag ggc atg ttt agg cgg caa gga ttc gta aat cag	240
Thr Tyr Phe Leu Glu Gly Met Phe Arg Arg Gln Gly Phe Val Asn Gln	
65 70 75 80	
gtg tcc aca tgc aac gta ttc cag cag cta ctg atg gca gtg acg ggc	288
Val Ser Thr Cys Asn Val Phe Gln Gln Leu Leu Met Ala Val Thr Gly	
85 90 95	
aca tgg ttg cac ttt cta ttt gaa cgg cac gtg tgt cag acg tac aac	336

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Thr	Trp	Leu	His	Phe	Leu	Phe	Glu	Arg	His	Val	Cys	Gln	Thr	Tyr	Asn	
			100					105					110			
gag	ttg	tcc	aga	att	ttg	aag	cat	gac	ctg	aag	ctc	aag	gag	cac	agt	384
Glu	Leu	Ser	Arg	Ile	Leu	Lys	His	Asp	Leu	Lys	Leu	Lys	Glu	His	Ser	
		115					120					125				
cgc	ttc	tac	tgc	ctg	gcc	ttt	ctg	gcc	aaa	gtc	tac	aat	ttt	ttc	cac	432
Arg	Phe	Tyr	Cys	Leu	Ala	Phe	Leu	Ala	Lys	Val	Tyr	Asn	Phe	Phe	His	
	130					135					140					
aac	ttc	aac	ttt	gcc	cta	agt	gcc	atc	atg	cat	tgg	ggc	ctg	cga	ccc	480
Asn	Phe	Asn	Phe	Ala	Leu	Ser	Ala	Ile	Met	His	Trp	Gly	Leu	Arg	Pro	
145					150					155					160	
ttc	aat	gtt	tgg	gac	tta	ctg	gcc	aat	ctg	tac	ttt	gtc	tac	aac	tca	528
Phe	Asn	Val	Trp	Asp	Leu	Leu	Ala	Asn	Leu	Tyr	Phe	Val	Tyr	Asn	Ser	
				165					170					175		
ctg	gct	agg	gat	gcc	att	ctg	gtg	gcc	tat	gtt	ctg	ttg	ctg	ctc	aac	576
Leu	Ala	Arg	Asp	Ala	Ile	Leu	Val	Ala	Tyr	Val	Leu	Leu	Leu	Leu	Asn	
			180					185						190		
ctg	tcg	gag	gca	ctg	cgt	ctg	aat	ggc	cag	cag	gag	cac	gac	acc	tac	624
Leu	Ser	Glu	Ala	Leu	Arg	Leu	Asn	Gly	Gln	Gln	Glu	His	Asp	Thr	Tyr	
		195					200					205				
agc	gac	ctc	atg	aag	cag	ctg	cgc	aga	cgg	gag	cga	ttg	ctg	agg	att	672
Ser	Asp	Leu	Met	Lys	Gln	Leu	Arg	Arg	Arg	Glu	Arg	Leu	Leu	Arg	Ile	
	210					215					220					
gga	agg	cga	gtg	cat	cgc	atg	ttc	gcc	tgg	ctg	gtg	gcc	ata	gcc	tta	720
Gly	Arg	Arg	Val	His	Arg	Met	Phe	Ala	Trp	Leu	Val	Ala	Ile	Ala	Leu	
225					230					235					240	
ata	tat	ctg	gtg	ttt	ttc	aac	acg	gcc	acc	att	tac	ctg	ggc	tac	acc	768
Ile	Tyr	Leu	Val	Phe	Phe	Asn	Thr	Ala	Thr	Ile	Tyr	Leu	Gly	Tyr	Thr	
				245					250					255		
atg	ttc	att	cag	aag	cac	gac	gcc	ttg	ggc	ctg	cgt	ggc	cga	ggc	ttg	816
Met	Phe	Ile	Gln	Lys	His	Asp	Ala	Leu	Gly	Leu	Arg	Gly	Arg	Gly	Leu	
			260					265					270			
aag	atg	ctg	ctc	acg	gtc	gtc	tcc	ttt	ttg	gtc	atc	cta	tgg	gac	gtc	864
Lys	Met	Leu	Leu	Thr	Val	Val	Ser	Phe	Leu	Val	Ile	Leu	Trp	Asp	Val	
		275					280					285				
gtg	cta	ctg	cag	gtc	atc	tgt	gaa	aag	ctt	ttg	gcc	gag	gaa	aac	aaa	912
Val	Leu	Leu	Gln	Val	Ile	Cys	Glu	Lys	Leu	Leu	Ala	Glu	Glu	Asn	Lys	
	290					295					300					
att	tgc	gac	tgt	cca	gag	gat	gtg	gcc	tct	tcc	agg	acg	act	tac	aga	960
Ile	Cys	Asp	Cys	Pro	Glu	Asp	Val	Ala	Ser	Ser	Arg	Thr	Thr	Tyr	Arg	
305					310					315					320	
cag	tgg	gaa	atg	tcc	gct	tta	aga	cga	gct	att	aca	cga	tca	tcg	ccg	1008

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<400> 8
Met Arg Val Gly Lys Leu Cys Arg Leu Ala Leu Arg Phe Trp Met Gly
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Leu Ile Leu Val Leu Gly Phe Ser Ser His Tyr Tyr Asn Pro Thr Arg
      20              25              30

Arg Arg Leu Val Tyr Ser Arg Ile Leu Gln Thr Tyr Asp Trp Leu Leu
      35              40              45

Met Val Ile Asn Leu Gly Ala Phe Tyr Leu Tyr Tyr Arg Tyr Ala Met
      50              55              60

Thr Tyr Phe Leu Glu Gly Met Phe Arg Arg Gln Gly Phe Val Asn Gln
      65              70              75              80

Val Ser Thr Cys Asn Val Phe Gln Gln Leu Leu Met Ala Val Thr Gly
      85              90              95

Thr Trp Leu His Phe Leu Phe Glu Arg His Val Cys Gln Thr Tyr Asn
      100              105              110

Glu Leu Ser Arg Ile Leu Lys His Asp Leu Lys Leu Lys Glu His Ser
      115              120              125

Arg Phe Tyr Cys Leu Ala Phe Leu Ala Lys Val Tyr Asn Phe Phe His
      130              135              140

Asn Phe Asn Phe Ala Leu Ser Ala Ile Met His Trp Gly Leu Arg Pro
      145              150              155              160

Phe Asn Val Trp Asp Leu Leu Ala Asn Leu Tyr Phe Val Tyr Asn Ser
      165              170              175

Leu Ala Arg Asp Ala Ile Leu Val Ala Tyr Val Leu Leu Leu Leu Asn

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180					185					190						
Leu	Ser	Glu	Ala	Leu	Arg	Leu	Asn	Gly	Gln	Gln	Glu	His	Asp	Thr	Tyr	
195					200					205						
Ser	Asp	Leu	Met	Lys	Gln	Leu	Arg	Arg	Arg	Glu	Arg	Leu	Leu	Arg	Ile	
210					215					220						
Gly	Arg	Arg	Val	His	Arg	Met	Phe	Ala	Trp	Leu	Val	Ala	Ile	Ala	Leu	
225					230					235					240	
Ile	Tyr	Leu	Val	Phe	Phe	Asn	Thr	Ala	Thr	Ile	Tyr	Leu	Gly	Tyr	Thr	
245					250					255						
Met	Phe	Ile	Gln	Lys	His	Asp	Ala	Leu	Gly	Leu	Arg	Gly	Arg	Gly	Leu	
260					265					270						
Lys	Met	Leu	Leu	Thr	Val	Val	Ser	Phe	Leu	Val	Ile	Leu	Trp	Asp	Val	
275					280					285						
Val	Leu	Leu	Gln	Val	Ile	Cys	Glu	Lys	Leu	Leu	Ala	Glu	Glu	Asn	Lys	
290					295					300						
Ile	Cys	Asp	Cys	Pro	Glu	Asp	Val	Ala	Ser	Ser	Arg	Thr	Thr	Tyr	Arg	
305					310					315					320	
Gln	Trp	Glu	Met	Ser	Ala	Leu	Arg	Arg	Ala	Ile	Thr	Arg	Ser	Ser	Pro	
325					330					335						
Glu	Asn	Asn	Val	Leu	Gly	Met	Phe	Arg	Met	Asp	Met	Arg	Cys	Ala	Phe	
340					345					350						
Ala	Leu	Ile	Ser	Cys	Ser	Leu	Ser	Tyr	Gly	Ile	Ile	Ile	Ile	Gln	Ile	
355					360					365						
Gly	Tyr	Ile	Pro	Gly												
370																

<210> 9
 <211> 1092
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1092)
 <223> Coding region GR21D.1

<220>
 <221> misc_feature
 <222> (505)..(766)
 <223> Splice sites before bases 505, 562 and 766.

<400> 9

WO 00/77208

PCT/US00/16211

atg ggc gta atg ccc att cac cgc aat ccg ccc gag aag aac ctg cct	48
Met Gly Val Met Pro Ile His Arg Asn Pro Pro Glu Lys Asn Leu Pro	
1 5 10 15	
aga acg ggc tac tcc tgg ggc tcc aag cag gtc atg tgg gcc atc ttc	96
Arg Thr Gly Tyr Ser Trp Gly Ser Lys Gln Val Met Trp Ala Ile Phe	
20 25 30	
atc tac agc tgc cag acg acc att gtt gtt ctg gtg ctg cgt gag cgc	144
Ile Tyr Ser Cys Gln Thr Thr Ile Val Val Leu Val Leu Arg Glu Arg	
35 40 45	
gtg aaa aaa ttc gtc acc agc ccg gac aag cgc ttc gat gag gcc atc	192
Val Lys Lys Phe Val Thr Ser Pro Asp Lys Arg Phe Asp Glu Ala Ile	
50 55 60	
tac aat gtc att ttc atc agt ctg ctc ttc acc aac ttt ctg ctc ccg	240
Tyr Asn Val Ile Phe Ile Ser Leu Leu Phe Thr Asn Phe Leu Leu Pro	
65 70 75 80	
gtg gcc agc tgg cgg cac ggt ccc cag gtg gct atc ttc aag aac atg	288
Val Ala Ser Trp Arg His Gly Pro Gln Val Ala Ile Phe Lys Asn Met	
85 90 95	
tgg acc aac tac cag tat aag ttc ttc aaa act acc ggc tcg ccg atc	336
Trp Thr Asn Tyr Gln Tyr Lys Phe Phe Lys Thr Thr Gly Ser Pro Ile	
100 105 110	
gtc ttt ccg aat ctc tac cca ctc acc tgg tcg ctg tgc gtc ttc tcc	384
Val Phe Pro Asn Leu Tyr Pro Leu Thr Trp Ser Leu Cys Val Phe Ser	
115 120 125	
tgg ctc cta agc atc gcc atc aac ctg tcg cag tac ttc ctg cag ccg	432
Trp Leu Leu Ser Ile Ala Ile Asn Leu Ser Gln Tyr Phe Leu Gln Pro	
130 135 140	
gac ttc cgg ctg tgg tac aca ttc gcc tac tac ccc atc atc gcc atg	480
Asp Phe Arg Leu Trp Tyr Thr Phe Ala Tyr Tyr Pro Ile Ile Ala Met	
145 150 155 160	
ctc aac tgc ttc tgc agc ttg tgg tac atc aac tgc aat gca ttc gga	528
Leu Asn Cys Phe Cys Ser Leu Trp Tyr Ile Asn Cys Asn Ala Phe Gly	
165 170 175	
act gca agt cgc gct ctt tcc gac gct ctg cag aca acc atc cgg ggc	576
Thr Ala Ser Arg Ala Leu Ser Asp Ala Leu Gln Thr Thr Ile Arg Gly	
180 185 190	
gag aag ccc gcc caa aaa ctc act gag tac cgc cat cta tgg gtg gat	624
Glu Lys Pro Ala Gln Lys Leu Thr Glu Tyr Arg His Leu Trp Val Asp	
195 200 205	
ctg agc cac atg atg cag cag ctg gga cga gct tac tcc aac atg tac	672
Leu Ser His Met Met Gln Gln Leu Gly Arg Ala Tyr Ser Asn Met Tyr	
210 215 220	

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PCT/US00/16211

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ggc atg tac tgt cta gtc atc ttc ttc aca acg atc atc gcc act tac 720
Gly Met Tyr Cys Leu Val Ile Phe Phe Thr Thr Ile Ile Ala Thr Tyr
225                      230                      235                      240

ggc agc atc agc gaa atc atc gac cac ggg gca acc tac aag gag gtg 768
Gly Ser Ile Ser Glu Ile Ile Asp His Gly Ala Thr Tyr Lys Glu Val
                      245                      250                      255

ggg ctg ttc gtc atc gtg ttc tac tgc atg ggt ctg ctg tac att atc 816
Gly Leu Phe Val Ile Val Phe Tyr Cys Met Gly Leu Leu Tyr Ile Ile
                      260                      265                      270

tgc aac gag gcg cac tac gcc tcc cga aag gtc gga ctt gac ttc cag 864
Cys Asn Glu Ala His Tyr Ala Ser Arg Lys Val Gly Leu Asp Phe Gln
                      275                      280                      285

acg aag ctg ctc aat atc aac ctg act gcc gtg gac gct gcc acc cag 912
Thr Lys Leu Leu Asn Ile Asn Leu Thr Ala Val Asp Ala Ala Thr Gln
                      290                      295                      300

aag gaa gtg gag atg ctg ctt gtg gcc ata aac aag aac ccg ccc atc 960
Lys Glu Val Glu Met Leu Leu Val Ala Ile Asn Lys Asn Pro Pro Ile
305                      310                      315                      320

atg aat ctg gac ggg tat gca aac atc aac cgc gag ctg atc acg acc 1008
Met Asn Leu Asp Gly Tyr Ala Asn Ile Asn Arg Glu Leu Ile Thr Thr
                      325                      330                      335

aac atc tcg ttc atg gcc acc tac ctc gtg gtc ctg ctg cag ttt aag 1056
Asn Ile Ser Phe Met Ala Thr Tyr Leu Val Val Leu Leu Gln Phe Lys
                      340                      345                      350

atc acg gag cag aga cgc att ggt cag cag cag gcc 1092
Ile Thr Glu Gln Arg Arg Ile Gly Gln Gln Gln Ala
                      355                      360

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<210> 10

<211> 364

<212> PRT

<213> *Drosophila melanogaster*

<400> 10

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Met Gly Val Met Pro Ile His Arg Asn Pro Pro Glu Lys Asn Leu Pro
  1                      5                      10                      15

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Arg Thr Gly Tyr Ser Trp Gly Ser Lys Gln Val Met Trp Ala Ile Phe
      20                      25                      30

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Ile Tyr Ser Cys Gln Thr Thr Ile Val Val Leu Val Leu Arg Glu Arg
  35                      40                      45

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Val Lys Lys Phe Val Thr Ser Pro Asp Lys Arg Phe Asp Glu Ala Ile
  50                      55                      60

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Tyr Asn Val Ile Phe Ile Ser Leu Leu Phe Thr Asn Phe Leu Leu Pro

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WO 00/77208

PCT/US00/16211

65	70	75	80
Val Ala Ser Trp Arg His Gly Pro Gln Val Ala Ile Phe Lys Asn Met	85	90	95
Trp Thr Asn Tyr Gln Tyr Lys Phe Phe Lys Thr Thr Gly Ser Pro Ile	100	105	110
Val Phe Pro Asn Leu Tyr Pro Leu Thr Trp Ser Leu Cys Val Phe Ser	115	120	125
Trp Leu Leu Ser Ile Ala Ile Asn Leu Ser Gln Tyr Phe Leu Gln Pro	130	135	140
Asp Phe Arg Leu Trp Tyr Thr Phe Ala Tyr Tyr Pro Ile Ile Ala Met	145	150	155
Leu Asn Cys Phe Cys Ser Leu Trp Tyr Ile Asn Cys Asn Ala Phe Gly	165	170	175
Thr Ala Ser Arg Ala Leu Ser Asp Ala Leu Gln Thr Thr Ile Arg Gly	180	185	190
Glu Lys Pro Ala Gln Lys Leu Thr Glu Tyr Arg His Leu Trp Val Asp	195	200	205
Leu Ser His Met Met Gln Gln Leu Gly Arg Ala Tyr Ser Asn Met Tyr	210	215	220
Gly Met Tyr Cys Leu Val Ile Phe Phe Thr Thr Ile Ile Ala Thr Tyr	225	230	235
Gly Ser Ile Ser Glu Ile Ile Asp His Gly Ala Thr Tyr Lys Glu Val	245	250	255
Gly Leu Phe Val Ile Val Phe Tyr Cys Met Gly Leu Leu Tyr Ile Ile	260	265	270
Cys Asn Glu Ala His Tyr Ala Ser Arg Lys Val Gly Leu Asp Phe Gln	275	280	285
Thr Lys Leu Leu Asn Ile Asn Leu Thr Ala Val Asp Ala Ala Thr Gln	290	295	300
Lys Glu Val Glu Met Leu Leu Val Ala Ile Asn Lys Asn Pro Pro Ile	305	310	315
Met Asn Leu Asp Gly Tyr Ala Asn Ile Asn Arg Glu Leu Ile Thr Thr	325	330	335
Asn Ile Ser Phe Met Ala Thr Tyr Leu Val Val Leu Leu Gln Phe Lys	340	345	350
Ile Thr Glu Gln Arg Arg Ile Gly Gln Gln Gln Ala	355	360	

<210> 11
 <211> 1134
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1134)
 <223> Coding region GR22B.1

<220>
 <221> misc_feature
 <222> (985)
 <223> Splice site

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 1 5 10 15
 ttc atg ctg cag acg acc ctc tac gca tcc tgg cta ctg gga ctg ttc 96
 Phe Met Leu Gln Thr Thr Leu Tyr Ala Ser Trp Leu Leu Gly Leu Phe
 20 25 30
 ccc ttc act ttc gat tcc cgg aga aag cag ttg aaa cgc tcc cga tgg 144
 Pro Phe Thr Phe Asp Ser Arg Arg Lys Gln Leu Lys Arg Ser Arg Trp
 35 40 45
 ctt ctc ctc tac ggt ttc gtt ctg cat tct ctg gcc atg tgc cta gcc 192
 Leu Leu Leu Tyr Gly Phe Val Leu His Ser Leu Ala Met Cys Leu Ala
 50 55 60
 atg agt agc cac ttg gca tcc aag cag cga agg aaa tat aat gca ttt 240
 Met Ser Ser His Leu Ala Ser Lys Gln Arg Arg Lys Tyr Asn Ala Phe
 65 70 75 80
 gag cgc aat ccg ctg ttg gag aaa ata tat atg caa ttt cag gtt act 288
 Glu Arg Asn Pro Leu Leu Glu Lys Ile Tyr Met Gln Phe Gln Val Thr
 85 90 95
 aca ttc ttc act ata agc gta cta ctg ctc atg aat gtt tgg aaa agc 336
 Thr Phe Phe Thr Ile Ser Val Leu Leu Leu Met Asn Val Trp Lys Ser
 100 105 110
 aac acg gtt cgg aaa att gcc aat gaa cta ctc acc ctt gag ggc cag 384
 Asn Thr Val Arg Lys Ile Ala Asn Glu Leu Leu Thr Leu Glu Gly Gln
 115 120 125
 gta aaa gac ctt ctc act ctg aag aac tgt ccc aac ttt aac tgt ttc 432
 Val Lys Asp Leu Leu Thr Leu Lys Asn Cys Pro Asn Phe Asn Cys Phe
 130 135 140
 gtg att aaa aaa cat gtg gct gca ata ggt cag ttc gtg att tca att 480
 Val Ile Lys Lys His Val Ala Ala Ile Gly Gln Phe Val Ile Ser Ile
 145 150 155 160

WO 00/77208

PCT/US00/16211

tac ttc tgc cta tgc caa gaa aat tcg tac ccg aag atc ctt aag atc	528
Tyr Phe Cys Leu Cys Gln Glu Asn Ser Tyr Pro Lys Ile Leu Lys Ile	
165 170 175	
ctt tgc tgc ctg cca tcg gtg ggc ttg cag ctg att ata atg cac ttt	576
Leu Cys Cys Leu Pro Ser Val Gly Leu Gln Leu Ile Ile Met His Phe	
180 185 190	
cat acc gaa atc att ttg gtc tac cgc tat gtg tgg ctg gtc aat gaa	624
His Thr Glu Ile Ile Leu Val Tyr Arg Tyr Val Trp Leu Val Asn Glu	
195 200 205	
acc ctc gaa gat tca cac cat cta agc tcc tca aga att cac gca cta	672
Thr Leu Glu Asp Ser His His Leu Ser Ser Ser Arg Ile His Ala Leu	
210 215 220	
gca tcc ttg tac gat cgc ctg ctg aag ctg agt gaa ttg gtg gta gcg	720
Ala Ser Leu Tyr Asp Arg Leu Leu Lys Leu Ser Glu Leu Val Val Ala	
225 230 235 240	
tgc aac gat ttg caa ctg atc ctt atg cta att att tat tta atc gga	768
Cys Asn Asp Leu Gln Leu Ile Leu Met Leu Ile Ile Tyr Leu Ile Gly	
245 250 255	
aac act gtg caa atc ttt ttc ctc att gtg ctc gga gta agc atg aat	816
Asn Thr Val Gln Ile Phe Phe Leu Ile Val Leu Gly Val Ser Met Asn	
260 265 270	
aag cgg tat att tac tta gtg gct tcc cca caa ttg atc atc aat ttc	864
Lys Arg Tyr Ile Tyr Leu Val Ala Ser Pro Gln Leu Ile Ile Asn Phe	
275 280 285	
tgg gac ttc tgg ctg aat atc gtg gtg tgt gat ctt gcc gga aag tgt	912
Trp Asp Phe Trp Leu Asn Ile Val Val Cys Asp Leu Ala Gly Lys Cys	
290 295 300	
gga gac caa aca tca aag gtc ctg aaa ctg ttc act gat ctg gag cac	960
Gly Asp Gln Thr Ser Lys Val Leu Lys Leu Phe Thr Asp Leu Glu His	
305 310 315 320	
gac gat gaa gag tta gag aga agt ttg aat gaa ttc gca tgg ctg tgc	1008
Asp Asp Glu Glu Leu Glu Arg Ser Leu Asn Glu Phe Ala Trp Leu Cys	
325 330 335	
acc cac cgc aag ttt cgg ttt cag ctg tgt ggt ctc ttt tcc att aac	1056
Thr His Arg Lys Phe Arg Phe Gln Leu Cys Gly Leu Phe Ser Ile Asn	
340 345 350	
cac aac atg ggc ttt caa atg atc atc acc agt ttt cta tac ctg gtt	1104
His Asn Met Gly Phe Gln Met Ile Ile Thr Ser Phe Leu Tyr Leu Val	
355 360 365	
tac ctg ctt cag ttt gac ttc atg aac ttg	1134
Tyr Leu Leu Gln Phe Asp Phe Met Asn Leu	
370 375	

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<210> 12

<211> 378

<212> PRT

<213> Drosophila melanogaster

<400> 12

Met	Lys	Met	Phe	Gln	Pro	Arg	Arg	Gly	Phe	Ser	Cys	His	Leu	Ala	Trp
1				5					10					15	
Phe	Met	Leu	Gln	Thr	Thr	Leu	Tyr	Ala	Ser	Trp	Leu	Leu	Gly	Leu	Phe
			20					25					30		
Pro	Phe	Thr	Phe	Asp	Ser	Arg	Arg	Lys	Gln	Leu	Lys	Arg	Ser	Arg	Trp
		35					40					45			
Leu	Leu	Leu	Tyr	Gly	Phe	Val	Leu	His	Ser	Leu	Ala	Met	Cys	Leu	Ala
	50					55					60				
Met	Ser	Ser	His	Leu	Ala	Ser	Lys	Gln	Arg	Arg	Lys	Tyr	Asn	Ala	Phe
65					70					75					80
Glu	Arg	Asn	Pro	Leu	Leu	Glu	Lys	Ile	Tyr	Met	Gln	Phe	Gln	Val	Thr
				85					90					95	
Thr	Phe	Phe	Thr	Ile	Ser	Val	Leu	Leu	Leu	Met	Asn	Val	Trp	Lys	Ser
			100					105					110		
Asn	Thr	Val	Arg	Lys	Ile	Ala	Asn	Glu	Leu	Leu	Thr	Leu	Glu	Gly	Gln
		115					120					125			
Val	Lys	Asp	Leu	Leu	Thr	Leu	Lys	Asn	Cys	Pro	Asn	Phe	Asn	Cys	Phe
	130					135					140				
Val	Ile	Lys	Lys	His	Val	Ala	Ala	Ile	Gly	Gln	Phe	Val	Ile	Ser	Ile
145					150					155					160
Tyr	Phe	Cys	Leu	Cys	Gln	Glu	Asn	Ser	Tyr	Pro	Lys	Ile	Leu	Lys	Ile
			165						170					175	
Leu	Cys	Cys	Leu	Pro	Ser	Val	Gly	Leu	Gln	Leu	Ile	Ile	Met	His	Phe
			180					185					190		
His	Thr	Glu	Ile	Ile	Leu	Val	Tyr	Arg	Tyr	Val	Trp	Leu	Val	Asn	Glu
		195					200					205			
Thr	Leu	Glu	Asp	Ser	His	His	Leu	Ser	Ser	Ser	Arg	Ile	His	Ala	Leu
	210					215					220				
Ala	Ser	Leu	Tyr	Asp	Arg	Leu	Leu	Lys	Leu	Ser	Glu	Leu	Val	Val	Ala
225					230					235					240
Cys	Asn	Asp	Leu	Gln	Leu	Ile	Leu	Met	Leu	Ile	Ile	Tyr	Leu	Ile	Gly
			245						250					255	
Asn	Thr	Val	Gln	Ile	Phe	Phe	Leu	Ile	Val	Leu	Gly	Val	Ser	Met	Asn
		260						265					270		

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Lys Arg Tyr Ile Tyr Leu Val Ala Ser Pro Gln Leu Ile Ile Asn Phe
 275 280 285
 Trp Asp Phe Trp Leu Asn Ile Val Val Cys Asp Leu Ala Gly Lys Cys
 290 295 300
 Gly Asp Gln Thr Ser Lys Val Leu Lys Leu Phe Thr Asp Leu Glu His
 305 310 315 320
 Asp Asp Glu Glu Leu Glu Arg Ser Leu Asn Glu Phe Ala Trp Leu Cys
 325 330 335
 Thr His Arg Lys Phe Arg Phe Gln Leu Cys Gly Leu Phe Ser Ile Asn
 340 345 350
 His Asn Met Gly Phe Gln Met Ile Ile Thr Ser Phe Leu Tyr Leu Val
 355 360 365
 Tyr Leu Leu Gln Phe Asp Phe Met Asn Leu
 370 375

<210> 13
 <211> 1149
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1149)
 <223> Coding region GR23A.1a

<220>
 <221> misc_feature
 <222> (910)..(1068)
 <223> Splice sites before positions 910 and 1068

<400> 13
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 Met Val Met Val Gln Ser Val Ser Val Tyr Lys Ala Asn Met Lys Thr
 1 5 10 15
 ttg gag tgc ctg acc cgc cgt ttc ctg gaa gtt atc ttc tct gta ctc 96
 Leu Glu Cys Leu Thr Arg Arg Phe Leu Glu Val Ile Phe Ser Val Leu
 20 25 30
 gcc ttg gtt cca ctt cct cct att tcg cag ttg gga tgg ctg ttt tta 144
 Ala Leu Val Pro Leu Pro Pro Ile Ser Gln Leu Gly Trp Leu Phe Leu
 35 40 45
 tca ttg gcc att cgc tgc tgt tgg ata gtt tac ttt ata tat ttg ctg 192
 Ser Leu Ala Ile Arg Cys Cys Trp Ile Val Tyr Phe Ile Tyr Leu Leu
 50 55 60
 gac gtt gcc atc agc ttt tcg tgg gtg gcc atc gaa aat gtt gga aat 240

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Asp	Val	Ala	Ile	Ser	Phe	Ser	Trp	Val	Ala	Ile	Glu	Asn	Val	Gly	Asn		
65					70					75					80		
gcc	gtg	ggc	acc	atg	ctg	ttc	gtg	gga	aac	tcc	gtg	ctg	gga	ttt	gcg	288	
Ala	Val	Gly	Thr	Met	Leu	Phe	Val	Gly	Asn	Ser	Val	Leu	Gly	Phe	Ala		
				85					90					95			
ctc	ctg	ctg	gag	agt	gtc	ctt	aag	cag	aag	acc	cac	agc	cag	ctg	gag	336	
Leu	Leu	Leu	Glu	Ser	Val	Leu	Lys	Gln	Lys	Thr	His	Ser	Gln	Leu	Glu		
			100					105					110				
gat	ctg	cga	gtc	cag	acg	gag	ttg	caa	ctg	caa	aga	ctt	gga	atg	ttc	384	
Asp	Leu	Arg	Val	Gln	Thr	Glu	Leu	Gln	Leu	Gln	Arg	Leu	Gly	Met	Phe		
		115					120					125					
ggg	aga	tct	cgc	cac	gcg	gca	tac	cta	ttg	cca	cta	att	gga	gtt	cag	432	
Gly	Arg	Ser	Arg	His	Ala	Ala	Tyr	Leu	Leu	Pro	Leu	Ile	Gly	Val	Gln		
	130					135					140						
ttt	act	tgt	gat	ctt	gtg	aga	ctt	gcg	acc	aat	ttt	ggg	gag	acg	gta	480	
Phe	Thr	Cys	Asp	Leu	Val	Arg	Leu	Ala	Thr	Asn	Phe	Gly	Glu	Thr	Val		
145					150					155					160		
tcg	cct	gtg	ttt	tgt	ata	tcc	tta	cca	ctg	atg	tgg	cta	cta	cgg	tat	528	
Ser	Pro	Val	Phe	Cys	Ile	Ser	Leu	Pro	Leu	Met	Trp	Leu	Leu	Arg	Tyr		
				165					170					175			
cgc	tat	gtt	caa	ctg	gtg	cag	cac	gtc	atg	gat	ctg	aat	cag	aga	tcc	576	
Arg	Tyr	Val	Gln	Leu	Val	Gln	His	Val	Met	Asp	Leu	Asn	Gln	Arg	Ser		
			180					185					190				
atc	cac	ttg	cgc	cga	tcc	ctg	ttg	tcc	atg	gcc	tcc	gga	aac	gat	ctg	624	
Ile	His	Leu	Arg	Arg	Ser	Leu	Leu	Ser	Met	Ala	Ser	Gly	Asn	Asp	Leu		
		195					200					205					
tgg	cag	ccc	tac	gga	gtc	caa	gag	tgc	ctt	caa	ctc	cag	acc	ctg	cgc	672	
Trp	Gln	Pro	Tyr	Gly	Val	Gln	Glu	Cys	Leu	Gln	Leu	Gln	Thr	Leu	Arg		
	210					215					220						
acc	acc	tac	gaa	agg	atc	ttc	gag	tgc	tac	gaa	aca	ttc	agc	gac	tgc	720	
Thr	Thr	Tyr	Glu	Arg	Ile	Phe	Glu	Cys	Tyr	Glu	Thr	Phe	Ser	Asp	Cys		
225					230					235					240		
tat	gga	tgg	gga	atg	ctg	gga	ctc	cat	ttg	ctg	acc	agc	ttt	cag	ttc	768	
Tyr	Gly	Trp	Gly	Met	Leu	Gly	Leu	His	Leu	Leu	Thr	Ser	Phe	Gln	Phe		
				245					250					255			
gtg	acc	aat	gcc	tac	tgg	atg	atc	atg	ggc	att	tac	gat	ggc	ggc	aat	816	
Val	Thr	Asn	Ala	Tyr	Trp	Met	Ile	Met	Gly	Ile	Tyr	Asp	Gly	Gly	Asn		
			260					265					270				
gtc	cgt	tca	ctg	atc	ttc	aac	gga	gcc	acg	ggg	atc	gac	ttc	ggc	act	864	
Val	Arg	Ser	Leu	Ile	Phe	Asn	Gly	Ala	Thr	Gly	Ile	Asp	Phe	Gly	Thr		
		275					280					285					
cca	att	gcc	act	ctt	ttt	tgg	cac	ggc	gat	tca	ggg	gcg	gaa	aat	ggc	912	

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Pro Ile Ala Thr Leu Phe Trp His Gly Asp Ser Gly Ala Glu Asn Gly
 290 295 300

cgg caa atc ggt tgt cta att tcg aag ttg gta aaa ccc cag ggc agc 960
 Arg Gln Ile Gly Cys Leu Ile Ser Lys Leu Val Lys Pro Gln Gly Ser
 305 310 315 320

aaa cta tac aat gat ttg gta agt gaa ttt tca ctt caa aca ctg cac 1008
 Lys Leu Tyr Asn Asp Leu Val Ser Glu Phe Ser Leu Gln Thr Leu His
 325 330 335

cag cga ttt gtg gtg acc gcc aag gat ttc ttc agt ctc aat ctg cat 1056
 Gln Arg Phe Val Val Thr Ala Lys Asp Phe Phe Ser Leu Asn Leu His
 340 345 350

cta ctg agt agt atg ttt gca gct gtg gtc aca tat ctg gtt att ctc 1104
 Leu Leu Ser Ser Met Phe Ala Ala Val Val Thr Tyr Leu Val Ile Leu
 355 360 365

ata cag ttc atg ttc gcc gaa agg agt tca acg cga ggc agc gga 1149
 Ile Gln Phe Met Phe Ala Glu Arg Ser Ser Thr Arg Gly Ser Gly
 370 375 380

<210> 14

<211> 383

<212> PRT

<213> Drosophila melanogaster

<400> 14

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

Ala Leu Val Pro Leu Pro Pro Ile Ser Gln Leu Gly Trp Leu Phe Leu
 35 40 45

Ser Leu Ala Ile Arg Cys Cys Trp Ile Val Tyr Phe Ile Tyr Leu Leu
 50 55 60

Asp Val Ala Ile Ser Phe Ser Trp Val Ala Ile Glu Asn Val Gly Asn
 65 70 75 80

Ala Val Gly Thr Met Leu Phe Val Gly Asn Ser Val Leu Gly Phe Ala
 85 90 95

Leu Leu Leu Glu Ser Val Leu Lys Gln Lys Thr His Ser Gln Leu Glu
 100 105 110

Asp Leu Arg Val Gln Thr Glu Leu Gln Leu Gln Arg Leu Gly Met Phe
 115 120 125

Gly Arg Ser Arg His Ala Ala Tyr Leu Leu Pro Leu Ile Gly Val Gln
 130 135 140

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Phe	Thr	Cys	Asp	Leu	Val	Arg	Leu	Ala	Thr	Asn	Phe	Gly	Glu	Thr	Val	145	150	155	160
Ser	Pro	Val	Phe	Cys	Ile	Ser	Leu	Pro	Leu	Met	Trp	Leu	Leu	Arg	Tyr	165	170	175	
Arg	Tyr	Val	Gln	Leu	Val	Gln	His	Val	Met	Asp	Leu	Asn	Gln	Arg	Ser	180	185	190	
Ile	His	Leu	Arg	Arg	Ser	Leu	Leu	Ser	Met	Ala	Ser	Gly	Asn	Asp	Leu	195	200	205	
Trp	Gln	Pro	Tyr	Gly	Val	Gln	Glu	Cys	Leu	Gln	Leu	Gln	Thr	Leu	Arg	210	215	220	
Thr	Thr	Tyr	Glu	Arg	Ile	Phe	Glu	Cys	Tyr	Glu	Thr	Phe	Ser	Asp	Cys	225	230	235	240
Tyr	Gly	Trp	Gly	Met	Leu	Gly	Leu	His	Leu	Leu	Thr	Ser	Phe	Gln	Phe	245	250	255	
Val	Thr	Asn	Ala	Tyr	Trp	Met	Ile	Met	Gly	Ile	Tyr	Asp	Gly	Gly	Asn	260	265	270	
Val	Arg	Ser	Leu	Ile	Phe	Asn	Gly	Ala	Thr	Gly	Ile	Asp	Phe	Gly	Thr	275	280	285	
Pro	Ile	Ala	Thr	Leu	Phe	Trp	His	Gly	Asp	Ser	Gly	Ala	Glu	Asn	Gly	290	295	300	
Arg	Gln	Ile	Gly	Cys	Leu	Ile	Ser	Lys	Leu	Val	Lys	Pro	Gln	Gly	Ser	305	310	315	320
Lys	Leu	Tyr	Asn	Asp	Leu	Val	Ser	Glu	Phe	Ser	Leu	Gln	Thr	Leu	His	325	330	335	
Gln	Arg	Phe	Val	Val	Thr	Ala	Lys	Asp	Phe	Phe	Ser	Leu	Asn	Leu	His	340	345	350	
Leu	Leu	Ser	Ser	Met	Phe	Ala	Ala	Val	Val	Thr	Tyr	Leu	Val	Ile	Leu	355	360	365	
Ile	Gln	Phe	Met	Phe	Ala	Glu	Arg	Ser	Ser	Thr	Arg	Gly	Ser	Gly		370	375	380	

<210> 15

<211> 1122

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1122)

<223> Coding region GR23A.1b

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PCT/US00/16211

<220>

<221> misc_feature

<222> (901)..(1042)

<223> Splice sites before positions 901 and 1042

<400> 15

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Met	Phe	Pro	Pro	Thr	Arg	Val	Gln	Ala	Ser	Ser	Arg	Val	Val	Leu	Lys	
1				5					10					15		
att	ttc	cat	ttc	att	ttg	gtg	gca	ttt	tct	ttg	aga	tca	agg	aga	cta	96
Ile	Phe	His	Phe	Ile	Leu	Val	Ala	Phe	Ser	Leu	Arg	Ser	Arg	Arg	Leu	
			20					25					30			
tct	cgt	ttg	gtc	ctg	tgg	tta	cag	ttt	ctg	ggc	tgg	cta	acc	tgg	ttt	144
Ser	Arg	Leu	Val	Leu	Trp	Leu	Gln	Phe	Leu	Gly	Trp	Leu	Thr	Trp	Phe	
		35					40					45				
att	tcc	atg	tgg	act	caa	agt	gtg	ata	tat	gcc	caa	acg	att	gac	tgc	192
Ile	Ser	Met	Trp	Thr	Gln	Ser	Val	Ile	Tyr	Ala	Gln	Thr	Ile	Asp	Cys	
	50					55					60					
aca	ttg	gac	tgc	tca	ctg	cgg	cat	ata	ctc	aca	ttt	ttc	cag	acg	gtc	240
Thr	Leu	Asp	Cys	Ser	Leu	Arg	His	Ile	Leu	Thr	Phe	Phe	Gln	Thr	Val	
65					70					75					80	
tca	cat	gcc	ttc	att	gtg	gtt	acc	tcc	ttt	ctt	gat	ggc	ttc	aga	atc	288
Ser	His	Ala	Phe	Ile	Val	Val	Thr	Ser	Phe	Leu	Asp	Gly	Phe	Arg	Ile	
				85					90					95		
aag	cag	gac	cag	ttg	gac	gaa	ccg	att	gcg	ttc	gag	gac	tcc	gat	ccc	336
Lys	Gln	Asp	Gln	Leu	Asp	Glu	Pro	Ile	Ala	Phe	Glu	Asp	Ser	Asp	Pro	
			100					105					110			
tgg	ttg	gcc	ttc	act	gtg	ctg	gcg	atg	ctg	gtt	ccc	act	ttg	gga	gta	384
Trp	Leu	Ala	Phe	Thr	Val	Leu	Ala	Met	Leu	Val	Pro	Thr	Leu	Gly	Val	
		115					120					125				
gag	tat	ttg	gtg	tgc	tcg	aac	gcg	cca	gaa	tat	gcc	ttt	cgt	atc	agg	432
Glu	Tyr	Leu	Val	Cys	Ser	Asn	Ala	Pro	Glu	Tyr	Ala	Phe	Arg	Ile	Arg	
	130					135					140					
atc	tat	cac	ctg	aaa	acg	ctg	ccc	agt	ttt	ctg	gct	ctg	cag	gtg	cag	480
Ile	Tyr	His	Leu	Lys	Thr	Leu	Pro	Ser	Phe	Leu	Ala	Leu	Gln	Val	Gln	
145					150					155				160		
att	ata	tcc	ttt	atc	ctg	gag	gtc	atg	aag	gtg	aac	ata	agg	gtt	cgc	528
Ile	Ile	Ser	Phe	Ile	Leu	Glu	Val	Met	Lys	Val	Asn	Ile	Arg	Val	Arg	
				165					170					175		
cag	acc	aag	ctg	cag	ctg	ctg	att	ctg	gcc	agg	gaa	tta	tcc	tgt	cgt	576
Gln	Thr	Lys	Leu	Gln	Leu	Leu	Ile	Leu	Ala	Arg	Glu	Leu	Ser	Cys	Arg	
			180					185					190			
tgg	cca	cag	aga	aag	caa	aag	ccg	cag	ttt	tcc	gac	caa	cag	gcc	cat	624
Trp	Pro	Gln	Arg	Lys	Gln	Lys	Pro	Gln	Phe	Ser	Asp	Gln	Gln	Ala	His	

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195	200	205	
cga gtg aaa gac ctg aaa agg cgc tat aat gac cta cat tat ttg ttt			672
Arg Val Lys Asp Leu Lys Arg Arg Tyr Asn Asp Leu His Tyr Leu Phe			
210	215	220	
gtt cgc att aat ggc tat ttt gga ggc agc ctt ctg acc atc atc att			720
Val Arg Ile Asn Gly Tyr Phe Gly Gly Ser Leu Leu Thr Ile Ile Ile			
225	230	235	240
gtt cac ttt gcg atc ttt gtt tcc aac tcc tat tgg cta ttc gtg gat			768
Val His Phe Ala Ile Phe Val Ser Asn Ser Tyr Trp Leu Phe Val Asp			
245	250	255	
atc aga aca aga ccc tgg agg ata tat gcc atc ttg ctc aac ttg gga			816
Ile Arg Thr Arg Pro Trp Arg Ile Tyr Ala Ile Leu Leu Asn Leu Gly			
260	265	270	
ttt att ttc aat gta gcc ctg caa atg gca gct gct tgt tgg cac tgt			864
Phe Ile Phe Asn Val Ala Leu Gln Met Ala Ala Ala Cys Trp His Cys			
275	280	285	
caa caa agc tat aat cta ggc cgg caa atc ggt tgt cta att tcg aag			912
Gln Gln Ser Tyr Asn Leu Gly Arg Gln Ile Gly Cys Leu Ile Ser Lys			
290	295	300	
ttg gta aaa ccc cag ggc agc aaa cta tac aat gat ttg gta agt gaa			960
Leu Val Lys Pro Gln Gly Ser Lys Leu Tyr Asn Asp Leu Val Ser Glu			
305	310	315	320
ttt tca ctt caa aca ctg cac cag cga ttt gtg gtg acc gcc aag gat			1008
Phe Ser Leu Gln Thr Leu His Gln Arg Phe Val Val Thr Ala Lys Asp			
325	330	335	
ttc ttc agt ctc aat ctg cat cta ctg agt agt atg ttt gca gct gtg			1056
Phe Phe Ser Leu Asn Leu His Leu Leu Ser Ser Met Phe Ala Ala Val			
340	345	350	
gtc aca tat ctg gtt att ctc ata cag ttc atg ttc gcc gaa agg agt			1104
Val Thr Tyr Leu Val Ile Leu Ile Gln Phe Met Phe Ala Glu Arg Ser			
355	360	365	
tca acg cga ggc agc gga			1122
Ser Thr Arg Gly Ser Gly			
370			

<210> 16

<211> 374

<212> PRT

<213> Drosophila melanogaster

<400> 16

Met	Phe	Pro	Pro	Thr	Arg	Val	Gln	Ala	Ser	Ser	Arg	Val	Val	Leu	Lys
1				5					10					15	

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Ile	Phe	His	Phe	Ile	Leu	Val	Ala	Phe	Ser	Leu	Arg	Ser	Arg	Arg	Leu			
			20					25					30					
Ser	Arg	Leu	Val	Leu	Trp	Leu	Gln	Phe	Leu	Gly	Trp	Leu	Thr	Trp	Phe			
		35					40					45						
Ile	Ser	Met	Trp	Thr	Gln	Ser	Val	Ile	Tyr	Ala	Gln	Thr	Ile	Asp	Cys			
	50					55					60							
Thr	Leu	Asp	Cys	Ser	Leu	Arg	His	Ile	Leu	Thr	Phe	Phe	Gln	Thr	Val			
65					70					75					80			
Ser	His	Ala	Phe	Ile	Val	Val	Thr	Ser	Phe	Leu	Asp	Gly	Phe	Arg	Ile			
				85					90					95				
Lys	Gln	Asp	Gln	Leu	Asp	Glu	Pro	Ile	Ala	Phe	Glu	Asp	Ser	Asp	Pro			
			100					105					110					
Trp	Leu	Ala	Phe	Thr	Val	Leu	Ala	Met	Leu	Val	Pro	Thr	Leu	Gly	Val			
		115					120					125						
Glu	Tyr	Leu	Val	Cys	Ser	Asn	Ala	Pro	Glu	Tyr	Ala	Phe	Arg	Ile	Arg			
	130					135					140							
Ile	Tyr	His	Leu	Lys	Thr	Leu	Pro	Ser	Phe	Leu	Ala	Leu	Gln	Val	Gln			
145					150					155					160			
Ile	Ile	Ser	Phe	Ile	Leu	Glu	Val	Met	Lys	Val	Asn	Ile	Arg	Val	Arg			
				165					170					175				
Gln	Thr	Lys	Leu	Gln	Leu	Leu	Ile	Leu	Ala	Arg	Glu	Leu	Ser	Cys	Arg			
			180					185					190					
Trp	Pro	Gln	Arg	Lys	Gln	Lys	Pro	Gln	Phe	Ser	Asp	Gln	Gln	Ala	His			
		195					200					205						
Arg	Val	Lys	Asp	Leu	Lys	Arg	Arg	Tyr	Asn	Asp	Leu	His	Tyr	Leu	Phe			
	210					215					220							
Val	Arg	Ile	Asn	Gly	Tyr	Phe	Gly	Gly	Ser	Leu	Leu	Thr	Ile	Ile	Ile			
225					230					235					240			
Val	His	Phe	Ala	Ile	Phe	Val	Ser	Asn	Ser	Tyr	Trp	Leu	Phe	Val	Asp			
				245					250					255				
Ile	Arg	Thr	Arg	Pro	Trp	Arg	Ile	Tyr	Ala	Ile	Leu	Leu	Asn	Leu	Gly			
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Phe	Ile	Phe	Asn	Val	Ala	Leu	Gln	Met	Ala	Ala	Ala	Cys	Trp	His	Cys			
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Gln	Gln	Ser	Tyr	Asn	Leu	Gly	Arg	Gln	Ile	Gly	Cys	Leu	Ile	Ser	Lys			
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Met	Ala	Phe	Lys	Leu	Trp	Glu	Arg	Phe	Ser	Gln	Ala	Asp	Asn	Val	Phe	
1				5					10					15		
cag	gca	ctt	cga	ccg	cta	aca	ttc	ata	tcg	cta	ttg	ggc	ctg	gct	cca	96
Gln	Ala	Leu	Arg	Pro	Leu	Thr	Phe	Ile	Ser	Leu	Leu	Gly	Leu	Ala	Pro	
			20					25					30			
ttt	cgt	ttg	aat	ttg	aat	cct	cgc	aag	gag	gtg	caa	aca	tcg	aag	ttc	144
Phe	Arg	Leu	Asn	Leu	Asn	Pro	Arg	Lys	Glu	Val	Gln	Thr	Ser	Lys	Phe	
		35					40					45				
tcc	ttc	ttt	gcc	ggc	ata	gtg	cac	ttc	ctg	ttc	ttc	gtc	ctg	tgt	ttt	192
Ser	Phe	Phe	Ala	Gly	Ile	Val	His	Phe	Leu	Phe	Phe	Val	Leu	Cys	Phe	
	50					55					60					
ggt	atc	tcc	gta	aag	gag	gga	gat	tcc	ata	ata	ggg	tac	ttc	ttt	cag	240
Gly	Ile	Ser	Val	Lys	Glu	Gly	Asp	Ser	Ile	Ile	Gly	Tyr	Phe	Phe	Gln	
65				70					75						80	
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Thr	Asn	Ile	Thr	Arg	Phe	Ser	Asp	Gly	Thr	Leu	Arg	Leu	Thr	Gly	Ile	
				85					90					95		
ctg	gcc	atg	tcc	act	att	ttt	ggc	ttt	gcc	atg	ttc	aag	aga	caa	cgt	336
Leu	Ala	Met	Ser	Thr	Ile	Phe	Gly	Phe	Ala	Met	Phe	Lys	Arg	Gln	Arg	
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ttg	gtc	agc	ata	ata	cag	aac	aac	ata	gtg	gtg	gac	gag	ata	ttt	gtg	384
Leu	Val	Ser	Ile	Ile	Gln	Asn	Asn	Ile	Val	Val	Asp	Glu	Ile	Phe	Val	
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agg ctg ggc atg aag ttg gac tac cgc agg ata ctg ttg tcc agc ttt	432
Arg Leu Gly Met Lys Leu Asp Tyr Arg Arg Ile Leu Leu Ser Ser Phe	
130 135 140	
ctc ata tcc ttg ggc atg ctg ctg ttc aac gtc att tac ttg tgt gtg	480
Leu Ile Ser Leu Gly Met Leu Leu Phe Asn Val Ile Tyr Leu Cys Val	
145 150 155 160	
agc tac agc ctg ctg gtc agt gcc acc ata tcg ccc tca ttt gtg act	528
Ser Tyr Ser Leu Leu Val Ser Ala Thr Ile Ser Pro Ser Phe Val Thr	
165 170 175	
ttc aca acc ttc gcc ctg ccg cac atc aat atc agc ctg atg gtc ttc	576
Phe Thr Thr Phe Ala Leu Pro His Ile Asn Ile Ser Leu Met Val Phe	
180 185 190	
aag ttt ctt tgc acc acg gac ttg gcc agg agc cgg ttt agt atg tta	624
Lys Phe Leu Cys Thr Thr Asp Leu Ala Arg Ser Arg Phe Ser Met Leu	
195 200 205	
aac gaa atc ctg cag gat att ttg gat gcc cat ata gag caa tta agc	672
Asn Glu Ile Leu Gln Asp Ile Leu Asp Ala His Ile Glu Gln Leu Ser	
210 215 220	
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Ala Leu Glu Leu Ser Pro Met His Ser Val Val Asn His Arg Arg Tyr	
225 230 235 240	
tca cat cgc cta cga aat ttg att agt acg cca atg aag cgg tac agt	768
Ser His Arg Leu Arg Asn Leu Ile Ser Thr Pro Met Lys Arg Tyr Ser	
245 250 255	
gtt acc tcc gtc ata cgc ctc aat ccc gaa tac gca atc aaa cag gtg	816
Val Thr Ser Val Ile Arg Leu Asn Pro Glu Tyr Ala Ile Lys Gln Val	
260 265 270	
tcc aac ata cac aat ctg ctc tgc gac att tgc cag acc atc gag gaa	864
Ser Asn Ile His Asn Leu Leu Cys Asp Ile Cys Gln Thr Ile Glu Glu	
275 280 285	
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Tyr Phe Thr Tyr Pro Leu Leu Gly Ile Ile Ala Ile Ser Phe Leu Phe	
290 295 300	
att ctc ttt gat gac ttt tac att ttg gaa gcc att ctg aat ccc aaa	960
Ile Leu Phe Asp Asp Phe Tyr Ile Leu Glu Ala Ile Leu Asn Pro Lys	
305 310 315 320	
cga ctg gat gtc ttt gag gcc gat gag ttc ttt gcc ttc ttc ctg atg	1008
Arg Leu Asp Val Phe Glu Ala Asp Glu Phe Phe Ala Phe Phe Leu Met	
325 330 335	
cag ctc atc tgg tat ata gtg atc ata gtg ctg atc gtg gag ggc agc	1056
Gln Leu Ile Trp Tyr Ile Val Ile Ile Val Leu Ile Val Glu Gly Ser	
340 345 350	

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Ser Arg Thr Ile Leu His Ser Ser Tyr Thr Ala Ala Ile Val His Lys
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att ctc aat atc acc gat gat cca gaa ctc aga gat cga ctt ttc cgt 1152
Ile Leu Asn Ile Thr Asp Asp Pro Glu Leu Arg Asp Arg Leu Phe Arg
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ctg tcc ttg cag ctg tcg cat cgg aag gtc ctt ttc aca gcc gca gga 1200
Leu Ser Leu Gln Leu Ser His Arg Lys Val Leu Phe Thr Ala Ala Gly
385                390                395                400

ctt ttt cgt ctg gat cgc aca ctg att ttt acg att act ggt gct gcc 1248
Leu Phe Arg Leu Asp Arg Thr Leu Ile Phe Thr Ile Thr Gly Ala Ala
      405                410                415

acg tgc tac ctc att atc cta att cag ttt cga ttc aca cat cac atg 1296
Thr Cys Tyr Leu Ile Ile Leu Ile Gln Phe Arg Phe Thr His His Met
      420                425                430

gac gac acc agc tcc aat tca aca aat aat tta cat tcc att cat ctc 1344
Asp Asp Thr Ser Ser Asn Ser Thr Asn Asn Leu His Ser Ile His Leu
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ggc ga
Gly
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<212> PRT

<213> *Drosophila melanogaster*

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Phe Arg Leu Asn Leu Asn Pro Arg Lys Glu Val Gln Thr Ser Lys Phe
      35              40              45

Ser Phe Phe Ala Gly Ile Val His Phe Leu Phe Phe Val Leu Cys Phe
      50              55              60

Gly Ile Ser Val Lys Glu Gly Asp Ser Ile Ile Gly Tyr Phe Phe Gln
      65              70              75              80

Thr Asn Ile Thr Arg Phe Ser Asp Gly Thr Leu Arg Leu Thr Gly Ile
      85              90              95

Leu Ala Met Ser Thr Ile Phe Gly Phe Ala Met Phe Lys Arg Gln Arg
      100             105             110

Leu Val Ser Ile Ile Gln Asn Asn Ile Val Val Asp Glu Ile Phe Val

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115	120	125
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Leu Ile Ser Leu Gly Met Leu Leu Phe Asn Val Ile Tyr Leu Cys Val 145 150 155 160		
Ser Tyr Ser Leu Leu Val Ser Ala Thr Ile Ser Pro Ser Phe Val Thr 165 170 175		
Phe Thr Thr Phe Ala Leu Pro His Ile Asn Ile Ser Leu Met Val Phe 180 185 190		
Lys Phe Leu Cys Thr Thr Asp Leu Ala Arg Ser Arg Phe Ser Met Leu 195 200 205		
Asn Glu Ile Leu Gln Asp Ile Leu Asp Ala His Ile Glu Gln Leu Ser 210 215 220		
Ala Leu Glu Leu Ser Pro Met His Ser Val Val Asn His Arg Arg Tyr 225 230 235 240		
Ser His Arg Leu Arg Asn Leu Ile Ser Thr Pro Met Lys Arg Tyr Ser 245 250 255		
Val Thr Ser Val Ile Arg Leu Asn Pro Glu Tyr Ala Ile Lys Gln Val 260 265 270		
Ser Asn Ile His Asn Leu Leu Cys Asp Ile Cys Gln Thr Ile Glu Glu 275 280 285		
Tyr Phe Thr Tyr Pro Leu Leu Gly Ile Ile Ala Ile Ser Phe Leu Phe 290 295 300		
Ile Leu Phe Asp Asp Phe Tyr Ile Leu Glu Ala Ile Leu Asn Pro Lys 305 310 315 320		
Arg Leu Asp Val Phe Glu Ala Asp Glu Phe Phe Ala Phe Phe Leu Met 325 330 335		
Gln Leu Ile Trp Tyr Ile Val Ile Ile Val Leu Ile Val Glu Gly Ser 340 345 350		
Ser Arg Thr Ile Leu His Ser Ser Tyr Thr Ala Ala Ile Val His Lys 355 360 365		
Ile Leu Asn Ile Thr Asp Asp Pro Glu Leu Arg Asp Arg Leu Phe Arg 370 375 380		
Leu Ser Leu Gln Leu Ser His Arg Lys Val Leu Phe Thr Ala Ala Gly 385 390 395 400		
Leu Phe Arg Leu Asp Arg Thr Leu Ile Phe Thr Ile Thr Gly Ala Ala 405 410 415		

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Thr Cys Tyr Leu Ile Ile Leu Ile Gln Phe Arg Phe Thr His His Met
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Asp Asp Thr Ser Ser Asn Ser Thr Asn Asn Leu His Ser Ile His Leu
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Gly

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 <223> Coding region GR32D.1

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 <222> (931)..(1084)
 <223> Splice sites before positions 931, 994 and 1084.

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 Lys Thr Asn Glu Phe Tyr Ser Phe Phe Val Arg Gly Val Val His Ala
 20 25 30
 ctg acc atc ttc aat gtc tac agc tta ttt aca ccg ata tcg gcg caa 144
 Leu Thr Ile Phe Asn Val Tyr Ser Leu Phe Thr Pro Ile Ser Ala Gln
 35 40 45
 tta ttt ttc tcc tac cgc gag acg gac aat gtg aac cag tgg atc gag 192
 Leu Phe Phe Ser Tyr Arg Glu Thr Asp Asn Val Asn Gln Trp Ile Glu
 50 55 60
 ctg ctg ctc tgc atc cta acc tat acc ctt acg gtt ttc gtt tgt gcc 240
 Leu Leu Leu Cys Ile Leu Thr Tyr Thr Leu Thr Val Phe Val Cys Ala
 65 70 75 80
 cac aat acc acg agc atg ttg cgg ata atg aat gaa atc ctt caa ctc 288
 His Asn Thr Thr Ser Met Leu Arg Ile Met Asn Glu Ile Leu Gln Leu
 85 90 95
 gac gag gaa gtg cgt cgc cag ttt ggt gcc aat ttg agc caa aat ttt 336
 Asp Glu Glu Val Arg Arg Gln Phe Gly Ala Asn Leu Ser Gln Asn Phe
 100 105 110
 ggg ttc ttg gta aag ttt tta gta gga atc acc gct tgc cag gct tat 384

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Gly	Phe	Leu	Val	Lys	Phe	Leu	Val	Gly	Ile	Thr	Ala	Cys	Gln	Ala	Tyr	
		115					120					125				
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Ile	Ile	Val	Leu	Lys	Ile	Tyr	Ala	Val	Gln	Gly	Glu	Ile	Thr	Pro	Thr	
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tcc	tat	ata	cta	ttg	gcc	ttc	tat	ggc	atc	cag	aac	ggg	ctg	acc	gcc	480
Ser	Tyr	Ile	Leu	Leu	Ala	Phe	Tyr	Gly	Ile	Gln	Asn	Gly	Leu	Thr	Ala	
145					150				155					160		
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Thr	Tyr	Ile	Val	Phe	Ala	Ser	Ala	Leu	Leu	Arg	Ile	Val	Tyr	Ile	Arg	
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ttt	cat	ttc	atc	aac	cag	ctg	cta	aat	ggg	tac	acc	tat	ggg	cag	cag	576
Phe	His	Phe	Ile	Asn	Gln	Leu	Leu	Asn	Gly	Tyr	Thr	Tyr	Gly	Gln	Gln	
			180					185					190			
cat	agg	cgc	aaa	gaa	ggg	gga	gca	cga	gcg	agg	cgg	cag	cgt	ggg	gac	624
His	Arg	Arg	Lys	Glu	Gly	Gly	Ala	Arg	Ala	Arg	Arg	Gln	Arg	Gly	Asp	
		195					200					205				
gtc	aat	ccc	aat	gtc	aat	cct	gct	cta	atg	gaa	cat	ttc	ccg	gaa	gac	672
Val	Asn	Pro	Asn	Val	Asn	Pro	Ala	Leu	Met	Glu	His	Phe	Pro	Glu	Asp	
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tcg	cta	ttc	ata	tac	cgc	atg	cac	aac	aaa	ctg	ctg	cgt	atc	tac	aag	720
Ser	Leu	Phe	Ile	Tyr	Arg	Met	His	Asn	Lys	Leu	Leu	Arg	Ile	Tyr	Lys	
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Gly	Ile	Asn	Asp	Cys	Cys	Asn	Leu	Ile	Leu	Val	Ser	Phe	Leu	Gly	Tyr	
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Ser	Phe	Tyr	Thr	Val	Thr	Thr	Asn	Cys	Tyr	Asn	Leu	Phe	Val	Gln	Ile	
			260					265					270			
acc	ggc	aag	ggc	atg	ggt	tca	cca	aac	ata	ttg	cag	tgg	tgc	ttc	gcc	864
Thr	Gly	Lys	Gly	Met	Val	Ser	Pro	Asn	Ile	Leu	Gln	Trp	Cys	Phe	Ala	
		275					280					285				
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Trp	Leu	Cys	Leu	His	Val	Ser	Leu	Leu	Ala	Leu	Leu	Ser	Arg	Ser	Cys	
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Gly	Leu	Thr	Thr	Thr	Glu	Ala	Asn	Ala	Thr	Ser	Gln	Ile	Leu	Ala	Arg	
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gtg	tat	gcc	aag	tcg	aag	gag	tat	cag	aat	atc	att	gat	aag	ttc	ctt	1008
Val	Tyr	Ala	Lys	Ser	Lys	Glu	Tyr	Gln	Asn	Ile	Ile	Asp	Lys	Phe	Leu	
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acg	aag	agc	att	aaa	cag	gag	gtg	caa	ttc	acg	gca	tat	gga	ttt	ttt	1056

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 Ala Ile Asp Asn Ser Thr Leu Phe Lys Ile Phe Ser Ala Val Thr Thr
 355 360 365
 tac ttg gta atc ttg att cag ttc aaa cag ctc gaa gac tcg aaa gta 1152
 Tyr Leu Val Ile Leu Ile Gln Phe Lys Gln Leu Glu Asp Ser Lys Val
 370 375 380
 gag gat cct gta cca gaa caa act 1176
 Glu Asp Pro Val Pro Glu Gln Thr
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 35 40 45
 Leu Phe Phe Ser Tyr Arg Glu Thr Asp Asn Val Asn Gln Trp Ile Glu
 50 55 60
 Leu Leu Leu Cys Ile Leu Thr Tyr Thr Leu Thr Val Phe Val Cys Ala
 65 70 75 80
 His Asn Thr Thr Ser Met Leu Arg Ile Met Asn Glu Ile Leu Gln Leu
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 Asp Glu Glu Val Arg Arg Gln Phe Gly Ala Asn Leu Ser Gln Asn Phe
 100 105 110
 Gly Phe Leu Val Lys Phe Leu Val Gly Ile Thr Ala Cys Gln Ala Tyr
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 Ile Ile Val Leu Lys Ile Tyr Ala Val Gln Gly Glu Ile Thr Pro Thr
 130 135 140
 Ser Tyr Ile Leu Leu Ala Phe Tyr Gly Ile Gln Asn Gly Leu Thr Ala
 145 150 155 160
 Thr Tyr Ile Val Phe Ala Ser Ala Leu Leu Arg Ile Val Tyr Ile Arg
 165 170 175
 Phe His Phe Ile Asn Gln Leu Leu Asn Gly Tyr Thr Tyr Gly Gln Gln

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180								185				190			
His	Arg	Arg	Lys	Glu	Gly	Gly	Ala	Arg	Ala	Arg	Arg	Gln	Arg	Gly	Asp
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Val	Asn	Pro	Asn	Val	Asn	Pro	Ala	Leu	Met	Glu	His	Phe	Pro	Glu	Asp
210								215				220			
Ser	Leu	Phe	Ile	Tyr	Arg	Met	His	Asn	Lys	Leu	Leu	Arg	Ile	Tyr	Lys
225								230				235			
Gly	Ile	Asn	Asp	Cys	Cys	Asn	Leu	Ile	Leu	Val	Ser	Phe	Leu	Gly	Tyr
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Ser	Phe	Tyr	Thr	Val	Thr	Thr	Asn	Cys	Tyr	Asn	Leu	Phe	Val	Gln	Ile
260								265				270			
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275								280				285			
Trp	Leu	Cys	Leu	His	Val	Ser	Leu	Leu	Ala	Leu	Leu	Ser	Arg	Ser	Cys
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Gly	Leu	Thr	Thr	Thr	Glu	Ala	Asn	Ala	Thr	Ser	Gln	Ile	Leu	Ala	Arg
305								310				315			
Val	Tyr	Ala	Lys	Ser	Lys	Glu	Tyr	Gln	Asn	Ile	Ile	Asp	Lys	Phe	Leu
325								330				335			
Thr	Lys	Ser	Ile	Lys	Gln	Glu	Val	Gln	Phe	Thr	Ala	Tyr	Gly	Phe	Phe
340								345				350			
Ala	Ile	Asp	Asn	Ser	Thr	Leu	Phe	Lys	Ile	Phe	Ser	Ala	Val	Thr	Thr
355								360				365			
Tyr	Leu	Val	Ile	Leu	Ile	Gln	Phe	Lys	Gln	Leu	Glu	Asp	Ser	Lys	Val
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Glu	Asp	Pro	Val	Pro	Glu	Gln	Thr								
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Gln Gln Ser Glu Thr Asn Phe Ile Leu Asp Tyr Ala Met Met Cys Ile				
	20	25	30	
gtg ccc atc ttc tat gtg gct tgc tat ctt ctc ata aat ctt agc cac				144
Val Pro Ile Phe Tyr Val Ala Cys Tyr Leu Leu Ile Asn Leu Ser His				
	35	40	45	
att att ggc ctc tgt tta ctg gac tct tgc aat agt gtt tgc aag ctg				192
Ile Ile Gly Leu Cys Leu Leu Asp Ser Cys Asn Ser Val Cys Lys Leu				
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agc agc cat ctc ttt atg cat ttg ggc gca ttt cta tat ctg acc atc				240
Ser Ser His Leu Phe Met His Leu Gly Ala Phe Leu Tyr Leu Thr Ile				
	65	70	75	80
acc ctg ctg tca ctt tat cgc cga aag gag ttt ttc cag cag ttt gat				288
Thr Leu Leu Ser Leu Tyr Arg Arg Lys Glu Phe Phe Gln Gln Phe Asp				
	85	90	95	
gcg aga ctt aat gac att gat gca gtt atc cag aaa tgc cag cgg gtg				336
Ala Arg Leu Asn Asp Ile Asp Ala Val Ile Gln Lys Cys Gln Arg Val				
	100	105	110	
gcg gaa atg gac aag gtg aag gtt act gcg gtg aaa cac agt gtg gcc				384
Ala Glu Met Asp Lys Val Lys Val Thr Ala Val Lys His Ser Val Ala				
	115	120	125	
tat cac ttc acc tgg ctt ttc cta ttc tgc gtt ttc acc ttt gcc ctt				432
Tyr His Phe Thr Trp Leu Phe Leu Phe Cys Val Phe Thr Phe Ala Leu				
	130	135	140	
tac tat gac gtc aga tct ttg tac ttg acc ttc ggc aat ctc gcc ttc				480
Tyr Tyr Asp Val Arg Ser Leu Tyr Leu Thr Phe Gly Asn Leu Ala Phe				
	145	150	155	160
att ccg ttc atg gtg tcc agt ttc cca tat ttg gcc ggc agc atc att				528
Ile Pro Phe Met Val Ser Ser Phe Pro Tyr Leu Ala Gly Ser Ile Ile				
	165	170	175	
cag ggt gag ttc atc tat cac gtg tcg gtc atc tcg cag cgc ttc gag				576
Gln Gly Glu Phe Ile Tyr His Val Ser Val Ile Ser Gln Arg Phe Glu				
	180	185	190	
cag att aac atg ctg ctg gag aag att aac cag gag gcg cgc cat cgc				624
Gln Ile Asn Met Leu Leu Glu Lys Ile Asn Gln Glu Ala Arg His Arg				
	195	200	205	
cac gca ccc ctt acc gtg ttc gat atc gag agc gag ggc aaa aag gag				672
His Ala Pro Leu Thr Val Phe Asp Ile Glu Ser Glu Gly Lys Lys Glu				
	210	215	220	
cgg aag acc gtt aca ccg att acg gtc atg gac ggc agg acg acg aca				720
Arg Lys Thr Val Thr Pro Ile Thr Val Met Asp Gly Arg Thr Thr Thr				

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225	230	235	240	
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Gly Phe Gly Asn Glu Asn Lys Phe Ala Gly Glu Met Lys Arg Gln Glu				
	245	250	255	
ggg caa caa aag aac gac gat gac gat ttg gac acc agc aac gac gag				816
Gly Gln Gln Lys Asn Asp Asp Asp Leu Asp Thr Ser Asn Asp Glu				
	260	265	270	
gac gag gat gac ttt gat tat gac aat gcc acc atc gcg gaa aat act				864
Asp Glu Asp Asp Phe Asp Tyr Asp Asn Ala Thr Ile Ala Glu Asn Thr				
	275	280	285	
gga aac aca tcg gaa gcc aat tta cca gat ctc ttc aag ctg cat gat				912
Gly Asn Thr Ser Glu Ala Asn Leu Pro Asp Leu Phe Lys Leu His Asp				
	290	295	300	
aaa atc ctg gcg ctc agc gtg att aca aac ggc gag ttt gga cca cag				960
Lys Ile Leu Ala Leu Ser Val Ile Thr Asn Gly Glu Phe Gly Pro Gln				
	305	310	315	320
tgt gta ccc tat atg gcg gcc tgc ttt gtg gtg agc atc ttt ggc att				1008
Cys Val Pro Tyr Met Ala Ala Cys Phe Val Val Ser Ile Phe Gly Ile				
	325	330	335	
ttc ctg gag acc aag gtc aac ttc att gtg ggc ggc aag agt cga ctg				1056
Phe Leu Glu Thr Lys Val Asn Phe Ile Val Gly Gly Lys Ser Arg Leu				
	340	345	350	
ctg gac tat atg acc tat ttg tac gtg att tgg agc ttc acc acc atg				1104
Leu Asp Tyr Met Thr Tyr Leu Tyr Val Ile Trp Ser Phe Thr Thr Met				
	355	360	365	
atg gtg gcc tac ata gtg ctt cga cta tgc tgc aat gcc aac aat cat				1152
Met Val Ala Tyr Ile Val Leu Arg Leu Cys Cys Asn Ala Asn Asn His				
	370	375	380	
tcc aaa caa tcg gcg atg att gtc cat gag att atg caa aag aaa ccg				1200
Ser Lys Gln Ser Ala Met Ile Val His Glu Ile Met Gln Lys Lys Pro				
	385	390	395	400
gca ttt atg ttg agc aac gat ctg ttc tac aac aaa atg aag tca ttc				1248
Ala Phe Met Leu Ser Asn Asp Leu Phe Tyr Asn Lys Met Lys Ser Phe				
	405	410	415	
aca ctg cag ttt ctt cac tgg gag ggt ttc ttt caa ttc aac ggc gtg				1296
Thr Leu Gln Phe Leu His Trp Glu Gly Phe Phe Gln Phe Asn Gly Val				
	420	425	430	
gga ttg ttt gct ctg gac tac aca ttc att ttc tcg act gta agt gca				1344
Gly Leu Phe Ala Leu Asp Tyr Thr Phe Ile Phe Ser Thr Val Ser Ala				
	435	440	445	
gcc aca tcc tat tta att gtc ctg ctg cag ttt gac atg act gca att				1392
Ala Thr Ser Tyr Leu Ile Val Leu Leu Gln Phe Asp Met Thr Ala Ile				

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450 455 460
 ttg cgc aac gag ggg cta atg tca taa 1419
 Leu Arg Asn Glu Gly Leu Met Ser
 465 470

 <210> 22
 <211> 472
 <212> PRT
 <213> *Drosophila melanogaster*

 <400> 22
 Met Lys Arg Lys Ala Val Glu Val Ile Gly Leu Ile Pro Leu Asn Arg
 1 5 10 15
 Gln Gln Ser Glu Thr Asn Phe Ile Leu Asp Tyr Ala Met Met Cys Ile
 20 25 30
 Val Pro Ile Phe Tyr Val Ala Cys Tyr Leu Leu Ile Asn Leu Ser His
 35 40 45
 Ile Ile Gly Leu Cys Leu Leu Asp Ser Cys Asn Ser Val Cys Lys Leu
 50 55 60
 Ser Ser His Leu Phe Met His Leu Gly Ala Phe Leu Tyr Leu Thr Ile
 65 70 75 80
 Thr Leu Leu Ser Leu Tyr Arg Arg Lys Glu Phe Phe Gln Gln Phe Asp
 85 90 95
 Ala Arg Leu Asn Asp Ile Asp Ala Val Ile Gln Lys Cys Gln Arg Val
 100 105 110
 Ala Glu Met Asp Lys Val Lys Val Thr Ala Val Lys His Ser Val Ala
 115 120 125
 Tyr His Phe Thr Trp Leu Phe Leu Phe Cys Val Phe Thr Phe Ala Leu
 130 135 140
 Tyr Tyr Asp Val Arg Ser Leu Tyr Leu Thr Phe Gly Asn Leu Ala Phe
 145 150 155 160
 Ile Pro Phe Met Val Ser Ser Phe Pro Tyr Leu Ala Gly Ser Ile Ile
 165 170 175
 Gln Gly Glu Phe Ile Tyr His Val Ser Val Ile Ser Gln Arg Phe Glu
 180 185 190
 Gln Ile Asn Met Leu Leu Glu Lys Ile Asn Gln Glu Ala Arg His Arg
 195 200 205
 His Ala Pro Leu Thr Val Phe Asp Ile Glu Ser Glu Gly Lys Lys Glu
 210 215 220
 Arg Lys Thr Val Thr Pro Ile Thr Val Met Asp Gly Arg Thr Thr Thr

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225		230		235		240
Gly Phe Gly Asn Glu Asn Lys Phe Ala Gly Glu Met Lys Arg Gln Glu						
		245		250		255
Gly Gln Gln Lys Asn Asp Asp Asp Asp Leu Asp Thr Ser Asn Asp Glu						
		260		265		270
Asp Glu Asp Asp Phe Asp Tyr Asp Asn Ala Thr Ile Ala Glu Asn Thr						
		275		280		285
Gly Asn Thr Ser Glu Ala Asn Leu Pro Asp Leu Phe Lys Leu His Asp						
		290		295		300
Lys Ile Leu Ala Leu Ser Val Ile Thr Asn Gly Glu Phe Gly Pro Gln						
		305		310		315
Cys Val Pro Tyr Met Ala Ala Cys Phe Val Val Ser Ile Phe Gly Ile						
		325		330		335
Phe Leu Glu Thr Lys Val Asn Phe Ile Val Gly Gly Lys Ser Arg Leu						
		340		345		350
Leu Asp Tyr Met Thr Tyr Leu Tyr Val Ile Trp Ser Phe Thr Thr Met						
		355		360		365
Met Val Ala Tyr Ile Val Leu Arg Leu Cys Cys Asn Ala Asn Asn His						
		370		375		380
Ser Lys Gln Ser Ala Met Ile Val His Glu Ile Met Gln Lys Lys Pro						
		385		390		395
Ala Phe Met Leu Ser Asn Asp Leu Phe Tyr Asn Lys Met Lys Ser Phe						
		405		410		415
Thr Leu Gln Phe Leu His Trp Glu Gly Phe Phe Gln Phe Asn Gly Val						
		420		425		430
Gly Leu Phe Ala Leu Asp Tyr Thr Phe Ile Phe Ser Thr Val Ser Ala						
		435		440		445
Ala Thr Ser Tyr Leu Ile Val Leu Leu Gln Phe Asp Met Thr Ala Ile						
		450		455		460
Leu Arg Asn Glu Gly Leu Met Ser						
		465		470		

<210> 23

<211> 1113

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

WO 00/77208

PCT/US00/16211

<222> (1)..(1113)

<223> Coding region GR36B.1

<400> 23

atg ttt gac tgg gtc ggt ttg ttg tta aag gta ctc tac tac tat ggg	48
Met Phe Asp Trp Val Gly Leu Leu Leu Lys Val Leu Tyr Tyr Tyr Gly	
1 5 10 15	
cag atc att gga ctt atc aac ttc gaa att gac tgg caa aga ggt cgt	96
Gln Ile Ile Gly Leu Ile Asn Phe Glu Ile Asp Trp Gln Arg Gly Arg	
20 25 30	
gtc gtt gca gcc caa aga ggc att ctt ttc gca atc gca att aac gtc	144
Val Val Ala Ala Gln Arg Gly Ile Leu Phe Ala Ile Ala Ile Asn Val	
35 40 45	
tta att tgc atg gtg ctg ctt ttg caa ata tcc aag aaa ttc aat ctc	192
Leu Ile Cys Met Val Leu Leu Leu Gln Ile Ser Lys Lys Phe Asn Leu	
50 55 60	
gat gtg tac ttc ggt agg gct aac cag ctg cat caa tat gtg atc atc	240
Asp Val Tyr Phe Gly Arg Ala Asn Gln Leu His Gln Tyr Val Ile Ile	
65 70 75 80	
cga gca caa cta atg cgc ctt gtt gaa tgt gta ctt cgg cta ttt ctg	288
Arg Ala Gln Leu Met Arg Leu Val Glu Cys Val Leu Arg Leu Phe Leu	
85 90 95	
aaa aaa ccg cat gta aag caa atg tcc cga tgg gca att ctg gta aag	336
Lys Lys Pro His Val Lys Gln Met Ser Arg Trp Ala Ile Leu Val Lys	
100 105 110	
ttc tct gta ggt gtc gtc agc aat ttc cta caa atg gcc atc tct atg	384
Phe Ser Val Gly Val Val Ser Asn Phe Leu Gln Met Ala Ile Ser Met	
115 120 125	
gaa tca ttg gat cgc ttg ggg ttc aac gaa ttc gtg gga atg gct tcg	432
Glu Ser Leu Asp Arg Leu Gly Phe Asn Glu Phe Val Gly Met Ala Ser	
130 135 140	
gat ttc tgg atg tcg gcc att ata aat atg gcc ata tca caa cac tat	480
Asp Phe Trp Met Ser Ala Ile Ile Asn Met Ala Ile Ser Gln His Tyr	
145 150 155 160	
ttg gta ata ctt ttc gtt cga gcc tat tac cat ttg ctc aag aca gag	528
Leu Val Ile Leu Phe Val Arg Ala Tyr Tyr His Leu Leu Lys Thr Glu	
165 170 175	
gtg cgg cag gcg atc cat gaa agc caa atg tta agt gag att tac cca	576
Val Arg Gln Ala Ile His Glu Ser Gln Met Leu Ser Glu Ile Tyr Pro	
180 185 190	
cgg aga gcg gct ttc atg acc aag tgt tgt tac ttg gct gat cga ata	624
Arg Arg Ala Ala Phe Met Thr Lys Cys Cys Tyr Leu Ala Asp Arg Ile	
195 200 205	

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gat aat ata gca aaa ctt cag aat caa ctg caa tcg att gtg acc cag	672
Asp Asn Ile Ala Lys Leu Gln Asn Gln Leu Gln Ser Ile Val Thr Gln	
210 215 220	
ttg aac caa gtg ttt ggc atc caa ggg ata atg gtt tat ggc gga tac	720
Leu Asn Gln Val Phe Gly Ile Gln Gly Ile Met Val Tyr Gly Gly Tyr	
225 230 235 240	
tat ata ttc tca gta gct aca act tac ata acg tac agt tta gct ata	768
Tyr Ile Phe Ser Val Ala Thr Thr Tyr Ile Thr Tyr Ser Leu Ala Ile	
245 250 255	
aat ggt ata gaa gaa ctg cac ttg agt gtc aga gca gcg gca ctg gta	816
Asn Gly Ile Glu Glu Leu His Leu Ser Val Arg Ala Ala Leu Val	
260 265 270	
ttt agt tgg ttt tta ttc tac tac acg agt gca ata cta aat ctg ttt	864
Phe Ser Trp Phe Leu Phe Tyr Tyr Thr Ser Ala Ile Leu Asn Leu Phe	
275 280 285	
gtt atg ctc aaa ctc ttc gat gat cac aag gag atg gaa cgg ata cta	912
Val Met Leu Lys Leu Phe Asp Asp His Lys Glu Met Glu Arg Ile Leu	
290 295 300	
gaa gag aga act ctg ttt act tcc gcc ttg gat gtc cgc ttg gag caa	960
Glu Glu Arg Thr Leu Phe Thr Ser Ala Leu Asp Val Arg Leu Glu Gln	
305 310 315 320	
tcc ttt gaa agc att caa ttg cag cta att aga aac ccg ttg aaa att	1008
Ser Phe Glu Ser Ile Gln Leu Gln Leu Ile Arg Asn Pro Leu Lys Ile	
325 330 335	
gaa gta ttg gat ata ttt acc att act cgc agt tca tct gct gcc atg	1056
Glu Val Leu Asp Ile Phe Thr Ile Thr Arg Ser Ser Ser Ala Ala Met	
340 345 350	
att gga tct ata ata acg aat tcg ata ttt ctt att caa tac gat atg	1104
Ile Gly Ser Ile Ile Thr Asn Ser Ile Phe Leu Ile Gln Tyr Asp Met	
355 360 365	
gaa tat ttt	1113
Glu Tyr Phe	
370	

<210> 24

<211> 371

<212> PRT

<213> Drosophila melanogaster

<400> 24

Met Phe Asp Trp Val Gly Leu Leu Leu Lys Val Leu Tyr Tyr Tyr Gly
1 5 10 15

Gln Ile Ile Gly Leu Ile Asn Phe Glu Ile Asp Trp Gln Arg Gly Arg
20 25 30

43

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PCT/US00/16211

Glu Val Leu Asp Ile Phe Thr Ile Thr Arg Ser Ser Ser Ala Ala Met
 340 345 350

Ile Gly Ser Ile Ile Thr Asn Ser Ile Phe Leu Ile Gln Tyr Asp Met
 355 360 365

Glu Tyr Phe
 370

<210> 25
 <211> 1134
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1134)
 <223> Coding region GR36B.2

<400> 25
 atg gtc gat tgg gtc gtg ttg ttg ctg aag gca gtc cac ata tac tgc 48
 Met Val Asp Trp Val Val Leu Leu Leu Lys Ala Val His Ile Tyr Cys
 1 5 10 15

tac ttg ata gga tta agt aac ttt gag ttc gat tgc cga aca gga cgc 96
 Tyr Leu Ile Gly Leu Ser Asn Phe Glu Phe Asp Cys Arg Thr Gly Arg
 20 25 30

gta ttt aaa tca agg cga tgt act atc tac gcc ttc atg gcc aac atc 144
 Val Phe Lys Ser Arg Arg Cys Thr Ile Tyr Ala Phe Met Ala Asn Ile
 35 40 45

ttt att ttg att aca ata att tat aat ttt acc gct cat ggt gat acc 192
 Phe Ile Leu Ile Thr Ile Ile Tyr Asn Phe Thr Ala His Gly Asp Thr
 50 55 60

aat tta ctt ttt caa agc gca aat aag ctg cat gaa tat gtt atc atc 240
 Asn Leu Leu Phe Gln Ser Ala Asn Lys Leu His Glu Tyr Val Ile Ile
 65 70 75 80

ata atg tcc ggc ctc aag atc cgt ggc caa atg atg cag cta gtt aaa 288
 Ile Met Ser Gly Leu Lys Ile Arg Gly Gln Met Met Gln Leu Val Lys
 85 90 95

gac gtt atc cgt cta tat atg atc aat ccg cag tta aag agt atg att 336
 Asp Val Ile Arg Leu Tyr Met Ile Asn Pro Gln Leu Lys Ser Met Ile
 100 105 110

cgc tgg gga att cta ttg aaa gct ttc att agt ttt gca ata gag ctc 384
 Arg Trp Gly Ile Leu Leu Lys Ala Phe Ile Ser Phe Ala Ile Glu Leu
 115 120 125

ctt caa gtg aca ctc tcc gtg gat gca ttg gac cgc caa gga aca gcg 432
 Leu Gln Val Thr Leu Ser Val Asp Ala Leu Asp Arg Gln Gly Thr Ala

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130	135	140	
gaa atg atg ggc ttg ctt gta aaa tta tgc gtt tcg ttc att atg aat			480
Glu Met Met Gly Leu Leu Val Lys Leu Cys Val Ser Phe Ile Met Asn			
145	150	155	160
ttg gcc ata tca cag cat ttt ttg gta ata ctt tta att cgg gca caa			528
Leu Ala Ile Ser Gln His Phe Leu Val Ile Leu Leu Ile Arg Ala Gln			
	165	170	175
tat cgg att atg aac gca aag ctg cga atg gtg atc gag gaa agc agg			576
Tyr Arg Ile Met Asn Ala Lys Leu Arg Met Val Ile Glu Glu Ser Arg			
	180	185	190
agg ttg agt ttc ctg cag ctc cga aat gga gct ttt atg acg aga tgc			624
Arg Leu Ser Phe Leu Gln Leu Arg Asn Gly Ala Phe Met Thr Arg Cys			
	195	200	205
tgc tat cta tct gat cag ttg gaa gat ata ggt gag gtt cag agc caa			672
Cys Tyr Leu Ser Asp Gln Leu Glu Asp Ile Gly Glu Val Gln Ser Gln			
	210	215	220
cta caa tcg atg gtg ggt caa ctt gat gag gta ttt ggc atg caa ggg			720
Leu Gln Ser Met Val Gly Gln Leu Asp Glu Val Phe Gly Met Gln Gly			
225	230	235	240
ctt atg gct tat agt gag tac tac cta tcc att gtg ggt aca tct tac			768
Leu Met Ala Tyr Ser Glu Tyr Tyr Leu Ser Ile Val Gly Thr Ser Tyr			
	245	250	255
atg tcg tat agc att tat aaa tat ggc ccg cat aat ctg aaa cta tca			816
Met Ser Tyr Ser Ile Tyr Lys Tyr Gly Pro His Asn Leu Lys Leu Ser			
	260	265	270
gct aag acc tcg atc att gtc tgc att ttg ata acc cta ttt tac ctt			864
Ala Lys Thr Ser Ile Ile Val Cys Ile Leu Ile Thr Leu Phe Tyr Leu			
	275	280	285
gat gcc ttg gtc aac tgc aac aat atg cta cgt gtg ttg gac cat cac			912
Asp Ala Leu Val Asn Cys Asn Asn Met Leu Arg Val Leu Asp His His			
290	295	300	
aag gat ttt ttg ggt cta ttg gag gaa cga act gtg ttt gct tcc agc			960
Lys Asp Phe Leu Gly Leu Leu Glu Glu Arg Thr Val Phe Ala Ser Ser			
305	310	315	320
ttg gac att cga ctg gag gaa tcc ttt gaa agt cta cag ttg caa cta			1008
Leu Asp Ile Arg Leu Glu Glu Ser Phe Glu Ser Leu Gln Leu Gln Leu			
	325	330	335
gct cga aac cca tta aaa att aat gta atg ggt atg ttc cct atc acg			1056
Ala Arg Asn Pro Leu Lys Ile Asn Val Met Gly Met Phe Pro Ile Thr			
	340	345	350
cgt ggc tca act gcg gct atg tgt gct tct gtt ata gtg aat tcg ata			1104
Arg Gly Ser Thr Ala Ala Met Cys Ala Ser Val Ile Val Asn Ser Ile			

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PCT/US00/16211

355

360

365

ttt cta att caa ttt gac atg gaa ttc ttt
 Phe Leu Ile Gln Phe Asp Met Glu Phe Phe
 370 375

1134

<210> 26

<211> 378

<212> PRT

<213> *Drosophila melanogaster*

<400> 26

Met Val Asp Trp Val Val Leu Leu Leu Lys Ala Val His Ile Tyr Cys
 1 5 10 15

Tyr Leu Ile Gly Leu Ser Asn Phe Glu Phe Asp Cys Arg Thr Gly Arg
 20 25 30

Val Phe Lys Ser Arg Arg Cys Thr Ile Tyr Ala Phe Met Ala Asn Ile
 35 40 45

Phe Ile Leu Ile Thr Ile Ile Tyr Asn Phe Thr Ala His Gly Asp Thr
 50 55 60

Asn Leu Leu Phe Gln Ser Ala Asn Lys Leu His Glu Tyr Val Ile Ile
 65 70 75 80

Ile Met Ser Gly Leu Lys Ile Arg Gly Gln Met Met Gln Leu Val Lys
 85 90 95

Asp Val Ile Arg Leu Tyr Met Ile Asn Pro Gln Leu Lys Ser Met Ile
 100 105 110

Arg Trp Gly Ile Leu Leu Lys Ala Phe Ile Ser Phe Ala Ile Glu Leu
 115 120 125

Leu Gln Val Thr Leu Ser Val Asp Ala Leu Asp Arg Gln Gly Thr Ala
 130 135 140

Glu Met Met Gly Leu Leu Val Lys Leu Cys Val Ser Phe Ile Met Asn
 145 150 155 160

Leu Ala Ile Ser Gln His Phe Leu Val Ile Leu Leu Ile Arg Ala Gln
 165 170 175

Tyr Arg Ile Met Asn Ala Lys Leu Arg Met Val Ile Glu Glu Ser Arg
 180 185 190

Arg Leu Ser Phe Leu Gln Leu Arg Asn Gly Ala Phe Met Thr Arg Cys
 195 200 205

Cys Tyr Leu Ser Asp Gln Leu Glu Asp Ile Gly Glu Val Gln Ser Gln
 210 215 220

Leu Gln Ser Met Val Gly Gln Leu Asp Glu Val Phe Gly Met Gln Gly

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PCT/US00/16211

225		230		235		240
Leu Met Ala Tyr Ser Glu Tyr Tyr Leu Ser Ile Val Gly Thr Ser Tyr						
	245			250		255
Met Ser Tyr Ser Ile Tyr Lys Tyr Gly Pro His Asn Leu Lys Leu Ser						
	260			265		270
Ala Lys Thr Ser Ile Ile Val Cys Ile Leu Ile Thr Leu Phe Tyr Leu						
	275			280		285
Asp Ala Leu Val Asn Cys Asn Asn Met Leu Arg Val Leu Asp His His						
	290			295		300
Lys Asp Phe Leu Gly Leu Leu Glu Glu Arg Thr Val Phe Ala Ser Ser						
305		310		315		320
Leu Asp Ile Arg Leu Glu Glu Ser Phe Glu Ser Leu Gln Leu Gln Leu						
	325			330		335
Ala Arg Asn Pro Leu Lys Ile Asn Val Met Gly Met Phe Pro Ile Thr						
	340			345		350
Arg Gly Ser Thr Ala Ala Met Cys Ala Ser Val Ile Val Asn Ser Ile						
	355			360		365
Phe Leu Ile Gln Phe Asp Met Glu Phe Phe						
	370			375		

<210> 27

<211> 1131

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1131)

<223> Coding region GR36B.3

<400> 27

atg gac ttg gaa agt ttt ttg ttg gga gcg gtt tac tac tat gga ctc	48
Met Asp Leu Glu Ser Phe Leu Leu Gly Ala Val Tyr Tyr Tyr Gly Leu	
1 5 10 15	
ttc atc ggt ctc agt aac ttt gag ttc gac tgg aac aca gga cgt gta	96
Phe Ile Gly Leu Ser Asn Phe Glu Phe Asp Trp Asn Thr Gly Arg Val	
20 25 30	
ttt aca aaa aaa tgg agt act ttg tac gca att gcg ttg gat tct tgt	144
Phe Thr Lys Lys Trp Ser Thr Leu Tyr Ala Ile Ala Leu Asp Ser Cys	
35 40 45	
ata ttt gca cta tat att tat cac tgg acc gga aac aca aac att gtt	192
Ile Phe Ala Leu Tyr Ile Tyr His Trp Thr Gly Asn Thr Asn Ile Val	

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50	55	60	
aat gca att ttc ggc aga gca aac atg ttg cac gaa tat gtt gtc gcc			240
Asn Ala Ile Phe Gly Arg Ala Asn Met Leu His Glu Tyr Val Val Ala			
65	70	75	80
ata ttg acc gga ctt aga att cgt tgc aag atg atg gat ttg gcg tca			288
Ile Leu Thr Gly Leu Arg Ile Arg Cys Lys Met Met Asp Leu Ala Ser			
	85	90	95
aaa gtg gtc cga atg tat gta gct agg ccg cag gta agg aga atg tct			336
Lys Val Val Arg Met Tyr Val Ala Arg Pro Gln Val Arg Arg Met Ser			
	100	105	110
cgc tgg ggc att ctc acc aag ttt att ttt ggt tct atc acc gat ggc			384
Arg Trp Gly Ile Leu Thr Lys Phe Ile Phe Gly Ser Ile Thr Asp Gly			
	115	120	125
ctc caa atg gcc atg gtc ttg agt gca atg ggg agt gtg gac tct caa			432
Leu Gln Met Ala Met Val Leu Ser Ala Met Gly Ser Val Asp Ser Gln			
	130	135	140
ttc tac ctg gga ctg ggc ttg cag tac tgg atg ttt gtc att ctc aac			480
Phe Tyr Leu Gly Leu Gly Leu Gln Tyr Trp Met Phe Val Ile Leu Asn			
145	150	155	160
atg gct atg atg cag caa cac atg ata atg ctt ttc gtt cgg aca cag			528
Met Ala Met Met Gln Gln His Met Ile Met Leu Phe Val Arg Thr Gln			
	165	170	175
ttc cag ctc att aat acg gaa ctg cgt cag gtg atc gat gaa gcc aag			576
Phe Gln Leu Ile Asn Thr Glu Leu Arg Gln Val Ile Asp Glu Ala Lys			
	180	185	190
gat ctg ctc tta agt ccc cgg cat cag gga gtt ttc atg acc aag tgt			624
Asp Leu Leu Leu Ser Pro Arg His Gln Gly Val Phe Met Thr Lys Cys			
	195	200	205
tgt tcg ttg gcg gat cag ata gag aat ata gca aga att cag agc caa			672
Cys Ser Leu Ala Asp Gln Ile Glu Asn Ile Ala Arg Ile Gln Ser Gln			
210	215	220	
ctg cag acg att atg aac caa atg gaa gaa gta ttc ggc att cag ggg			720
Leu Gln Thr Ile Met Asn Gln Met Glu Glu Val Phe Gly Ile Gln Gly			
225	230	235	240
gcc atg acc tat ggg ggc tac tac ttg tcc tcg gtt ggc acc tgt tac			768
Ala Met Thr Tyr Gly Gly Tyr Tyr Leu Ser Ser Val Gly Thr Cys Tyr			
	245	250	255
ttg gca tat agt atc ctc aag cat ggc tat gag aat ttg agc atg aca			816
Leu Ala Tyr Ser Ile Leu Lys His Gly Tyr Glu Asn Leu Ser Met Thr			
	260	265	270
ctg agt act gta atc ctg gcg tac tct tgg tgt ttt ttt tac tac ctt			864
Leu Ser Thr Val Ile Leu Ala Tyr Ser Trp Cys Phe Phe Tyr Tyr Leu			

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275	280	285	
gat ggt atg ctc aat tta tcg gtc atg ctc cac gta cag gat gac tac			912
Asp Gly Met Leu Asn Leu Ser Val Met Leu His Val Gln Asp Asp Tyr			
290	295	300	
tggtg gaa atg cta caa ata ctc ggg aag cgg aca ata ttc gtt ggc ttg			960
Trp Glu Met Leu Gln Ile Leu Gly Lys Arg Thr Ile Phe Val Gly Leu			
305	310	315	320
gat gtc cgc ctc gaa gaa gcc ttt gag aac ctt aat ttg cag ttg ata			1008
Asp Val Arg Leu Glu Glu Ala Phe Glu Asn Leu Asn Leu Gln Leu Ile			
	325	330	335
cga aat ccg tta aaa ata acg gtt gtt aag tta tat gat gta act cgc			1056
Arg Asn Pro Leu Lys Ile Thr Val Val Lys Leu Tyr Asp Val Thr Arg			
	340	345	350
agc aat aca atg gcc atg ttc gga aac ctg att acg cat tca att ttt			1104
Ser Asn Thr Met Ala Met Phe Gly Asn Leu Ile Thr His Ser Ile Phe			
	355	360	365
tta att cag tat gat att gaa cat ttt			1131
Leu Ile Gln Tyr Asp Ile Glu His Phe			
370	375		

<210> 28

<211> 377

<212> PRT

<213> Drosophila melanogaster

<400> 28

Met Asp Leu Glu Ser Phe Leu Leu Gly Ala Val Tyr Tyr Tyr Gly Leu			
1	5	10	15
Phe Ile Gly Leu Ser Asn Phe Glu Phe Asp Trp Asn Thr Gly Arg Val			
	20	25	30
Phe Thr Lys Lys Trp Ser Thr Leu Tyr Ala Ile Ala Leu Asp Ser Cys			
	35	40	45
Ile Phe Ala Leu Tyr Ile Tyr His Trp Thr Gly Asn Thr Asn Ile Val			
	50	55	60
Asn Ala Ile Phe Gly Arg Ala Asn Met Leu His Glu Tyr Val Val Ala			
	65	70	75
Ile Leu Thr Gly Leu Arg Ile Arg Cys Lys Met Met Asp Leu Ala Ser			
	85	90	95
Lys Val Val Arg Met Tyr Val Ala Arg Pro Gln Val Arg Arg Met Ser			
	100	105	110
Arg Trp Gly Ile Leu Thr Lys Phe Ile Phe Gly Ser Ile Thr Asp Gly			
	115	120	125

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Leu Gln Met Ala Met Val Leu Ser Ala Met Gly Ser Val Asp Ser Gln
 130 135 140
 Phe Tyr Leu Gly Leu Gly Leu Gln Tyr Trp Met Phe Val Ile Leu Asn
 145 150 155 160
 Met Ala Met Met Gln Gln His Met Ile Met Leu Phe Val Arg Thr Gln
 165 170 175
 Phe Gln Leu Ile Asn Thr Glu Leu Arg Gln Val Ile Asp Glu Ala Lys
 180 185 190
 Asp Leu Leu Leu Ser Pro Arg His Gln Gly Val Phe Met Thr Lys Cys
 195 200 205
 Cys Ser Leu Ala Asp Gln Ile Glu Asn Ile Ala Arg Ile Gln Ser Gln
 210 215 220
 Leu Gln Thr Ile Met Asn Gln Met Glu Glu Val Phe Gly Ile Gln Gly
 225 230 235 240
 Ala Met Thr Tyr Gly Gly Tyr Tyr Leu Ser Ser Val Gly Thr Cys Tyr
 245 250 255
 Leu Ala Tyr Ser Ile Leu Lys His Gly Tyr Glu Asn Leu Ser Met Thr
 260 265 270
 Leu Ser Thr Val Ile Leu Ala Tyr Ser Trp Cys Phe Phe Tyr Tyr Leu
 275 280 285
 Asp Gly Met Leu Asn Leu Ser Val Met Leu His Val Gln Asp Asp Tyr
 290 295 300
 Trp Glu Met Leu Gln Ile Leu Gly Lys Arg Thr Ile Phe Val Gly Leu
 305 310 315 320
 Asp Val Arg Leu Glu Glu Ala Phe Glu Asn Leu Asn Leu Gln Leu Ile
 325 330 335
 Arg Asn Pro Leu Lys Ile Thr Val Val Lys Leu Tyr Asp Val Thr Arg
 340 345 350
 Ser Asn Thr Met Ala Met Phe Gly Asn Leu Ile Thr His Ser Ile Phe
 355 360 365
 Leu Ile Gln Tyr Asp Ile Glu His Phe
 370 375

<210> 29

<211> 1044

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1044)

<223> Coding region GR39D.1

<220>

<221> misc_feature

<222> (232)..(991)

<223> Splice sites before positions 232, 823 and 991

<400> 29

atg ctc tat tcc ttt cat ccg tac ctc aaa tac ttt gcc ctt ttg ggg	48
Met Leu Tyr Ser Phe His Pro Tyr Leu Lys Tyr Phe Ala Leu Leu Gly	
1 5 10 15	
ctt gtg cct tgg tca gag agt tgt gcc caa tct aag ttc gta cag aaa	96
Leu Val Pro Trp Ser Glu Ser Cys Ala Gln Ser Lys Phe Val Gln Lys	
20 25 30	
gtg tac tca gcg atc cta ata att tta aat gca gtt cat ttc ggg att	144
Val Tyr Ser Ala Ile Leu Ile Ile Leu Asn Ala Val His Phe Gly Ile	
35 40 45	
tca att tat ttt cct caa agt gca gaa cta ttt ctt tct ctt atg ggt	192
Ser Ile Tyr Phe Pro Gln Ser Ala Glu Leu Phe Leu Ser Leu Met Gly	
50 55 60	
aac ggg att ggt ttc gta act agg att gcg tgt ggt act tac ttg gga	240
Asn Gly Ile Gly Phe Val Thr Arg Ile Ala Cys Gly Thr Tyr Leu Gly	
65 70 75 80	
ctt cga ttg cag tgc gaa ctt aaa ata cat gta ggg cgg tta aag tgg	288
Leu Arg Leu Gln Cys Glu Leu Lys Ile His Val Gly Arg Leu Lys Trp	
85 90 95	
cag tcg tat gct aaa att cta gca ctc ggt att gga ttt ttg gtg acg	336
Gln Ser Tyr Ala Lys Ile Leu Ala Leu Gly Ile Gly Phe Leu Val Thr	
100 105 110	
gta ttg cca tcc atc tat gtt gct cta agc ggt agc ctt ctc tac ttt	384
Val Leu Pro Ser Ile Tyr Val Ala Leu Ser Gly Ser Leu Leu Tyr Phe	
115 120 125	
tgg tcc tcc ctc ctg tca atc ctt att ata agg atg caa ttc gta ttg	432
Trp Ser Ser Leu Leu Ser Ile Leu Ile Ile Arg Met Gln Phe Val Leu	
130 135 140	
gtt ctt ttg aac gta gaa ttg ctg ggt cac cac gtg agt ctg tta ggc	480
Val Leu Leu Asn Val Glu Leu Leu Gly His His Val Ser Leu Leu Gly	
145 150 155 160	
ata cga ctt caa aac gta cta gag tgt cat ctg atg ggc gcc aac tgc	528
Ile Arg Leu Gln Asn Val Leu Glu Cys His Leu Met Gly Ala Asn Cys	
165 170 175	
aca ttg gac ggc aat gcc aat cgg ctt tgc tcc cta gag ttt ctg tta	576
Thr Leu Asp Gly Asn Ala Asn Arg Leu Cys Ser Leu Glu Phe Leu Leu	

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180						185						190						
gca	ctt	aag	cag	agc	cat	atg	caa	ctg	cat	tat	ctg	ttt	acc	cac	ttc	624		
Ala	Leu	Lys	Gln	Ser	His	Met	Gln	Leu	His	Tyr	Leu	Phe	Thr	His	Phe			
195						200						205						
aac	gat	ctt	ttc	ggc	tgg	tcc	ata	ctt	ggc	acc	tac	gtg	ggt	ctg	ttt	672		
Asn	Asp	Leu	Phe	Gly	Trp	Ser	Ile	Leu	Gly	Thr	Tyr	Val	Val	Leu	Phe			
210						215						220						
tca	gat	agt	acc	gtc	aat	att	tac	tgg	acc	cag	cag	ggt	ctg	gta	gag	720		
Ser	Asp	Ser	Thr	Val	Asn	Ile	Tyr	Trp	Thr	Gln	Gln	Val	Leu	Val	Glu			
225						230						235						240
ggt	tat	gaa	tac	aaa	tac	ctt	tac	gca	aca	ttt	tcc	ggt	ttt	gta	ccc	768		
Val	Tyr	Glu	Tyr	Lys	Tyr	Leu	Tyr	Ala	Thr	Phe	Ser	Val	Phe	Val	Pro			
245						250						255						
tca	ttc	ttc	aac	atc	tta	gtg	ttt	tgc	cgt	tgt	gga	gag	ttt	tgc	caa	816		
Ser	Phe	Phe	Asn	Ile	Leu	Val	Phe	Cys	Arg	Cys	Gly	Glu	Phe	Cys	Gln			
260						265						270						
cga	cag	agt	gtc	ttg	att	gga	agt	tat	tta	agg	aac	ttg	tcc	tgc	cat	864		
Arg	Gln	Ser	Val	Leu	Ile	Gly	Ser	Tyr	Leu	Arg	Asn	Leu	Ser	Cys	His			
275						280						285						
ccc	tcg	att	gga	aga	gaa	act	tcg	tat	aaa	gat	ctg	ctg	atg	gag	ttt	912		
Pro	Ser	Ile	Gly	Arg	Glu	Thr	Ser	Tyr	Lys	Asp	Leu	Leu	Met	Glu	Phe			
290						295						300						
att	ttg	caa	gtg	gaa	caa	aat	gta	ttg	gct	atc	aat	gct	gag	ggc	ttt	960		
Ile	Leu	Gln	Val	Glu	Gln	Asn	Val	Leu	Ala	Ile	Asn	Ala	Glu	Gly	Phe			
305						310						315						320
atg	agc	act	gat	aat	tcg	ctt	cta	atg	tcg	att	ttg	gct	gcg	aaa	ggt	1008		
Met	Ser	Thr	Asp	Asn	Ser	Leu	Leu	Met	Ser	Ile	Leu	Ala	Ala	Lys	Val			
325						330						335						
acc	tat	tta	atc	gtg	ctt	atg	caa	ttt	agt	tca	gtc					1044		
Thr	Tyr	Leu	Ile	Val	Leu	Met	Gln	Phe	Ser	Ser	Val							
340						345												

<210> 30

<211> 348

<212> PRT

<213> Drosophila melanogaster

<400> 30

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

Leu	Val	Pro	Trp	Ser	Glu	Ser	Cys	Ala	Gln	Ser	Lys	Phe	Val	Gln	Lys
			20					25					30		

Val	Tyr	Ser	Ala	Ile	Leu	Ile	Ile	Leu	Asn	Ala	Val	His	Phe	Gly	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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35					40					45						
Ser	Ile	Tyr	Phe	Pro	Gln	Ser	Ala	Glu	Leu	Phe	Leu	Ser	Leu	Met	Gly	
50					55					60						
Asn	Gly	Ile	Gly	Phe	Val	Thr	Arg	Ile	Ala	Cys	Gly	Thr	Tyr	Leu	Gly	
65					70					75					80	
Leu	Arg	Leu	Gln	Cys	Glu	Leu	Lys	Ile	His	Val	Gly	Arg	Leu	Lys	Trp	
					85					90					95	
Gln	Ser	Tyr	Ala	Lys	Ile	Leu	Ala	Leu	Gly	Ile	Gly	Phe	Leu	Val	Thr	
100					105					110						
Val	Leu	Pro	Ser	Ile	Tyr	Val	Ala	Leu	Ser	Gly	Ser	Leu	Leu	Tyr	Phe	
115					120					125						
Trp	Ser	Ser	Leu	Leu	Ser	Ile	Leu	Ile	Ile	Arg	Met	Gln	Phe	Val	Leu	
130					135					140						
Val	Leu	Leu	Asn	Val	Glu	Leu	Leu	Gly	His	His	Val	Ser	Leu	Leu	Gly	
145					150					155					160	
Ile	Arg	Leu	Gln	Asn	Val	Leu	Glu	Cys	His	Leu	Met	Gly	Ala	Asn	Cys	
					165					170					175	
Thr	Leu	Asp	Gly	Asn	Ala	Asn	Arg	Leu	Cys	Ser	Leu	Glu	Phe	Leu	Leu	
180					185					190						
Ala	Leu	Lys	Gln	Ser	His	Met	Gln	Leu	His	Tyr	Leu	Phe	Thr	His	Phe	
195					200					205						
Asn	Asp	Leu	Phe	Gly	Trp	Ser	Ile	Leu	Gly	Thr	Tyr	Val	Val	Leu	Phe	
210					215					220						
Ser	Asp	Ser	Thr	Val	Asn	Ile	Tyr	Trp	Thr	Gln	Gln	Val	Leu	Val	Glu	
225					230					235					240	
Val	Tyr	Glu	Tyr	Lys	Tyr	Leu	Tyr	Ala	Thr	Phe	Ser	Val	Phe	Val	Pro	
					245					250					255	
Ser	Phe	Phe	Asn	Ile	Leu	Val	Phe	Cys	Arg	Cys	Gly	Glu	Phe	Cys	Gln	
260					265					270						
Arg	Gln	Ser	Val	Leu	Ile	Gly	Ser	Tyr	Leu	Arg	Asn	Leu	Ser	Cys	His	
275					280					285						
Pro	Ser	Ile	Gly	Arg	Glu	Thr	Ser	Tyr	Lys	Asp	Leu	Leu	Met	Glu	Phe	
290					295					300						
Ile	Leu	Gln	Val	Glu	Gln	Asn	Val	Leu	Ala	Ile	Asn	Ala	Glu	Gly	Phe	
305					310					315					320	
Met	Ser	Thr	Asp	Asn	Ser	Leu	Leu	Met	Ser	Ile	Leu	Ala	Ala	Lys	Val	
					325					330					335	

Thr Tyr Leu Ile Val Leu Met Gln Phe Ser Ser Val
 340 345

<210> 31
 <211> 1116
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1116)
 <223> Coding region GR39D.2a

<220>
 <221> misc_feature
 <222> (880)..(1033)
 <223> Splice sites before positions 880, 943 and 1033

<400> 31
 atg ggc aca aga aat cga aag ctt ctg ttt ttc ctg cac tat cag cgc 48
 Met Gly Thr Arg Asn Arg Lys Leu Leu Phe Phe Leu His Tyr Gln Arg
 1 5 10 15

 tac ttg ggc ctt aca aac ttg gac ttc tca aaa tcg ctg cat att tac 96
 Tyr Leu Gly Leu Thr Asn Leu Asp Phe Ser Lys Ser Leu His Ile Tyr
 20 25 30

 tgg ctc cat ggt act tgg tct tca act gcg att caa att gtg gtc gtt 144
 Trp Leu His Gly Thr Trp Ser Ser Thr Ala Ile Gln Ile Val Val Val
 35 40 45

 ggg gtt ttt atg gcc gct ctg ttg gga gca ctg gcc gaa tct ctt tac 192
 Gly Val Phe Met Ala Ala Leu Leu Gly Ala Leu Ala Glu Ser Leu Tyr
 50 55 60

 tac atg gag act aaa tcc cag act ggc aac acc ttt gac aat gca gtg 240
 Tyr Met Glu Thr Lys Ser Gln Thr Gly Asn Thr Phe Asp Asn Ala Val
 65 70 75 80

 ata cta acc acc tcg gtc act caa ttg cta gcc aat ctt tgg ctc cgt 288
 Ile Leu Thr Thr Ser Val Thr Gln Leu Leu Ala Asn Leu Trp Leu Arg
 85 90 95

 tcg cag cag aaa tca caa gta aac cta ctt caa cga ctt tcg cag gtg 336
 Ser Gln Gln Lys Ser Gln Val Asn Leu Leu Gln Arg Leu Ser Gln Val
 100 105 110

 gta gaa ctt ttg caa ttt gag cct tat gca gtt cca cag ttc cgt tgg 384
 Val Glu Leu Leu Gln Phe Glu Pro Tyr Ala Val Pro Gln Phe Arg Trp
 115 120 125

 tta tac cgt atc tgg cta tta gtg tgc ctt atc tat ggg gcc atg gtg 432
 Leu Tyr Arg Ile Trp Leu Leu Val Cys Leu Ile Tyr Gly Ala Met Val
 130 135 140

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acg cat ttt ggc ata aat tgg ttg aca act atg cag atc agc cgt gtc	480
Thr His Phe Gly Ile Asn Trp Leu Thr Thr Met Gln Ile Ser Arg Val	
145 150 155 160	
ctg act ttg ata gga ttt gta tat agg tgc gtt ttg gcc aac ttt caa	528
Leu Thr Leu Ile Gly Phe Val Tyr Arg Cys Val Leu Ala Asn Phe Gln	
165 170 175	
ttc acc tgt tat acc ggg atg gtg gtg atc ttg aaa aag ctg ctt caa	576
Phe Thr Cys Tyr Thr Gly Met Val Val Ile Leu Lys Lys Leu Leu Gln	
180 185 190	
gtt cag gtt aag caa ctg gag cac ttg gtg tcc acc acc acc atc tca	624
Val Gln Val Lys Gln Leu Glu His Leu Val Ser Thr Thr Thr Ile Ser	
195 200 205	
atg gct gga gta gcc ggt tgt ttg aga acc cac gat gaa atc cta ctg	672
Met Ala Gly Val Ala Gly Cys Leu Arg Thr His Asp Glu Ile Leu Leu	
210 215 220	
ttg ggt caa aga gaa ctg att gcc gtt tat ggt gga gtt ata cta ttt	720
Leu Gly Gln Arg Glu Leu Ile Ala Val Tyr Gly Gly Val Ile Leu Phe	
225 230 235 240	
ctc ttt att tac caa gtc atg cag tgt ata tta ata ttt tac atc agc	768
Leu Phe Ile Tyr Gln Val Met Gln Cys Ile Leu Ile Phe Tyr Ile Ser	
245 250 255	
aac cta gag ggg ttt cat tca agc aat gac ctg gtt ctc att ttc tgt	816
Asn Leu Glu Gly Phe His Ser Ser Asn Asp Leu Val Leu Ile Phe Cys	
260 265 270	
tgg ctg gca ccg atg ctc ttc tat ctc atc cta cct tta gtc gtt aat	864
Trp Leu Ala Pro Met Leu Phe Tyr Leu Ile Leu Pro Leu Val Val Asn	
275 280 285	
gac ata cat aat cag gca aat aaa aca gca aag atg ctg aca aaa gta	912
Asp Ile His Asn Gln Ala Asn Lys Thr Ala Lys Met Leu Thr Lys Val	
290 295 300	
ccc cga acc ggg act ggg ttg gat aga atg att gaa aaa ttc tta ctc	960
Pro Arg Thr Gly Thr Gly Leu Asp Arg Met Ile Glu Lys Phe Leu Leu	
305 310 315 320	
aag aac ctt cga cag aag ccc att tta acc gct tat gga ttt ttc gct	1008
Lys Asn Leu Arg Gln Lys Pro Ile Leu Thr Ala Tyr Gly Phe Phe Ala	
325 330 335	
ctg gat aaa agt act ttg ttt aag cta ttt act gca atc ttc acg tat	1056
Leu Asp Lys Ser Thr Leu Phe Lys Leu Phe Thr Ala Ile Phe Thr Tyr	
340 345 350	
atg gtt att ctg gtc caa ttc aag gag atg gaa aat tcc aca aag tct	1104
Met Val Ile Leu Val Gln Phe Lys Glu Met Glu Asn Ser Thr Lys Ser	
355 360 365	

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att aat aaa ttt
 Ile Asn Lys Phe
 370

1116

<210> 32
 <211> 372
 <212> PRT
 <213> Drosophila melanogaster

<400> 32

Met	Gly	Thr	Arg	Asn	Arg	Lys	Leu	Leu	Phe	Phe	Leu	His	Tyr	Gln	Arg
1				5					10					15	
Tyr	Leu	Gly	Leu	Thr	Asn	Leu	Asp	Phe	Ser	Lys	Ser	Leu	His	Ile	Tyr
			20					25					30		
Trp	Leu	His	Gly	Thr	Trp	Ser	Ser	Thr	Ala	Ile	Gln	Ile	Val	Val	Val
			35				40					45			
Gly	Val	Phe	Met	Ala	Ala	Leu	Leu	Gly	Ala	Leu	Ala	Glu	Ser	Leu	Tyr
	50					55					60				
Tyr	Met	Glu	Thr	Lys	Ser	Gln	Thr	Gly	Asn	Thr	Phe	Asp	Asn	Ala	Val
65					70				75						80
Ile	Leu	Thr	Thr	Ser	Val	Thr	Gln	Leu	Leu	Ala	Asn	Leu	Trp	Leu	Arg
				85					90					95	
Ser	Gln	Gln	Lys	Ser	Gln	Val	Asn	Leu	Leu	Gln	Arg	Leu	Ser	Gln	Val
			100					105					110		
Val	Glu	Leu	Leu	Gln	Phe	Glu	Pro	Tyr	Ala	Val	Pro	Gln	Phe	Arg	Trp
		115					120					125			
Leu	Tyr	Arg	Ile	Trp	Leu	Leu	Val	Cys	Leu	Ile	Tyr	Gly	Ala	Met	Val
	130					135					140				
Thr	His	Phe	Gly	Ile	Asn	Trp	Leu	Thr	Thr	Met	Gln	Ile	Ser	Arg	Val
145					150					155					160
Leu	Thr	Leu	Ile	Gly	Phe	Val	Tyr	Arg	Cys	Val	Leu	Ala	Asn	Phe	Gln
				165					170					175	
Phe	Thr	Cys	Tyr	Thr	Gly	Met	Val	Val	Ile	Leu	Lys	Lys	Leu	Leu	Gln
			180					185					190		
Val	Gln	Val	Lys	Gln	Leu	Glu	His	Leu	Val	Ser	Thr	Thr	Thr	Ile	Ser
			195				200					205			
Met	Ala	Gly	Val	Ala	Gly	Cys	Leu	Arg	Thr	His	Asp	Glu	Ile	Leu	Leu
	210					215					220				
Leu	Gly	Gln	Arg	Glu	Leu	Ile	Ala	Val	Tyr	Gly	Gly	Val	Ile	Leu	Phe
225					230					235					240

Leu	Phe	Ile	Tyr	Gln	Val	Met	Gln	Cys	Ile	Leu	Ile	Phe	Tyr	Ile	Ser			
				245							250					255		
Asn	Leu	Glu	Gly	Phe	His	Ser	Ser	Asn	Asp	Leu	Val	Leu	Ile	Phe	Cys			
				260							265					270		
Trp	Leu	Ala	Pro	Met	Leu	Phe	Tyr	Leu	Ile	Leu	Pro	Leu	Val	Val	Asn			
				275							280					285		
Asp	Ile	His	Asn	Gln	Ala	Asn	Lys	Thr	Ala	Lys	Met	Leu	Thr	Lys	Val			
				290							295					300		
Pro	Arg	Thr	Gly	Thr	Gly	Leu	Asp	Arg	Met	Ile	Glu	Lys	Phe	Leu	Leu			
305							310							315			320	
Lys	Asn	Leu	Arg	Gln	Lys	Pro	Ile	Leu	Thr	Ala	Tyr	Gly	Phe	Phe	Ala			
				325							330					335		
Leu	Asp	Lys	Ser	Thr	Leu	Phe	Lys	Leu	Phe	Thr	Ala	Ile	Phe	Thr	Tyr			
				340							345					350		
Met	Val	Ile	Leu	Val	Gln	Phe	Lys	Glu	Met	Glu	Asn	Ser	Thr	Lys	Ser			
				355							360					365		
Ile	Asn	Lys	Phe															
370																		

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<210> 33
<211> 1143
<212> DNA
<213> Drosophila melanogaster
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<220>
<221> CDS
<222> (1)..(1143)
<223> Coding region GR39D.2b
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<220>
<221> misc_feature
<222> (907)..(1060)
<223> Splice sites before positions 907, 970 and 1060
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<400> 33																
atg	gac	ttc	caa	cca	ggt	gaa	ctc	tgt	gct	tac	tac	cgc	ctt	tgc	cga	48
Met	Asp	Phe	Gln	Pro	Gly	Glu	Leu	Cys	Ala	Tyr	Tyr	Arg	Leu	Cys	Arg	
1				5					10					15		
tat	cta	ggg	ata	ttc	tgt	att	gat	tat	aat	ccc	act	aaa	aag	aaa	ttc	96
Tyr	Leu	Gly	Ile	Phe	Cys	Ile	Asp	Tyr	Asn	Pro	Thr	Lys	Lys	Lys	Phe	
			20					25					30			
cga	ctg	cgg	cgc	agt	gtt	ctc	tgt	tac	ata	gtt	cat	ttt	gcc	ttg	caa	144
Arg	Leu	Arg	Arg	Ser	Val	Leu	Cys	Tyr	Ile	Val	His	Phe	Ala	Leu	Gln	
		35					40					45				

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gcc	cac	cca	gct	ggt	tgc	atc	tcc	gtc	atg	gtc	aca	tac	ggg	ggg	ggg	---
Ala	Tyr	Leu	Val	Gly	Cys	Ile	Ser	Val	Met	Val	Thr	Tyr	Trp	Arg	Arg	
	50					55					60					
tgc	ttc	aaa	agc	gag	ctt	acc	acg	act	gga	aac	cac	ttc	gac	cgt	ctt	240
Cys	Phe	Lys	Ser	Glu	Leu	Thr	Thr	Thr	Gly	Asn	His	Phe	Asp	Arg	Leu	
	65				70					75					80	
gta	atg	gta	att	gcc	ctt	ggt	att	ctg	gtt	gtc	cag	aat	gcg	tgg	ctc	288
Val	Met	Val	Ile	Ala	Leu	Gly	Ile	Leu	Val	Val	Gln	Asn	Ala	Trp	Leu	
				85				90						95		
atc	tgg	ctg	caa	gcc	cca	cac	cta	cga	att	gtc	agg	caa	ata	gag	ttt	336
Ile	Trp	Leu	Gln	Ala	Pro	His	Leu	Arg	Ile	Val	Arg	Gln	Ile	Glu	Phe	
			100					105					110			
tat	cga	agg	aat	cac	ttg	gct	aat	gtt	cga	ctg	ctc	ctc	ccc	aaa	cgt	384
Tyr	Arg	Arg	Asn	His	Leu	Ala	Asn	Val	Arg	Leu	Leu	Leu	Pro	Lys	Arg	
		115					120					125				
ctg	ctt	tgg	cta	att	att	gca	acc	aat	gtt	gtc	tac	atg	gct	aac	ttc	432
Leu	Leu	Trp	Leu	Ile	Ile	Ala	Thr	Asn	Val	Val	Tyr	Met	Ala	Asn	Phe	
	130					135					140					
att	aag	acg	tgc	ata	ttc	gaa	tgg	ctg	acg	gat	gct	tct	cga	ctt	ttt	480
Ile	Lys	Thr	Cys	Ile	Phe	Glu	Trp	Leu	Thr	Asp	Ala	Ser	Arg	Leu	Phe	
	145				150					155					160	
gtc	att	acc	tcc	ttg	gga	ttt	cct	tta	cga	tat	ctg	gtt	act	agc	ttt	528
Val	Ile	Thr	Ser	Leu	Gly	Phe	Pro	Leu	Arg	Tyr	Leu	Val	Thr	Ser	Phe	
				165					170					175		
aca	atg	ggc	aca	tat	ttt	tgc	atg	gtg	cat	att	gta	cgc	ctg	gtg	ctc	576
Thr	Met	Gly	Thr	Tyr	Phe	Cys	Met	Val	His	Ile	Val	Arg	Leu	Val	Leu	
			180					185					190			
gac	tgg	aat	cag	tcg	cag	att	aac	gcg	ata	ata	gat	gaa	tcg	gca	gac	624
Asp	Trp	Asn	Gln	Ser	Gln	Ile	Asn	Ala	Ile	Ile	Asp	Glu	Ser	Ala	Asp	
		195					200					205				
ctc	aaa	atg	act	agc	ccc	aat	cgt	ctg	cgt	tta	cgt	gta	tgc	ctg	gag	672
Leu	Lys	Met	Thr	Ser	Pro	Asn	Arg	Leu	Arg	Leu	Arg	Val	Cys	Leu	Glu	
	210					215					220					
atg	cac	gat	cgc	ctg	atg	ctg	ctc	tgc	aat	gat	gag	atc	agt	ctt	gtc	720
Met	His	Asp	Arg	Leu	Met	Leu	Leu	Cys	Asn	Asp	Glu	Ile	Ser	Leu	Val	
	225				230					235					240	
tac	ggg	ttt	ata	gcc	tgg	ctg	tct	tgg	atg	ttt	gcc	tcg	ctt	gat	gta	768
Tyr	Gly	Phe	Ile	Ala	Trp	Leu	Ser	Trp	Met	Phe	Ala	Ser	Leu	Asp	Val	
				245				250						255		
act	ggc	gta	att	tat	ctg	act	atg	gtt	att	caa	act	aaa	aaa	tca	atc	816
Thr	Gly	Val	Ile	Tyr	Leu	Thr	Met	Val	Ile	Gln	Thr	Lys	Lys	Ser	Ile	
			260					265					270			

WO 00/77208

PCT/US00/16211

gtt cta aaa ttg ata aca aac gta gtg tgg ctt tcg cca act ttt atg 864
 Val Leu Lys Leu Ile Thr Asn Val Val Trp Leu Ser Pro Thr Phe Met
 275 280 285

acg tgc gcc gct agc ttc atg agt aat cgt gtt act att cag gca aat 912
 Thr Cys Ala Ala Ser Phe Met Ser Asn Arg Val Thr Ile Gln Ala Asn
 290 295 300

aaa aca gca aag atg ctg aca aaa gta ccc cga acc ggg act ggg ttg 960
 Lys Thr Ala Lys Met Leu Thr Lys Val Pro Arg Thr Gly Thr Gly Leu
 305 310 315 320

gat aga atg att gaa aaa ttc tta ctc aag aac ctt cga cag aag ccc 1008
 Asp Arg Met Ile Glu Lys Phe Leu Leu Lys Asn Leu Arg Gln Lys Pro
 325 330 335

att tta acc gct tat gga ttt ttc gct ctg gat aaa agt act ttg ttt 1056
 Ile Leu Thr Ala Tyr Gly Phe Phe Ala Leu Asp Lys Ser Thr Leu Phe
 340 345 350

aag cta ttt act gca atc ttc acg tat atg gtt att ctg gtc caa ttc 1104
 Lys Leu Phe Thr Ala Ile Phe Thr Tyr Met Val Ile Leu Val Gln Phe
 355 360 365

aag gag atg gaa aat tcc aca aag tct att aat aaa ttt 1143
 Lys Glu Met Glu Asn Ser Thr Lys Ser Ile Asn Lys Phe
 370 375 380

<210> 34

<211> 381

<212> PRT

<213> *Drosophila melanogaster*

<400> 34

Met Asp Phe Gln Pro Gly Glu Leu Cys Ala Tyr Tyr Arg Leu Cys Arg
 1 5 10 15

Tyr Leu Gly Ile Phe Cys Ile Asp Tyr Asn Pro Thr Lys Lys Lys Phe
 20 25 30

Arg Leu Arg Arg Ser Val Leu Cys Tyr Ile Val His Phe Ala Leu Gln
 35 40 45

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

Cys Phe Lys Ser Glu Leu Thr Thr Thr Gly Asn His Phe Asp Arg Leu
 65 70 75 80

Val Met Val Ile Ala Leu Gly Ile Leu Val Val Gln Asn Ala Trp Leu
 85 90 95

Ile Trp Leu Gln Ala Pro His Leu Arg Ile Val Arg Gln Ile Glu Phe
 100 105 110

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PCT/US00/16211

Tyr Arg Arg Asn His Leu Ala Asn Val Arg Leu Leu Leu Pro Lys Arg
 115 120 125
 Leu Leu Trp Leu Ile Ile Ala Thr Asn Val Val Tyr Met Ala Asn Phe
 130 135 140
 Ile Lys Thr Cys Ile Phe Glu Trp Leu Thr Asp Ala Ser Arg Leu Phe
 145 150 155 160
 Val Ile Thr Ser Leu Gly Phe Pro Leu Arg Tyr Leu Val Thr Ser Phe
 165 170 175
 Thr Met Gly Thr Tyr Phe Cys Met Val His Ile Val Arg Leu Val Leu
 180 185 190
 Asp Trp Asn Gln Ser Gln Ile Asn Ala Ile Ile Asp Glu Ser Ala Asp
 195 200 205
 Leu Lys Met Thr Ser Pro Asn Arg Leu Arg Leu Arg Val Cys Leu Glu
 210 215 220
 Met His Asp Arg Leu Met Leu Leu Cys Asn Asp Glu Ile Ser Leu Val
 225 230 235 240
 Tyr Gly Phe Ile Ala Trp Leu Ser Trp Met Phe Ala Ser Leu Asp Val
 245 250 255
 Thr Gly Val Ile Tyr Leu Thr Met Val Ile Gln Thr Lys Lys Ser Ile
 260 265 270
 Val Leu Lys Leu Ile Thr Asn Val Val Trp Leu Ser Pro Thr Phe Met
 275 280 285
 Thr Cys Ala Ala Ser Phe Met Ser Asn Arg Val Thr Ile Gln Ala Asn
 290 295 300
 Lys Thr Ala Lys Met Leu Thr Lys Val Pro Arg Thr Gly Thr Gly Leu
 305 310 315 320
 Asp Arg Met Ile Glu Lys Phe Leu Leu Lys Asn Leu Arg Gln Lys Pro
 325 330 335
 Ile Leu Thr Ala Tyr Gly Phe Phe Ala Leu Asp Lys Ser Thr Leu Phe
 340 345 350
 Lys Leu Phe Thr Ala Ile Phe Thr Tyr Met Val Ile Leu Val Gln Phe
 355 360 365
 Lys Glu Met Glu Asn Ser Thr Lys Ser Ile Asn Lys Phe
 370 375 380

<210> 35

<211> 1143

<212> DNA

WO 00/77208

PCT/US00/16211

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1143)

<223> Coding region GR39D.2c

<220>

<221> misc_feature

<222> (907)..(1060)

<223> Splice sites before positions 907, 970 and 1060

<400> 35

atg	aaa	cgc	aac	gca	ttt	gaa	gag	ttg	agg	gtt	cag	ttg	cga	acc	tta	48
Met	Lys	Arg	Asn	Ala	Phe	Glu	Glu	Leu	Arg	Val	Gln	Leu	Arg	Thr	Leu	
1				5					10					15		
aaa	tgg	ctt	gga	gtc	ctg	cgg	ttc	act	atc	gac	ttt	aat	aag	tgc	tta	96
Lys	Trp	Leu	Gly	Val	Leu	Arg	Phe	Thr	Ile	Asp	Phe	Asn	Lys	Cys	Leu	
			20					25					30			
gta	cgg	gaa	aat	gcg	tct	gag	gag	cgc	agt	gcc	tgg	ctg	tat	ttg	ata	144
Val	Arg	Glu	Asn	Ala	Ser	Glu	Glu	Arg	Ser	Ala	Trp	Leu	Tyr	Leu	Ile	
			35					40					45			
ggt	gta	gtg	gga	att	acg	tgc	agc	ttg	atc	gtc	tac	agc	act	tac	ttt	192
Gly	Val	Val	Gly	Ile	Thr	Cys	Ser	Leu	Ile	Val	Tyr	Ser	Thr	Tyr	Phe	
	50					55					60					
ccc	agt	cac	ttt	att	atg	gga	aaa	cac	aac	acc	acg	ggc	aat	tgc	tat	240
Pro	Ser	His	Phe	Ile	Met	Gly	Lys	His	Asn	Thr	Thr	Gly	Asn	Cys	Tyr	
65					70				75					80		
gcc	cta	atc	aac	atc	agg	tcc	tgt	tcc	att	gta	aca	atg	ctg	att	tac	288
Ala	Leu	Ile	Asn	Ile	Arg	Ser	Cys	Ser	Ile	Val	Thr	Met	Leu	Ile	Tyr	
			85						90					95		
aca	cag	ctc	tac	ata	caa	cgt	ttt	cga	ttc	gtc	gcc	ctc	tta	cag	tcc	336
Thr	Gln	Leu	Tyr	Ile	Gln	Arg	Phe	Arg	Phe	Val	Ala	Leu	Leu	Gln	Ser	
			100					105					110			
att	cta	cgt	ttt	aac	cag	atc	tct	ggg	agt	cac	aga	gaa	gaa	gga	aga	384
Ile	Leu	Arg	Phe	Asn	Gln	Ile	Ser	Gly	Ser	His	Arg	Glu	Glu	Gly	Arg	
		115					120					125				
ttt	gct	ttt	tat	tat	tat	aca	cat	tta	tcc	cta	cta	atc	att	tgt	atg	432
Phe	Ala	Phe	Tyr	Tyr	Tyr	Thr	His	Leu	Ser	Leu	Leu	Ile	Ile	Cys	Met	
	130					135						140				
ctg	aac	tat	gct	tat	ggt	tac	tgg	aca	gca	ggt	gtt	cgc	ttg	acc	aca	480
Leu	Asn	Tyr	Ala	Tyr	Gly	Tyr	Trp	Thr	Ala	Gly	Val	Arg	Leu	Thr	Thr	
145					150					155				160		
att	cct	att	tat	ctg	ctt	caa	tac	gga	ttt	tca	tac	ctc	ttc	ctc	gga	528
Ile	Pro	Ile	Tyr	Leu	Leu	Gln	Tyr	Gly	Phe	Ser	Tyr	Leu	Phe	Leu	Gly	
				165				170						175		

WO 00/77208

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cag	gtg	gtg	gtc	ctg	ttt	gcc	tgc	att	caa	caa	ata	tta	ctt	tcg	att	576
Gln	Val	Val	Val	Leu	Phe	Ala	Cys	Ile	Gln	Gln	Ile	Leu	Leu	Ser	Ile	
			180					185					190			
tta	aag	tac	tat	aac	caa	gta	gtt	ctt	aaa	aat	att	aaa	tca	agc	aag	624
Leu	Lys	Tyr	Tyr	Asn	Gln	Val	Val	Leu	Lys	Asn	Ile	Lys	Ser	Ser	Lys	
		195					200					205				
gag	agt	cgc	gaa	ttc	tat	tac	aac	ttt	tgc	aaa	tac	aac	caa	gta	ata	672
Glu	Ser	Arg	Glu	Phe	Tyr	Tyr	Asn	Phe	Cys	Lys	Tyr	Asn	Gln	Val	Ile	
	210					215					220					
tgg	cta	agc	tat	acc	gag	atc	aac	cat	tgt	ttc	ggg	ttg	cta	cta	tta	720
Trp	Leu	Ser	Tyr	Thr	Glu	Ile	Asn	His	Cys	Phe	Gly	Leu	Leu	Leu	Leu	
225					230					235					240	
ctc	gta	acc	gga	tta	att	ctg	cta	atc	acc	cct	tct	ggg	ccg	ttc	tat	768
Leu	Val	Thr	Gly	Leu	Ile	Leu	Leu	Ile	Thr	Pro	Ser	Gly	Pro	Phe	Tyr	
			245					250						255		
ttg	gta	tct	acc	ata	ttt	gaa	gga	cga	ttt	cgt	cag	aat	tgg	cag	ttc	816
Leu	Val	Ser	Thr	Ile	Phe	Glu	Gly	Arg	Phe	Arg	Gln	Asn	Trp	Gln	Phe	
		260						265					270			
agc	tta	atg	tcg	ttc	act	gcc	ata	ctt	tgg	agc	tta	cca	tgg	ata	gtt	864
Ser	Leu	Met	Ser	Phe	Thr	Ala	Ile	Leu	Trp	Ser	Leu	Pro	Trp	Ile	Val	
		275					280					285				
ttg	ctg	gtt	ttg	gca	atg	ggc	agg	aat	gat	gta	cag	aag	gag	gca	aat	912
Leu	Leu	Val	Leu	Ala	Met	Gly	Arg	Asn	Asp	Val	Gln	Lys	Glu	Ala	Asn	
	290					295					300					
aaa	aca	gca	aag	atg	ctg	aca	aaa	gta	ccc	cga	acc	ggg	act	ggg	ttg	960
Lys	Thr	Ala	Lys	Met	Leu	Thr	Lys	Val	Pro	Arg	Thr	Gly	Thr	Gly	Leu	
305					310					315					320	
gat	aga	atg	att	gaa	aaa	ttc	tta	ctc	aag	aac	ctt	cga	cag	aag	ccc	1008
Asp	Arg	Met	Ile	Glu	Lys	Phe	Leu	Leu	Lys	Asn	Leu	Arg	Gln	Lys	Pro	
				325					330					335		
att	tta	acc	gct	tat	gga	ttt	ttc	gct	ctg	gat	aaa	agt	act	ttg	ttt	1056
Ile	Leu	Thr	Ala	Tyr	Gly	Phe	Phe	Ala	Leu	Asp	Lys	Ser	Thr	Leu	Phe	
			340					345					350			
aag	cta	ttt	act	gca	atc	ttc	acg	tat	atg	gtt	att	ctg	gtc	caa	ttc	1104
Lys	Leu	Phe	Thr	Ala	Ile	Phe	Thr	Tyr	Met	Val	Ile	Leu	Val	Gln	Phe	
		355					360					365				
aag	gag	atg	gaa	aat	tcc	aca	aag	tct	att	aat	aaa	ttt				1143
Lys	Glu	Met	Glu	Asn	Ser	Thr	Lys	Ser	Ile	Asn	Lys	Phe				
	370					375					380					

<210> 36

<211> 381

<212> PRT

WO 00/77208

PCT/US00/16211

Leu Leu Val Leu Ala Met Gly Arg Asn Asp Val Gln Lys Glu Ala Asn
 290 295 300
 Lys Thr Ala Lys Met Leu Thr Lys Val Pro Arg Thr Gly Thr Gly Leu
 305 310 315 320
 Asp Arg Met Ile Glu Lys Phe Leu Leu Lys Asn Leu Arg Gln Lys Pro
 325 330 335
 Ile Leu Thr Ala Tyr Gly Phe Phe Ala Leu Asp Lys Ser Thr Leu Phe
 340 345 350
 Lys Leu Phe Thr Ala Ile Phe Thr Tyr Met Val Ile Leu Val Gln Phe
 355 360 365
 Lys Glu Met Glu Asn Ser Thr Lys Ser Ile Asn Lys Phe
 370 375 380

<210> 37
 <211> 1113
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1113)
 <223> Coding region GR39D.2d

<220>
 <221> misc_feature
 <222> (877)..(1030)
 <223> Splice sites before positions 877, 940 and 1030

<400> 37
 atg tca aaa gtc tgc cgg gac cta cgt atc tat ctc cgt ctt ctt cac 48
 Met Ser Lys Val Cys Arg Asp Leu Arg Ile Tyr Leu Arg Leu Leu His
 1 5 10 15
 atc atg ggc atg atg tgc tgg cat ttc gat tcc gac cac tgt caa cta 96
 Ile Met Gly Met Met Cys Trp His Phe Asp Ser Asp His Cys Gln Leu
 20 25 30
 gtg gcc aca tct gga agc gag cgc tat gcc gtc gtt tat gct ggc tgt 144
 Val Ala Thr Ser Gly Ser Glu Arg Tyr Ala Val Val Tyr Ala Gly Cys
 35 40 45
 att tta gtt tct act acg gct ggc ttt atc ttt gcg ctt tta cat ccg 192
 Ile Leu Val Ser Thr Thr Ala Gly Phe Ile Phe Ala Leu Leu His Pro
 50 55 60
 agt cga ttc cac ata gcc att tat aac cag acg gga aat ttt tac gag 240
 Ser Arg Phe His Ile Ala Ile Tyr Asn Gln Thr Gly Asn Phe Tyr Glu
 65 70 75 80

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PCT/US00/16211

gcc gtc ata ttt cgc agc acg tgt gtg gtg ctt ttc ttg gtt tat gtg	288
Ala Val Ile Phe Arg Ser Thr Cys Val Val Leu Phe Leu Val Tyr Val	
85 90 95	
ata ttg tat gca tgg cgg cat cgg tac agg gat ttg gtt caa cat ata	336
Ile Leu Tyr Ala Trp Arg His Arg Tyr Arg Asp Leu Val Gln His Ile	
100 105 110	
ttg cgt ctt aac aga cgc tgt gct agc agt tgc aca aac caa cag ttt	384
Leu Arg Leu Asn Arg Arg Cys Ala Ser Ser Cys Thr Asn Gln Gln Phe	
115 120 125	
ctg cac aac ata ata ctt tac ggt atg ctt acg atc ctc tgc ttc ggc	432
Leu His Asn Ile Ile Leu Tyr Gly Met Leu Thr Ile Leu Cys Phe Gly	
130 135 140	
aac tat ctc cac ggc tat act cgc gct gga ctg gcc aca ctt ccg ctg	480
Asn Tyr Leu His Gly Tyr Thr Arg Ala Gly Leu Ala Thr Leu Pro Leu	
145 150 155 160	
gcc ctt tgt atg ttg gtc tat atc ttc gcc ttt ttg gtt tta tgc ctt	528
Ala Leu Cys Met Leu Val Tyr Ile Phe Ala Phe Leu Val Leu Cys Leu	
165 170 175	
ctt ctg atg ttc ttt gtt agt cta aag caa gtc atg acc gcg gga ttg	576
Leu Leu Met Phe Phe Val Ser Leu Lys Gln Val Met Thr Ala Gly Leu	
180 185 190	
att cac tac aac caa cag ctt tgt cag ggc gat ctg atc tct ggt ctt	624
Ile His Tyr Asn Gln Gln Leu Cys Gln Gly Asp Leu Ile Ser Gly Leu	
195 200 205	
cga ggc agg cag cag att ctg aaa tta tgc ggc ggc gaa cta aac gag	672
Arg Gly Arg Gln Gln Ile Leu Lys Leu Cys Gly Gly Glu Leu Asn Glu	
210 215 220	
tgc ttc ggc tta ctt atg ctc ccc att gta gcc ctg gtg ctc ctg atg	720
Cys Phe Gly Leu Leu Met Leu Pro Ile Val Ala Leu Val Leu Leu Met	
225 230 235 240	
gca cct tcg ggg ccg ttc ttc tta atc agt acc gtt tta gag gga aaa	768
Ala Pro Ser Gly Pro Phe Phe Leu Ile Ser Thr Val Leu Glu Gly Lys	
245 250 255	
ttt cga ccc gac gaa tgc ttg atc atg ctt ttg acc tcc tct act tgg	816
Phe Arg Pro Asp Glu Cys Leu Ile Met Leu Leu Thr Ser Ser Thr Trp	
260 265 270	
gat act ccg tgg atg att atg ttg gtt ctc atg tta cgc act aat ggc	864
Asp Thr Pro Trp Met Ile Met Leu Val Leu Met Leu Arg Thr Asn Gly	
275 280 285	
att tca gag gaa gca aat aaa aca gca aag atg ctg aca aaa gta ccc	912
Ile Ser Glu Glu Ala Asn Lys Thr Ala Lys Met Leu Thr Lys Val Pro	
290 295 300	

WO 00/77208

PCT/US00/16211

cga acc ggg act ggg ttg gat aga atg att gaa aaa ttc tta ctc aag 960
 Arg Thr Gly Thr Gly Leu Asp Arg Met Ile Glu Lys Phe Leu Leu Lys
 305 310 315 320

aac ctt cga cag aag ccc att tta acc gct tat gga ttt ttc gct ctg 1008
 Asn Leu Arg Gln Lys Pro Ile Leu Thr Ala Tyr Gly Phe Phe Ala Leu
 325 330 335

gat aaa agt act ttg ttt aag cta ttt act gca atc ttc acg tat atg 1056
 Asp Lys Ser Thr Leu Phe Lys Leu Phe Thr Ala Ile Phe Thr Tyr Met
 340 345 350

gtt att ctg gtc caa ttc aag gag atg gaa aat tcc aca aag tct att 1104
 Val Ile Leu Val Gln Phe Lys Glu Met Glu Asn Ser Thr Lys Ser Ile
 355 360 365

aat aaa ttt 1113
 Asn Lys Phe
 370

<210> 38
 <211> 371
 <212> PRT
 <213> Drosophila melanogaster

<400> 38
 Met Ser Lys Val Cys Arg Asp Leu Arg Ile Tyr Leu Arg Leu Leu His
 1 5 10 15
 Ile Met Gly Met Met Cys Trp His Phe Asp Ser Asp His Cys Gln Leu
 20 25 30
 Val Ala Thr Ser Gly Ser Glu Arg Tyr Ala Val Val Tyr Ala Gly Cys
 35 40 45
 Ile Leu Val Ser Thr Thr Ala Gly Phe Ile Phe Ala Leu Leu His Pro
 50 55 60
 Ser Arg Phe His Ile Ala Ile Tyr Asn Gln Thr Gly Asn Phe Tyr Glu
 65 70 75 80
 Ala Val Ile Phe Arg Ser Thr Cys Val Val Leu Phe Leu Val Tyr Val
 85 90 95
 Ile Leu Tyr Ala Trp Arg His Arg Tyr Arg Asp Leu Val Gln His Ile
 100 105 110
 Leu Arg Leu Asn Arg Arg Cys Ala Ser Ser Cys Thr Asn Gln Gln Phe
 115 120 125
 Leu His Asn Ile Ile Leu Tyr Gly Met Leu Thr Ile Leu Cys Phe Gly
 130 135 140
 Asn Tyr Leu His Gly Tyr Thr Arg Ala Gly Leu Ala Thr Leu Pro Leu
 145 150 155 160

WO 00/77208

PCT/US00/16211

Ala Leu Cys Met Leu Val Tyr Ile Phe Ala Phe Leu Val Leu Cys Leu
 165 170 175
 Leu Leu Met Phe Phe Val Ser Leu Lys Gln Val Met Thr Ala Gly Leu
 180 185 190
 Ile His Tyr Asn Gln Gln Leu Cys Gln Gly Asp Leu Ile Ser Gly Leu
 195 200 205
 Arg Gly Arg Gln Gln Ile Leu Lys Leu Cys Gly Gly Glu Leu Asn Glu
 210 215 220
 Cys Phe Gly Leu Leu Met Leu Pro Ile Val Ala Leu Val Leu Leu Met
 225 230 235 240
 Ala Pro Ser Gly Pro Phe Phe Leu Ile Ser Thr Val Leu Glu Gly Lys
 245 250 255
 Phe Arg Pro Asp Glu Cys Leu Ile Met Leu Leu Thr Ser Ser Thr Trp
 260 265 270
 Asp Thr Pro Trp Met Ile Met Leu Val Leu Met Leu Arg Thr Asn Gly
 275 280 285
 Ile Ser Glu Glu Ala Asn Lys Thr Ala Lys Met Leu Thr Lys Val Pro
 290 295 300
 Arg Thr Gly Thr Gly Leu Asp Arg Met Ile Glu Lys Phe Leu Leu Lys
 305 310 315 320
 Asn Leu Arg Gln Lys Pro Ile Leu Thr Ala Tyr Gly Phe Phe Ala Leu
 325 330 335
 Asp Lys Ser Thr Leu Phe Lys Leu Phe Thr Ala Ile Phe Thr Tyr Met
 340 345 350
 Val Ile Leu Val Gln Phe Lys Glu Met Glu Asn Ser Thr Lys Ser Ile
 355 360 365
 Asn Lys Phe
 370

<210> 39
 <211> 1137
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1137)
 <223> Coding region GR43C.1

<220>
 <221> misc_feature

WO 00/77208

PCT/US00/16211

<222> (133)..(1078)

<223> Splice sites before positions 133, 301, 442, 727
and 1078

<400> 39

atg aag tcg gct acg tcg aag gtg gtg acg gcc ctg gac gtg tct gtg	48
Met Lys Ser Ala Thr Ser Lys Val Val Thr Ala Leu Asp Val Ser Val	
1 5 10 15	
gtg gtc atg gcc att gta tcc ggt gtt tac tgt ggc ctt ttc agc ctg	96
Val Val Met Ala Ile Val Ser Gly Val Tyr Cys Gly Leu Phe Ser Leu	
20 25 30	
aac gac act ctc gag ctc aac gat cga cta aac aag atc gat aat acc	144
Asn Asp Thr Leu Glu Leu Asn Asp Arg Leu Asn Lys Ile Asp Asn Thr	
35 40 45	
cta aat gcc tac aat aac ttt cga aga gat cga tgg cga gcc ttg ggc	192
Leu Asn Ala Tyr Asn Asn Phe Arg Arg Asp Arg Trp Arg Ala Leu Gly	
50 55 60	
atg gct gcc gtc tct ctg ctg gcc att tcg att ctg gtc ggc ctg gat	240
Met Ala Ala Val Ser Leu Leu Ala Ile Ser Ile Leu Val Gly Leu Asp	
65 70 75 80	
gta ggg acg tgg atg cgc att gcc cag gat atg aac ata gct cag tcg	288
Val Gly Thr Trp Met Arg Ile Ala Gln Asp Met Asn Ile Ala Gln Ser	
85 90 95	
gat acg gag ctc aat gtg cac tgg tac att cca ttc tat agt ctt tac	336
Asp Thr Glu Leu Asn Val His Trp Tyr Ile Pro Phe Tyr Ser Leu Tyr	
100 105 110	
ttc atc ctc acg ggc ttg cag gtt aac att gcc aac acg gcc tat gga	384
Phe Ile Leu Thr Gly Leu Gln Val Asn Ile Ala Asn Thr Ala Tyr Gly	
115 120 125	
cta gga agg cgc ttt ggc cgt ctg aac cga atg ctt tcg agc agc ttt	432
Leu Gly Arg Arg Phe Gly Arg Leu Asn Arg Met Leu Ser Ser Ser Phe	
130 135 140	
ctt gca gag aac aat gca acc agt gcc atc aag cca caa aag gtc agc	480
Leu Ala Glu Asn Asn Ala Thr Ser Ala Ile Lys Pro Gln Lys Val Ser	
145 150 155 160	
acc gtg aag aac gtt agc gta aat cgg cca gcg atg cca tcg gca ctc	528
Thr Val Lys Asn Val Ser Val Asn Arg Pro Ala Met Pro Ser Ala Leu	
165 170 175	
cac gcg agc ctg acg aag ctg aac ggc gaa acc ttg ccc agt gaa gcc	576
His Ala Ser Leu Thr Lys Leu Asn Gly Glu Thr Leu Pro Ser Glu Ala	
180 185 190	
gca ggt gac aag gca gcc gca cgc agt cta atc ctc aac gtg gag tta	624
Ala Gly Asp Lys Ala Ala Ala Arg Ser Leu Ile Leu Asn Val Glu Leu	
195 200 205	

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ctc aaa ttg ggt tat ttt cca gcc aag aac aag ggg ttg ctc ctc aaa 672
Leu Lys Leu Gly Tyr Phe Pro Ala Lys Asn Lys Gly Leu Leu Leu Lys
210 215 220

tcc ctg gcg gac agt cac gag tcg ctg gga aaa tgt gtc cac ctc ctg 720
Ser Leu Ala Asp Ser His Glu Ser Leu Gly Lys Cys Val His Leu Leu
225 230 235 240

tcc aac tcc ttc ggc att gcg gtt ctc ttc atc ctg gtg tcc tgt ctg 768
Ser Asn Ser Phe Gly Ile Ala Val Leu Phe Ile Leu Val Ser Cys Leu
245 250 255

ctg cac ctc gtg gct acg gcc tac ttc ctc ttt ctg gaa ctg ctc agc 816
Leu His Leu Val Ala Thr Ala Tyr Phe Leu Phe Leu Glu Leu Leu Ser
260 265 270

aag cgg gat aac ggc tac ctg tgg gtg cag atg ctc tgg att tgc ttt 864
Lys Arg Asp Asn Gly Tyr Leu Trp Val Gln Met Leu Trp Ile Cys Phe
275 280 285

cac ttc ctg cga ctg ctc atg gtg gtg gag ccg tgc cac ttg gct gcc 912
His Phe Leu Arg Leu Leu Met Val Val Glu Pro Cys His Leu Ala Ala
290 295 300

cga gag tcc cgt aaa acg atc cag att gtt tgc gaa atc gag cgg aaa 960
Arg Glu Ser Arg Lys Thr Ile Gln Ile Val Cys Glu Ile Glu Arg Lys
305 310 315 320

gtg cac gag ccc att ctc gcg gag gca gtt aag aag ttt tgg cag cag 1008
Val His Glu Pro Ile Leu Ala Glu Ala Val Lys Lys Phe Trp Gln Gln
325 330 335

tta ctc gtc gta gat gct gac ttc tcc gcc tgc gga ttg tgc cgc gtg 1056
Leu Leu Val Val Asp Ala Asp Phe Ser Ala Cys Gly Leu Cys Arg Val
340 345 350

aac cgc acc att ctg aca tcg ttt gca tcc gcc ata gcc acc tat ctc 1104
Asn Arg Thr Ile Leu Thr Ser Phe Ala Ser Ala Ile Ala Thr Tyr Leu
355 360 365

gtg att ctc att cag ttt caa cgg acc aat ggc 1137
Val Ile Leu Ile Gln Phe Gln Arg Thr Asn Gly
370 375

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<210> 40

<211> 379

<212> PRT

<213> Drosophila melanogaster

<400> 40

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Met Lys Ser Ala Thr Ser Lys Val Val Thr Ala Leu Asp Val Ser Val
1 5 10 15

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Val Val Met Ala Ile Val Ser Gly Val Tyr Cys Gly Leu Phe Ser Leu
20 25 30

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WO 00/77208

PCT/US00/16211

Asn Asp Thr Leu Glu Leu Asn Asp Arg Leu Asn Lys Ile Asp Asn Thr
 35 40 45
 Leu Asn Ala Tyr Asn Asn Phe Arg Arg Asp Arg Trp Arg Ala Leu Gly
 50 55 60
 Met Ala Ala Val Ser Leu Leu Ala Ile Ser Ile Leu Val Gly Leu Asp
 65 70 75 80
 Val Gly Thr Trp Met Arg Ile Ala Gln Asp Met Asn Ile Ala Gln Ser
 85 90 95
 Asp Thr Glu Leu Asn Val His Trp Tyr Ile Pro Phe Tyr Ser Leu Tyr
 100 105 110
 Phe Ile Leu Thr Gly Leu Gln Val Asn Ile Ala Asn Thr Ala Tyr Gly
 115 120 125
 Leu Gly Arg Arg Phe Gly Arg Leu Asn Arg Met Leu Ser Ser Ser Phe
 130 135 140
 Leu Ala Glu Asn Asn Ala Thr Ser Ala Ile Lys Pro Gln Lys Val Ser
 145 150 155 160
 Thr Val Lys Asn Val Ser Val Asn Arg Pro Ala Met Pro Ser Ala Leu
 165 170 175
 His Ala Ser Leu Thr Lys Leu Asn Gly Glu Thr Leu Pro Ser Glu Ala
 180 185 190
 Ala Gly Asp Lys Ala Ala Ala Arg Ser Leu Ile Leu Asn Val Glu Leu
 195 200 205
 Leu Lys Leu Gly Tyr Phe Pro Ala Lys Asn Lys Gly Leu Leu Leu Lys
 210 215 220
 Ser Leu Ala Asp Ser His Glu Ser Leu Gly Lys Cys Val His Leu Leu
 225 230 235 240
 Ser Asn Ser Phe Gly Ile Ala Val Leu Phe Ile Leu Val Ser Cys Leu
 245 250 255
 Leu His Leu Val Ala Thr Ala Tyr Phe Leu Phe Leu Glu Leu Leu Ser
 260 265 270
 Lys Arg Asp Asn Gly Tyr Leu Trp Val Gln Met Leu Trp Ile Cys Phe
 275 280 285
 His Phe Leu Arg Leu Leu Met Val Val Glu Pro Cys His Leu Ala Ala
 290 295 300
 Arg Glu Ser Arg Lys Thr Ile Gln Ile Val Cys Glu Ile Glu Arg Lys
 305 310 315 320
 Val His Glu Pro Ile Leu Ala Glu Ala Val Lys Lys Phe Trp Gln Gln
 325 330 335

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PCT/US00/16211

Leu Leu Val Val Asp Ala Asp Phe Ser Ala Cys Gly Leu Cys Arg Val
 340 345 350

Asn Arg Thr Ile Leu Thr Ser Phe Ala Ser Ala Ile Ala Thr Tyr Leu
 355 360 365

Val Ile Leu Ile Gln Phe Gln Arg Thr Asn Gly
 370 375

<210> 41

<211> 1083

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1083)

<223> Coding region GR47A.1

<220>

<221> misc_feature

<222> (928)

<223> Splice site

<400> 41

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 1 5 10 15

gcg ctc aat gga cta aat acc tac tat ttc gat aca aag acg aat gcg 96
 Ala Leu Asn Gly Leu Asn Thr Tyr Tyr Phe Asp Thr Lys Thr Asn Ala
 20 25 30

ttc cga gtc tcc tcg aag ctc aag ata tac tgc gct atc cat cat gcc 144
 Phe Arg Val Ser Ser Lys Leu Lys Ile Tyr Cys Ala Ile His His Ala
 35 40 45

ctc tgt gtg ctg gca ctg gca cac atg tcc tat agc act gct agt aat 192
 Leu Cys Val Leu Ala Leu Ala His Met Ser Tyr Ser Thr Ala Ser Asn
 50 55 60

ttg cgt gtg agt gtg act gtt ctg acg att ggt gga acc atg gcc tgc 240
 Leu Arg Val Ser Val Thr Val Leu Thr Ile Gly Gly Thr Met Ala Cys
 65 70 75 80

tgt gtg aag tcg tgc tgg gaa aag gcg cag ggc att cga aac ttg gcc 288
 Cys Val Lys Ser Cys Trp Glu Lys Ala Gln Gly Ile Arg Asn Leu Ala
 85 90 95

cgc gga ctt gtc aca atg gag cag aag tat ttc gct ggc aga ccc agc 336
 Arg Gly Leu Val Thr Met Glu Gln Lys Tyr Phe Ala Gly Arg Pro Ser
 100 105 110

ggg ctg cta ttg aag tgc cga tac tac att aaa att act ttt ggt tcg 384

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Gly	Leu	Leu	Leu	Lys	Cys	Arg	Tyr	Tyr	Ile	Lys	Ile	Thr	Phe	Gly	Ser	
	115						120					125				
ata	acc	ctg	ctg	cgt	atc	cat	ttg	atc	caa	ccg	atc	tac	atg	agg	aga	432
Ile	Thr	Leu	Leu	Arg	Ile	His	Leu	Ile	Gln	Pro	Ile	Tyr	Met	Arg	Arg	
	130					135					140					
ctg	cta	cca	tcg	cag	ttt	tat	cta	aat	gtg	gga	gcg	tat	tgg	cta	ctc	480
Leu	Leu	Pro	Ser	Gln	Phe	Tyr	Leu	Asn	Val	Gly	Ala	Tyr	Trp	Leu	Leu	
145					150					155					160	
tac	aac	atg	ctt	ttg	gca	gct	gtg	ctg	ggc	ttt	tac	ttt	ctg	ctc	tgg	528
Tyr	Asn	Met	Leu	Leu	Ala	Ala	Val	Leu	Gly	Phe	Tyr	Phe	Leu	Leu	Trp	
				165					170					175		
gaa	atg	tgt	cgc	ata	caa	aag	ctc	ata	aat	gat	caa	atg	aca	ctc	att	576
Glu	Met	Cys	Arg	Ile	Gln	Lys	Leu	Ile	Asn	Asp	Gln	Met	Thr	Leu	Ile	
			180					185					190			
ttg	gcc	agg	tcg	ggc	cag	aga	aat	cgg	ctg	aaa	aag	atg	cag	cac	tgc	624
Leu	Ala	Arg	Ser	Gly	Gln	Arg	Asn	Arg	Leu	Lys	Lys	Met	Gln	His	Cys	
	195						200					205				
ctt	aga	ctc	tac	tcc	aag	ctt	cta	ctg	cta	tgt	gac	cag	ttc	aat	agt	672
Leu	Arg	Leu	Tyr	Ser	Lys	Leu	Leu	Leu	Leu	Cys	Asp	Gln	Phe	Asn	Ser	
	210					215					220					
cag	ctt	gga	cat	gtt	gcg	att	tgg	gtt	ttg	gct	tgc	aaa	agc	tgg	tgc	720
Gln	Leu	Gly	His	Val	Ala	Ile	Trp	Val	Leu	Ala	Cys	Lys	Ser	Trp	Cys	
225					230					235					240	
cag	atc	acc	ttt	ggc	tac	gaa	ata	ttc	cag	atg	gtg	gct	gcc	cca	aag	768
Gln	Ile	Thr	Phe	Gly	Tyr	Glu	Ile	Phe	Gln	Met	Val	Ala	Ala	Pro	Lys	
				245					250					255		
tca	atc	gat	tta	act	atg	tcc	atg	aga	gtg	ttt	gta	att	ttc	acc	tac	816
Ser	Ile	Asp	Leu	Thr	Met	Ser	Met	Arg	Val	Phe	Val	Ile	Phe	Thr	Tyr	
			260					265					270			
att	ttt	gat	gcc	atg	aac	cta	ttt	ctt	gga	aca	gac	att	tcc	gag	ttg	864
Ile	Phe	Asp	Ala	Met	Asn	Leu	Phe	Leu	Gly	Thr	Asp	Ile	Ser	Glu	Leu	
	275					280						285				
ttc	agt	act	ttt	aga	gcg	gac	tct	caa	cga	att	ttg	agg	gag	acc	agt	912
Phe	Ser	Thr	Phe	Arg	Ala	Asp	Ser	Gln	Arg	Ile	Leu	Arg	Glu	Thr	Ser	
	290					295					300					
cgc	ttg	gat	cgt	ttg	ctc	tcc	atg	ttc	gcc	ttg	aag	ttg	gcc	ctc	cat	960
Arg	Leu	Asp	Arg	Leu	Leu	Ser	Met	Phe	Ala	Leu	Lys	Leu	Ala	Leu	His	
305					310					315					320	
ccc	aag	cgg	gtc	gtc	tta	ctc	aac	gtg	ttt	acc	ttt	gac	cga	aag	ctg	1008
Pro	Lys	Arg	Val	Val	Leu	Leu	Asn	Val	Phe	Thr	Phe	Asp	Arg	Lys	Leu	
				325					330					335		
act	cta	acg	ctt	ctg	gcc	aag	tcg	acg	ttg	tac	aca	ata	tgc	tgt	ctg	1056

WO 00/77208

PCT/US00/16211

Thr Leu Thr Leu Leu Ala Lys Ser Thr Leu Tyr Thr Ile Cys Cys Leu
 340 345 350

caa aac gac tac aac aaa ctc aag gcg 1083
 Gln Asn Asp Tyr Asn Lys Leu Lys Ala
 355 360

<210> 42

<211> 361

<212> PRT

<213> Drosophila melanogaster

<400> 42

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

Phe Arg Val Ser Ser Lys Leu Lys Ile Tyr Cys Ala Ile His His Ala
 35 40 45

Leu Cys Val Leu Ala Leu Ala His Met Ser Tyr Ser Thr Ala Ser Asn
 50 55 60

Leu Arg Val Ser Val Thr Val Leu Thr Ile Gly Gly Thr Met Ala Cys
 65 70 75 80

Cys Val Lys Ser Cys Trp Glu Lys Ala Gln Gly Ile Arg Asn Leu Ala
 85 90 95

Arg Gly Leu Val Thr Met Glu Gln Lys Tyr Phe Ala Gly Arg Pro Ser
 100 105 110

Gly Leu Leu Leu Lys Cys Arg Tyr Tyr Ile Lys Ile Thr Phe Gly Ser
 115 120 125

Ile Thr Leu Leu Arg Ile His Leu Ile Gln Pro Ile Tyr Met Arg Arg
 130 135 140

Leu Leu Pro Ser Gln Phe Tyr Leu Asn Val Gly Ala Tyr Trp Leu Leu
 145 150 155 160

Tyr Asn Met Leu Leu Ala Ala Val Leu Gly Phe Tyr Phe Leu Leu Trp
 165 170 175

Glu Met Cys Arg Ile Gln Lys Leu Ile Asn Asp Gln Met Thr Leu Ile
 180 185 190

Leu Ala Arg Ser Gly Gln Arg Asn Arg Leu Lys Lys Met Gln His Cys
 195 200 205

Leu Arg Leu Tyr Ser Lys Leu Leu Leu Leu Cys Asp Gln Phe Asn Ser
 210 215 220

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PCT/US00/16211

Gln Leu Gly His Val Ala Ile Trp Val Leu Ala Cys Lys Ser Trp Cys
 225 230 235 240

Gln Ile Thr Phe Gly Tyr Glu Ile Phe Gln Met Val Ala Ala Pro Lys
 245 250 255

Ser Ile Asp Leu Thr Met Ser Met Arg Val Phe Val Ile Phe Thr Tyr
 260 265 270

Ile Phe Asp Ala Met Asn Leu Phe Leu Gly Thr Asp Ile Ser Glu Leu
 275 280 285

Phe Ser Thr Phe Arg Ala Asp Ser Gln Arg Ile Leu Arg Glu Thr Ser
 290 295 300

Arg Leu Asp Arg Leu Leu Ser Met Phe Ala Leu Lys Leu Ala Leu His
 305 310 315 320

Pro Lys Arg Val Val Leu Leu Asn Val Phe Thr Phe Asp Arg Lys Leu
 325 330 335

Thr Leu Thr Leu Leu Ala Lys Ser Thr Leu Tyr Thr Ile Cys Cys Leu
 340 345 350

Gln Asn Asp Tyr Asn Lys Leu Lys Ala
 355 360

<210> 43

<211> 1206

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1206)

<223> Coding region GR47F.1

<400> 43

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 1 5 10 15

ctc ctg ctc tac tgg gga ttg gtc aca atc cgg gtg aga agt cct gat 96
 Leu Leu Leu Tyr Trp Gly Leu Val Thr Ile Arg Val Arg Ser Pro Asp
 20 25 30

cgt gga ggt gcg ttt tca aac agg tgg act gtg tgc tat gcc ctt ttc 144
 Arg Gly Gly Ala Phe Ser Asn Arg Trp Thr Val Cys Tyr Ala Leu Phe
 35 40 45

acg cgc tcc ttt atg gtt atc tgc ttt atg gct acc gtg atg act aag 192
 Thr Arg Ser Phe Met Val Ile Cys Phe Met Ala Thr Val Met Thr Lys
 50 55 60

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PCT/US00/16211

ctg	agg	gat	ccc	gag	atg	tcc	gct	gcc	atg	ttt	gga	cac	ctt	agc	ccg	240
Leu	Arg	Asp	Pro	Glu	Met	Ser	Ala	Ala	Met	Phe	Gly	His	Leu	Ser	Pro	
65					70					75					80	
ttg	gtc	aag	gca	ata	ttc	acc	tgg	gag	tgc	ctc	agt	tgc	tcg	gtc	acc	288
Leu	Val	Lys	Ala	Ile	Phe	Thr	Trp	Glu	Cys	Leu	Ser	Cys	Ser	Val	Thr	
				85					90					95		
tac	att	gag	tac	tgc	ctt	tcg	ctg	gac	ttg	cag	aag	gac	aga	cac	ctg	336
Tyr	Ile	Glu	Tyr	Cys	Leu	Ser	Leu	Asp	Leu	Gln	Lys	Asp	Arg	His	Leu	
			100					105					110			
aaa	ctc	gtg	gct	agg	atg	caa	gag	ttc	gat	cgt	tcc	gtt	ttg	atg	gtg	384
Lys	Leu	Val	Ala	Arg	Met	Gln	Glu	Phe	Asp	Arg	Ser	Val	Leu	Met	Val	
		115					120					125				
ttc	cct	cat	gtt	cag	tgg	aac	tat	cga	cgc	gct	cgc	ttg	aag	tat	tgg	432
Phe	Pro	His	Val	Gln	Trp	Asn	Tyr	Arg	Arg	Ala	Arg	Leu	Lys	Tyr	Trp	
	130					135					140					
tat	ggc	act	gtg	att	gtc	ggc	ttt	tgc	ttt	ttc	tcc	ttt	tcc	atc	tca	480
Tyr	Gly	Thr	Val	Ile	Val	Gly	Phe	Cys	Phe	Phe	Ser	Phe	Ser	Ile	Ser	
145					150					155					160	
ctg	atc	ttc	gat	acg	acg	cgt	tgc	aca	tgc	ggc	ata	ccg	tcc	acc	ttg	528
Leu	Ile	Phe	Asp	Thr	Thr	Arg	Cys	Thr	Cys	Gly	Ile	Pro	Ser	Thr	Leu	
				165					170					175		
ctg	atg	gcc	ttc	acc	tac	acc	ttg	ctg	acc	agt	tcc	gta	gga	ttg	ctg	576
Leu	Met	Ala	Phe	Thr	Tyr	Thr	Leu	Leu	Thr	Ser	Ser	Val	Gly	Leu	Leu	
			180					185					190			
ggg	ttc	gtg	cac	ata	ggg	att	atg	gac	ttt	ata	agg	gtt	cgt	ctg	cgt	624
Gly	Phe	Val	His	Ile	Gly	Ile	Met	Asp	Phe	Ile	Arg	Val	Arg	Leu	Arg	
		195					200					205				
ctg	gtg	cag	cag	ctg	ctt	cac	caa	ctt	tac	caa	gcg	gat	gac	agt	tca	672
Leu	Val	Gln	Gln	Leu	Leu	His	Gln	Leu	Tyr	Gln	Ala	Asp	Asp	Ser	Ser	
	210					215					220					
gag	gtg	cac	gaa	agg	att	gct	tat	ctt	ttc	gaa	atg	tcc	aag	cgc	tgt	720
Glu	Val	His	Glu	Arg	Ile	Ala	Tyr	Leu	Phe	Glu	Met	Ser	Lys	Arg	Cys	
225					230					235					240	
tcg	ttt	ctc	ctg	gcg	gag	tta	aac	gga	gtt	ttt	gga	ttc	gcc	gca	gct	768
Ser	Phe	Leu	Leu	Ala	Glu	Leu	Asn	Gly	Val	Phe	Gly	Phe	Ala	Ala	Ala	
				245				250						255		
gct	ggg	atc	ttt	tat	gat	ttc	act	atc	atg	acc	tgc	ttc	gtg	tac	gtt	816
Ala	Gly	Ile	Phe	Tyr	Asp	Phe	Thr	Ile	Met	Thr	Cys	Phe	Val	Tyr	Val	
			260					265					270			
atc	tgc	caa	aag	ctg	ctg	gag	aga	gag	ccc	tgg	gat	ccc	gag	tac	gtg	864
Ile	Cys	Gln	Lys	Leu	Leu	Glu	Arg	Glu	Pro	Trp	Asp	Pro	Glu	Tyr	Val	
		275					280					285				

WO 00/77208

PCT/US00/16211

tac atg ttg ctg cac gtg gcc ata cac acc tac aaa gtg gtc att act	912
Tyr Met Leu Leu His Val Ala Ile His Thr Tyr Lys Val Val Ile Thr	
290 295 300	
agc acc tat ggg tat tta ctt ctg cga gag gtg ggt gac ctt att tcc	960
Ser Thr Tyr Gly Tyr Leu Leu Leu Arg Glu Val Gly Asp Leu Ile Ser	
305 310 315 320	
gat gtg gct cgc cgg aaa acg gag gac ttt cag cat tgg cgc atg cac	1008
Asp Val Ala Arg Arg Lys Thr Glu Asp Phe Gln His Trp Arg Met His	
325 330 335	
aat cgg caa gcg gca atg gtg ggc agc aca acc ttg cta agt gtt tct	1056
Asn Arg Gln Ala Ala Met Val Gly Ser Thr Thr Leu Leu Ser Val Ser	
340 345 350	
acc att tac ctg gtg tac aac gga atg gcc aac tat gtg att atc ctg	1104
Thr Ile Tyr Leu Val Tyr Asn Gly Met Ala Asn Tyr Val Ile Ile Leu	
355 360 365	
gtg cag ctg cta ttt caa caa cag caa atc aaa gat cac cag ttg aca	1152
Val Gln Leu Leu Phe Gln Gln Gln Gln Ile Lys Asp His Gln Leu Thr	
370 375 380	
tcg ggc aaa gat gtg gac att gtg ggc cca atg gga ccc atc act cac	1200
Ser Gly Lys Asp Val Asp Ile Val Gly Pro Met Gly Pro Ile Thr His	
385 390 395 400	
atg gat	1206
Met Asp	

<210> 44

<211> 402

<212> PRT

<213> Drosophila melanogaster

<400> 44

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Arg Gly Gly Ala Phe Ser Asn Arg Trp Thr Val Cys Tyr Ala Leu Phe	
35 40 45	
Thr Arg Ser Phe Met Val Ile Cys Phe Met Ala Thr Val Met Thr Lys	
50 55 60	
Leu Arg Asp Pro Glu Met Ser Ala Ala Met Phe Gly His Leu Ser Pro	
65 70 75 80	
Leu Val Lys Ala Ile Phe Thr Trp Glu Cys Leu Ser Cys Ser Val Thr	
85 90 95	

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Tyr	Ile	Glu	Tyr	Cys	Leu	Ser	Leu	Asp	Leu	Gln	Lys	Asp	Arg	His	Leu			
			100					105					110					
Lys	Leu	Val	Ala	Arg	Met	Gln	Glu	Phe	Asp	Arg	Ser	Val	Leu	Met	Val			
		115					120					125						
Phe	Pro	His	Val	Gln	Trp	Asn	Tyr	Arg	Arg	Ala	Arg	Leu	Lys	Tyr	Trp			
	130					135					140							
Tyr	Gly	Thr	Val	Ile	Val	Gly	Phe	Cys	Phe	Phe	Ser	Phe	Ser	Ile	Ser			
145					150					155					160			
Leu	Ile	Phe	Asp	Thr	Thr	Arg	Cys	Thr	Cys	Gly	Ile	Pro	Ser	Thr	Leu			
				165					170					175				
Leu	Met	Ala	Phe	Thr	Tyr	Thr	Leu	Leu	Thr	Ser	Ser	Val	Gly	Leu	Leu			
			180					185					190					
Gly	Phe	Val	His	Ile	Gly	Ile	Met	Asp	Phe	Ile	Arg	Val	Arg	Leu	Arg			
		195					200					205						
Leu	Val	Gln	Gln	Leu	Leu	His	Gln	Leu	Tyr	Gln	Ala	Asp	Asp	Ser	Ser			
	210					215					220							
Glu	Val	His	Glu	Arg	Ile	Ala	Tyr	Leu	Phe	Glu	Met	Ser	Lys	Arg	Cys			
225					230					235					240			
Ser	Phe	Leu	Leu	Ala	Glu	Leu	Asn	Gly	Val	Phe	Gly	Phe	Ala	Ala	Ala			
				245				250						255				
Ala	Gly	Ile	Phe	Tyr	Asp	Phe	Thr	Ile	Met	Thr	Cys	Phe	Val	Tyr	Val			
			260					265					270					
Ile	Cys	Gln	Lys	Leu	Leu	Glu	Arg	Glu	Pro	Trp	Asp	Pro	Glu	Tyr	Val			
		275					280					285						
Tyr	Met	Leu	Leu	His	Val	Ala	Ile	His	Thr	Tyr	Lys	Val	Val	Ile	Thr			
	290					295					300							
Ser	Thr	Tyr	Gly	Tyr	Leu	Leu	Leu	Arg	Glu	Val	Gly	Asp	Leu	Ile	Ser			
305					310					315					320			
Asp	Val	Ala	Arg	Arg	Lys	Thr	Glu	Asp	Phe	Gln	His	Trp	Arg	Met	His			
				325					330					335				
Asn	Arg	Gln	Ala	Ala	Met	Val	Gly	Ser	Thr	Thr	Leu	Leu	Ser	Val	Ser			
			340					345					350					
Thr	Ile	Tyr	Leu	Val	Tyr	Asn	Gly	Met	Ala	Asn	Tyr	Val	Ile	Ile	Leu			
		355					360					365						
Val	Gln	Leu	Leu	Phe	Gln	Gln	Gln	Gln	Ile	Lys	Asp	His	Gln	Leu	Thr			
	370					375					380							
Ser	Gly	Lys	Asp	Val	Asp	Ile	Val	Gly	Pro	Met	Gly	Pro	Ile	Thr	His			
385					390					395					400			

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PCT/US00/16211

Met Asp

<210> 45
 <211> 1251
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1248)
 <223> Coding region 57B.1

<400> 45
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 Met Ala Val Leu Tyr Phe Phe Arg Glu Pro Glu Thr Val Phe Asp Cys
 1 5 10 15

gcc gca ttc att tgc atc ctg cag ttc ctt atg ggc tgc aat ggg ttc 96
 Ala Ala Phe Ile Cys Ile Leu Gln Phe Leu Met Gly Cys Asn Gly Phe
 20 25 30

ggc att cgt cga tcg acc ttt agg atc agt tgg gca agc aga atc tat 144
 Gly Ile Arg Arg Ser Thr Phe Arg Ile Ser Trp Ala Ser Arg Ile Tyr
 35 40 45

tcc atg tcg gtg gcc att gcg gca ttt tgc tgt ctc ttt ggt tcc ctg 192
 Ser Met Ser Val Ala Ile Ala Ala Phe Cys Cys Leu Phe Gly Ser Leu
 50 55 60

agt gtc ctt ttg gca gag gaa gat ata aga gaa cgc ctg gca aag gcc 240
 Ser Val Leu Leu Ala Glu Glu Asp Ile Arg Glu Arg Leu Ala Lys Ala
 65 70 75 80

gat aat cta gtg ctg agc ata tca gcc ttg gaa ctg ctg atg tcc aca 288
 Asp Asn Leu Val Leu Ser Ile Ser Ala Leu Glu Leu Leu Met Ser Thr
 85 90 95

ttg gtc ttt ggg gtg act gtg ata tcc ttg caa gta ttt gca cgc cgg 336
 Leu Val Phe Gly Val Thr Val Ile Ser Leu Gln Val Phe Ala Arg Arg
 100 105 110

cac ttg gga atc tat caa aga ttg gct gcc ttg gat gcc agg ctg atg 384
 His Leu Gly Ile Tyr Gln Arg Leu Ala Ala Leu Asp Ala Arg Leu Met
 115 120 125

agc gac ttc gga gct aat ctg aac tat aga aaa atg ctg aga aag aac 432
 Ser Asp Phe Gly Ala Asn Leu Asn Tyr Arg Lys Met Leu Arg Lys Asn
 130 135 140

ata gca gtg ctg gga ata gtg acc act att tac ctg atg gcc atc aac 480
 Ile Ala Val Leu Gly Ile Val Thr Thr Ile Tyr Leu Met Ala Ile Asn
 145 150 155 160

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PCT/US00/16211

agt gcc gcc gtc caa gtg gcc agc ggt cat cga gct ctg ttc ctt cta	528
Ser Ala Ala Val Gln Val Ala Ser Gly His Arg Ala Leu Phe Leu Leu	
165 170 175	
ttc gct ctg tgc tat aca att gtc acc gga gga ccc cac ttt acg ggc	576
Phe Ala Leu Cys Tyr Thr Ile Val Thr Gly Gly Pro His Phe Thr Gly	
180 185 190	
tat gtg cac atg acc ctg gcc gag atg ttg ggc ata cgt ttc cgt ttg	624
Tyr Val His Met Thr Leu Ala Glu Met Leu Gly Ile Arg Phe Arg Leu	
195 200 205	
ctg cag caa ctg cta cag ccg gaa ttt ctt aac tgg cga ttt cct cag	672
Leu Gln Gln Leu Leu Gln Pro Glu Phe Leu Asn Trp Arg Phe Pro Gln	
210 215 220	
ctg cac gta cag gag tta cgc ata cgc cag gtg gtt tcc atg atc cag	720
Leu His Val Gln Glu Leu Arg Ile Arg Gln Val Val Ser Met Ile Gln	
225 230 235 240	
gag ctg cac tat ctc atc cag gag att aac cga gtt tac gcc ctc agt	768
Glu Leu His Tyr Leu Ile Gln Glu Ile Asn Arg Val Tyr Ala Leu Ser	
245 250 255	
ctg tgg gca gcc atg gcc cat gat ctg gcc atg agc acg agt gag ttg	816
Leu Trp Ala Ala Met Ala His Asp Leu Ala Met Ser Thr Ser Glu Leu	
260 265 270	
tac atc ctg ttt ggc cag tcc gtg ggc att ggc caa cag aat gag gag	864
Tyr Ile Leu Phe Gly Gln Ser Val Gly Ile Gly Gln Gln Asn Glu Glu	
275 280 285	
gag aac ggc agt tgc tat cga atg ctc ggc tat ttg gcc cta gtc atg	912
Glu Asn Gly Ser Cys Tyr Arg Met Leu Gly Tyr Leu Ala Leu Val Met	
290 295 300	
atc cca ccg ctc tac aag ctt ctg ata gct cca ttc tat tgc gat cgc	960
Ile Pro Pro Leu Tyr Lys Leu Leu Ile Ala Pro Phe Tyr Cys Asp Arg	
305 310 315 320	
acc ata tac gag gca agg aga tgc ctt cgc ctc gtc gaa aag ttg gac	1008
Thr Ile Tyr Glu Ala Arg Arg Cys Leu Arg Leu Val Glu Lys Leu Asp	
325 330 335	
gat tgg ttc ccc caa aag tct tct ctg cga ccc ctg gtc gaa tcc cta	1056
Asp Trp Phe Pro Gln Lys Ser Ser Leu Arg Pro Leu Val Glu Ser Leu	
340 345 350	
atg tcg tgg cgc att cag gcc aag att cag ttc acc agt ggc cta gat	1104
Met Ser Trp Arg Ile Gln Ala Lys Ile Gln Phe Thr Ser Gly Leu Asp	
355 360 365	
gtt gtg ctt agc cgc aaa gtt atc ggt ttg ttt aca tcg att ctg gtc	1152
Val Val Leu Ser Arg Lys Val Ile Gly Leu Phe Thr Ser Ile Leu Val	
370 375 380	

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aat tac ctg ctc ata ctc atc cag ttc gcc atg acc cag aag atg ggc 1200
 Asn Tyr Leu Leu Ile Leu Ile Gln Phe Ala Met Thr Gln Lys Met Gly
 385 390 395 400

gag caa atc gag cag cag aag att gca ctg cag gaa tgg att gga ttc 1248
 Glu Gln Ile Glu Gln Gln Lys Ile Ala Leu Gln Glu Trp Ile Gly Phe
 405 410 415

taa 1251

<210> 46

<211> 416

<212> PRT

<213> Drosophila melanogaster

<400> 46

Met Ala Val Leu Tyr Phe Phe Arg Glu Pro Glu Thr Val Phe Asp Cys
 1 5 10 15

Ala Ala Phe Ile Cys Ile Leu Gln Phe Leu Met Gly Cys Asn Gly Phe
 20 25 30

Gly Ile Arg Arg Ser Thr Phe Arg Ile Ser Trp Ala Ser Arg Ile Tyr
 35 40 45

Ser Met Ser Val Ala Ile Ala Ala Phe Cys Cys Leu Phe Gly Ser Leu
 50 55 60

Ser Val Leu Leu Ala Glu Glu Asp Ile Arg Glu Arg Leu Ala Lys Ala
 65 70 75 80

Asp Asn Leu Val Leu Ser Ile Ser Ala Leu Glu Leu Leu Met Ser Thr
 85 90 95

Leu Val Phe Gly Val Thr Val Ile Ser Leu Gln Val Phe Ala Arg Arg
 100 105 110

His Leu Gly Ile Tyr Gln Arg Leu Ala Ala Leu Asp Ala Arg Leu Met
 115 120 125

Ser Asp Phe Gly Ala Asn Leu Asn Tyr Arg Lys Met Leu Arg Lys Asn
 130 135 140

Ile Ala Val Leu Gly Ile Val Thr Thr Ile Tyr Leu Met Ala Ile Asn
 145 150 155 160

Ser Ala Ala Val Gln Val Ala Ser Gly His Arg Ala Leu Phe Leu Leu
 165 170 175

Phe Ala Leu Cys Tyr Thr Ile Val Thr Gly Gly Pro His Phe Thr Gly
 180 185 190

Tyr Val His Met Thr Leu Ala Glu Met Leu Gly Ile Arg Phe Arg Leu
 195 200 205

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Leu Gln Gln Leu Leu Gln Pro Glu Phe Leu Asn Trp Arg Phe Pro Gln
 210 215 220
 Leu His Val Gln Glu Leu Arg Ile Arg Gln Val Val Ser Met Ile Gln
 225 230 235 240
 Glu Leu His Tyr Leu Ile Gln Glu Ile Asn Arg Val Tyr Ala Leu Ser
 245 250 255
 Leu Trp Ala Ala Met Ala His Asp Leu Ala Met Ser Thr Ser Glu Leu
 260 265 270
 Tyr Ile Leu Phe Gly Gln Ser Val Gly Ile Gly Gln Gln Asn Glu Glu
 275 280 285
 Glu Asn Gly Ser Cys Tyr Arg Met Leu Gly Tyr Leu Ala Leu Val Met
 290 295 300
 Ile Pro Pro Leu Tyr Lys Leu Leu Ile Ala Pro Phe Tyr Cys Asp Arg
 305 310 315 320
 Thr Ile Tyr Glu Ala Arg Arg Cys Leu Arg Leu Val Glu Lys Leu Asp
 325 330 335
 Asp Trp Phe Pro Gln Lys Ser Ser Leu Arg Pro Leu Val Glu Ser Leu
 340 345 350
 Met Ser Trp Arg Ile Gln Ala Lys Ile Gln Phe Thr Ser Gly Leu Asp
 355 360 365
 Val Val Leu Ser Arg Lys Val Ile Gly Leu Phe Thr Ser Ile Leu Val
 370 375 380
 Asn Tyr Leu Leu Ile Leu Ile Gln Phe Ala Met Thr Gln Lys Met Gly
 385 390 395 400
 Glu Gln Ile Glu Gln Gln Lys Ile Ala Leu Gln Glu Trp Ile Gly Phe
 405 410 415

<210> 47
 <211> 1185
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1185)
 <223> Coding region GR58A.1

<220>
 <221> misc_feature
 <222> (1021)
 <223> Splice site

WO 00/77208

PCT/US00/16211

<400> 47

atg ctg ttg aaa ttc atg tac ata tat gga ata ggc tgt ggt ctg atg	48
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1 5 10 15	
cct gct cct ctg aag aaa gga cag ttt ctt ttg gga tat aag cag aga	96
Pro Ala Pro Leu Lys Lys Gly Gln Phe Leu Leu Gly Tyr Lys Gln Arg	
20 25 30	
tgg tac ctc atc tat acg gcc tgc ctg cac ggc ggt cta ctg acc gtc	144
Trp Tyr Leu Ile Tyr Thr Ala Cys Leu His Gly Gly Leu Leu Thr Val	
35 40 45	
ctg ccc ttc aca ttt ccc cac tac atg tac gac gac agc tac atg agc	192
Leu Pro Phe Thr Phe Pro His Tyr Met Tyr Asp Asp Ser Tyr Met Ser	
50 55 60	
agc aat cca gtc ctg aaa tgg aca ttt aat cta acc aac atc acc cgt	240
Ser Asn Pro Val Leu Lys Trp Thr Phe Asn Leu Thr Asn Ile Thr Arg	
65 70 75 80	
att atg gcc atg ttt tcg ggc gtt ctc ctg atg tgg ttc aga aga aaa	288
Ile Met Ala Met Phe Ser Gly Val Leu Leu Met Trp Phe Arg Arg Lys	
85 90 95	
agg atc ttg aat ttg ggt gaa aac tta ata ctt cac tgt ctt aag tgc	336
Arg Ile Leu Asn Leu Gly Glu Asn Leu Ile Leu His Cys Leu Lys Cys	
100 105 110	
aaa aca ctg gat aat cgt tct aag aag tat tct aaa ttg cgg aaa aga	384
Lys Thr Leu Asp Asn Arg Ser Lys Lys Tyr Ser Lys Leu Arg Lys Arg	
115 120 125	
gtt cga aat gta ctt ttc cag atg tta ctc gtc gca aat ctc agc att	432
Val Arg Asn Val Leu Phe Gln Met Leu Leu Val Ala Asn Leu Ser Ile	
130 135 140	
ctg ctg ggg gct tta att ttg ttt aga att cat tca gta caa aga att	480
Leu Leu Gly Ala Leu Ile Leu Phe Arg Ile His Ser Val Gln Arg Ile	
145 150 155 160	
agt aaa act gca atg att gta gcc cat att aca cag ttt ata tat gtg	528
Ser Lys Thr Ala Met Ile Val Ala His Ile Thr Gln Phe Ile Tyr Val	
165 170 175	
gtc ttt atg atg acg gga ata tgt gtg atc cta tta gtt ctc cac tgg	576
Val Phe Met Met Thr Gly Ile Cys Val Ile Leu Leu Val Leu His Trp	
180 185 190	
caa agt gag aga ctt caa ata gca ctc aag gac ttg tgc tcc ttt ctt	624
Gln Ser Glu Arg Leu Gln Ile Ala Leu Lys Asp Leu Cys Ser Phe Leu	
195 200 205	
aat cat gaa gaa cgc aac tcc ttg act tta tca gaa aac aag gcc aat	672
Asn His Glu Glu Arg Asn Ser Leu Thr Leu Ser Glu Asn Lys Ala Asn	
210 215 220	

WO 00/77208

PCT/US00/16211

aga tcc ctc gga aaa ttg gct aag ctc ttt aaa ctt ttt gcg gaa aat 720
 Arg Ser Leu Gly Lys Leu Ala Lys Leu Phe Lys Leu Phe Ala Glu Asn
 225 230 235 240

cag cga tta gtc cga gaa gtt ttt cga acc ttt gac ttg ccc atc gcc 768
 Gln Arg Leu Val Arg Glu Val Phe Arg Thr Phe Asp Leu Pro Ile Ala
 245 250 255

ctt ctt ttg ctg aaa atg ttt gtt aca aac gtg aat ctg gtt tat cat 816
 Leu Leu Leu Leu Lys Met Phe Val Thr Asn Val Asn Leu Val Tyr His
 260 265 270

gga gtg caa ttt ggc aac gat acc ata gaa acc tca agt tac aca aga 864
 Gly Val Gln Phe Gly Asn Asp Thr Ile Glu Thr Ser Ser Tyr Thr Arg
 275 280 285

atc gtg gga cag tgg gtg gtg att tct cat tac tgg agt gct gtt ttg 912
 Ile Val Gly Gln Trp Val Val Ile Ser His Tyr Trp Ser Ala Val Leu
 290 295 300

ctc atg aat gtt gtg gat gac gtg acg cgg aga agt gac ctg aaa atg 960
 Leu Met Asn Val Val Asp Asp Val Thr Arg Arg Ser Asp Leu Lys Met
 305 310 315 320

gga gac ctc ctg cga gaa ttc agt cat ctg gag ctg gtc aaa agg gac 1008
 Gly Asp Leu Leu Arg Glu Phe Ser His Leu Glu Leu Val Lys Arg Asp
 325 330 335

ttt cat ttg cag ctg gaa ctt ttc tcg gat cac ctt cgt tgt cat ccg 1056
 Phe His Leu Gln Leu Glu Leu Phe Ser Asp His Leu Arg Cys His Pro
 340 345 350

tca acg tat aag gtc tgt gga cta ttt att ttc aat aag caa acg agt 1104
 Ser Thr Tyr Lys Val Cys Gly Leu Phe Ile Phe Asn Lys Gln Thr Ser
 355 360 365

ttg gct tat ttt ttc tat gtg ctg gtt caa gtt ttg gtg ctt gta caa 1152
 Leu Ala Tyr Phe Phe Tyr Val Leu Val Gln Val Leu Val Leu Val Gln
 370 375 380

ttt gat tta aaa aat aaa gtt gaa aaa aga aat 1185
 Phe Asp Leu Lys Asn Lys Val Glu Lys Arg Asn
 385 390 395

<210> 48

<211> 395

<212> PRT

<213> Drosophila melanogaster

<400> 48

Met Leu Leu Lys Phe Met Tyr Ile Tyr Gly Ile Gly Cys Gly Leu Met
 1 5 10 15

Pro Ala Pro Leu Lys Lys Gly Gln Phe Leu Leu Gly Tyr Lys Gln Arg
 20 25 30

WO 00/77208

PCT/US00/16211

Trp Tyr Leu Ile Tyr Thr Ala Cys Leu His Gly Gly Leu Leu Thr Val
 35 40 45
 Leu Pro Phe Thr Phe Pro His Tyr Met Tyr Asp Asp Ser Tyr Met Ser
 50 55 60
 Ser Asn Pro Val Leu Lys Trp Thr Phe Asn Leu Thr Asn Ile Thr Arg
 65 70 75 80
 Ile Met Ala Met Phe Ser Gly Val Leu Leu Met Trp Phe Arg Arg Lys
 85 90 95
 Arg Ile Leu Asn Leu Gly Glu Asn Leu Ile Leu His Cys Leu Lys Cys
 100 105 110
 Lys Thr Leu Asp Asn Arg Ser Lys Lys Tyr Ser Lys Leu Arg Lys Arg
 115 120 125
 Val Arg Asn Val Leu Phe Gln Met Leu Leu Val Ala Asn Leu Ser Ile
 130 135 140
 Leu Leu Gly Ala Leu Ile Leu Phe Arg Ile His Ser Val Gln Arg Ile
 145 150 155 160
 Ser Lys Thr Ala Met Ile Val Ala His Ile Thr Gln Phe Ile Tyr Val
 165 170 175
 Val Phe Met Met Thr Gly Ile Cys Val Ile Leu Leu Val Leu His Trp
 180 185 190
 Gln Ser Glu Arg Leu Gln Ile Ala Leu Lys Asp Leu Cys Ser Phe Leu
 195 200 205
 Asn His Glu Glu Arg Asn Ser Leu Thr Leu Ser Glu Asn Lys Ala Asn
 210 215 220
 Arg Ser Leu Gly Lys Leu Ala Lys Leu Phe Lys Leu Phe Ala Glu Asn
 225 230 235 240
 Gln Arg Leu Val Arg Glu Val Phe Arg Thr Phe Asp Leu Pro Ile Ala
 245 250 255
 Leu Leu Leu Leu Lys Met Phe Val Thr Asn Val Asn Leu Val Tyr His
 260 265 270
 Gly Val Gln Phe Gly Asn Asp Thr Ile Glu Thr Ser Ser Tyr Thr Arg
 275 280 285
 Ile Val Gly Gln Trp Val Val Ile Ser His Tyr Trp Ser Ala Val Leu
 290 295 300
 Leu Met Asn Val Val Asp Asp Val Thr Arg Arg Ser Asp Leu Lys Met
 305 310 315 320
 Gly Asp Leu Leu Arg Glu Phe Ser His Leu Glu Leu Val Lys Arg Asp
 325 330 335

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Phe His Leu Gln Leu Glu Leu Phe Ser Asp His Leu Arg Cys His Pro
 340 345 350

Ser Thr Tyr Lys Val Cys Gly Leu Phe Ile Phe Asn Lys Gln Thr Ser
 355 360 365

Leu Ala Tyr Phe Phe Tyr Val Leu Val Gln Val Leu Val Leu Val Gln
 370 375 380

Phe Asp Leu Lys Asn Lys Val Glu Lys Arg Asn
 385 390 395

<210> 49
 <211> 1224
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1224)
 <223> Coding region GR58A.2

<220>
 <221> misc_feature
 <222> (1015)
 <223> Splice site

<400> 49
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 Met Leu His Pro Lys Leu Gly Arg Val Met Asn Val Val Tyr Tyr His
 1 5 10 15

tcc gtt gtc ttc gcc cta atg agc act acc cta agg ata cgc tcc tgc 96
 Ser Val Val Phe Ala Leu Met Ser Thr Thr Leu Arg Ile Arg Ser Cys
 20 25 30

agg aaa tgc cta cgc ttg gaa aag gtc tcg cga act tac acc atc tac 144
 Arg Lys Cys Leu Arg Leu Glu Lys Val Ser Arg Thr Tyr Thr Ile Tyr
 35 40 45

agt ttc ttt gtg ggc ata ttc ctg ttt cta aac ttg tac ttc atg gtg 192
 Ser Phe Phe Val Gly Ile Phe Leu Phe Leu Asn Leu Tyr Phe Met Val
 50 55 60

cct cgg atc atg gaa gat ggc tac atg aag tac aac ata gtc ctg cag 240
 Pro Arg Ile Met Glu Asp Gly Tyr Met Lys Tyr Asn Ile Val Leu Gln
 65 70 75 80

tgg aac ttc ttt gtg atg ctc ttc ctt aga gcc atc gct gtg gtg agc 288
 Trp Asn Phe Phe Val Met Leu Phe Leu Arg Ala Ile Ala Val Val Ser
 85 90 95

tgc tat gga acc ctg tgg cta aag cgc cac aaa atc att cag ctc tat 336
 Cys Tyr Gly Thr Leu Trp Leu Lys Arg His Lys Ile Ile Gln Leu Tyr

100	105	110	
aaa tac tcg ctg ata tat tgg aag agg ttc gga cac ata acg agg gcc Lys Tyr Ser Leu Ile Tyr Trp Lys Arg Phe Gly His Ile Thr Arg Ala 115 120 125			384
ata gtg gac aag aaa gaa ctc ctt gac cta caa gag tcc ttg gcc aga Ile Val Asp Lys Lys Glu Leu Leu Asp Leu Gln Glu Ser Leu Ala Arg 130 135 140			432
ata atg atc cgg aaa ata ata tta ctc tat agt gct ttt ctg tgc tcc Ile Met Ile Arg Lys Ile Ile Leu Leu Tyr Ser Ala Phe Leu Cys Ser 145 150 155 160			480
act gtg ttg cag tat caa ttg ctc agt gtg att aac cca cag att ttc Thr Val Leu Gln Tyr Gln Leu Leu Ser Val Ile Asn Pro Gln Ile Phe 165 170 175			528
ctg gct ttc tgt gcc cgg ctc acg cac ttt ctg cac ttc ttg tgc gtg Leu Ala Phe Cys Ala Arg Leu Thr His Phe Leu His Phe Leu Cys Val 180 185 190			576
aaa atg ggt ttc ttc ggg gta ctg gtt cta ctg aat cat caa ttt ttg Lys Met Gly Phe Phe Gly Val Leu Val Leu Leu Asn His Gln Phe Leu 195 200 205			624
gta atc cat ctg gcc ata aac gct ctt cat ggt agg aaa gcc cgg aag Val Ile His Leu Ala Ile Asn Ala Leu His Gly Arg Lys Ala Arg Lys 210 215 220			672
aaa tgg aaa gct ctg cgt tcc gta gcc gcc atg cat ctg aaa acc ctt Lys Trp Lys Ala Leu Arg Ser Val Ala Ala Met His Leu Lys Thr Leu 225 230 235 240			720
cga tta gcc aga agg atc ttt gac atg ttt gac atc gct aat gcc acg Arg Leu Ala Arg Arg Ile Phe Asp Met Phe Asp Ile Ala Asn Ala Thr 245 250 255			768
gtg ttt atc aac atg ttt atg acc gct att aat atc ctt tat cat gcc Val Phe Ile Asn Met Phe Met Thr Ala Ile Asn Ile Leu Tyr His Ala 260 265 270			816
gtc cag tac agc aat agc agc atc aag tca aat ggt tgg ggc atc tta Val Gln Tyr Ser Asn Ser Ser Ile Lys Ser Asn Gly Trp Gly Ile Leu 275 280 285			864
ttt ggc aac gga ttg atc gtt ttc aac ttc tgg ggc acc atg gcg ctg Phe Gly Asn Gly Leu Ile Val Phe Asn Phe Trp Gly Thr Met Ala Leu 290 295 300			912
atg gaa atg ctg gat agt gtg gtg acc tcc tgc aac aac act ggc cag Met Glu Met Leu Asp Ser Val Val Thr Ser Cys Asn Asn Thr Gly Gln 305 310 315 320			960
caa cta agg caa ctt agc gat cta cca aaa gtg ggt cca aag atg caa Gln Leu Arg Gln Leu Ser Asp Leu Pro Lys Val Gly Pro Lys Met Gln			1008

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325	330	335	
agg gag ttg gat gtt ttt acc atg cag ctg agg cag aat cgg ttg gtc			1056
Arg Glu Leu Asp Val Phe Thr Met Gln Leu Arg Gln Asn Arg Leu Val			
340	345	350	
tac aaa ata tgc gga att gtg gag ctg gac aaa ccc gct tgc ctt agt			1104
Tyr Lys Ile Cys Gly Ile Val Glu Leu Asp Lys Pro Ala Cys Leu Ser			
355	360	365	
tat att ggc tcc att ctg agc aac gtc att atc ctc atg cag ttc gat			1152
Tyr Ile Gly Ser Ile Leu Ser Asn Val Ile Ile Leu Met Gln Phe Asp			
370	375	380	
ttg aga cgg caa aga caa ccc atc aat gat cgt caa tat ctc atc cat			1200
Leu Arg Arg Gln Arg Gln Pro Ile Asn Asp Arg Gln Tyr Leu Ile His			
385	390	395	400
ttg atg aag aac aaa aca aaa gtg			1224
Leu Met Lys Asn Lys Thr Lys Val			
405			

<210> 50

<211> 408

<212> PRT

<213> Drosophila melanogaster

<400> 50

Met	Leu	His	Pro	Lys	Leu	Gly	Arg	Val	Met	Asn	Val	Val	Tyr	Tyr	His
1				5					10					15	

Ser	Val	Val	Phe	Ala	Leu	Met	Ser	Thr	Thr	Leu	Arg	Ile	Arg	Ser	Cys
			20					25					30		

Arg	Lys	Cys	Leu	Arg	Leu	Glu	Lys	Val	Ser	Arg	Thr	Tyr	Thr	Ile	Tyr
		35					40					45			

Ser	Phe	Phe	Val	Gly	Ile	Phe	Leu	Phe	Leu	Asn	Leu	Tyr	Phe	Met	Val
	50					55					60				

Pro	Arg	Ile	Met	Glu	Asp	Gly	Tyr	Met	Lys	Tyr	Asn	Ile	Val	Leu	Gln
65					70					75					80

Trp	Asn	Phe	Phe	Val	Met	Leu	Phe	Leu	Arg	Ala	Ile	Ala	Val	Val	Ser
				85					90					95	

Cys	Tyr	Gly	Thr	Leu	Trp	Leu	Lys	Arg	His	Lys	Ile	Ile	Gln	Leu	Tyr
			100				105						110		

Lys	Tyr	Ser	Leu	Ile	Tyr	Trp	Lys	Arg	Phe	Gly	His	Ile	Thr	Arg	Ala
		115					120					125			

Ile	Val	Asp	Lys	Lys	Glu	Leu	Leu	Asp	Leu	Gln	Glu	Ser	Leu	Ala	Arg
	130					135					140				

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Ile Met Ile Arg Lys Ile Ile Leu Leu Tyr Ser Ala Phe Leu Cys Ser
 145 150 155 160
 Thr Val Leu Gln Tyr Gln Leu Leu Ser Val Ile Asn Pro Gln Ile Phe
 165 170 175
 Leu Ala Phe Cys Ala Arg Leu Thr His Phe Leu His Phe Leu Cys Val
 180 185 190
 Lys Met Gly Phe Phe Gly Val Leu Val Leu Leu Asn His Gln Phe Leu
 195 200 205
 Val Ile His Leu Ala Ile Asn Ala Leu His Gly Arg Lys Ala Arg Lys
 210 215 220
 Lys Trp Lys Ala Leu Arg Ser Val Ala Ala Met His Leu Lys Thr Leu
 225 230 235 240
 Arg Leu Ala Arg Arg Ile Phe Asp Met Phe Asp Ile Ala Asn Ala Thr
 245 250 255
 Val Phe Ile Asn Met Phe Met Thr Ala Ile Asn Ile Leu Tyr His Ala
 260 265 270
 Val Gln Tyr Ser Asn Ser Ser Ile Lys Ser Asn Gly Trp Gly Ile Leu
 275 280 285
 Phe Gly Asn Gly Leu Ile Val Phe Asn Phe Trp Gly Thr Met Ala Leu
 290 295 300
 Met Glu Met Leu Asp Ser Val Val Thr Ser Cys Asn Asn Thr Gly Gln
 305 310 315 320
 Gln Leu Arg Gln Leu Ser Asp Leu Pro Lys Val Gly Pro Lys Met Gln
 325 330 335
 Arg Glu Leu Asp Val Phe Thr Met Gln Leu Arg Gln Asn Arg Leu Val
 340 345 350
 Tyr Lys Ile Cys Gly Ile Val Glu Leu Asp Lys Pro Ala Cys Leu Ser
 355 360 365
 Tyr Ile Gly Ser Ile Leu Ser Asn Val Ile Ile Leu Met Gln Phe Asp
 370 375 380
 Leu Arg Arg Gln Arg Gln Pro Ile Asn Asp Arg Gln Tyr Leu Ile His
 385 390 395 400
 Leu Met Lys Asn Lys Thr Lys Val
 405

<210> 51
 <211> 1236
 <212> DNA

WO 00/77208

PCT/US00/16211

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1236)

<223> Coding region GR58A.3

<220>

<221> misc_feature

<222> (1066)

<223> Splice site

<400> 51

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ata gga ctc tgc aat ctg cac tac gat tcc tcg aat cat cgg ttc atc	96
Ile Gly Leu Cys Asn Leu His Tyr Asp Ser Ser Asn His Arg Phe Ile	
20 25 30	
ctc aat cat gtg ccc aca gtg gtt tac tgt gtt atc ctg aat gtg gtc	144
Leu Asn His Val Pro Thr Val Val Tyr Cys Val Ile Leu Asn Val Val	
35 40 45	
tat ctc ttg gtc ctt cca ttt gcc ctg ttc gtg cta act ggc aac att	192
Tyr Leu Leu Val Leu Pro Phe Ala Leu Phe Val Leu Thr Gly Asn Ile	
50 55 60	
tac cat tgt cca gat gcg ggc atg ttt gga gtg gtc tac aac gtg gtg	240
Tyr His Cys Pro Asp Ala Gly Met Phe Gly Val Val Tyr Asn Val Val	
65 70 75 80	
gct ctg acc aaa ctc ctg acc atg ctc ttc cta atg agc agt gtt tgg	288
Ala Leu Thr Lys Leu Leu Thr Met Leu Phe Leu Met Ser Ser Val Trp	
85 90 95	
ata cag aga cgt cga ctg tat aag ttg gga aac gac tta atg aag atg	336
Ile Gln Arg Arg Arg Leu Tyr Lys Leu Gly Asn Asp Leu Met Lys Met	
100 105 110	
ttg cac aaa ttc cga ttt aac ctt gga aac gat tgc agg aat aga tgc	384
Leu His Lys Phe Arg Phe Asn Leu Gly Asn Asp Cys Arg Asn Arg Cys	
115 120 125	
ctg tgc aag ggt ctg ctg acc agc tct cga ttt gtg ctc cta acc cag	432
Leu Cys Lys Gly Leu Leu Thr Ser Ser Arg Phe Val Leu Leu Thr Gln	
130 135 140	
cag ctg ttg acc cgg gat tcg gtg gtt aat tgc gag agt aac tcc agt	480
Gln Leu Leu Thr Arg Asp Ser Val Val Asn Cys Glu Ser Asn Ser Ser	
145 150 155 160	
ttg aga caa gct atg gtt ccg tac caa agt gct gcc ata gtg tat gcc	528
Leu Arg Gln Ala Met Val Pro Tyr Gln Ser Ala Ala Ile Val Tyr Ala	
165 170 175	

WO 00/77208

PCT/US00/16211

tta atc atg att cta tta atg agc tat gtg gat atg aca gtc tat atg	576
Leu Ile Met Ile Leu Leu Met Ser Tyr Val Asp Met Thr Val Tyr Met	
180 185 190	
gtc gaa gtg gct ggc aat tgg ctg ctg gta aat atg acc cag ggg gtt	624
Val Glu Val Ala Gly Asn Trp Leu Leu Val Asn Met Thr Gln Gly Val	
195 200 205	
cgg gaa atg gtc caa gat cta gag gtc ttg ccc gaa cgg aat ggc att	672
Arg Glu Met Val Gln Asp Leu Glu Val Leu Pro Glu Arg Asn Gly Ile	
210 215 220	
ccg cgg gag atg gga ctg atg caa atc ctt gcc gcc tgg cga aaa ctt	720
Pro Arg Glu Met Gly Leu Met Gln Ile Leu Ala Ala Trp Arg Lys Leu	
225 230 235 240	
tgg aga cgc tgt cgc cgt ttg gat gcg ttg ctc aag cag ttc gtt gac	768
Trp Arg Arg Cys Arg Arg Leu Asp Ala Leu Leu Lys Gln Phe Val Asp	
245 250 255	
atc ttc cag tgg cag gtg ctc ttc aac ctg cta acc act tat ata ttc	816
Ile Phe Gln Trp Gln Val Leu Phe Asn Leu Leu Thr Thr Tyr Ile Phe	
260 265 270	
agc att gct gtt ttg ttt cga ttg tgg att tat ttg gag ttc gat aaa	864
Ser Ile Ala Val Leu Phe Arg Leu Trp Ile Tyr Leu Glu Phe Asp Lys	
275 280 285	
aac ttt cat tta tgg aag ggc ata ttg tat gcg att att ttt ctg acc	912
Asn Phe His Leu Trp Lys Gly Ile Leu Tyr Ala Ile Ile Phe Leu Thr	
290 295 300	
cat cac gtc gaa atc gta atg caa ttt tcc att ttc gag atc aac cgc	960
His His Val Glu Ile Val Met Gln Phe Ser Ile Phe Glu Ile Asn Arg	
305 310 315 320	
tgt aag tgg ttg gga ctt tta gaa gat gtc gga aat ctg tgg gac atc	1008
Cys Lys Trp Leu Gly Leu Leu Glu Asp Val Gly Asn Leu Trp Asp Ile	
325 330 335	
aat tat tcg gga agg caa tgc att aaa agc agt gga acg att ctg tca	1056
Asn Tyr Ser Gly Arg Gln Cys Ile Lys Ser Ser Gly Thr Ile Leu Ser	
340 345 350	
aga aag tta gag ttt tcc ctg ctc tac atg aat cgc aaa ctt caa ctg	1104
Arg Lys Leu Glu Phe Ser Leu Leu Tyr Met Asn Arg Lys Leu Gln Leu	
355 360 365	
aat cca aaa cgt gtg aga cgt ctg cac atc gtt gga ttg ttc gat ttg	1152
Asn Pro Lys Arg Val Arg Arg Leu His Ile Val Gly Leu Phe Asp Leu	
370 375 380	
agt aat tta acc gtt cac aac atg acc aga agt ata ata acc aat gtg	1200
Ser Asn Leu Thr Val His Asn Met Thr Arg Ser Ile Ile Thr Asn Val	
385 390 395 400	

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tta gtt ctg tgt cag att gcc tat aaa aaa tat ggt 1236
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 405 410

<210> 52

<211> 412

<212> PRT

<213> Drosophila melanogaster

<400> 52

Met Asn Gln Tyr Phe Leu Leu His Thr Tyr Phe Gln Val Ser Arg Leu
 1 5 10 15

Ile Gly Leu Cys Asn Leu His Tyr Asp Ser Ser Asn His Arg Phe Ile
 20 25 30

Leu Asn His Val Pro Thr Val Val Tyr Cys Val Ile Leu Asn Val Val
 35 40 45

Tyr Leu Leu Val Leu Pro Phe Ala Leu Phe Val Leu Thr Gly Asn Ile
 50 55 60

Tyr His Cys Pro Asp Ala Gly Met Phe Gly Val Val Tyr Asn Val Val
 65 70 75 80

Ala Leu Thr Lys Leu Leu Thr Met Leu Phe Leu Met Ser Ser Val Trp
 85 90 95

Ile Gln Arg Arg Arg Leu Tyr Lys Leu Gly Asn Asp Leu Met Lys Met
 100 105 110

Leu His Lys Phe Arg Phe Asn Leu Gly Asn Asp Cys Arg Asn Arg Cys
 115 120 125

Leu Cys Lys Gly Leu Leu Thr Ser Ser Arg Phe Val Leu Leu Thr Gln
 130 135 140

Gln Leu Leu Thr Arg Asp Ser Val Val Asn Cys Glu Ser Asn Ser Ser
 145 150 155 160

Leu Arg Gln Ala Met Val Pro Tyr Gln Ser Ala Ala Ile Val Tyr Ala
 165 170 175

Leu Ile Met Ile Leu Leu Met Ser Tyr Val Asp Met Thr Val Tyr Met
 180 185 190

Val Glu Val Ala Gly Asn Trp Leu Leu Val Asn Met Thr Gln Gly Val
 195 200 205

Arg Glu Met Val Gln Asp Leu Glu Val Leu Pro Glu Arg Asn Gly Ile
 210 215 220

Pro Arg Glu Met Gly Leu Met Gln Ile Leu Ala Ala Trp Arg Lys Leu
 225 230 235 240

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Trp Arg Arg Cys Arg Arg Leu Asp Ala Leu Leu Lys Gln Phe Val Asp
 245 250 255
 Ile Phe Gln Trp Gln Val Leu Phe Asn Leu Leu Thr Thr Tyr Ile Phe
 260 265 270
 Ser Ile Ala Val Leu Phe Arg Leu Trp Ile Tyr Leu Glu Phe Asp Lys
 275 280 285
 Asn Phe His Leu Trp Lys Gly Ile Leu Tyr Ala Ile Ile Phe Leu Thr
 290 295 300
 His His Val Glu Ile Val Met Gln Phe Ser Ile Phe Glu Ile Asn Arg
 305 310 315 320
 Cys Lys Trp Leu Gly Leu Leu Glu Asp Val Gly Asn Leu Trp Asp Ile
 325 330 335
 Asn Tyr Ser Gly Arg Gln Cys Ile Lys Ser Ser Gly Thr Ile Leu Ser
 340 345 350
 Arg Lys Leu Glu Phe Ser Leu Leu Tyr Met Asn Arg Lys Leu Gln Leu
 355 360 365
 Asn Pro Lys Arg Val Arg Arg Leu His Ile Val Gly Leu Phe Asp Leu
 370 375 380
 Ser Asn Leu Thr Val His Asn Met Thr Arg Ser Ile Ile Thr Asn Val
 385 390 395 400
 Leu Val Leu Cys Gln Ile Ala Tyr Lys Lys Tyr Gly
 405 410

<210> 53

<211> 1098

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1098)

<223> Coding region GR59C.1

<400> 53

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 Met Lys Arg Ile Gly Gln Ala Tyr Asn Val Tyr Ala Val Phe Ile Gly
 1 5 10 15
 atg acg tca tac gaa aca atg ggt gga aaa ttc agg cag tcg cgg att 96
 Met Thr Ser Tyr Glu Thr Met Gly Gly Lys Phe Arg Gln Ser Arg Ile
 20 25 30
 act cgg ata tat tgc ttg ctt ata aat gcc atc ttc ttg act ttg cta 144
 Thr Arg Ile Tyr Cys Leu Leu Ile Asn Ala Ile Phe Leu Thr Leu Leu

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35	40	45	
ccg agt gct ttc tgg aaa tcg gcc aag ctt ttg agt acg gcg gac tgg			192
Pro Ser Ala Phe Trp Lys Ser Ala Lys Leu Leu Ser Thr Ala Asp Trp			
50	55	60	
atg cct tcc tac atg agg gtc act ccg tac atc atg tgt aca atc aac			240
Met Pro Ser Tyr Met Arg Val Thr Pro Tyr Ile Met Cys Thr Ile Asn			
65	70	75	80
tat gct gca ata gcc tac acc ttg atc tca aga tgc tac agg gac gcc			288
Tyr Ala Ala Ile Ala Tyr Thr Leu Ile Ser Arg Cys Tyr Arg Asp Ala			
85	90	95	
atg ttg atg gac ttg caa cgc att gtg ctg gaa gtg aat cgg gaa atg			336
Met Leu Met Asp Leu Gln Arg Ile Val Leu Glu Val Asn Arg Glu Met			
100	105	110	
ttg cgc acg gga aag aaa atg aac tca cta ctt cga cga atg ttt ttc			384
Leu Arg Thr Gly Lys Lys Met Asn Ser Leu Leu Arg Arg Met Phe Phe			
115	120	125	
ttg aac att tac att gac ctc tcg tgc ttg tcg tac att ctg gcg gtt			432
Leu Asn Ile Tyr Ile Asp Leu Ser Cys Leu Ser Tyr Ile Leu Ala Val			
130	135	140	
ttc att tac cag tgg aaa gct caa aac tgg tcg aat ctt tgc aat gga			480
Phe Ile Tyr Gln Trp Lys Ala Gln Asn Trp Ser Asn Leu Cys Asn Gly			
145	150	155	160
ctc ttg gtt aac att tcc cta act atc ctg ttt gtc aac aca ttc ttc			528
Leu Leu Val Asn Ile Ser Leu Thr Ile Leu Phe Val Asn Thr Phe Phe			
165	170	175	
tac ttc acc tct ttg tgg cac ata gcc agg gga tat gac ttt gta aac			576
Tyr Phe Thr Ser Leu Trp His Ile Ala Arg Gly Tyr Asp Phe Val Asn			
180	185	190	
cag caa ctg aat gag att gtc gcc tgc caa tcg atg gac ttg gag aga			624
Gln Gln Leu Asn Glu Ile Val Ala Cys Gln Ser Met Asp Leu Glu Arg			
195	200	205	
aag tca aaa gaa ctc cgc ggc ctg tgg gct ctg cac aga aat ctt agt			672
Lys Ser Lys Glu Leu Arg Gly Leu Trp Ala Leu His Arg Asn Leu Ser			
210	215	220	
tat aca gca cgc agg ata aac aag cac tac ggt ccc caa atg ctt gcc			720
Tyr Thr Ala Arg Arg Ile Asn Lys His Tyr Gly Pro Gln Met Leu Ala			
225	230	235	240
atg cga ttt gat tac ttc ata ttc tcc atc atc aac gct tgc ata ggc			768
Met Arg Phe Asp Tyr Phe Ile Phe Ser Ile Ile Asn Ala Cys Ile Gly			
245	250	255	
acg att tac tcg act acc gac cag gag ccc tcg ctt gaa aag att ttc			816
Thr Ile Tyr Ser Thr Thr Asp Gln Glu Pro Ser Leu Glu Lys Ile Phe			

260	265	270	
gga tct cta att tac tgg gtg cga agt ttc gat ttc ttt ctg aac gac			864
Gly Ser Leu Ile Tyr Trp Val Arg Ser Phe Asp Phe Phe Leu Asn Asp			
275	280	285	
tat atc tgc gat ctg gtc agc gag tac caa atg cag cca aag ttc ttc			912
Tyr Ile Cys Asp Leu Val Ser Glu Tyr Gln Met Gln Pro Lys Phe Phe			
290	295	300	
gcc ccc gaa agc agc atg tcc aat gag ttg agt tct tac ttg atc tac			960
Ala Pro Glu Ser Ser Met Ser Asn Glu Leu Ser Ser Tyr Leu Ile Tyr			
305	310	315	320
gag agc agc acg cga ttg gat ctg ttg gtc tgc gga ctc tat cgt gtc			1008
Glu Ser Ser Thr Arg Leu Asp Leu Leu Val Cys Gly Leu Tyr Arg Val			
325	330	335	
aat aag cgg aaa tgg ttg caa atg gtt ggc tcc atc gta gtc cac tca			1056
Asn Lys Arg Lys Trp Leu Gln Met Val Gly Ser Ile Val Val His Ser			
340	345	350	
agt atg ctg ttc cag ttc cat ctc gtc atg cga ggt ggt ctc			1098
Ser Met Leu Phe Gln Phe His Leu Val Met Arg Gly Gly Leu			
355	360	365	

<210> 54

<211> 366

<212> PRT

<213> Drosophila melanogaster

<400> 54

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Met Thr Ser Tyr Glu Thr Met Gly Gly Lys Phe Arg Gln Ser Arg Ile
20 25 30

Thr Arg Ile Tyr Cys Leu Leu Ile Asn Ala Ile Phe Leu Thr Leu Leu
35 40 45

Pro Ser Ala Phe Trp Lys Ser Ala Lys Leu Leu Ser Thr Ala Asp Trp
50 55 60

Met Pro Ser Tyr Met Arg Val Thr Pro Tyr Ile Met Cys Thr Ile Asn
65 70 75 80

Tyr Ala Ala Ile Ala Tyr Thr Leu Ile Ser Arg Cys Tyr Arg Asp Ala
85 90 95

Met Leu Met Asp Leu Gln Arg Ile Val Leu Glu Val Asn Arg Glu Met
100 105 110

Leu Arg Thr Gly Lys Lys Met Asn Ser Leu Leu Arg Arg Met Phe Phe
115 120 125

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Leu Asn Ile Tyr Ile Asp Leu Ser Cys Leu Ser Tyr Ile Leu Ala Val
 130 135 140
 Phe Ile Tyr Gln Trp Lys Ala Gln Asn Trp Ser Asn Leu Cys Asn Gly
 145 150 155 160
 Leu Leu Val Asn Ile Ser Leu Thr Ile Leu Phe Val Asn Thr Phe Phe
 165 170 175
 Tyr Phe Thr Ser Leu Trp His Ile Ala Arg Gly Tyr Asp Phe Val Asn
 180 185 190
 Gln Gln Leu Asn Glu Ile Val Ala Cys Gln Ser Met Asp Leu Glu Arg
 195 200 205
 Lys Ser Lys Glu Leu Arg Gly Leu Trp Ala Leu His Arg Asn Leu Ser
 210 215 220
 Tyr Thr Ala Arg Arg Ile Asn Lys His Tyr Gly Pro Gln Met Leu Ala
 225 230 235 240
 Met Arg Phe Asp Tyr Phe Ile Phe Ser Ile Ile Asn Ala Cys Ile Gly
 245 250 255
 Thr Ile Tyr Ser Thr Thr Asp Gln Glu Pro Ser Leu Glu Lys Ile Phe
 260 265 270
 Gly Ser Leu Ile Tyr Trp Val Arg Ser Phe Asp Phe Phe Leu Asn Asp
 275 280 285
 Tyr Ile Cys Asp Leu Val Ser Glu Tyr Gln Met Gln Pro Lys Phe Phe
 290 295 300
 Ala Pro Glu Ser Ser Met Ser Asn Glu Leu Ser Ser Tyr Leu Ile Tyr
 305 310 315 320
 Glu Ser Ser Thr Arg Leu Asp Leu Leu Val Cys Gly Leu Tyr Arg Val
 325 330 335
 Asn Lys Arg Lys Trp Leu Gln Met Val Gly Ser Ile Val Val His Ser
 340 345 350
 Ser Met Leu Phe Gln Phe His Leu Val Met Arg Gly Gly Leu
 355 360 365

<210> 55

<211> 1161

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1161)

<223> Coding region GR59C.2

WO 00/77208

PCT/US00/16211

<400> 55

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Met Val Tyr Trp Met Ile Lys Leu Tyr Phe Arg Tyr Ser Leu Ala Ile	
1 5 10 15	
gga att aca tca cag caa ttt tcg aat cga aag ttt ttc agt acc cta	96
Gly Ile Thr Ser Gln Gln Phe Ser Asn Arg Lys Phe Phe Ser Thr Leu	
20 25 30	
ttt tct cgg acg tat gct cta att gcc aac atc gtg acg ctc atc atg	144
Phe Ser Arg Thr Tyr Ala Leu Ile Ala Asn Ile Val Thr Leu Ile Met	
35 40 45	
ttg ccc atc gtg atg tgg cag gtt caa ttg gtt ttc cag cag aag aag	192
Leu Pro Ile Val Met Trp Gln Val Gln Leu Val Phe Gln Gln Lys Lys	
50 55 60	
acc ttt cca aag ctc att ttg atc acc aat aac gtg agg gaa gcg gtg	240
Thr Phe Pro Lys Leu Ile Leu Ile Thr Asn Asn Val Arg Glu Ala Val	
65 70 75 80	
tcc ttc ctg gtc ata ttg tac aca gtg ctg tcg cga gga ttt cgc gat	288
Ser Phe Leu Val Ile Leu Tyr Thr Val Leu Ser Arg Gly Phe Arg Asp	
85 90 95	
aca gcg ttt aag gag atg caa cca ttg ctg ctg acg cta ttt cga gaa	336
Thr Ala Phe Lys Glu Met Gln Pro Leu Leu Leu Thr Leu Phe Arg Glu	
100 105 110	
gag aag cga tgt ggc ttt aag ggc ata ggc ggt gta cga agg tcc ttg	384
Glu Lys Arg Cys Gly Phe Lys Gly Ile Gly Gly Val Arg Arg Ser Leu	
115 120 125	
cgg att ctt ctg ttt gtg aag ttc ttc acg ttg tct tgg ctg tgc gtc	432
Arg Ile Leu Leu Phe Val Lys Phe Phe Thr Leu Ser Trp Leu Cys Val	
130 135 140	
aca gac gtt ttg ttt cta ctc tac tcg acc gat gcg tta atc tgg gtt	480
Thr Asp Val Leu Phe Leu Leu Tyr Ser Thr Asp Ala Leu Ile Trp Val	
145 150 155 160	
aac gtg ctc agg ttt ttt ttc aag tgt aat acc aac aat att ttg gaa	528
Asn Val Leu Arg Phe Phe Phe Lys Cys Asn Thr Asn Asn Ile Leu Glu	
165 170 175	
atg gtg ccc atg ggc tac ttt ctc gcc ctg tgg cac att gct cgt ggc	576
Met Val Pro Met Gly Tyr Phe Leu Ala Leu Trp His Ile Ala Arg Gly	
180 185 190	
ttc gat tgc gtc aac agg cgt ctg gac caa att gtg aaa tcg aaa tcg	624
Phe Asp Cys Val Asn Arg Arg Leu Asp Gln Ile Val Lys Ser Lys Ser	
195 200 205	
act aga aaa cac agg gag ctg caa cat ctc tgg cta ctt cat gcc tgc	672
Thr Arg Lys His Arg Glu Leu Gln His Leu Trp Leu Leu His Ala Cys	
210 215 220	

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ctc acc aag aca gcg ctc aac ata aac aag atc tac gcc ccc cag atg 720
Leu Thr Lys Thr Ala Leu Asn Ile Asn Lys Ile Tyr Ala Pro Gln Met
225                230                235                240

ttg gcc tcc cgg ttc gat aac ttt gta aac ggt gta atc cag gcc tat 768
Leu Ala Ser Arg Phe Asp Asn Phe Val Asn Gly Val Ile Gln Ala Tyr
                245                250                255

tgg ggt gct gtg ttc acc ttt gac ctc tcc acg ccc ttc ttt tgg gtc 816
Trp Gly Ala Val Phe Thr Phe Asp Leu Ser Thr Pro Phe Phe Trp Val
                260                265                270

gtt tat gga agt gtc caa tac cac gtg cgc tgc ttg gac tac tat ctc 864
Val Tyr Gly Ser Val Gln Tyr His Val Arg Cys Leu Asp Tyr Tyr Leu
                275                280                285

atc gat aat atg tgc gat gtg gct gtg gag tac cac gat tca gcc aag 912
Ile Asp Asn Met Cys Asp Val Ala Val Glu Tyr His Asp Ser Ala Lys
                290                295                300

cac tcg tgg agt gaa gtt cgt tgg aca aaa gaa gta tct gca ttc ggt 960
His Ser Trp Ser Glu Val Arg Trp Thr Lys Glu Val Ser Ala Phe Gly
305                310                315                320

tct att cta ttg tac ata tgt atg ctc atg caa ctt ctt tca ttt cag 1008
Ser Ile Leu Leu Tyr Ile Cys Met Leu Met Gln Leu Leu Ser Phe Gln
                325                330                335

ata agc tcc tat gtg atc tat gcg aat agt acg aag ttg caa ctc tgg 1056
Ile Ser Ser Tyr Val Ile Tyr Ala Asn Ser Thr Lys Leu Gln Leu Trp
                340                345                350

agt tgt ggg ctt ttt caa gcc aat cgc agc atg tgg ttt gcc atg ata 1104
Ser Cys Gly Leu Phe Gln Ala Asn Arg Ser Met Trp Phe Ala Met Ile
                355                360                365

agc agc gtg ttg tat tac ata cta gtg cta ctg caa ttt cac cta gtt 1152
Ser Ser Val Leu Tyr Tyr Ile Leu Val Leu Leu Gln Phe His Leu Val
                370                375                380

atg agg aag 1161
Met Arg Lys
385

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<210> 56

<211> 387

<212> PRT

<213> Drosophila melanogaster

<400> 56

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Met Val Tyr Trp Met Ile Lys Leu Tyr Phe Arg Tyr Ser Leu Ala Ile
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Gly Ile Thr Ser Gln Gln Phe Ser Asn Arg Lys Phe Phe Ser Thr Leu
      20              25              30

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WO 00/77208

PCT/US00/16211

Phe Ser Arg Thr Tyr Ala Leu Ile Ala Asn Ile Val Thr Leu Ile Met
 35 40 45
 Leu Pro Ile Val Met Trp Gln Val Gln Leu Val Phe Gln Gln Lys Lys
 50 55 60
 Thr Phe Pro Lys Leu Ile Leu Ile Thr Asn Asn Val Arg Glu Ala Val
 65 70 75 80
 Ser Phe Leu Val Ile Leu Tyr Thr Val Leu Ser Arg Gly Phe Arg Asp
 85 90 95
 Thr Ala Phe Lys Glu Met Gln Pro Leu Leu Leu Thr Leu Phe Arg Glu
 100 105 110
 Glu Lys Arg Cys Gly Phe Lys Gly Ile Gly Gly Val Arg Arg Ser Leu
 115 120 125
 Arg Ile Leu Leu Phe Val Lys Phe Phe Thr Leu Ser Trp Leu Cys Val
 130 135 140
 Thr Asp Val Leu Phe Leu Leu Tyr Ser Thr Asp Ala Leu Ile Trp Val
 145 150 155 160
 Asn Val Leu Arg Phe Phe Phe Lys Cys Asn Thr Asn Asn Ile Leu Glu
 165 170 175
 Met Val Pro Met Gly Tyr Phe Leu Ala Leu Trp His Ile Ala Arg Gly
 180 185 190
 Phe Asp Cys Val Asn Arg Arg Leu Asp Gln Ile Val Lys Ser Lys Ser
 195 200 205
 Thr Arg Lys His Arg Glu Leu Gln His Leu Trp Leu Leu His Ala Cys
 210 215 220
 Leu Thr Lys Thr Ala Leu Asn Ile Asn Lys Ile Tyr Ala Pro Gln Met
 225 230 235 240
 Leu Ala Ser Arg Phe Asp Asn Phe Val Asn Gly Val Ile Gln Ala Tyr
 245 250 255
 Trp Gly Ala Val Phe Thr Phe Asp Leu Ser Thr Pro Phe Phe Trp Val
 260 265 270
 Val Tyr Gly Ser Val Gln Tyr His Val Arg Cys Leu Asp Tyr Tyr Leu
 275 280 285
 Ile Asp Asn Met Cys Asp Val Ala Val Glu Tyr His Asp Ser Ala Lys
 290 295 300
 His Ser Trp Ser Glu Val Arg Trp Thr Lys Glu Val Ser Ala Phe Gly
 305 310 315 320
 Ser Ile Leu Leu Tyr Ile Cys Met Leu Met Gln Leu Leu Ser Phe Gln
 325 330 335

WO 00/77208

PCT/US00/16211

Ile Ser Ser Tyr Val Ile Tyr Ala Asn Ser Thr Lys Leu Gln Leu Trp
 340 345 350

Ser Cys Gly Leu Phe Gln Ala Asn Arg Ser Met Trp Phe Ala Met Ile
 355 360 365

Ser Ser Val Leu Tyr Tyr Ile Leu Val Leu Leu Gln Phe His Leu Val
 370 375 380

Met Arg Lys
 385

<210> 57

<211> 1170

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1170)

<223> Coding region GR59D.1

<220>

<221> misc_feature

<222> (1021)

<223> Splice site

<400> 57

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cgg ttg acc ggc gta atc aac ttt aag att gat ttg aaa acg ggt caa 96
 Arg Leu Thr Gly Val Ile Asn Phe Lys Ile Asp Leu Lys Thr Gly Gln
 20 25 30

gcg cta gtt acc aga gga gct acg ctt att tca gtg agc aca cac ttg 144
 Ala Leu Val Thr Arg Gly Ala Thr Leu Ile Ser Val Ser Thr His Leu
 35 40 45

ctg atc ttt gcc cta ctc ctc tac caa aca atg cga aaa agt gtg gtg 192
 Leu Ile Phe Ala Leu Leu Leu Tyr Gln Thr Met Arg Lys Ser Val Val
 50 55 60

aac gtc atg tgg aag tat gcc aat tcc ctt cac gaa tac gtg ttc ctg 240
 Asn Val Met Trp Lys Tyr Ala Asn Ser Leu His Glu Tyr Val Phe Leu
 65 70 75 80

gtc ata gcc ggc ttt cgc gta gtc tgt gtc ttt ctg gag ctg gtc agt 288
 Val Ile Ala Gly Phe Arg Val Val Cys Val Phe Leu Glu Leu Val Ser
 85 90 95

cga tgg tcg cag cgt cgc acc ttt gtg agg ctc ttc aac tca ttc cgg 336
 Arg Trp Ser Gln Arg Arg Thr Phe Val Arg Leu Phe Asn Ser Phe Arg

100	105	110	
aga ctg tat cag aga aat ccg gat	ata atc cag tac tgc cga agg agc		384
Arg Leu Tyr Gln Arg Asn Pro Asp	Ile Ile Gln Tyr Cys Arg Arg Ser		
115	120	125	
atc gtt agc aaa ttc ttt tgc gtc aca atg aca gag aca ctg cac atc			432
Ile Val Ser Lys Phe Phe Cys Val Thr Met Thr Glu Thr Leu His Ile			
130	135	140	
ata gtc acc ttg gcc atg atg agg aat ccg ctg agc att gct ctg gct			480
Ile Val Thr Leu Ala Met Met Arg Asn Arg Leu Ser Ile Ala Leu Ala			
145	150	155	160
ctg cgc att tgg gcc gta ttg agt ctg acg gcc ata ata aat gta atc			528
Leu Arg Ile Trp Ala Val Leu Ser Leu Thr Ala Ile Ile Asn Val Ile			
165	170	175	
atc acg cag tac tat gtg gcc acc gcg tgt gtg cga gga cga tat gcg			576
Ile Thr Gln Tyr Tyr Val Ala Thr Ala Cys Val Arg Gly Arg Tyr Ala			
180	185	190	
ctc ctg aac aag gat ctt cag gcg att gtg acc gaa tcc cag tcg ctg			624
Leu Leu Asn Lys Asp Leu Gln Ala Ile Val Thr Glu Ser Gln Ser Leu			
195	200	205	
gtt ccc aac gga ggt ggc gtc ttt gtg acc aag tgt tgc tac cta gcg			672
Val Pro Asn Gly Gly Gly Val Phe Val Thr Lys Cys Cys Tyr Leu Ala			
210	215	220	
gat cgc ttg gag cga ata gcc aag tcc cag tcg gac cta cag gag ctc			720
Asp Arg Leu Glu Arg Ile Ala Lys Ser Gln Ser Asp Leu Gln Glu Leu			
225	230	235	240
gtc gaa aac ttg tcc acg gca tac gaa gga gaa gtg gtc tgc ctg gtc			768
Val Glu Asn Leu Ser Thr Ala Tyr Glu Gly Glu Val Val Cys Leu Val			
245	250	255	
atc aca tac tat ctg aat atg ctg ggc acc tcg tat ctg ctg ttc agc			816
Ile Thr Tyr Tyr Leu Asn Met Leu Gly Thr Ser Tyr Leu Leu Phe Ser			
260	265	270	
att agc aag tat ggc aat ttt ggg aat aac ctg ctc gtg atc atc act			864
Ile Ser Lys Tyr Gly Asn Phe Gly Asn Asn Leu Leu Val Ile Ile Thr			
275	280	285	
ctt tgt ggc att gtc tac ttc gta ttt tac gtc gtc gat tgc tgg atc			912
Leu Cys Gly Ile Val Tyr Phe Val Phe Tyr Val Val Asp Cys Trp Ile			
290	295	300	
aac gcg ttt aat gtg ttt tac ctt ttg gat gcc cat gat aag atg gtt			960
Asn Ala Phe Asn Val Phe Tyr Leu Leu Asp Ala His Asp Lys Met Val			
305	310	315	320
aag ttg ctg aat aag cga act ttg ttt cag cca ggt ctg gat cat cga			1008
Lys Leu Leu Asn Lys Arg Thr Leu Phe Gln Pro Gly Leu Asp His Arg			

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PCT/US00/16211

325	330	335	
ttg gaa atg gtt ttt gaa aac ttt gct ctg aac ttg gtg cgg aat cca			1056
Leu Glu Met Val Phe Glu Asn Phe Ala Leu Asn Leu Val Arg Asn Pro			
340	345	350	
ttg aag ctc cat atg tac ggc ctt ttc gag ttt ggt cga gga aca tcc			1104
Leu Lys Leu His Met Tyr Gly Leu Phe Glu Phe Gly Arg Gly Thr Ser			
355	360	365	
ttt gcc gtg ttt aac tcc ctg tta aca cac tcc ctt ctc ctc att caa			1152
Phe Ala Val Phe Asn Ser Leu Leu Thr His Ser Leu Leu Leu Ile Gln			
370	375	380	
tac gac gtg caa aac ttc			1170
Tyr Asp Val Gln Asn Phe			
385	390		
<210> 58			
<211> 390			
<212> PRT			
<213> Drosophila melanogaster			
<400> 58			
Met Ala Asp Leu Leu Lys Leu Cys Leu Arg Ile Ala Tyr Ala Tyr Gly			
1	5	10	15
Arg Leu Thr Gly Val Ile Asn Phe Lys Ile Asp Leu Lys Thr Gly Gln			
20	25	30	
Ala Leu Val Thr Arg Gly Ala Thr Leu Ile Ser Val Ser Thr His Leu			
35	40	45	
Leu Ile Phe Ala Leu Leu Leu Tyr Gln Thr Met Arg Lys Ser Val Val			
50	55	60	
Asn Val Met Trp Lys Tyr Ala Asn Ser Leu His Glu Tyr Val Phe Leu			
65	70	75	80
Val Ile Ala Gly Phe Arg Val Val Cys Val Phe Leu Glu Leu Val Ser			
85	90	95	
Arg Trp Ser Gln Arg Arg Thr Phe Val Arg Leu Phe Asn Ser Phe Arg			
100	105	110	
Arg Leu Tyr Gln Arg Asn Pro Asp Ile Ile Gln Tyr Cys Arg Arg Ser			
115	120	125	
Ile Val Ser Lys Phe Phe Cys Val Thr Met Thr Glu Thr Leu His Ile			
130	135	140	
Ile Val Thr Leu Ala Met Met Arg Asn Arg Leu Ser Ile Ala Leu Ala			
145	150	155	160
Leu Arg Ile Trp Ala Val Leu Ser Leu Thr Ala Ile Ile Asn Val Ile			

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<220>  
<221> CDS  
<222> (1)..(1191)  
<223> Coding region GR59D.2
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<220>

<221> misc_feature

<222> (1036)

<223> Splice site

<400> 59

atg gtt gac ttg gtg aag acg att ttg ctc att gcc tac tgg tat ggc	48
Met Val Asp Leu Val Lys Thr Ile Leu Leu Ile Ala Tyr Trp Tyr Gly	
1 5 10 15	
ctt gcc gtg gga gtg tcc aac ttc gag gtg gac tgg cta act gga gaa	96
Leu Ala Val Gly Val Ser Asn Phe Glu Val Asp Trp Leu Thr Gly Glu	
20 25 30	
gcc att gcc acc cga agg act acg atc tat gca gca gtg cat aat gcc	144
Ala Ile Ala Thr Arg Arg Thr Thr Ile Tyr Ala Ala Val His Asn Ala	
35 40 45	
agc ctt atc act ctg ctg att ctt ttc aat ctt ggc aat aac tca ctg	192
Ser Leu Ile Thr Leu Leu Ile Leu Phe Asn Leu Gly Asn Asn Ser Leu	
50 55 60	
aaa tcc gag ttc ata agt gct cga tat ctg cat gag tac ttc ttt atg	240
Lys Ser Glu Phe Ile Ser Ala Arg Tyr Leu His Glu Tyr Phe Phe Met	
65 70 75 80	
ctc atg act gcg gtt cga atc tcg gca gtt ctg ctc tca ctg ata acc	288
Leu Met Thr Ala Val Arg Ile Ser Ala Val Leu Leu Ser Leu Ile Thr	
85 90 95	
aga tgg tat cag cgt tcc aga ttc att cga att tgg aat cag ata cta	336
Arg Trp Tyr Gln Arg Ser Arg Phe Ile Arg Ile Trp Asn Gln Ile Leu	
100 105 110	
gcc cta gtt cgc gat aga cct caa gtg gtt cgt ggg cgc tgg tat cgt	384
Ala Leu Val Arg Asp Arg Pro Gln Val Val Arg Gly Arg Trp Tyr Arg	
115 120 125	
cgc agc att atc ctt aaa ttt gtg ttc tgt gtc ctg tca gat tct ctg	432
Arg Ser Ile Ile Leu Lys Phe Val Phe Cys Val Leu Ser Asp Ser Leu	
130 135 140	
cac acc ata tcg gat gtg agt gcg caa cga aag cgg atc act gct gac	480
His Thr Ile Ser Asp Val Ser Ala Gln Arg Lys Arg Ile Thr Ala Asp	
145 150 155 160	
ctg att gtc aaa ctg agc tta ctg gcc aca ctg acc acc att ttt aac	528
Leu Ile Val Lys Leu Ser Leu Leu Ala Thr Leu Thr Thr Ile Phe Asn	
165 170 175	
atg atc gtg tgc cag tac tac ttg gcc atg gtg cag gtg att ggg ctc	576
Met Ile Val Cys Gln Tyr Tyr Leu Ala Met Val Gln Val Ile Gly Leu	
180 185 190	
tac aag att ctg ctc caa gat ctg cga tgc ttg gtg cgc caa gct gaa	624
Tyr Lys Ile Leu Leu Gln Asp Leu Arg Cys Leu Val Arg Gln Ala Glu	

195	200	205	
tgc atc tgc tcc att cgc aat cgg cga ggt gga gtt tac tcc att cag			672
Cys Ile Cys Ser Ile Arg Asn Arg Arg Gly Gly Val Tyr Ser Ile Gln			
210	215	220	
tgc tgc tcg ttg gca gat cag ctg gat cta att gcc gaa agg cat tac			720
Cys Cys Ser Leu Ala Asp Gln Leu Asp Leu Ile Ala Glu Arg His Tyr			
225	230	235	240
ttt ctg aag gac aga ctt gat gag atg tcg gac ctt ttc cag ata cag			768
Phe Leu Lys Asp Arg Leu Asp Glu Met Ser Asp Leu Phe Gln Ile Gln			
	245	250	255
agc cta agc atg agc ctg gtg tac ttt ttc tcc acc atg ggc tcc atc			816
Ser Leu Ser Met Ser Leu Val Tyr Phe Phe Ser Thr Met Gly Ser Ile			
	260	265	270
tac ttt agc gtc tgt tcg atc ctg tac agc tcc aca gga ttc ggc tct			864
Tyr Phe Ser Val Cys Ser Ile Leu Tyr Ser Ser Thr Gly Phe Gly Ser			
	275	280	285
aca tac tgg ggt ctt ctg ctg att gta cta tcc acg gct tcc ttc tac			912
Thr Tyr Trp Gly Leu Leu Leu Ile Val Leu Ser Thr Ala Ser Phe Tyr			
290	295	300	
atg gac aat tgg ttg tcc gtt aac att ggg ttt cat att cga gat cag			960
Met Asp Asn Trp Leu Ser Val Asn Ile Gly Phe His Ile Arg Asp Gln			
305	310	315	320
cag gac gaa cta ttc cga gtg ctg gcg gat cga act ctg ttc tat cgg			1008
Gln Asp Glu Leu Phe Arg Val Leu Ala Asp Arg Thr Leu Phe Tyr Arg			
	325	330	335
gaa ttg gac aac cga ctg gag gca gcc ttt gag aac ttc caa ctg caa			1056
Glu Leu Asp Asn Arg Leu Glu Ala Ala Phe Glu Asn Phe Gln Leu Gln			
	340	345	350
ctg gcc agt aac cgg cat gaa ttc tac gtt atg ggt ctc ttt aaa atg			1104
Leu Ala Ser Asn Arg His Glu Phe Tyr Val Met Gly Leu Phe Lys Met			
	355	360	365
gaa cgt ggt cgt cta atc gct atg cta agc tca gtg atc act cat act			1152
Glu Arg Gly Arg Leu Ile Ala Met Leu Ser Ser Val Ile Thr His Thr			
370	375	380	
atg gtt ctt gtt cag tgg gaa att caa aac gat gaa tcg			1191
Met Val Leu Val Gln Trp Glu Ile Gln Asn Asp Glu Ser			
385	390	395	

<210> 60

<211> 397

<212> PRT

<213> Drosophila melanogaster

WO 00/77208

PCT/US00/16211

<400> 60

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Met Val Asp Leu Val Lys Thr Ile Leu Leu Ile Ala Tyr Trp Tyr Gly
 1              5              10              15

Leu Ala Val Gly Val Ser Asn Phe Glu Val Asp Trp Leu Thr Gly Glu
      20              25              30

Ala Ile Ala Thr Arg Arg Thr Thr Ile Tyr Ala Ala Val His Asn Ala
      35              40              45

Ser Leu Ile Thr Leu Leu Ile Leu Phe Asn Leu Gly Asn Asn Ser Leu
      50              55              60

Lys Ser Glu Phe Ile Ser Ala Arg Tyr Leu His Glu Tyr Phe Phe Met
 65              70              75              80

Leu Met Thr Ala Val Arg Ile Ser Ala Val Leu Leu Ser Leu Ile Thr
      85              90              95

Arg Trp Tyr Gln Arg Ser Arg Phe Ile Arg Ile Trp Asn Gln Ile Leu
      100              105              110

Ala Leu Val Arg Asp Arg Pro Gln Val Val Arg Gly Arg Trp Tyr Arg
      115              120              125

Arg Ser Ile Ile Leu Lys Phe Val Phe Cys Val Leu Ser Asp Ser Leu
      130              135              140

His Thr Ile Ser Asp Val Ser Ala Gln Arg Lys Arg Ile Thr Ala Asp
145              150              155              160

Leu Ile Val Lys Leu Ser Leu Leu Ala Thr Leu Thr Thr Ile Phe Asn
      165              170              175

Met Ile Val Cys Gln Tyr Tyr Leu Ala Met Val Gln Val Ile Gly Leu
      180              185              190

Tyr Lys Ile Leu Leu Gln Asp Leu Arg Cys Leu Val Arg Gln Ala Glu
      195              200              205

Cys Ile Cys Ser Ile Arg Asn Arg Arg Gly Gly Val Tyr Ser Ile Gln
      210              215              220

Cys Cys Ser Leu Ala Asp Gln Leu Asp Leu Ile Ala Glu Arg His Tyr
225              230              235              240

Phe Leu Lys Asp Arg Leu Asp Glu Met Ser Asp Leu Phe Gln Ile Gln
      245              250              255

Ser Leu Ser Met Ser Leu Val Tyr Phe Phe Ser Thr Met Gly Ser Ile
      260              265              270

Tyr Phe Ser Val Cys Ser Ile Leu Tyr Ser Ser Thr Gly Phe Gly Ser
      275              280              285

Thr Tyr Trp Gly Leu Leu Leu Ile Val Leu Ser Thr Ala Ser Phe Tyr

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290 295 300
 Met Asp Asn Trp Leu Ser Val Asn Ile Gly Phe His Ile Arg Asp Gln
 305 310 315 320
 Gln Asp Glu Leu Phe Arg Val Leu Ala Asp Arg Thr Leu Phe Tyr Arg
 325 330 335
 Glu Leu Asp Asn Arg Leu Glu Ala Ala Phe Glu Asn Phe Gln Leu Gln
 340 345 350
 Leu Ala Ser Asn Arg His Glu Phe Tyr Val Met Gly Leu Phe Lys Met
 355 360 365
 Glu Arg Gly Arg Leu Ile Ala Met Leu Ser Ser Val Ile Thr His Thr
 370 375 380
 Met Val Leu Val Gln Trp Glu Ile Gln Asn Asp Glu Ser
 385 390 395

<210> 61
 <211> 1089
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1089)
 <223> Coding region GR59E.1

<220>
 <221> misc_feature
 <222> (52)..(988)
 <223> Splice sites before positions 52, 835 and 988

<400> 61
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 1 5 10 15
 gaa aga ttc tat cga ttg gtc cac ttg agt tgg atg att ctg tgg tac 96
 Glu Arg Phe Tyr Arg Leu Val His Leu Ser Trp Met Ile Leu Trp Tyr
 20 25 30
 gga ttg ttc gtc ctg ggc tcc tac tgg gaa ttc gtg ctc gtc acc aca 144
 Gly Leu Phe Val Leu Gly Ser Tyr Trp Glu Phe Val Leu Val Thr Thr
 35 40 45
 cag agg gta tcc ttg gac cgc tac cta aat gct atc gag tcc gcc atc 192
 Gln Arg Val Ser Leu Asp Arg Tyr Leu Asn Ala Ile Glu Ser Ala Ile
 50 55 60
 tat gta gtt cac ata ttt tcc atc atg ctc ctc acc tgg cag tgc agg 240
 Tyr Val Val His Ile Phe Ser Ile Met Leu Leu Thr Trp Gln Cys Arg

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PCT/US00/16211

65	70	75	80	
aac tgg gct ccc aag ctg atg acg aac atc gtt aca tcc gac ctg aat				288
Asn Trp Ala Pro Lys Leu Met Thr Asn Ile Val Thr Ser Asp Leu Asn				
	85	90	95	
aga gct tat acc ata gac tgc aac aga acc aag aga ttt att agg ctc				336
Arg Ala Tyr Thr Ile Asp Cys Asn Arg Thr Lys Arg Phe Ile Arg Leu				
	100	105	110	
cag ctg ttt ctg gtg gga att ttt gcc tgt cta gcg atc ttc ttc aac				384
Gln Leu Phe Leu Val Gly Ile Phe Ala Cys Leu Ala Ile Phe Phe Asn				
	115	120	125	
atc tgg acc cac aaa ttc gtt gta tat aga tcg atc ctg agc atc aac				432
Ile Trp Thr His Lys Phe Val Val Tyr Arg Ser Ile Leu Ser Ile Asn				
	130	135	140	
agc tac gtg atg ccc aat atc ata agt agc ata tcc ttc gcc cag tac				480
Ser Tyr Val Met Pro Asn Ile Ile Ser Ser Ile Ser Phe Ala Gln Tyr				
	145	150	155	160
tac ctg ctg ctt caa gga atc gct tgg cgt caa agg agg cta act gaa				528
Tyr Leu Leu Leu Gln Gly Ile Ala Trp Arg Gln Arg Arg Leu Thr Glu				
	165	170	175	
ggc ctg gag cgg gaa cta act cat ttg cac agt ccc cga ata tca gag				576
Gly Leu Glu Arg Glu Leu Thr His Leu His Ser Pro Arg Ile Ser Glu				
	180	185	190	
gtc cag aaa atc cga atg cat cac gcg aat cta att gat ttt acc aag				624
Val Gln Lys Ile Arg Met His His Ala Asn Leu Ile Asp Phe Thr Lys				
	195	200	205	
gcg gtg aac cgg acg ttt cag tac tcc atc cta ctg ctc ttc gtg gga				672
Ala Val Asn Arg Thr Phe Gln Tyr Ser Ile Leu Leu Leu Phe Val Gly				
	210	215	220	
tgt ttc ctg aac ttc aac ctc gtc ctg ttc ctc gtc tat cag ggc att				720
Cys Phe Leu Asn Phe Asn Leu Val Leu Phe Leu Val Tyr Gln Gly Ile				
	225	230	235	240
gag aat cct tcc atg gcc gac ttc acc aag tgg gta tgc atg ctt ctc				768
Glu Asn Pro Ser Met Ala Asp Phe Thr Lys Trp Val Cys Met Leu Leu				
	245	250	255	
tgg ctg gcc atg cac gtg gga aag gtg tgc agc atc ctg cat ttc aac				816
Trp Leu Ala Met His Val Gly Lys Val Cys Ser Ile Leu His Phe Asn				
	260	265	270	
cag agt atc caa aat gag cat tcc acg tgc ttg acc tta ttg agt aga				864
Gln Ser Ile Gln Asn Glu His Ser Thr Cys Leu Thr Leu Leu Ser Arg				
	275	280	285	
gtg tcg tat gcc aga aaa gat att cag gat acc ata acc cat ttc atc				912
Val Ser Tyr Ala Arg Lys Asp Ile Gln Asp Thr Ile Thr His Phe Ile				

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PCT/US00/16211

290	295	300	
atc caa atg cgg acg aat gtg cgg cag cat gtc gtg tgt gga gtc ata			960
Ile Gln Met Arg Thr Asn Val Arg Gln His Val Val Cys Gly Val Ile			
305	310	315	320
aat ctg gac ctc aaa ttc tta acc act ttg ttg gtg gcc tct gct gat			1008
Asn Leu Asp Leu Lys Phe Leu Thr Thr Leu Leu Val Ala Ser Ala Asp			
	325	330	335
ttc ttc atc ttc ctg ctg caa tac gat gtc acc tac gaa gcg ttg tcc			1056
Phe Phe Ile Phe Leu Leu Gln Tyr Asp Val Thr Tyr Glu Ala Leu Ser			
	340	345	350
aag tcg gtt cag ggc aat gtc act aga tat aag			1089
Lys Ser Val Gln Gly Asn Val Thr Arg Tyr Lys			
	355	360	

<210> 62

<211> 363

<212> PRT

<213> Drosophila melanogaster

<400> 62

Met Arg Ser Ser Ala Thr Lys Gly Ala Lys Leu Lys Asn Ser Pro Arg	
1	15

Glu Arg Phe Tyr Arg Leu Val His Leu Ser Trp Met Ile Leu Trp Tyr	
20	30

Gly Leu Phe Val Leu Gly Ser Tyr Trp Glu Phe Val Leu Val Thr Thr	
35	45

Gln Arg Val Ser Leu Asp Arg Tyr Leu Asn Ala Ile Glu Ser Ala Ile	
50	60

Tyr Val Val His Ile Phe Ser Ile Met Leu Leu Thr Trp Gln Cys Arg	
65	80

Asn Trp Ala Pro Lys Leu Met Thr Asn Ile Val Thr Ser Asp Leu Asn	
85	95

Arg Ala Tyr Thr Ile Asp Cys Asn Arg Thr Lys Arg Phe Ile Arg Leu	
100	110

Gln Leu Phe Leu Val Gly Ile Phe Ala Cys Leu Ala Ile Phe Phe Asn	
115	125

Ile Trp Thr His Lys Phe Val Val Tyr Arg Ser Ile Leu Ser Ile Asn	
130	140

Ser Tyr Val Met Pro Asn Ile Ile Ser Ser Ile Ser Phe Ala Gln Tyr	
145	160

Tyr Leu Leu Leu Gln Gly Ile Ala Trp Arg Gln Arg Arg Leu Thr Glu	
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WO 00/77208

PCT/US00/16211

	165		170		175										
Gly	Leu	Glu	Arg	Glu	Leu	Thr	His	Leu	His	Ser	Pro	Arg	Ile	Ser	Glu
			180					185					190		
Val	Gln	Lys	Ile	Arg	Met	His	His	Ala	Asn	Leu	Ile	Asp	Phe	Thr	Lys
		195					200					205			
Ala	Val	Asn	Arg	Thr	Phe	Gln	Tyr	Ser	Ile	Leu	Leu	Leu	Phe	Val	Gly
	210					215					220				
Cys	Phe	Leu	Asn	Phe	Asn	Leu	Val	Leu	Phe	Leu	Val	Tyr	Gln	Gly	Ile
225					230					235				240	
Glu	Asn	Pro	Ser	Met	Ala	Asp	Phe	Thr	Lys	Trp	Val	Cys	Met	Leu	Leu
				245					250					255	
Trp	Leu	Ala	Met	His	Val	Gly	Lys	Val	Cys	Ser	Ile	Leu	His	Phe	Asn
			260					265					270		
Gln	Ser	Ile	Gln	Asn	Glu	His	Ser	Thr	Cys	Leu	Thr	Leu	Leu	Ser	Arg
		275					280					285			
Val	Ser	Tyr	Ala	Arg	Lys	Asp	Ile	Gln	Asp	Thr	Ile	Thr	His	Phe	Ile
	290					295					300				
Ile	Gln	Met	Arg	Thr	Asn	Val	Arg	Gln	His	Val	Val	Cys	Gly	Val	Ile
305					310					315				320	
Asn	Leu	Asp	Leu	Lys	Phe	Leu	Thr	Thr	Leu	Leu	Val	Ala	Ser	Ala	Asp
				325					330					335	
Phe	Phe	Ile	Phe	Leu	Leu	Gln	Tyr	Asp	Val	Thr	Tyr	Glu	Ala	Leu	Ser
			340					345					350		
Lys	Ser	Val	Gln	Gly	Asn	Val	Thr	Arg	Tyr	Lys					
		355					360								

<210> 63
 <211> 1197
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1197)
 <223> Coding region GR59E.2

<220>
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 <222> (937)..(1093)
 <223> Splice sites before positions 937 and 1093

<400> 63

WO 00/77208

PCT/US00/16211

atg gac agt tcg tac tgg gag aat ctg ctg ctg acc atc aat cgg ttc	48
Met Asp Ser Ser Tyr Trp Glu Asn Leu Leu Leu Thr Ile Asn Arg Phe	
1 5 10 15	
ctg ggc gtg tat ccc agt ggg aga gtg ggc gta ctc cgc tgg ctc cac	96
Leu Gly Val Tyr Pro Ser Gly Arg Val Gly Val Leu Arg Trp Leu His	
20 25 30	
acg ctc tgg agc ctg ttc ctg ctt atg tac atc tgg act ggc agc att	144
Thr Leu Trp Ser Leu Phe Leu Leu Met Tyr Ile Trp Thr Gly Ser Ile	
35 40 45	
gtt aag tgc ttg gag ttc aca gtg gag ata ccc act att gaa aaa ctg	192
Val Lys Cys Leu Glu Phe Thr Val Glu Ile Pro Thr Ile Glu Lys Leu	
50 55 60	
ctc tat ctg atg gag ttc cct gga aat atg gcc acc att gcc atc ctg	240
Leu Tyr Leu Met Glu Phe Pro Gly Asn Met Ala Thr Ile Ala Ile Leu	
65 70 75 80	
gta tac tat gcc gta ttg aac cgt cca ctt gct cac gga gcg gaa ctc	288
Val Tyr Tyr Ala Val Leu Asn Arg Pro Leu Ala His Gly Ala Glu Leu	
85 90 95	
cag att gag cgg atc atc aca gga ctc aaa ggc aaa gct aag cga ctg	336
Gln Ile Glu Arg Ile Ile Thr Gly Leu Lys Gly Lys Ala Lys Arg Leu	
100 105 110	
gtt tat aag aga cat ggt cag agg act ctt cat ctg atg gcg acc act	384
Val Tyr Lys Arg His Gly Gln Arg Thr Leu His Leu Met Ala Thr Thr	
115 120 125	
tta gtc ttc cat ggc ctg tgt gtc ctg gtt gac gtg gtc aac tat gac	432
Leu Val Phe His Gly Leu Cys Val Leu Val Asp Val Val Asn Tyr Asp	
130 135 140	
ttc gag ttc tgg acc act tgg agc agt aac agt gtc tac aat ttg cct	480
Phe Glu Phe Trp Thr Thr Trp Ser Ser Asn Ser Val Tyr Asn Leu Pro	
145 150 155 160	
ggt cta atg atg agt ctg ggg gtg ctc cag tat gcc cag ccc gtc cat	528
Gly Leu Met Met Ser Leu Gly Val Leu Gln Tyr Ala Gln Pro Val His	
165 170 175	
ttc cta tgg ctg gtg atg gac cag atg agg atg tgt ctc aag gag ctg	576
Phe Leu Trp Leu Val Met Asp Gln Met Arg Met Cys Leu Lys Glu Leu	
180 185 190	
aag ttg ctg cag aga cca ccg cag ggt tcg acc aag ttg gat gcc tgc	624
Lys Leu Leu Gln Arg Pro Pro Gln Gly Ser Thr Lys Leu Asp Ala Cys	
195 200 205	
tac gag tcc gcc ttt gct gtc cta gta gat gcg ggt gga gga tct gct	672
Tyr Glu Ser Ala Phe Ala Val Leu Val Asp Ala Gly Gly Gly Ser Ala	
210 215 220	

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PCT/US00/16211

ctg atg att gaa gag atg aga tac acc tgc aat ctt atc gag cag gtc 720
 Leu Met Ile Glu Glu Met Arg Tyr Thr Cys Asn Leu Ile Glu Gln Val
 225 230 235 240

cac agc cag ttt cta ctg aga ttt ggt ctc tat ctg gtg tta aac ctg 768
 His Ser Gln Phe Leu Leu Arg Phe Gly Leu Tyr Leu Val Leu Asn Leu
 245 250 255

ctc aat tcc ttg gtc agc atc tgt gtg gag tta tac ttg atc ttc aac 816
 Leu Asn Ser Leu Val Ser Ile Cys Val Glu Leu Tyr Leu Ile Phe Asn
 260 265 270

ttc ttt gag act cct ctc tgg gag gag tcc gtg ctc ctc gta tac cgc 864
 Phe Phe Glu Thr Pro Leu Trp Glu Glu Ser Val Leu Leu Val Tyr Arg
 275 280 285

ctg ctc tgg ttg gcc atg cat ggc ggt cgt atc tgg ttc atc ctg tcg 912
 Leu Leu Trp Leu Ala Met His Gly Gly Arg Ile Trp Phe Ile Leu Ser
 290 295 300

gtc aac gaa cag atc ctg gag cag aaa tgt aac ctt tgc cag ctg ctc 960
 Val Asn Glu Gln Ile Leu Glu Gln Lys Cys Asn Leu Cys Gln Leu Leu
 305 310 315 320

aac gag ttg gag gtc tgc agc tcc cgc ctg cag agg acc att aat cgc 1008
 Asn Glu Leu Glu Val Cys Ser Ser Arg Leu Gln Arg Thr Ile Asn Arg
 325 330 335

ttc ctg ctg cag ctc cag cgg agt att gac cag ccc ctg gaa gcc tgc 1056
 Phe Leu Leu Gln Leu Gln Arg Ser Ile Asp Gln Pro Leu Glu Ala Cys
 340 345 350

gga atc gtt acg ctg gac act cgc tca ttg ggc ggg ttt atc ggc gtc 1104
 Gly Ile Val Thr Leu Asp Thr Arg Ser Leu Gly Gly Phe Ile Gly Val
 355 360 365

ctg atg gcc att gtc att ttc ctc att caa atc gga ctg ggc aat aag 1152
 Leu Met Ala Ile Val Ile Phe Leu Ile Gln Ile Gly Leu Gly Asn Lys
 370 375 380

tcg cta atg ggc gtt gcc ctc aac aga tcc aat tgg gtt tac gtt 1197
 Ser Leu Met Gly Val Ala Leu Asn Arg Ser Asn Trp Val Tyr Val
 385 390 395

<210> 64

<211> 399

<212> PRT

<213> Drosophila melanogaster

<400> 64

Met Asp Ser Ser Tyr Trp Glu Asn Leu Leu Leu Thr Ile Asn Arg Phe
 1 5 10 15

Leu Gly Val Tyr Pro Ser Gly Arg Val Gly Val Leu Arg Trp Leu His
 20 25 30

Thr Leu Trp Ser Leu Phe Leu Leu Met Tyr Ile Trp Thr Gly Ser Ile
 35 40 45
 Val Lys Cys Leu Glu Phe Thr Val Glu Ile Pro Thr Ile Glu Lys Leu
 50 55 60
 Leu Tyr Leu Met Glu Phe Pro Gly Asn Met Ala Thr Ile Ala Ile Leu
 65 70 75 80
 Val Tyr Tyr Ala Val Leu Asn Arg Pro Leu Ala His Gly Ala Glu Leu
 85 90 95
 Gln Ile Glu Arg Ile Ile Thr Gly Leu Lys Gly Lys Ala Lys Arg Leu
 100 105 110
 Val Tyr Lys Arg His Gly Gln Arg Thr Leu His Leu Met Ala Thr Thr
 115 120 125
 Leu Val Phe His Gly Leu Cys Val Leu Val Asp Val Val Asn Tyr Asp
 130 135 140
 Phe Glu Phe Trp Thr Thr Trp Ser Ser Asn Ser Val Tyr Asn Leu Pro
 145 150 155 160
 Gly Leu Met Met Ser Leu Gly Val Leu Gln Tyr Ala Gln Pro Val His
 165 170 175
 Phe Leu Trp Leu Val Met Asp Gln Met Arg Met Cys Leu Lys Glu Leu
 180 185 190
 Lys Leu Leu Gln Arg Pro Pro Gln Gly Ser Thr Lys Leu Asp Ala Cys
 195 200 205
 Tyr Glu Ser Ala Phe Ala Val Leu Val Asp Ala Gly Gly Gly Ser Ala
 210 215 220
 Leu Met Ile Glu Glu Met Arg Tyr Thr Cys Asn Leu Ile Glu Gln Val
 225 230 235 240
 His Ser Gln Phe Leu Leu Arg Phe Gly Leu Tyr Leu Val Leu Asn Leu
 245 250 255
 Leu Asn Ser Leu Val Ser Ile Cys Val Glu Leu Tyr Leu Ile Phe Asn
 260 265 270
 Phe Phe Glu Thr Pro Leu Trp Glu Glu Ser Val Leu Leu Val Tyr Arg
 275 280 285
 Leu Leu Trp Leu Ala Met His Gly Gly Arg Ile Trp Phe Ile Leu Ser
 290 295 300
 Val Asn Glu Gln Ile Leu Glu Gln Lys Cys Asn Leu Cys Gln Leu Leu
 305 310 315 320
 Asn Glu Leu Glu Val Cys Ser Ser Arg Leu Gln Arg Thr Ile Asn Arg
 325 330 335

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Phe Leu Leu Gln Leu Gln Arg Ser Ile Asp Gln Pro Leu Glu Ala Cys
 340 345 350

Gly Ile Val Thr Leu Asp Thr Arg Ser Leu Gly Gly Phe Ile Gly Val
 355 360 365

Leu Met Ala Ile Val Ile Phe Leu Ile Gln Ile Gly Leu Gly Asn Lys
 370 375 380

Ser Leu Met Gly Val Ala Leu Asn Arg Ser Asn Trp Val Tyr Val
 385 390 395

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 <212> DNA
 <213> Drosophila melanogaster

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 <223> Coding region GR61D.1

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 1 5 10 15

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 Gln Lys Gln Arg Ala Ile Leu Ala Met Arg Trp Arg Cys Ala Gln Gly
 20 25 30

gga ttg gag ttc gag cag ctg gac acc ttc tac gga gcc atc agg cca 144
 Gly Leu Glu Phe Glu Gln Leu Asp Thr Phe Tyr Gly Ala Ile Arg Pro
 35 40 45

tgt aag acc act ttt cca aac cac ttt cat atg tgt cta aac ata tta 192
 Cys Lys Thr Thr Phe Pro Asn His Phe His Met Cys Leu Asn Ile Leu
 50 55 60

caa tgg aca ata gat ctg tgt gtg gcg cag ttc ttc ggc att atg cct 240
 Gln Trp Thr Ile Asp Leu Cys Val Ala Gln Phe Phe Gly Ile Met Pro
 65 70 75 80

ttg tcg aat atc cgg agt cgc gat ccc cag gat gtg aag ttc aag gta 288
 Leu Ser Asn Ile Arg Ser Arg Asp Pro Gln Asp Val Lys Phe Lys Val
 85 90 95

agg agc att ggc ctg gca gtc acc ggt ctc ttc ctt ttg ctc ggt ggc 336
 Arg Ser Ile Gly Leu Ala Val Thr Gly Leu Phe Leu Leu Leu Gly Gly
 100 105 110

atg aag acc ttg gtc ggt gcc aat att ctc ttc aca gag ggt ctg aat 384
 Met Lys Thr Leu Val Gly Ala Asn Ile Leu Phe Thr Glu Gly Leu Asn
 115 120 125

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gcc aag aat atc gtg ggt ttg gtt ttc ctt atc gtg ggc atg gtc aac	432
Ala Lys Asn Ile Val Gly Leu Val Phe Leu Ile Val Gly Met Val Asn	
130 135 140	
tggt cta aac ttc gtg ggc ttt gct cgc tcc tgg tcg cac ata atg ctg	480
Trp Leu Asn Phe Val Gly Phe Ala Arg Ser Trp Ser His Ile Met Leu	
145 150 155 160	
ccc tgg agt tcg gtg gac att ctg atg ctc ttt ccg ccc tac aaa cgt	528
Pro Trp Ser Ser Val Asp Ile Leu Met Leu Phe Pro Pro Tyr Lys Arg	
165 170 175	
ggc aag cga agc ctt cgg tca aag gtc aac gtc ctt gct ctg agt gtg	576
Gly Lys Arg Ser Leu Arg Ser Lys Val Asn Val Leu Ala Leu Ser Val	
180 185 190	
gtc gtc ctg gca gcg acc aca tgc tgt act acg cct ctg gct act gca	624
Val Val Leu Ala Ala Thr Thr Cys Cys Thr Thr Pro Leu Ala Thr Ala	
195 200 205	
gct ata gca tgc aca tcc tgc agt gcc aca caa acc act cgc gta tta	672
Ala Ile Ala Cys Thr Ser Cys Ser Ala Thr Gln Thr Thr Arg Val Leu	
210 215 220	
cct ttg gac ttt att tgg aga agg agt tct ccg aca tca tgt tca tca	720
Pro Leu Asp Phe Ile Trp Arg Arg Ser Ser Pro Thr Ser Cys Ser Ser	
225 230 235 240	
tgc cat tca ata tat ttt cca ttg gct aaa tgg agc ctt cac ctt tct	768
Cys His Ser Ile Tyr Phe Pro Leu Ala Lys Trp Ser Leu His Leu Ser	
245 250 255	
gtg gaa ctt cat gga cat ctt tat tgt gat gac cag tat tgg act ggc	816
Val Glu Leu His Gly His Leu Tyr Cys Asp Asp Gln Tyr Trp Thr Gly	
260 265 270	
gca aag gtt tca aca gtt tgc cgc tcg agt tgg cgc act gga ggg tcg	864
Ala Lys Val Ser Thr Val Cys Arg Ser Ser Trp Arg Thr Gly Gly Ser	
275 280 285	
tgt aaa ata atc caa act att tca atg tat ttc tct ttt aaa tcc cca	912
Cys Lys Ile Ile Gln Thr Ile Ser Met Tyr Phe Ser Phe Lys Ser Pro	
290 295 300	
tcc cat tta gca tgt tcc cga agc ctt gtg gta cga cat tcg gag gga	960
Ser His Leu Ala Cys Ser Arg Ser Leu Val Val Arg His Ser Glu Gly	
305 310 315 320	
tca cat tcg cct ttg cga gct ggc cac aaa ctg cgg cat ccc ata aac	1008
Ser His Ser Pro Leu Arg Ala Gly His Lys Leu Arg His Pro Ile Asn	
325 330 335	
tac gtt tac ttc tgg tac tcg ctg atc ttc ctg ctg gcc agg acg agt	1056
Tyr Val Tyr Phe Trp Tyr Ser Leu Ile Phe Leu Leu Ala Arg Thr Ser	
340 345 350	

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ctg gtt ttc atg act gcc tcc aag atc cac gat gcc tcg ctt ctg ccc 1104
 Leu Val Phe Met Thr Ala Ser Lys Ile His Asp Ala Ser Leu Leu Pro
 355 360 365

ctg agg tcc ttg tac ttg gtg ccc agc gat ggc tgg acg cag gag gtg 1152
 Leu Arg Ser Leu Tyr Leu Val Pro Ser Asp Gly Trp Thr Gln Glu Val
 370 375 380

cag aga ttt gcc gac cag ctg acc agc gag ttt gtc gga ttg tct gga 1200
 Gln Arg Phe Ala Asp Gln Leu Thr Ser Glu Phe Val Gly Leu Ser Gly
 385 390 395 400

tat cgt ctc ttc tgc ttg aca aga aag agt ctc ttc gga atg cta gcc 1248
 Tyr Arg Leu Phe Cys Leu Thr Arg Lys Ser Leu Phe Gly Met Leu Ala
 405 410 415

acc ctg gtg acc tac gaa ctt atg ctg ctg caa ata gat gct aag agc 1296
 Thr Leu Val Thr Tyr Glu Leu Met Leu Leu Gln Ile Asp Ala Lys Ser
 420 425 430

cac aag gga ctg cgg tgc gcg 1317
 His Lys Gly Leu Arg Cys Ala
 435

<210> 66

<211> 439

<212> PRT

<213> Drosophila melanogaster

<400> 66

Met Ser Arg Thr Ser Asp Asp Ile Arg Lys His Leu Lys Val Arg Arg
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Gln Lys Gln Arg Ala Ile Leu Ala Met Arg Trp Arg Cys Ala Gln Gly
 20 25 30

Gly Leu Glu Phe Glu Gln Leu Asp Thr Phe Tyr Gly Ala Ile Arg Pro
 35 40 45

Cys Lys Thr Thr Phe Pro Asn His Phe His Met Cys Leu Asn Ile Leu
 50 55 60

Gln Trp Thr Ile Asp Leu Cys Val Ala Gln Phe Phe Gly Ile Met Pro
 65 70 75 80

Leu Ser Asn Ile Arg Ser Arg Asp Pro Gln Asp Val Lys Phe Lys Val
 85 90 95

Arg Ser Ile Gly Leu Ala Val Thr Gly Leu Phe Leu Leu Leu Gly Gly
 100 105 110

Met Lys Thr Leu Val Gly Ala Asn Ile Leu Phe Thr Glu Gly Leu Asn
 115 120 125

Ala Lys Asn Ile Val Gly Leu Val Phe Leu Ile Val Gly Met Val Asn

130	135	140
Trp Leu Asn Phe Val Gly Phe Ala Arg Ser Trp Ser His Ile Met Leu		
145	150	155 160
Pro Trp Ser Ser Val Asp Ile Leu Met Leu Phe Pro Pro Tyr Lys Arg		
	165	170 175
Gly Lys Arg Ser Leu Arg Ser Lys Val Asn Val Leu Ala Leu Ser Val		
	180	185 190
Val Val Leu Ala Ala Thr Thr Cys Cys Thr Thr Pro Leu Ala Thr Ala		
	195	200 205
Ala Ile Ala Cys Thr Ser Cys Ser Ala Thr Gln Thr Thr Arg Val Leu		
	210	215 220
Pro Leu Asp Phe Ile Trp Arg Arg Ser Ser Pro Thr Ser Cys Ser Ser		
	225	230 235 240
Cys His Ser Ile Tyr Phe Pro Leu Ala Lys Trp Ser Leu His Leu Ser		
	245	250 255
Val Glu Leu His Gly His Leu Tyr Cys Asp Asp Gln Tyr Trp Thr Gly		
	260	265 270
Ala Lys Val Ser Thr Val Cys Arg Ser Ser Trp Arg Thr Gly Gly Ser		
	275	280 285
Cys Lys Ile Ile Gln Thr Ile Ser Met Tyr Phe Ser Phe Lys Ser Pro		
	290	295 300
Ser His Leu Ala Cys Ser Arg Ser Leu Val Val Arg His Ser Glu Gly		
	305	310 315 320
Ser His Ser Pro Leu Arg Ala Gly His Lys Leu Arg His Pro Ile Asn		
	325	330 335
Tyr Val Tyr Phe Trp Tyr Ser Leu Ile Phe Leu Leu Ala Arg Thr Ser		
	340	345 350
Leu Val Phe Met Thr Ala Ser Lys Ile His Asp Ala Ser Leu Leu Pro		
	355	360 365
Leu Arg Ser Leu Tyr Leu Val Pro Ser Asp Gly Trp Thr Gln Glu Val		
	370	375 380
Gln Arg Phe Ala Asp Gln Leu Thr Ser Glu Phe Val Gly Leu Ser Gly		
	385	390 395 400
Tyr Arg Leu Phe Cys Leu Thr Arg Lys Ser Leu Phe Gly Met Leu Ala		
	405	410 415
Thr Leu Val Thr Tyr Glu Leu Met Leu Leu Gln Ile Asp Ala Lys Ser		
	420	425 430

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His Lys Gly Leu Arg Cys Ala
435

<210> 67
<211> 1080
<212> DNA
<213> Drosophila melanogaster

<220>
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<222> (1)..(1080)
<223> Coding region GR65C.1

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cct cca ttc atg tcc ttg aag ggc ggc aaa tcg ggt ttc gga tca att 96
Pro Pro Phe Met Ser Leu Lys Gly Gly Lys Ser Gly Phe Gly Ser Ile
20 25 30

gtt tgg cca tcc gcg atg agg gaa gtg aat ctg ctc aac cgc ttt aca 144
Val Trp Pro Ser Ala Met Arg Glu Val Asn Leu Leu Asn Arg Phe Thr
35 40 45

cgc cag ttc ctg ttt ctc atc gtg ttg gtg acc cag atc tgc ggg gtc 192
Arg Gln Phe Leu Phe Leu Ile Val Leu Val Thr Gln Ile Cys Gly Val
50 55 60

gcc acc ttt gtg tac aac tcg aag gcg caa tgc ttt cgt cag tcc gga 240
Ala Thr Phe Val Tyr Asn Ser Lys Ala Gln Cys Phe Arg Gln Ser Gly
65 70 75 80

ttt ctg cgg ttc tac tcc agc tta gtt ctc att ttt ctg gca ctt ttc 288
Phe Leu Arg Phe Tyr Ser Ser Leu Val Leu Ile Phe Leu Ala Leu Phe
85 90 95

ctg att gtt acc acg agt aaa atg ttt cat aat ctg caa gct gtg tgg 336
Leu Ile Val Thr Thr Ser Lys Met Phe His Asn Leu Gln Ala Val Trp
100 105 110

cca tat gtg gta gga agt gtt atc ata ttg gtg gta aga ata cac gga 384
Pro Tyr Val Val Gly Ser Val Ile Ile Leu Val Val Arg Ile His Gly
115 120 125

ctt ttg gaa agt gca gag atc gtg gag ttg cta aac caa atg ctg aga 432
Leu Leu Glu Ser Ala Glu Ile Val Glu Leu Leu Asn Gln Met Leu Arg
130 135 140

atc atg agg cag gtg aat cta atg gcc agg cac ccg aat ctg ttt cgc 480
Ile Met Arg Gln Val Asn Leu Met Ala Arg His Pro Asn Leu Phe Arg
145 150 155 160

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ctg aaa cat ttg ctg ctc ctt ctt ttg gcc ctg caa aat ctt tta aga	528
Leu Lys His Leu Leu Leu Leu Leu Leu Ala Leu Gln Asn Leu Leu Arg	
165 170 175	
tca ctg aat acg ata gtg gga ata agt aac cac tct gct gaa gct tat	576
Ser Leu Asn Thr Ile Val Gly Ile Ser Asn His Ser Ala Glu Ala Tyr	
180 185 190	
gac tct ttt ctt aat agc gtt atc cta tta att ata ctg gcc gtc ctg	624
Asp Ser Phe Leu Asn Ser Val Ile Leu Leu Ile Ile Leu Ala Val Leu	
195 200 205	
ctg agc ttt ctt ctt cag atc acc atc aat att tgc ctc ttt gta gtg	672
Leu Ser Phe Leu Leu Gln Ile Thr Ile Asn Ile Cys Leu Phe Val Val	
210 215 220	
ctc att gcc acg tat agc gaa cta cac cat tgc act cga cga atc tca	720
Leu Ile Ala Thr Tyr Ser Glu Leu His His Cys Thr Arg Arg Ile Ser	
225 230 235 240	
aat gat atg gat aag ctc aga ctt cat tct gtc cat gaa agt ggt caa	768
Asn Asp Met Asp Lys Leu Arg Leu His Ser Val His Glu Ser Gly Gln	
245 250 255	
ttt atg gtg ttg gta aaa caa ctt caa gga atc act gaa aaa tta att	816
Phe Met Val Leu Val Lys Gln Leu Gln Gly Ile Thr Glu Lys Leu Ile	
260 265 270	
cga ctg cgt caa aat gtc ttt cat att acc gtc aga atc ata cgg cat	864
Arg Leu Arg Gln Asn Val Phe His Ile Thr Val Arg Ile Ile Arg His	
275 280 285	
ttc cga ttt cat tgg ctg tgt gct att atc tac gga tta tta cca ttc	912
Phe Arg Phe His Trp Leu Cys Ala Ile Ile Tyr Gly Leu Leu Pro Phe	
290 295 300	
ttt agt tta aca gct aaa gat caa aat ggt ttt aac ttc ctc atc att	960
Phe Ser Leu Thr Ala Lys Asp Gln Asn Gly Phe Asn Phe Leu Ile Ile	
305 310 315 320	
tcc gca ttg aac ata ata ttc cag tgg act att ttt gcg att ctt tct	1008
Ser Ala Leu Asn Ile Ile Phe Gln Trp Thr Ile Phe Ala Ile Leu Ser	
325 330 335	
cgt gaa tca aga atc acc cgg agt tta tgc act ttt cac ttg acc aat	1056
Arg Glu Ser Arg Ile Thr Arg Ser Leu Cys Thr Phe His Leu Thr Asn	
340 345 350	
tac cat aag gaa act gct aga acg	1080
Tyr His Lys Glu Thr Ala Arg Thr	
355 360	

<210> 68

<211> 360

<212> PRT

<213> Drosophila melanogaster

<400> 68

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 Pro Pro Phe Met Ser Leu Lys Gly Gly Lys Ser Gly Phe Gly Ser Ile
 20 25 30
 Val Trp Pro Ser Ala Met Arg Glu Val Asn Leu Leu Asn Arg Phe Thr
 35 40 45
 Arg Gln Phe Leu Phe Leu Ile Val Leu Val Thr Gln Ile Cys Gly Val
 50 55 60
 Ala Thr Phe Val Tyr Asn Ser Lys Ala Gln Cys Phe Arg Gln Ser Gly
 65 70 75 80
 Phe Leu Arg Phe Tyr Ser Ser Leu Val Leu Ile Phe Leu Ala Leu Phe
 85 90 95
 Leu Ile Val Thr Thr Ser Lys Met Phe His Asn Leu Gln Ala Val Trp
 100 105 110
 Pro Tyr Val Val Gly Ser Val Ile Ile Leu Val Val Arg Ile His Gly
 115 120 125
 Leu Leu Glu Ser Ala Glu Ile Val Glu Leu Leu Asn Gln Met Leu Arg
 130 135 140
 Ile Met Arg Gln Val Asn Leu Met Ala Arg His Pro Asn Leu Phe Arg
 145 150 155 160
 Leu Lys His Leu Leu Leu Leu Leu Leu Ala Leu Gln Asn Leu Leu Arg
 165 170 175
 Ser Leu Asn Thr Ile Val Gly Ile Ser Asn His Ser Ala Glu Ala Tyr
 180 185 190
 Asp Ser Phe Leu Asn Ser Val Ile Leu Leu Ile Ile Leu Ala Val Leu
 195 200 205
 Leu Ser Phe Leu Leu Gln Ile Thr Ile Asn Ile Cys Leu Phe Val Val
 210 215 220
 Leu Ile Ala Thr Tyr Ser Glu Leu His His Cys Thr Arg Arg Ile Ser
 225 230 235 240
 Asn Asp Met Asp Lys Leu Arg Leu His Ser Val His Glu Ser Gly Gln
 245 250 255
 Phe Met Val Leu Val Lys Gln Leu Gln Gly Ile Thr Glu Lys Leu Ile
 260 265 270
 Arg Leu Arg Gln Asn Val Phe His Ile Thr Val Arg Ile Ile Arg His
 275 280 285

Phe Arg Phe His Trp Leu Cys Ala Ile Ile Tyr Gly Leu Leu Pro Phe
 290 295 300
 Phe Ser Leu Thr Ala Lys Asp Gln Asn Gly Phe Asn Phe Leu Ile Ile
 305 310 315 320
 Ser Ala Leu Asn Ile Ile Phe Gln Trp Thr Ile Phe Ala Ile Leu Ser
 325 330 335
 Arg Glu Ser Arg Ile Thr Arg Ser Leu Cys Thr Phe His Leu Thr Asn
 340 345 350
 Tyr His Lys Glu Thr Ala Arg Thr
 355 360

<210> 69
 <211> 1431
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1431)
 <223> Coding region GR66C.1

<400> 69
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 1 5 10 15
 caa ctg ttc ttc ata tcc aag ata gct gga att ctg cca cag gat ctc 96
 Gln Leu Phe Phe Ile Ser Lys Ile Ala Gly Ile Leu Pro Gln Asp Leu
 20 25 30
 gag aag ttt cga tct agg aat ctg ctg gag aaa tcc cgt aat ggc atg 144
 Glu Lys Phe Arg Ser Arg Asn Leu Leu Glu Lys Ser Arg Asn Gly Met
 35 40 45
 att tac atg ctg agt act tta ata ctc tac gtt gtg ctc tat aat att 192
 Ile Tyr Met Leu Ser Thr Leu Ile Leu Tyr Val Val Leu Tyr Asn Ile
 50 55 60
 ttg ata tat tcc ttt gga gag gag gac cgc agc cta aag gcc tcg cag 240
 Leu Ile Tyr Ser Phe Gly Glu Glu Asp Arg Ser Leu Lys Ala Ser Gln
 65 70 75 80
 agc acc ttg act ttc gtg att ggc ttg ttc ctg acc tat atc ggt ctg 288
 Ser Thr Leu Thr Phe Val Ile Gly Leu Phe Leu Thr Tyr Ile Gly Leu
 85 90 95
 att atg atg gtc tcc gac cag ttg acc gcg tta cga aac cag ggt aga 336
 Ile Met Met Val Ser Asp Gln Leu Thr Ala Leu Arg Asn Gln Gly Arg
 100 105 110

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att gga gag ctt tac gag cgc atc cgt ctg gtg gat gag cgc ctt tac      384
Ile Gly Glu Leu Tyr Glu Arg Ile Arg Leu Val Asp Glu Arg Leu Tyr
      115                      120                      125

aaa gag ggg tgt gtt atg gac aac agt aca att gga cgg cgc ata cga      432
Lys Glu Gly Cys Val Met Asp Asn Ser Thr Ile Gly Arg Arg Ile Arg
      130                      135                      140

att atg ctg atc atg acg gtc atc ttt gag ttg tcc att ttg gtg agc      480
Ile Met Leu Ile Met Thr Val Ile Phe Glu Leu Ser Ile Leu Val Ser
      145                      150                      155                      160

acc tat gtc aag ctg gtg gac tat agt caa tgg atg tcc ttg tta tgg      528
Thr Tyr Val Lys Leu Val Asp Tyr Ser Gln Trp Met Ser Leu Leu Trp
      165                      170                      175

ata gtg tcc gcc att ccc acg ttc atc aac acg cta gac aag atc tgg      576
Ile Val Ser Ala Ile Pro Thr Phe Ile Asn Thr Leu Asp Lys Ile Trp
      180                      185                      190

ttc gct gtt tcg tta tat gcg ttg aaa gaa cgc ttc gag gcc ata aac      624
Phe Ala Val Ser Leu Tyr Ala Leu Lys Glu Arg Phe Glu Ala Ile Asn
      195                      200                      205

gcc acc cta gag gaa ctg gtg gac acg cac gag aag cat aag ctg tgg      672
Ala Thr Leu Glu Glu Leu Val Asp Thr His Glu Lys His Lys Leu Trp
      210                      215                      220

ctg cga ggc aat caa gag gtt ccg cct cct ctg gac agc tcc cag ccg      720
Leu Arg Gly Asn Gln Glu Val Pro Pro Pro Leu Asp Ser Ser Gln Pro
      225                      230                      235                      240

cct cag tat gac agc aac ctg gag tat ctg tac aag gaa cta gga ggt      768
Pro Gln Tyr Asp Ser Asn Leu Glu Tyr Leu Tyr Lys Glu Leu Gly Gly
      245                      250                      255

atg gac ata ggt tcc att ggc aag agt tca gta gag gag aaa cta aac      816
Met Asp Ile Gly Ser Ile Gly Lys Ser Ser Val Glu Glu Lys Leu Asn
      260                      265                      270

aac ctg tgc cag gtg cac gac gag atc tgt gaa atc gga aaa gct ttg      864
Asn Leu Cys Gln Val His Asp Glu Ile Cys Glu Ile Gly Lys Ala Leu
      275                      280                      285

aac gag ctg tgg agc tat ccc att cta tct cta atg gcc tat ggt ttt      912
Asn Glu Leu Trp Ser Tyr Pro Ile Leu Ser Leu Met Ala Tyr Gly Phe
      290                      295                      300

ctg att ttc act gct caa ctt tat ttc ctc tac tgc gct aca cag tac      960
Leu Ile Phe Thr Ala Gln Leu Tyr Phe Leu Tyr Cys Ala Thr Gln Tyr
      305                      310                      315                      320

caa tcg ata cca tcg ctt ttc cgt tcc gcc aag aat ccc ttc atc act      1008
Gln Ser Ile Pro Ser Leu Phe Arg Ser Ala Lys Asn Pro Phe Ile Thr
      325                      330                      335

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gtt ata gtt cta agt tat acg tct gga aaa tgc gtg tac ctc atc tac 1056
 Val Ile Val Leu Ser Tyr Thr Ser Gly Lys Cys Val Tyr Leu Ile Tyr
 340 345 350

ctg agt tgg aaa acg tcg cag gcc tcc aag cgc acc gga atc agt ctg 1104
 Leu Ser Trp Lys Thr Ser Gln Ala Ser Lys Arg Thr Gly Ile Ser Leu
 355 360 365

cac aaa tgt ggc gtg gtg gcc gat gat aat ctt ctc tac gaa att gtt 1152
 His Lys Cys Gly Val Val Ala Asp Asp Asn Leu Leu Tyr Glu Ile Val
 370 375 380

aac cac cta tcg cta aaa ttg ctc aac cac tcg gtg gac ttt tcg gct 1200
 Asn His Leu Ser Leu Lys Leu Leu Asn His Ser Val Asp Phe Ser Ala
 385 390 395 400

tgc ggc ttc ttt acc ctg gac atg gaa aca ttg tat ggt gtg agt ggc 1248
 Cys Gly Phe Phe Thr Leu Asp Met Glu Thr Leu Tyr Gly Val Ser Gly
 405 410 415

ggg atc act agc tac ctg atc atc ctg att cag ttc aat ttg gcc gcc 1296
 Gly Ile Thr Ser Tyr Leu Ile Ile Leu Ile Gln Phe Asn Leu Ala Ala
 420 425 430

cag cag gcc aaa gag gct ata cag acg ttc aac tcg ctt aat gac acc 1344
 Gln Gln Ala Lys Glu Ala Ile Gln Thr Phe Asn Ser Leu Asn Asp Thr
 435 440 445

gcc ggc ttg gtt ggt gcc gcc acc gat atg gat aat att agc tcc acg 1392
 Ala Gly Leu Val Gly Ala Ala Thr Asp Met Asp Asn Ile Ser Ser Thr
 450 455 460

ctg cgt gat ttc gtc acc acg acc atg aca ccg gcg gtc 1431
 Leu Arg Asp Phe Val Thr Thr Thr Met Thr Pro Ala Val
 465 470 475

<210> 70

<211> 477

<212> PRT

<213> Drosophila melanogaster

<400> 70

Met Ala Gln Ala Glu Asp Ala Val Gln Pro Leu Leu Gln Gln Phe Gln
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Gln Leu Phe Phe Ile Ser Lys Ile Ala Gly Ile Leu Pro Gln Asp Leu
 20 25 30

Glu Lys Phe Arg Ser Arg Asn Leu Leu Glu Lys Ser Arg Asn Gly Met
 35 40 45

Ile Tyr Met Leu Ser Thr Leu Ile Leu Tyr Val Val Leu Tyr Asn Ile
 50 55 60

Leu Ile Tyr Ser Phe Gly Glu Glu Asp Arg Ser Leu Lys Ala Ser Gln

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65					70						75				80
Ser	Thr	Leu	Thr	Phe	Val	Ile	Gly	Leu	Phe	Leu	Thr	Tyr	Ile	Gly	Leu
				85					90					95	
Ile	Met	Met	Val	Ser	Asp	Gln	Leu	Thr	Ala	Leu	Arg	Asn	Gln	Gly	Arg
			100					105					110		
Ile	Gly	Glu	Leu	Tyr	Glu	Arg	Ile	Arg	Leu	Val	Asp	Glu	Arg	Leu	Tyr
		115					120					125			
Lys	Glu	Gly	Cys	Val	Met	Asp	Asn	Ser	Thr	Ile	Gly	Arg	Arg	Ile	Arg
	130					135					140				
Ile	Met	Leu	Ile	Met	Thr	Val	Ile	Phe	Glu	Leu	Ser	Ile	Leu	Val	Ser
145					150					155					160
Thr	Tyr	Val	Lys	Leu	Val	Asp	Tyr	Ser	Gln	Trp	Met	Ser	Leu	Leu	Trp
				165					170					175	
Ile	Val	Ser	Ala	Ile	Pro	Thr	Phe	Ile	Asn	Thr	Leu	Asp	Lys	Ile	Trp
			180					185					190		
Phe	Ala	Val	Ser	Leu	Tyr	Ala	Leu	Lys	Glu	Arg	Phe	Glu	Ala	Ile	Asn
		195					200					205			
Ala	Thr	Leu	Glu	Glu	Leu	Val	Asp	Thr	His	Glu	Lys	His	Lys	Leu	Trp
	210					215					220				
Leu	Arg	Gly	Asn	Gln	Glu	Val	Pro	Pro	Pro	Leu	Asp	Ser	Ser	Gln	Pro
225					230					235				240	
Pro	Gln	Tyr	Asp	Ser	Asn	Leu	Glu	Tyr	Leu	Tyr	Lys	Glu	Leu	Gly	Gly
				245					250					255	
Met	Asp	Ile	Gly	Ser	Ile	Gly	Lys	Ser	Ser	Val	Glu	Glu	Lys	Leu	Asn
		260					265						270		
Asn	Leu	Cys	Gln	Val	His	Asp	Glu	Ile	Cys	Glu	Ile	Gly	Lys	Ala	Leu
		275					280					285			
Asn	Glu	Leu	Trp	Ser	Tyr	Pro	Ile	Leu	Ser	Leu	Met	Ala	Tyr	Gly	Phe
	290					295					300				
Leu	Ile	Phe	Thr	Ala	Gln	Leu	Tyr	Phe	Leu	Tyr	Cys	Ala	Thr	Gln	Tyr
305					310					315				320	
Gln	Ser	Ile	Pro	Ser	Leu	Phe	Arg	Ser	Ala	Lys	Asn	Pro	Phe	Ile	Thr
				325					330					335	
Val	Ile	Val	Leu	Ser	Tyr	Thr	Ser	Gly	Lys	Cys	Val	Tyr	Leu	Ile	Tyr
			340					345					350		
Leu	Ser	Trp	Lys	Thr	Ser	Gln	Ala	Ser	Lys	Arg	Thr	Gly	Ile	Ser	Leu
		355					360					365			

His Lys Cys Gly Val Val Ala Asp Asp Asn Leu Leu Tyr Glu Ile Val
 370 375 380
 Asn His Leu Ser Leu Lys Leu Leu Asn His Ser Val Asp Phe Ser Ala
 385 390 395 400
 Cys Gly Phe Phe Thr Leu Asp Met Glu Thr Leu Tyr Gly Val Ser Gly
 405 410 415
 Gly Ile Thr Ser Tyr Leu Ile Ile Leu Ile Gln Phe Asn Leu Ala Ala
 420 425 430
 Gln Gln Ala Lys Glu Ala Ile Gln Thr Phe Asn Ser Leu Asn Asp Thr
 435 440 445
 Ala Gly Leu Val Gly Ala Ala Thr Asp Met Asp Asn Ile Ser Ser Thr
 450 455 460
 Leu Arg Asp Phe Val Thr Thr Thr Met Thr Pro Ala Val
 465 470 475

<210> 71
 <211> 1126
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1125)
 <223> Coding region GR68D.1

<400> 71
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 ttt gct ata tta cca ttc tat agt gga gac gtc gat gat ggc ttt cgc 96
 Phe Ala Ile Leu Pro Phe Tyr Ser Gly Asp Val Asp Asp Gly Phe Arg
 20 25 30
 ttt gga gga ttg ggt cgc tgg tac gga cga ctg gtg gcc ctg att ata 144
 Phe Gly Gly Leu Gly Arg Trp Tyr Gly Arg Leu Val Ala Leu Ile Ile
 35 40 45
 cta atc gga tca ctg aca ttg ggg gaa gat gtg ctc ttc gcc tcc aag 192
 Leu Ile Gly Ser Leu Thr Leu Gly Glu Asp Val Leu Phe Ala Ser Lys
 50 55 60
 gag tac aga ttg gtg gcc agt gcc caa ggt gat acc gag gag atc aac 240
 Glu Tyr Arg Leu Val Ala Ser Ala Gln Gly Asp Thr Glu Glu Ile Asn
 65 70 75 80
 agg acc atc gag acg ctt ctg tgt atc atc agc tat acc atg gtg gta 288
 Arg Thr Ile Glu Thr Leu Leu Cys Ile Ile Ser Tyr Thr Met Val Val

85					90					95						
tta	tcg	agt	gtg	cag	aat	gca	tcc	aga	cac	ttt	cgc	act	ctt	cac	gat	336
Leu	Ser	Ser	Val	Gln	Asn	Ala	Ser	Arg	His	Phe	Arg	Thr	Leu	His	Asp	
			100					105					110			
att	gcc	aaa	atc	gat	gag	tat	ctg	ctg	gcc	aat	gga	ttc	cgg	gaa	acc	384
Ile	Ala	Lys	Ile	Asp	Glu	Tyr	Leu	Leu	Ala	Asn	Gly	Phe	Arg	Glu	Thr	
		115					120					125				
tac	agt	tgt	cgc	aat	ctg	acc	att	ctg	gtc	acc	tct	gca	gca	ggc	ggc	432
Tyr	Ser	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Val	Thr	Ser	Ala	Ala	Gly	Gly	
	130					135					140					
gtc	ctc	gct	gtg	gcc	ttc	tac	tat	att	cac	tat	cga	agt	ggc	att	ggc	480
Val	Leu	Ala	Val	Ala	Phe	Tyr	Tyr	Ile	His	Tyr	Arg	Ser	Gly	Ile	Gly	
145					150					155					160	
gcc	aaa	agg	caa	atc	atc	ctg	ctt	ctg	atc	tac	ttc	ctc	caa	ctg	ctg	528
Ala	Lys	Arg	Gln	Ile	Ile	Leu	Leu	Leu	Ile	Tyr	Phe	Leu	Gln	Leu	Leu	
				165					170					175		
tac	tcc	act	ctc	ctg	gcc	tta	tat	cta	agg	aca	ctc	atg	atg	aat	ttg	576
Tyr	Ser	Thr	Leu	Leu	Ala	Leu	Tyr	Leu	Arg	Thr	Leu	Met	Met	Asn	Leu	
			180					185					190			
gca	cag	aga	att	gga	ttt	ctt	aac	cag	aaa	ctg	gat	acg	ttt	aat	ctt	624
Ala	Gln	Arg	Ile	Gly	Phe	Leu	Asn	Gln	Lys	Leu	Asp	Thr	Phe	Asn	Leu	
		195					200					205				
cag	gat	tgt	ggc	cac	atg	gaa	aac	tgg	cgt	gag	ttg	agc	aac	ctc	ata	672
Gln	Asp	Cys	Gly	His	Met	Glu	Asn	Trp	Arg	Glu	Leu	Ser	Asn	Leu	Ile	
	210					215					220					
gag	gtc	ctt	tgc	aaa	ttc	cgc	tac	atc	acc	gag	aat	att	aac	tgc	gtg	720
Glu	Val	Leu	Cys	Lys	Phe	Arg	Tyr	Ile	Thr	Glu	Asn	Ile	Asn	Cys	Val	
225					230					235					240	
gcc	gga	gtt	tca	ttg	cta	ttc	tac	ttt	ggc	ttc	tcc	ttc	tac	acg	gtc	768
Ala	Gly	Val	Ser	Leu	Leu	Phe	Tyr	Phe	Gly	Phe	Ser	Phe	Tyr	Thr	Val	
				245					250					255		
aca	aat	cag	agt	tac	ttg	gcc	ttt	gcc	aca	ttg	aca	gcc	ggc	tcg	ttg	816
Thr	Asn	Gln	Ser	Tyr	Leu	Ala	Phe	Ala	Thr	Leu	Thr	Ala	Gly	Ser	Leu	
			260					265					270			
agt	tcc	aaa	aca	gaa	gtg	gct	gat	acc	ata	gga	cta	tca	tgt	atc	tgg	864
Ser	Ser	Lys	Thr	Glu	Val	Ala	Asp	Thr	Ile	Gly	Leu	Ser	Cys	Ile	Trp	
		275					280					285				
gtt	ttg	gct	gaa	act	atc	aca	atg	att	gtg	att	tgc	agc	gca	tgt	gac	912
Val	Leu	Ala	Glu	Thr	Ile	Thr	Met	Ile	Val	Ile	Cys	Ser	Ala	Cys	Asp	
	290					295					300					
ggc	ctg	gca	tcc	gag	gtg	aat	ggc	acg	gca	cag	atc	ctg	gcg	aga	att	960
Gly	Leu	Ala	Ser	Glu	Val	Asn	Gly	Thr	Ala	Gln	Ile	Leu	Ala	Arg	Ile	

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<400> 72
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Phe Gly Gly Leu Gly Arg Trp Tyr Gly Arg Leu Val Ala Leu Ile Ile
      35             40             45
Leu Ile Gly Ser Leu Thr Leu Gly Glu Asp Val Leu Phe Ala Ser Lys
  50             55             60
Glu Tyr Arg Leu Val Ala Ser Ala Gln Gly Asp Thr Glu Glu Ile Asn
  65             70             75             80
Arg Thr Ile Glu Thr Leu Leu Cys Ile Ile Ser Tyr Thr Met Val Val
      85             90             95
Leu Ser Ser Val Gln Asn Ala Ser Arg His Phe Arg Thr Leu His Asp
      100            105            110
Ile Ala Lys Ile Asp Glu Tyr Leu Leu Ala Asn Gly Phe Arg Glu Thr
      115            120            125
Tyr Ser Cys Arg Asn Leu Thr Ile Leu Val Thr Ser Ala Ala Gly Gly
      130            135            140
Val Leu Ala Val Ala Phe Tyr Tyr Ile His Tyr Arg Ser Gly Ile Gly
  145            150            155            160
Ala Lys Arg Gln Ile Ile Leu Leu Leu Ile Tyr Phe Leu Gln Leu Leu

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165								170				175					
Tyr	Ser	Thr	Leu	Leu	Ala	Leu	Tyr	Leu	Arg	Thr	Leu	Met	Met	Asn	Leu		
180								185				190					
Ala	Gln	Arg	Ile	Gly	Phe	Leu	Asn	Gln	Lys	Leu	Asp	Thr	Phe	Asn	Leu		
195								200				205					
Gln	Asp	Cys	Gly	His	Met	Glu	Asn	Trp	Arg	Glu	Leu	Ser	Asn	Leu	Ile		
210								215				220					
Glu	Val	Leu	Cys	Lys	Phe	Arg	Tyr	Ile	Thr	Glu	Asn	Ile	Asn	Cys	Val		
225								230				235				240	
Ala	Gly	Val	Ser	Leu	Leu	Phe	Tyr	Phe	Gly	Phe	Ser	Phe	Tyr	Thr	Val		
245								250				255					
Thr	Asn	Gln	Ser	Tyr	Leu	Ala	Phe	Ala	Thr	Leu	Thr	Ala	Gly	Ser	Leu		
260								265				270					
Ser	Ser	Lys	Thr	Glu	Val	Ala	Asp	Thr	Ile	Gly	Leu	Ser	Cys	Ile	Trp		
275								280				285					
Val	Leu	Ala	Glu	Thr	Ile	Thr	Met	Ile	Val	Ile	Cys	Ser	Ala	Cys	Asp		
290								295				300					
Gly	Leu	Ala	Ser	Glu	Val	Asn	Gly	Thr	Ala	Gln	Ile	Leu	Ala	Arg	Ile		
305								310				315				320	
Tyr	Gly	Lys	Ser	Lys	Gln	Phe	Gln	Asn	Leu	Ile	Asp	Lys	Phe	Leu	Thr		
325								330				335					
Lys	Ser	Ile	Lys	Gln	Asp	Leu	Gln	Phe	Thr	Ala	Tyr	Gly	Phe	Phe	Ser		
340								345				350					
Ile	Asp	Asn	Ser	Thr	Leu	Phe	Lys	Ile	Phe	Ser	Ala	Val	Thr	Thr	Tyr		
355								360				365					
Leu	Val	Ile	Leu	Ile	Gln	Phe											
370								375									

<210> 73

<211> 1347

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1347)

<223> Coding region GR77E.1

<400> 73

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 Met Pro Leu Pro Leu Gly Asp Pro Leu Ala Leu Ala Val Ser Pro Gln

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1	5	10	15	
ctc gga tac att cga atc aca gcg atg ccg cgt tgg ctt caa ctc ccg	96			
Leu Gly Tyr Ile Arg Ile Thr Ala Met Pro Arg Trp Leu Gln Leu Pro				
20 25 30				
ggt atg tcg gcc ctg ggt ata ctg tac agt ctg acc agg gtg ttt ggc	144			
Gly Met Ser Ala Leu Gly Ile Leu Tyr Ser Leu Thr Arg Val Phe Gly				
35 40 45				
cta atg gcc acc gcc aat tgg agt cct cga ggc att aag agg gtc aga	192			
Leu Met Ala Thr Ala Asn Trp Ser Pro Arg Gly Ile Lys Arg Val Arg				
50 55 60				
cag agc ctc tat ctt cgc atc cac ggc tgc gtg atg ctg atc ttt gtg	240			
Gln Ser Leu Tyr Leu Arg Ile His Gly Cys Val Met Leu Ile Phe Val				
65 70 75 80				
ggc tgt ttc tcg ccc ttc gcc ttc tgg tgc att ttc caa agg atg gcc	288			
Gly Cys Phe Ser Pro Phe Ala Phe Trp Cys Ile Phe Gln Arg Met Ala				
85 90 95				
ttt ctg cgc caa aac cga att ctg cta atg att ggc ttt aat cga tat	336			
Phe Leu Arg Gln Asn Arg Ile Leu Leu Met Ile Gly Phe Asn Arg Tyr				
100 105 110				
gtc ctg ctg ctg gtc tgt gct ttt atg act ctg tgg ata cac tgc ttc	384			
Val Leu Leu Leu Val Cys Ala Phe Met Thr Leu Trp Ile His Cys Phe				
115 120 125				
aag cag gcg gag att att ggg tgt ctc aat cga ttg ctg aag tgt cga	432			
Lys Gln Ala Glu Ile Ile Gly Cys Leu Asn Arg Leu Leu Lys Cys Arg				
130 135 140				
agg cgg tta aga aga ctc atg cac act cgg aag ctg aag gat tcc atg	480			
Arg Arg Leu Arg Arg Leu Met His Thr Arg Lys Leu Lys Asp Ser Met				
145 150 155 160				
gat tgt ctg gcc act aag gga cac ctg cta gaa gtg gtg gtg cta ctc	528			
Asp Cys Leu Ala Thr Lys Gly His Leu Leu Glu Val Val Val Leu Leu				
165 170 175				
agt tcc tat ctg ctc tcc atg gct cag ccc att cag ata ctc aag gat	576			
Ser Ser Tyr Leu Leu Ser Met Ala Gln Pro Ile Gln Ile Leu Lys Asp				
180 185 190				
gat ccg gaa gtg cga agg aac ttc atg tac gcc tgc tct ttg gtt ttc	624			
Asp Pro Glu Val Arg Arg Asn Phe Met Tyr Ala Cys Ser Leu Val Phe				
195 200 205				
gta tcc gta tgc cag gcc atc ctg cag ctt tcc ctg ggg atg tac aca	672			
Val Ser Val Cys Gln Ala Ile Leu Gln Leu Ser Leu Gly Met Tyr Thr				
210 215 220				
atg gcc ata cta ttt ctg ggt cac ctc gtt cgt cac tcc aat ctg ctg	720			
Met Ala Ile Leu Phe Leu Gly His Leu Val Arg His Ser Asn Leu Leu				

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225					230					235					240		
ctg gcc aaa att	ctg gcg gat gcc gag cat att ttt gaa agt tcc cag	Leu Ala Lys Ile	Leu Ala Asp Ala Glu His Ile Phe Glu Ser Ser Gln	245	250	255	768										
aag gcc gga ttt	tgg ccc aac cgc cag gag ctg tac aaa ggc caa caa	Lys Ala Gly Phe	Trp Pro Asn Arg Gln Glu Leu Tyr Lys Gly Gln Gln	260	265	270	816										
aag tgg ttg gcc ctc	gaa ttg tgg aga tta ctt cat gta cat cat caa	Lys Trp Leu Ala Leu Glu Leu Trp Arg Leu Leu His Val His His Gln	275	280	285	864											
ttg ttg aag ctc	cat cgg tcc ata tgc tcg ttg tgc gca gtt cag gcc	Leu Leu Lys Leu His Arg Ser Ile Cys Ser Leu Cys Ala Val Gln Ala	290	295	300	912											
gtc tgc ttt ttg	gga ttt gtg ccc ttg gag tgc acg att cac ctg ttc	Val Cys Phe Leu Gly Phe Val Pro Leu Glu Cys Thr Ile His Leu Phe	305	310	315	960											
ttc aca tac ttc	atg aag tac agc aag ttt att ttg cga aaa tat gga	Phe Thr Tyr Phe Met Lys Tyr Ser Lys Phe Ile Leu Arg Lys Tyr Gly	325	330	335	1008											
aga tcg ttt ccg	ttg aac tac ttc gcc atc gcc ttt ttg gtg ggg ctc	Arg Ser Phe Pro Leu Asn Tyr Phe Ala Ile Ala Phe Leu Val Gly Leu	340	345	350	1056											
ttc acc aac ctt	ttg ctg gtc att tta ccc acc tac tac tca gaa aga	Phe Thr Asn Leu Leu Leu Val Ile Leu Pro Thr Tyr Tyr Ser Glu Arg	355	360	365	1104											
aga ttc aac tgt	acc agg gaa atc atc aaa ggc gga gga ttg gcc ttt	Arg Phe Asn Cys Thr Arg Glu Ile Ile Lys Gly Gly Gly Leu Ala Phe	370	375	380	1152											
cca tcc agg atc	act gtt aag caa ctc agg cac act atg cac ttc tac	Pro Ser Arg Ile Thr Val Lys Gln Leu Arg His Thr Met His Phe Tyr	385	390	395	1200											
ggc ctg tat ctg	aag aat gtg gag cat gta ttt gcc gtc agc gcc tgt	Gly Leu Tyr Leu Lys Asn Val Glu His Val Phe Ala Val Ser Ala Cys	405	410	415	1248											
gga ctg ttt aag	ctg aac aat gcg ata ctc ttt tgc atc gtg ggt gca	Gly Leu Phe Lys Leu Asn Asn Ala Ile Leu Phe Cys Ile Val Gly Ala	420	425	430	1296											
ata cta gaa tac	ctt atg ata ctg ata cag ttt gat aaa gtc cta aac	Ile Leu Glu Tyr Leu Met Ile Leu Ile Gln Phe Asp Lys Val Leu Asn	435	440	445	1344											
aaa							1347										
Lys																	

130

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260	265	270
Lys Trp Leu Ala Leu Glu Leu Trp Arg Leu Leu His Val His His Gln 275	280	285
Leu Leu Lys Leu His Arg Ser Ile Cys Ser Leu Cys Ala Val Gln Ala 290	295	300
Val Cys Phe Leu Gly Phe Val Pro Leu Glu Cys Thr Ile His Leu Phe 305	310	315
Phe Thr Tyr Phe Met Lys Tyr Ser Lys Phe Ile Leu Arg Lys Tyr Gly 325	330	335
Arg Ser Phe Pro Leu Asn Tyr Phe Ala Ile Ala Phe Leu Val Gly Leu 340	345	350
Phe Thr Asn Leu Leu Leu Val Ile Leu Pro Thr Tyr Tyr Ser Glu Arg 355	360	365
Arg Phe Asn Cys Thr Arg Glu Ile Ile Lys Gly Gly Gly Leu Ala Phe 370	375	380
Pro Ser Arg Ile Thr Val Lys Gln Leu Arg His Thr Met His Phe Tyr 385	390	395
Gly Leu Tyr Leu Lys Asn Val Glu His Val Phe Ala Val Ser Ala Cys 405	410	415
Gly Leu Phe Lys Leu Asn Asn Ala Ile Leu Phe Cys Ile Val Gly Ala 420	425	430
Ile Leu Glu Tyr Leu Met Ile Leu Ile Gln Phe Asp Lys Val Leu Asn 435	440	445

Lys

<210> 75

<211> 1165

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1164)

<223> Coding region GR94E.1

<400> 75

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1 5 10 15	

acg atc ata ctg ata ggc ttt atg acc gtc ttc gga ctc ctg gcc aat	96
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Thr	Ile	Ile	Leu	Ile	Gly	Phe	Met	Thr	Val	Phe	Gly	Leu	Leu	Ala	Asn	
			20					25					30			
cga	tat	cgg	gcg	ggc	cgt	cgt	gaa	aga	ttc	cgc	ttc	tca	aag	gca	aat	144
Arg	Tyr	Arg	Ala	Gly	Arg	Arg	Glu	Arg	Phe	Arg	Phe	Ser	Lys	Ala	Asn	
		35					40					45				
ctg	gcc	ttt	gct	tcg	ctg	tgg	gca	att	gca	ttc	agc	ttg	gtt	tac	ggg	192
Leu	Ala	Phe	Ala	Ser	Leu	Trp	Ala	Ile	Ala	Phe	Ser	Leu	Val	Tyr	Gly	
	50					55					60					
cgg	caa	atc	tac	aag	gag	tac	cag	gag	ggc	cag	atc	aac	ctg	aag	gac	240
Arg	Gln	Ile	Tyr	Lys	Glu	Tyr	Gln	Glu	Gly	Gln	Ile	Asn	Leu	Lys	Asp	
	65				70					75					80	
gcc	acc	act	ctg	tac	agc	tat	atg	aac	att	acg	gtg	gct	gtt	att	aac	288
Ala	Thr	Thr	Leu	Tyr	Ser	Tyr	Met	Asn	Ile	Thr	Val	Ala	Val	Ile	Asn	
				85					90					95		
tat	gtg	tcg	caa	atg	ata	atc	agt	gac	cat	gtg	gcc	aag	gtg	ttg	agc	336
Tyr	Val	Ser	Gln	Met	Ile	Ile	Ser	Asp	His	Val	Ala	Lys	Val	Leu	Ser	
			100					105					110			
aaa	gtg	ccc	ttc	ttt	gat	acc	cta	aaa	gaa	ttc	cgt	ctg	gac	agc	agg	384
Lys	Val	Pro	Phe	Phe	Asp	Thr	Leu	Lys	Glu	Phe	Arg	Leu	Asp	Ser	Arg	
		115					120					125				
tcg	ctg	tac	ata	tcc	atc	gtt	ttg	gct	ctg	gtc	aag	acc	gtg	gct	ttt	432
Ser	Leu	Tyr	Ile	Ser	Ile	Val	Leu	Ala	Leu	Val	Lys	Thr	Val	Ala	Phe	
	130					135					140					
cct	cta	aca	att	gaa	gtg	gct	ttc	ata	ctg	caa	cag	agg	cgg	cag	cat	480
Pro	Leu	Thr	Ile	Glu	Val	Ala	Phe	Ile	Leu	Gln	Gln	Arg	Arg	Gln	His	
	145				150					155					160	
ccc	gag	atg	agc	ttg	atc	tgg	acc	ttg	tac	cgg	ctg	ttt	ccc	tta	att	528
Pro	Glu	Met	Ser	Leu	Ile	Trp	Thr	Leu	Tyr	Arg	Leu	Phe	Pro	Leu	Ile	
				165				170						175		
att	tcg	aat	ttt	ctc	aat	aac	tgc	tac	ttt	ggc	gca	atg	gtg	gtg	gtg	576
Ile	Ser	Asn	Phe	Leu	Asn	Asn	Cys	Tyr	Phe	Gly	Ala	Met	Val	Val	Val	
			180					185					190			
aag	gag	att	ctg	tac	gct	ctg	aac	aga	cgg	ctg	gaa	gcg	cag	ctg	cag	624
Lys	Glu	Ile	Leu	Tyr	Ala	Leu	Asn	Arg	Arg	Leu	Glu	Ala	Gln	Leu	Gln	
		195					200					205				
gag	gtg	aat	ctg	ctg	cag	agg	aag	gac	cag	cta	aag	ttg	tac	act	aaa	672
Glu	Val	Asn	Leu	Leu	Gln	Arg	Lys	Asp	Gln	Leu	Lys	Leu	Tyr	Thr	Lys	
	210					215					220					
tac	tac	cgc	atg	cag	cga	ttt	tgc	gcc	ttg	gcg	gat	gaa	ctc	gac	cag	720
Tyr	Tyr	Arg	Met	Gln	Arg	Phe	Cys	Ala	Leu	Ala	Asp	Glu	Leu	Asp	Gln	
	225				230					235					240	
ctg	gcg	tat	cgc	tat	agg	ttg	ata	tat	gtg	cat	tcg	gga	aag	tat	ctg	768

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<400> 76
Met Asp Phe Thr Ser Asp Tyr Ala His Arg Arg Met Val Lys Phe Leu
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Thr Ile Ile Leu Ile Gly Phe Met Thr Val Phe Gly Leu Leu Ala Asn
      20             25             30

Arg Tyr Arg Ala Gly Arg Arg Glu Arg Phe Arg Phe Ser Lys Ala Asn
      35             40             45

Leu Ala Phe Ala Ser Leu Trp Ala Ile Ala Phe Ser Leu Val Tyr Gly

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50	55	60
Arg Gln Ile Tyr Lys Glu Tyr Gln Glu Gly Gln Ile Asn Leu Lys Asp 65 70 75 80		
Ala Thr Thr Leu Tyr Ser Tyr Met Asn Ile Thr Val Ala Val Ile Asn 85 90 95		
Tyr Val Ser Gln Met Ile Ile Ser Asp His Val Ala Lys Val Leu Ser 100 105 110		
Lys Val Pro Phe Phe Asp Thr Leu Lys Glu Phe Arg Leu Asp Ser Arg 115 120 125		
Ser Leu Tyr Ile Ser Ile Val Leu Ala Leu Val Lys Thr Val Ala Phe 130 135 140		
Pro Leu Thr Ile Glu Val Ala Phe Ile Leu Gln Gln Arg Arg Gln His 145 150 155 160		
Pro Glu Met Ser Leu Ile Trp Thr Leu Tyr Arg Leu Phe Pro Leu Ile 165 170 175		
Ile Ser Asn Phe Leu Asn Asn Cys Tyr Phe Gly Ala Met Val Val Val 180 185 190		
Lys Glu Ile Leu Tyr Ala Leu Asn Arg Arg Leu Glu Ala Gln Leu Gln 195 200 205		
Glu Val Asn Leu Leu Gln Arg Lys Asp Gln Leu Lys Leu Tyr Thr Lys 210 215 220		
Tyr Tyr Arg Met Gln Arg Phe Cys Ala Leu Ala Asp Glu Leu Asp Gln 225 230 235 240		
Leu Ala Tyr Arg Tyr Arg Leu Ile Tyr Val His Ser Gly Lys Tyr Leu 245 250 255		
Thr Pro Met Ser Leu Ser Met Ile Leu Ser Leu Ile Cys His Leu Leu 260 265 270		
Gly Ile Thr Val Gly Phe Tyr Ser Leu Tyr Tyr Ala Ile Ala Asp Thr 275 280 285		
Leu Ile Met Gly Lys Pro Val Gln Trp Ser Trp Ile Ala Asp Gln Ser 290 295 300		
Gly Phe Pro Leu His Leu Ala Gly Gly Asp His Ile Ala His Ala Phe 305 310 315 320		
Glu Met Asn Leu Gln His Ala Asp Ser Arg Tyr Arg Gln Ala Val His 325 330 335		
Gly Phe Thr Leu Leu Val Thr Val Thr Lys Tyr Gln Ile Lys Pro Leu 340 345 350		

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Gly Leu Tyr Glu Leu Asp Met Arg Leu Ile Ser Asn Val Phe Ser Ala
 355 360 365

Val Ala Ser Phe Leu Leu Ile Leu Val Gln Ala Asp Leu Ser Gln Arg
 370 375 380

Phe Lys Met Gln
 385

<210> 77

<211> 1269

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1269)

<223> Coding region GR97D.1

<400> 77

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cga agc ctt ccc gtt cgt ttc cgg cga gga aaa ctc cat acc caa ctg 96
 Arg Ser Leu Pro Val Arg Phe Arg Arg Gly Lys Leu His Thr Gln Leu
 20 25 30

gtc acg att tgt ctt tac gcg acc gtt ttc ctt aac ata ctt tac ggc 144
 Val Thr Ile Cys Leu Tyr Ala Thr Val Phe Leu Asn Ile Leu Tyr Gly
 35 40 45

gtt tat ctc ggc cgc ttt tcc ttc agg cgc aag aag ttt gtg ttt tcc 192
 Val Tyr Leu Gly Arg Phe Ser Phe Arg Arg Lys Lys Phe Val Phe Ser
 50 55 60

aaa ggg ctc act atc tat agc tta ttt gtg gcc acg ttc ttt gcg ctg 240
 Lys Gly Leu Thr Ile Tyr Ser Leu Phe Val Ala Thr Phe Phe Ala Leu
 65 70 75 80

ttt tac atc tgg aat att tat aat gaa att tcc act ggt cag atc aat 288
 Phe Tyr Ile Trp Asn Ile Tyr Asn Glu Ile Ser Thr Gly Gln Ile Asn
 85 90 95

ctt cgc gat aca att gga ata tat tgt tat atg aac gtc tgc gtt tgc 336
 Leu Arg Asp Thr Ile Gly Ile Tyr Cys Tyr Met Asn Val Cys Val Cys
 100 105 110

cta ttc aac tat gtg acc caa tgg gaa aaa aca ctg caa ata att cgg 384
 Leu Phe Asn Tyr Val Thr Gln Trp Glu Lys Thr Leu Gln Ile Ile Arg
 115 120 125

ttt cag aat agt gtg cct ctt ttc aag gtc ctc gat tca ctg gac att 432
 Phe Gln Asn Ser Val Pro Leu Phe Lys Val Leu Asp Ser Leu Asp Ile

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130	135	140	
tcg gcg atg att gtg tgg cgg gca ttt ata tat ggc ttg ctc aag atc			480
Ser Ala Met Ile Val Trp Arg Ala Phe Ile Tyr Gly Leu Leu Lys Ile			
145	150	155	160
gtg ttc tgt ccc ctt atc acc tat ata acg ctg att cta tat cat aga			528
Val Phe Cys Pro Leu Ile Thr Tyr Ile Thr Leu Ile Leu Tyr His Arg			
	165	170	175
cgc tcc att tcg gaa agt caa tgg acg agt gta acg acc acg aag acc			576
Arg Ser Ile Ser Glu Ser Gln Trp Thr Ser Val Thr Thr Thr Lys Thr			
	180	185	190
atg ttg cca ctg att gtt tcc aat cag ata aat aat tgc ttc ttc ggc			624
Met Leu Pro Leu Ile Val Ser Asn Gln Ile Asn Asn Cys Phe Phe Gly			
	195	200	205
ggc ctg gta ctt gca aat ttg ata ttt gcc gcg gtg aat cgt aag ctg			672
Gly Leu Val Leu Ala Asn Leu Ile Phe Ala Ala Val Asn Arg Lys Leu			
	210	215	220
cac ggc att gtc aag gag gcc aat atg ctg cag tca cct gtc cag atg			720
His Gly Ile Val Lys Glu Ala Asn Met Leu Gln Ser Pro Val Gln Met			
	225	230	235
aat ctc cat aag ccc tac tac cgg atg cgt cgc ttc tgc gag tta gcc			768
Asn Leu His Lys Pro Tyr Tyr Arg Met Arg Arg Phe Cys Glu Leu Ala			
	245	250	255
gat ctt ctg gat gag ttg gct agg aaa tat ggc ttc act gcc agc cgc			816
Asp Leu Leu Asp Glu Leu Ala Arg Lys Tyr Gly Phe Thr Ala Ser Arg			
	260	265	270
tca aag aat tac ctt cgg ttc acg gac tgg tcc atg gtg cta tcg atg			864
Ser Lys Asn Tyr Leu Arg Phe Thr Asp Trp Ser Met Val Leu Ser Met			
	275	280	285
cta atg aac ctt ctc ggt atc acc atg gga tgc tac aat cag tat ctg			912
Leu Met Asn Leu Leu Gly Ile Thr Met Gly Cys Tyr Asn Gln Tyr Leu			
	290	295	300
gcc att gcg gat cac tac atc aac gag gag cct ttc gat ctc ttt ctg			960
Ala Ile Ala Asp His Tyr Ile Asn Glu Glu Pro Phe Asp Leu Phe Leu			
	305	310	315
gcc att gtt ctg gtc gta ttt ctg gct gtt ccc ttc ctg gaa ctc gtc			1008
Ala Ile Val Leu Val Val Phe Leu Ala Val Pro Phe Leu Glu Leu Val			
	325	330	335
atg gtg gct cgg ata agt aac caa acc ctc acc agg aga act gga gaa			1056
Met Val Ala Arg Ile Ser Asn Gln Thr Leu Thr Arg Arg Thr Gly Glu			
	340	345	350
cta ttg cag cga ttc gat ctg cag cac gcc gat gcc cgt ttc aag caa			1104
Leu Leu Gln Arg Phe Asp Leu Gln His Ala Asp Ala Arg Phe Lys Gln			

355	360	365	
gtg gtg aat gct ttc tgg ctg cag gtc gtc acc atc aac tac aag ctt			1152
Val Val Asn Ala Phe Trp Leu Gln Val Val Thr Ile Asn Tyr Lys Leu			
370	375	380	
atg cca ttg ggc ctc ctg gaa ctg aat acc tcg ctg gtc aat aag gta			1200
Met Pro Leu Gly Leu Leu Glu Leu Asn Thr Ser Leu Val Asn Lys Val			
385	390	395	400
ttc tcg tca gct att gga agc ctg ctg att ctc att caa agt gat ttg			1248
Phe Ser Ser Ala Ile Gly Ser Leu Leu Ile Leu Ile Gln Ser Asp Leu			
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aca tta agg ttt tct cta aaa			1269
Thr Leu Arg Phe Ser Leu Lys			
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<210> 78

<211> 423

<212> PRT

<213> Drosophila melanogaster

<400> 78

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Val Thr Ile Cys Leu Tyr Ala Thr Val Phe Leu Asn Ile Leu Tyr Gly			
	35	40	45
Val Tyr Leu Gly Arg Phe Ser Phe Arg Arg Lys Lys Phe Val Phe Ser			
	50	55	60
Lys Gly Leu Thr Ile Tyr Ser Leu Phe Val Ala Thr Phe Phe Ala Leu			
65	70	75	80
Phe Tyr Ile Trp Asn Ile Tyr Asn Glu Ile Ser Thr Gly Gln Ile Asn			
	85	90	95
Leu Arg Asp Thr Ile Gly Ile Tyr Cys Tyr Met Asn Val Cys Val Cys			
	100	105	110
Leu Phe Asn Tyr Val Thr Gln Trp Glu Lys Thr Leu Gln Ile Ile Arg			
	115	120	125
Phe Gln Asn Ser Val Pro Leu Phe Lys Val Leu Asp Ser Leu Asp Ile			
	130	135	140
Ser Ala Met Ile Val Trp Arg Ala Phe Ile Tyr Gly Leu Leu Lys Ile			
145	150	155	160
Val Phe Cys Pro Leu Ile Thr Tyr Ile Thr Leu Ile Leu Tyr His Arg			

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	165		170		175
Arg Ser Ile	Ser Glu Ser Gln Trp Thr Ser Val Thr Thr Thr Lys Thr				
	180		185		190
Met Leu Pro Leu Ile Val Ser Asn Gln Ile Asn Asn Cys Phe Phe Gly					
	195		200		205
Gly Leu Val Leu Ala Asn Leu Ile Phe Ala Ala Val Asn Arg Lys Leu					
	210		215		220
His Gly Ile Val Lys Glu Ala Asn Met Leu Gln Ser Pro Val Gln Met					
	225		230		235
					240
Asn Leu His Lys Pro Tyr Tyr Arg Met Arg Arg Phe Cys Glu Leu Ala					
	245		250		255
Asp Leu Leu Asp Glu Leu Ala Arg Lys Tyr Gly Phe Thr Ala Ser Arg					
	260		265		270
Ser Lys Asn Tyr Leu Arg Phe Thr Asp Trp Ser Met Val Leu Ser Met					
	275		280		285
Leu Met Asn Leu Leu Gly Ile Thr Met Gly Cys Tyr Asn Gln Tyr Leu					
	290		295		300
Ala Ile Ala Asp His Tyr Ile Asn Glu Glu Pro Phe Asp Leu Phe Leu					
	305		310		315
					320
Ala Ile Val Leu Val Val Phe Leu Ala Val Pro Phe Leu Glu Leu Val					
	325		330		335
Met Val Ala Arg Ile Ser Asn Gln Thr Leu Thr Arg Arg Thr Gly Glu					
	340		345		350
Leu Leu Gln Arg Phe Asp Leu Gln His Ala Asp Ala Arg Phe Lys Gln					
	355		360		365
Val Val Asn Ala Phe Trp Leu Gln Val Val Thr Ile Asn Tyr Lys Leu					
	370		375		380
Met Pro Leu Gly Leu Leu Glu Leu Asn Thr Ser Leu Val Asn Lys Val					
	385		390		395
					400
Phe Ser Ser Ala Ile Gly Ser Leu Leu Ile Leu Ile Gln Ser Asp Leu					
	405		410		415
Thr Leu Arg Phe Ser Leu Lys					
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<210> 79

<211> 1299

<212> DNA

<213> Drosophila melanogaster

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PCT/US00/16211

<220>

<221> CDS

<222> (1)..(1299)

<223> Coding region GR98B.1

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cag att tat tcc att ttc gga ctc acg ccg cca att cag ttt ttt acc	96
Gln Ile Tyr Ser Ile Phe Gly Leu Thr Pro Pro Ile Gln Phe Phe Thr	
20 25 30	
agg acc tta cat aag cga cgt aga gga att gtg ata ttg ggc tac gcc	144
Arg Thr Leu His Lys Arg Arg Arg Gly Ile Val Ile Leu Gly Tyr Ala	
35 40 45	
tgc tat tta att agc att tcc ctg atg gtc atc tat gag tgc tac gcg	192
Cys Tyr Leu Ile Ser Ile Ser Leu Met Val Ile Tyr Glu Cys Tyr Ala	
50 55 60	
aac att gtg gct ctg caa aag gat ata cat aag ttt cac gcc gag gac	240
Asn Ile Val Ala Leu Gln Lys Asp Ile His Lys Phe His Ala Glu Asp	
65 70 75 80	
tct agc aaa gtt atg ggg gaa tac gca gaa agg tcc tgg tgg gta gcc	288
Ser Ser Lys Val Met Gly Glu Tyr Ala Glu Arg Ser Trp Trp Val Ala	
85 90 95	
atg ttc gtt tgg aat caa ttg aac att ctg ctt aac ttt cgg cgc ctt	336
Met Phe Val Trp Asn Gln Leu Asn Ile Leu Leu Asn Phe Arg Arg Leu	
100 105 110	
gct agg att tat gat gat att gcg gat ctg gaa ata gat ttg aat aac	384
Ala Arg Ile Tyr Asp Asp Ile Ala Asp Leu Glu Ile Asp Leu Asn Asn	
115 120 125	
gcc tct agc ggt ttt gtt ggc caa cgg cac tgg tgg cgc ttc cgt ttc	432
Ala Ser Ser Gly Phe Val Gly Gln Arg His Trp Trp Arg Phe Arg Phe	
130 135 140	
cgg ttg gcc ctc tct gtg ggc ctg tgg ata gtg ttg ctg gtg ggt ctc	480
Arg Leu Ala Leu Ser Val Gly Leu Trp Ile Val Leu Leu Val Gly Leu	
145 150 155 160	
acg cca cga ttc acc ctc gtg gca ctc gga ccc tac ctc cac tgg aca	528
Thr Pro Arg Phe Thr Leu Val Ala Leu Gly Pro Tyr Leu His Trp Thr	
165 170 175	
aat aaa gtg ctc acc gaa atc att ctg ata atg cta caa ctt aag tgt	576
Asn Lys Val Leu Thr Glu Ile Ile Leu Ile Met Leu Gln Leu Lys Cys	
180 185 190	
aca gag tat tgt gtg ttt gtg ctc ctg atc tat gaa ctg atc ctc cga	624
Thr Glu Tyr Cys Val Phe Val Leu Leu Ile Tyr Glu Leu Ile Leu Arg	

195					200					205							
ggg	cgc	cac	atc	ctt	cag	cag	atc	agt	gtg	gag	ctc	gag	ggt	aac	cag	672	
Gly	Arg	His	Ile	Leu	Gln	Gln	Ile	Ser	Val	Glu	Leu	Glu	Gly	Asn	Gln		
210					215					220							
tca	agg	gac	agt	gtt	cag	gag	ctg	tgt	gtg	gcc	ttg	aaa	cgc	aat	cag	720	
Ser	Arg	Asp	Ser	Val	Gln	Glu	Leu	Cys	Val	Ala	Leu	Lys	Arg	Asn	Gln		
225					230					235					240		
ttg	ctg	gct	gga	cgc	att	tgg	ggc	ttg	gtg	aat	gag	gtc	agc	ttg	tat	768	
Leu	Leu	Ala	Gly	Arg	Ile	Trp	Gly	Leu	Val	Asn	Glu	Val	Ser	Leu	Tyr		
					245					250					255		
ttt	acc	cta	tcc	ttg	acg	ctt	ttg	ttt	ctc	tac	aat	gaa	ctg	acc	att	816	
Phe	Thr	Leu	Ser	Leu	Thr	Leu	Leu	Phe	Leu	Tyr	Asn	Glu	Leu	Thr	Ile		
					260					265					270		
ctg	caa	att	gtc	aat	tgg	gct	ctc	att	aaa	tcc	gtc	aat	cca	aac	gaa	864	
Leu	Gln	Ile	Val	Asn	Trp	Ala	Leu	Ile	Lys	Ser	Val	Asn	Pro	Asn	Glu		
275					280					285							
tgc	tgt	caa	tat	agt	aag	tta	gtt	ttc	aag	ttc	aaa	aga	aac	ttt	acc	912	
Cys	Cys	Gln	Tyr	Ser	Lys	Leu	Val	Phe	Lys	Phe	Lys	Arg	Asn	Phe	Thr		
290					295					300							
tat	aaa	caa	gtt	att	ttc	ata	ata	ggg	cgc	gtt	ggg	act	tgc	ctc	ttg	960	
Tyr	Lys	Gln	Val	Ile	Phe	Ile	Ile	Gly	Arg	Val	Gly	Thr	Cys	Leu	Leu		
305					310					315					320		
ctg	tca	atc	aat	att	ttt	cta	tcc	tgt	tta	tac	agc	gag	ttc	tgc	att	1008	
Leu	Ser	Ile	Asn	Ile	Phe	Leu	Ser	Cys	Leu	Tyr	Ser	Glu	Phe	Cys	Ile		
					325					330					335		
caa	aca	tat	aat	agc	att	tca	cga	gtt	ctt	cac	caa	atg	tat	tgc	ctt	1056	
Gln	Thr	Tyr	Asn	Ser	Ile	Ser	Arg	Val	Leu	His	Gln	Met	Tyr	Cys	Leu		
340					345					350							
tct	gca	gcc	gaa	gat	tat	cta	ata	tta	aaa	atg	ggc	ctg	agg	gaa	tac	1104	
Ser	Ala	Ala	Glu	Asp	Tyr	Leu	Ile	Leu	Lys	Met	Gly	Leu	Arg	Glu	Tyr		
355					360					365							
tcg	ctg	caa	atg	gag	cat	tta	aag	ctg	att	ttc	aca	tgc	ggt	ggc	ctc	1152	
Ser	Leu	Gln	Met	Glu	His	Leu	Lys	Leu	Ile	Phe	Thr	Cys	Gly	Gly	Leu		
370					375					380							
ttt	gac	atc	aat	ctt	aag	ttc	ttc	gga	ggg	atg	gta	gtc	acc	tta	ttc	1200	
Phe	Asp	Ile	Asn	Leu	Lys	Phe	Phe	Gly	Gly	Met	Val	Val	Thr	Leu	Phe		
385					390					395					400		
ggt	tat	atc	att	att	ctc	gtg	caa	ttt	aaa	att	caa	ttt	ttt	gct	caa	1248	
Gly	Tyr	Ile	Ile	Ile	Leu	Val	Gln	Phe	Lys	Ile	Gln	Phe	Phe	Ala	Gln		
					405					410					415		
tca	aat	ttt	atg	caa	aat	att	aac	agc	acc	gaa	ctg	aaa	gca	tat	acc	1296	
Ser	Asn	Phe	Met	Gln	Asn	Ile	Asn	Ser	Thr	Glu	Leu	Lys	Ala	Tyr	Thr		

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420

425

430

1299

gcg
Ala

<210> 80

<211> 433

<212> PRT

<213> Drosophila melanogaster

<400> 80

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Gln	Ile	Tyr	Ser	Ile	Phe	Gly	Leu	Thr	Pro	Pro	Ile	Gln	Phe	Phe	Thr
			20					25					30		

Arg	Thr	Leu	His	Lys	Arg	Arg	Arg	Gly	Ile	Val	Ile	Leu	Gly	Tyr	Ala
		35					40						45		

Cys	Tyr	Leu	Ile	Ser	Ile	Ser	Leu	Met	Val	Ile	Tyr	Glu	Cys	Tyr	Ala
	50					55					60				

Asn	Ile	Val	Ala	Leu	Gln	Lys	Asp	Ile	His	Lys	Phe	His	Ala	Glu	Asp
65					70					75					80

Ser	Ser	Lys	Val	Met	Gly	Glu	Tyr	Ala	Glu	Arg	Ser	Trp	Trp	Val	Ala
				85					90					95	

Met	Phe	Val	Trp	Asn	Gln	Leu	Asn	Ile	Leu	Leu	Asn	Phe	Arg	Arg	Leu
		100						105					110		

Ala	Arg	Ile	Tyr	Asp	Asp	Ile	Ala	Asp	Leu	Glu	Ile	Asp	Leu	Asn	Asn
		115					120					125			

Ala	Ser	Ser	Gly	Phe	Val	Gly	Gln	Arg	His	Trp	Trp	Arg	Phe	Arg	Phe
	130					135					140				

Arg	Leu	Ala	Leu	Ser	Val	Gly	Leu	Trp	Ile	Val	Leu	Leu	Val	Gly	Leu
145					150					155					160

Thr	Pro	Arg	Phe	Thr	Leu	Val	Ala	Leu	Gly	Pro	Tyr	Leu	His	Trp	Thr
				165					170					175	

Asn	Lys	Val	Leu	Thr	Glu	Ile	Ile	Leu	Ile	Met	Leu	Gln	Leu	Lys	Cys
			180					185					190		

Thr	Glu	Tyr	Cys	Val	Phe	Val	Leu	Leu	Ile	Tyr	Glu	Leu	Ile	Leu	Arg
	195						200					205			

Gly	Arg	His	Ile	Leu	Gln	Gln	Ile	Ser	Val	Glu	Leu	Glu	Gly	Asn	Gln
	210					215						220			

Ser	Arg	Asp	Ser	Val	Gln	Glu	Leu	Cys	Val	Ala	Leu	Lys	Arg	Asn	Gln
225					230					235					240

Leu	Leu	Ala	Gly	Arg	Ile	Trp	Gly	Leu	Val	Asn	Glu	Val	Ser	Leu	Tyr
			245						250					255	
Phe	Thr	Leu	Ser	Leu	Thr	Leu	Leu	Phe	Leu	Tyr	Asn	Glu	Leu	Thr	Ile
			260					265					270		
Leu	Gln	Ile	Val	Asn	Trp	Ala	Leu	Ile	Lys	Ser	Val	Asn	Pro	Asn	Glu
		275					280					285			
Cys	Cys	Gln	Tyr	Ser	Lys	Leu	Val	Phe	Lys	Phe	Lys	Arg	Asn	Phe	Thr
	290					295					300				
Tyr	Lys	Gln	Val	Ile	Phe	Ile	Ile	Gly	Arg	Val	Gly	Thr	Cys	Leu	Leu
305					310					315					320
Leu	Ser	Ile	Asn	Ile	Phe	Leu	Ser	Cys	Leu	Tyr	Ser	Glu	Phe	Cys	Ile
				325					330					335	
Gln	Thr	Tyr	Asn	Ser	Ile	Ser	Arg	Val	Leu	His	Gln	Met	Tyr	Cys	Leu
			340					345					350		
Ser	Ala	Ala	Glu	Asp	Tyr	Leu	Ile	Leu	Lys	Met	Gly	Leu	Arg	Glu	Tyr
		355					360					365			
Ser	Leu	Gln	Met	Glu	His	Leu	Lys	Leu	Ile	Phe	Thr	Cys	Gly	Gly	Leu
	370					375					380				
Phe	Asp	Ile	Asn	Leu	Lys	Phe	Phe	Gly	Gly	Met	Val	Val	Thr	Leu	Phe
385					390					395					400
Gly	Tyr	Ile	Ile	Ile	Leu	Val	Gln	Phe	Lys	Ile	Gln	Phe	Phe	Ala	Gln
				405					410					415	
Ser	Asn	Phe	Met	Gln	Asn	Ile	Asn	Ser	Thr	Glu	Leu	Lys	Ala	Tyr	Thr
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Ala

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<210> 81
<211> 1068
<212> DNA
<213> Drosophila melanogaster
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<220>  
<221> CDS  
<222> (1)..(1068)  
<223> Coding region GR98B.4
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Arg Arg Leu Met Lys Cys Leu Gly Met Leu Pro Phe Gly Gln Asn Leu	
20 25 30	
ttc tcg aaa ggg ttt tgc tat gtg cta ctc ttt gtg tca ctg gga ttt	144
Phe Ser Lys Gly Phe Cys Tyr Val Leu Leu Phe Val Ser Leu Gly Phe	
35 40 45	
tcg agc tac tgg cgc ttc agc ttc gat tat gaa ttt gac tat gat ttc	192
Ser Ser Tyr Trp Arg Phe Ser Phe Asp Tyr Glu Phe Asp Tyr Asp Phe	
50 55 60	
cta aac gat cga ttc tcc agc acc atc gac ctg agc aac ttt gtt gcc	240
Leu Asn Asp Arg Phe Ser Ser Thr Ile Asp Leu Ser Asn Phe Val Ala	
65 70 75 80	
cta gtt ttg ggt cat gct att atc gta ttg gag cta ttg tgg gga aat	288
Leu Val Leu Gly His Ala Ile Ile Val Leu Glu Leu Leu Trp Gly Asn	
85 90 95	
tgc agc aag gat gtg gat agg caa ctg cag gcg atc cat tcc caa ata	336
Cys Ser Lys Asp Val Asp Arg Gln Leu Gln Ala Ile His Ser Gln Ile	
100 105 110	
aaa ctg caa ctg ggt act tcg aat agc acg gat cgt gtg cgg aaa tac	384
Lys Leu Gln Leu Gly Thr Ser Asn Ser Thr Asp Arg Val Arg Lys Tyr	
115 120 125	
tgc aat tgg atc tat gga tcc cta atc ata cga tgg cta ata ttt atc	432
Cys Asn Trp Ile Tyr Gly Ser Leu Ile Ile Arg Trp Leu Ile Phe Ile	
130 135 140	
gtg ggg act ata tat aaa ctt atc gtt gga ggc tcc aat gtt ctg gat	480
Val Gly Thr Ile Tyr Lys Leu Ile Val Gly Gly Ser Asn Val Leu Asp	
145 150 155 160	
gaa ttg tac aga acc cga tat gag atg tgg tcc ata cgc cgt tta tcc	528
Glu Leu Tyr Arg Thr Arg Tyr Glu Met Trp Ser Ile Arg Arg Leu Ser	
165 170 175	
ctg cag aaa ttg gcc aag tta cag gca atc cat aac tct ttg tgg cag	576
Leu Gln Lys Leu Ala Lys Leu Gln Ala Ile His Asn Ser Leu Trp Gln	
180 185 190	
gct atc cgt tgt ctg gag tgc tac ttt caa ctg agc ctg atc aca ctg	624
Ala Ile Arg Cys Leu Glu Cys Tyr Phe Gln Leu Ser Leu Ile Thr Leu	
195 200 205	
ctc atg aag ttc ttc atc gat act tct gct ttg cca tac tgg ctc tac	672
Leu Met Lys Phe Phe Ile Asp Thr Ser Ala Leu Pro Tyr Trp Leu Tyr	
210 215 220	
ctc agc aga gtt gag cac aca agg gtg gct gtg cag cac tac gtc gct	720
Leu Ser Arg Val Glu His Thr Arg Val Ala Val Gln His Tyr Val Ala	
225 230 235 240	

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acg gtt gag tgc atc aaa ctc tta gag att gta gtg ccc tgc tat ctc 768
 Thr Val Glu Cys Ile Lys Leu Leu Glu Ile Val Val Pro Cys Tyr Leu
 245 250 255

tgc acg cga tgt gat gca atg cag cga aag ttc cta tcg atg ttc tac 816
 Cys Thr Arg Cys Asp Ala Met Gln Arg Lys Phe Leu Ser Met Phe Tyr
 260 265 270

aca gtc act acc gat cga cgt agt agt caa cta aat gca gct cta aga 864
 Thr Val Thr Thr Asp Arg Arg Ser Ser Gln Leu Asn Ala Ala Leu Arg
 275 280 285

agt cta aac ctt cag ttg agt cag gag aaa tat aaa ttt agt gcc gga 912
 Ser Leu Asn Leu Gln Leu Ser Gln Glu Lys Tyr Lys Phe Ser Ala Gly
 290 295 300

gga atg gtg gac ata aac aca gaa atg ctg gga aag ttc ttt ttt gga 960
 Gly Met Val Asp Ile Asn Thr Glu Met Leu Gly Lys Phe Phe Phe Gly
 305 310 315 320

atg atc agc tat att gta atc tgc att cag ttc agc atc aac ttc agg 1008
 Met Ile Ser Tyr Ile Val Ile Cys Ile Gln Phe Ser Ile Asn Phe Arg
 325 330 335

gcc aaa aaa atg agc aat gag caa atg agt caa aac atc aca tcc aca 1056
 Ala Lys Lys Met Ser Asn Glu Gln Met Ser Gln Asn Ile Thr Ser Thr
 340 345 350

agt gcc ccc att
 Ser Ala Pro Ile 1068
 355

<210> 82

<211> 356

<212> PRT

<213> *Drosophila melanogaster*

<400> 82

Met Glu Gln Met Ser Gly Glu Leu His Ala Ala Ser Leu Leu Tyr Met
 1 5 10 15

Arg Arg Leu Met Lys Cys Leu Gly Met Leu Pro Phe Gly Gln Asn Leu
 20 25 30

Phe Ser Lys Gly Phe Cys Tyr Val Leu Leu Phe Val Ser Leu Gly Phe
 35 40 45

Ser Ser Tyr Trp Arg Phe Ser Phe Asp Tyr Glu Phe Asp Tyr Asp Phe
 50 55 60

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

Leu Val Leu Gly His Ala Ile Ile Val Leu Glu Leu Leu Trp Gly Asn
 85 90 95

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Cys	Ser	Lys	Asp	Val	Asp	Arg	Gln	Leu	Gln	Ala	Ile	His	Ser	Gln	Ile	100	105	110	
Lys	Leu	Gln	Leu	Gly	Thr	Ser	Asn	Ser	Thr	Asp	Arg	Val	Arg	Lys	Tyr	115	120	125	
Cys	Asn	Trp	Ile	Tyr	Gly	Ser	Leu	Ile	Ile	Arg	Trp	Leu	Ile	Phe	Ile	130	135	140	
Val	Gly	Thr	Ile	Tyr	Lys	Leu	Ile	Val	Gly	Gly	Ser	Asn	Val	Leu	Asp	145	150	155	160
Glu	Leu	Tyr	Arg	Thr	Arg	Tyr	Glu	Met	Trp	Ser	Ile	Arg	Arg	Leu	Ser	165	170	175	
Leu	Gln	Lys	Leu	Ala	Lys	Leu	Gln	Ala	Ile	His	Asn	Ser	Leu	Trp	Gln	180	185	190	
Ala	Ile	Arg	Cys	Leu	Glu	Cys	Tyr	Phe	Gln	Leu	Ser	Leu	Ile	Thr	Leu	195	200	205	
Leu	Met	Lys	Phe	Phe	Ile	Asp	Thr	Ser	Ala	Leu	Pro	Tyr	Trp	Leu	Tyr	210	215	220	
Leu	Ser	Arg	Val	Glu	His	Thr	Arg	Val	Ala	Val	Gln	His	Tyr	Val	Ala	225	230	235	240
Thr	Val	Glu	Cys	Ile	Lys	Leu	Leu	Glu	Ile	Val	Val	Pro	Cys	Tyr	Leu	245	250	255	
Cys	Thr	Arg	Cys	Asp	Ala	Met	Gln	Arg	Lys	Phe	Leu	Ser	Met	Phe	Tyr	260	265	270	
Thr	Val	Thr	Thr	Asp	Arg	Arg	Ser	Ser	Gln	Leu	Asn	Ala	Ala	Leu	Arg	275	280	285	
Ser	Leu	Asn	Leu	Gln	Leu	Ser	Gln	Glu	Lys	Tyr	Lys	Phe	Ser	Ala	Gly	290	295	300	
Gly	Met	Val	Asp	Ile	Asn	Thr	Glu	Met	Leu	Gly	Lys	Phe	Phe	Phe	Gly	305	310	315	320
Met	Ile	Ser	Tyr	Ile	Val	Ile	Cys	Ile	Gln	Phe	Ser	Ile	Asn	Phe	Arg	325	330	335	
Ala	Lys	Lys	Met	Ser	Asn	Glu	Gln	Met	Ser	Gln	Asn	Ile	Thr	Ser	Thr	340	345	350	
Ser	Ala	Pro	Ile													355			

<210> 83
 <211> 381
 <212> DNA

WO 00/77208

PCT/US00/16211

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(381)

<223> Partial coding region GR27F.1

<400> 83

cac	tgt	gct	ttt	gtg	ccc	tct	ttc	tcg	tcc	cac	ttg	ctc	tcg	tat	ctg	48
His	Cys	Ala	Phe	Val	Pro	Ser	Phe	Ser	Ser	His	Leu	Leu	Ser	Tyr	Leu	
1				5					10					15		

atc	gcc	acc	att	ccc	atc	gtc	gag	gac	agt	aat	cga	gcc	atc	aca	aag	96
Ile	Ala	Thr	Ile	Pro	Ile	Val	Glu	Asp	Ser	Asn	Arg	Ala	Ile	Thr	Lys	
			20					25					30			

agc	gag	aaa	act	gga	ggc	ata	gtg	cac	tcc	cta	ctc	aat	aaa	ccc	aaa	144
Ser	Glu	Lys	Thr	Gly	Gly	Ile	Val	His	Ser	Leu	Leu	Asn	Lys	Pro	Lys	
		35				40						45				

agt	gct	gag	tac	aag	gag	aaa	ctg	cag	caa	ttc	tcc	atg	cag	ttg	atg	192
Ser	Ala	Glu	Tyr	Lys	Glu	Lys	Leu	Gln	Gln	Phe	Ser	Met	Gln	Leu	Met	
	50					55				60						

cat	ctg	aaa	atc	aat	ttt	act	gca	gct	ggc	ctg	ttc	aac	atc	gac	cgc	240
His	Leu	Lys	Ile	Asn	Phe	Thr	Ala	Ala	Gly	Leu	Phe	Asn	Ile	Asp	Arg	
65					70					75					80	

aca	ttg	tat	ttc	acg	atc	agc	ggg	gcc	ttg	acc	act	tat	ctc	atc	atc	288
Thr	Leu	Tyr	Phe	Thr	Ile	Ser	Gly	Ala	Leu	Thr	Thr	Tyr	Leu	Ile	Ile	
				85				90					95			

ttg	ctg	cag	ttc	aca	tcc	aat	tcc	ccg	aac	aat	ggc	tat	ggg	aat	ggc	336
Leu	Leu	Gln	Phe	Thr	Ser	Asn	Ser	Pro	Asn	Asn	Gly	Tyr	Gly	Asn	Gly	
		100						105					110			

agc	tct	tgc	tgt	gag	ccc	ttc	aat	aat	atg	acg	aat	cat	acg	ctt		381
Ser	Ser	Cys	Cys	Glu	Pro	Phe	Asn	Asn	Met	Thr	Asn	His	Thr	Leu		
		115				120					125					

<210> 84

<211> 127

<212> PRT

<213> *Drosophila melanogaster*

<400> 84

His	Cys	Ala	Phe	Val	Pro	Ser	Phe	Ser	Ser	His	Leu	Leu	Ser	Tyr	Leu
1				5					10					15	

Ile	Ala	Thr	Ile	Pro	Ile	Val	Glu	Asp	Ser	Asn	Arg	Ala	Ile	Thr	Lys
			20					25					30		

Ser	Glu	Lys	Thr	Gly	Gly	Ile	Val	His	Ser	Leu	Leu	Asn	Lys	Pro	Lys
		35				40						45			

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Ser Ala Glu Tyr Lys Glu Lys Leu Gln Gln Phe Ser Met Gln Leu Met
 50 55 60

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

Thr Leu Tyr Phe Thr Ile Ser Gly Ala Leu Thr Thr Tyr Leu Ile Ile
 85 90 95

Leu Leu Gln Phe Thr Ser Asn Ser Pro Asn Asn Gly Tyr Gly Asn Gly
 100 105 110

Ser Ser Cys Cys Glu Pro Phe Asn Asn Met Thr Asn His Thr Leu
 115 120 125

<210> 85

<211> 186

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(186)

<223> Partial coding region GR93F.1

<400> 85

gtt gaa aca ttt ctc ggt cag ctg caa acc caa cga ctg gag atc aaa 48
 Val Glu Thr Phe Leu Gly Gln Leu Gln Thr Gln Arg Leu Glu Ile Lys
 1 5 10 15

gta ttg gga ttt ttc cat cta aat aat gag ttc att ctt ctc att ctg 96
 Val Leu Gly Phe Phe His Leu Asn Asn Glu Phe Ile Leu Leu Ile Leu
 20 25 30

tct gcc ata ata tcg tac ctg ttt atc ctt att cag ttc ggc att aca 144
 Ser Ala Ile Ile Ser Tyr Leu Phe Ile Leu Ile Gln Phe Gly Ile Thr
 35 40 45

ggt ggc ttt gag gcg tcc gag gac att aaa aat cgt ttt gat 186
 Gly Gly Phe Glu Ala Ser Glu Asp Ile Lys Asn Arg Phe Asp
 50 55 60

<210> 86

<211> 62

<212> PRT

<213> Drosophila melanogaster

<400> 86

Val Glu Thr Phe Leu Gly Gln Leu Gln Thr Gln Arg Leu Glu Ile Lys
 1 5 10 15

Val Leu Gly Phe Phe His Leu Asn Asn Glu Phe Ile Leu Leu Ile Leu
 20 25 30

Ser Ala Ile Ile Ser Tyr Leu Phe Ile Leu Ile Gln Phe Gly Ile Thr
 35 40 45

Gly Gly Phe Glu Ala Ser Glu Asp Ile Lys Asn Arg Phe Asp
 50 55 60

<210> 87

<211> 864

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(864)

<223> Partial coding region GR93F.4

<400> 87

tac tta tcg ata att cac ttg aag atc tgt cat ggc ccg gaa gtg acc	48
Tyr Leu Ser Ile Ile His Leu Lys Ile Cys His Gly Pro Glu Val Thr	
1 5 10 15	
aag ttg gtt aac caa tat ctg cac atc ttt cgc ctg gga acc ctg gac	96
Lys Leu Val Asn Gln Tyr Leu His Ile Phe Arg Leu Gly Thr Leu Asp	
20 25 30	
atc cgt aga aga agt caa ttt gga ggc ggt aga gag ttg ttc ctg cta	144
Ile Arg Arg Arg Ser Gln Phe Gly Gly Gly Arg Glu Leu Phe Leu Leu	
35 40 45	
att ctt tcg gtt tgt tgt cag att cat gaa tat gtt ttt ata ttg gtc	192
Ile Leu Ser Val Cys Cys Gln Ile His Glu Tyr Val Phe Ile Leu Val	
50 55 60	
ata gcg agc aga ctt tgt ggt ttt caa cat att att tgg tgg gtt agc	240
Ile Ala Ser Arg Leu Cys Gly Phe Gln His Ile Ile Trp Trp Val Ser	
65 70 75 80	
tat aca tat gtg ttt att ata tgt aat tcg atc atg tgt ttc ggt ttt	288
Tyr Thr Tyr Val Phe Ile Ile Cys Asn Ser Ile Met Cys Phe Gly Phe	
85 90 95	
att tgg cac cta agc ctg gga gtt ctc tat gct gag ctg aac gat aat	336
Ile Trp His Leu Ser Leu Gly Val Leu Tyr Ala Glu Leu Asn Asp Asn	
100 105 110	
ctt cgc ttt gag tca ggc ttc caa acg gca ttt tta agg aaa cag caa	384
Leu Arg Phe Glu Ser Gly Phe Gln Thr Ala Phe Leu Arg Lys Gln Gln	
115 120 125	
aga att agg gta caa aaa tct atg gca ctt ttc aag gag ata tcc tct	432
Arg Ile Arg Val Gln Lys Ser Met Ala Leu Phe Lys Glu Ile Ser Ser	
130 135 140	
gtg gtt acc tcc ttg cag gac att ttc aat gta cac cta ttt ttg agc	480

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Val	Val	Thr	Ser	Leu	Gln	Asp	Ile	Phe	Asn	Val	His	Leu	Phe	Leu	Ser	
145					150				155						160	
gca	ctc	ttg	aca	ctt	ctg	caa	gtt	cta	gtc	gtt	tgg	tat	aaa	atg	atc	528
Ala	Leu	Leu	Thr	Leu	Leu	Gln	Val	Leu	Val	Val	Trp	Tyr	Lys	Met	Ile	
				165				170						175		
atc	gat	tta	ggg	ttt	tct	gac	ttt	cgg	att	tgg	tca	ttc	tcg	ctt	aaa	576
Ile	Asp	Leu	Gly	Phe	Ser	Asp	Phe	Arg	Ile	Trp	Ser	Phe	Ser	Leu	Lys	
			180					185					190			
aat	ttg	atc	caa	acg	ctc	ctt	cct	gtt	ttg	gcc	att	caa	gaa	gcg	gca	624
Asn	Leu	Ile	Gln	Thr	Leu	Leu	Pro	Val	Leu	Ala	Ile	Gln	Glu	Ala	Ala	
		195					200					205				
aat	caa	ttt	aaa	caa	act	cgg	gaa	cgt	gct	ctg	gat	att	ttc	ctc	gtt	672
Asn	Gln	Phe	Lys	Gln	Thr	Arg	Glu	Arg	Ala	Leu	Asp	Ile	Phe	Leu	Val	
	210					215					220					
gga	aag	tca	aag	cat	tgg	atg	aaa	tcg	gtg	gaa	ata	ttt	gtc	acc	cat	720
Gly	Lys	Ser	Lys	His	Trp	Met	Lys	Ser	Val	Glu	Ile	Phe	Val	Thr	His	
225					230				235						240	
ctc	aac	cta	agc	gag	ttc	agg	gtt	aac	ttg	ttg	ggc	ctc	ttc	aat	gtt	768
Leu	Asn	Leu	Ser	Glu	Phe	Arg	Val	Asn	Leu	Leu	Gly	Leu	Phe	Asn	Val	
				245				250						255		
tcc	aac	gaa	cta	ttt	cta	ata	att	gta	tct	gca	atg	ttt	tgc	tat	ctg	816
Ser	Asn	Glu	Leu	Phe	Leu	Ile	Ile	Val	Ser	Ala	Met	Phe	Cys	Tyr	Leu	
			260					265					270			
gtt	ttt	gta	aca	caa	tgt	gta	atc	gtg	tat	cgc	aga	cgc	tat	gtt	att	864
Val	Phe	Val	Thr	Gln	Cys	Val	Ile	Val	Tyr	Arg	Arg	Arg	Tyr	Val	Ile	
		275					280					285				

<210> 88

<211> 288

<212> PRT

<213> Drosophila melanogaster

<400> 88

Tyr	Leu	Ser	Ile	Ile	His	Leu	Lys	Ile	Cys	His	Gly	Pro	Glu	Val	Thr	
1				5				10						15		
Lys	Leu	Val	Asn	Gln	Tyr	Leu	His	Ile	Phe	Arg	Leu	Gly	Thr	Leu	Asp	
			20					25					30			
Ile	Arg	Arg	Arg	Ser	Gln	Phe	Gly	Gly	Gly	Arg	Glu	Leu	Phe	Leu	Leu	
			35				40					45				
Ile	Leu	Ser	Val	Cys	Cys	Gln	Ile	His	Glu	Tyr	Val	Phe	Ile	Leu	Val	
	50					55					60					
Ile	Ala	Ser	Arg	Leu	Cys	Gly	Phe	Gln	His	Ile	Ile	Trp	Trp	Val	Ser	
65					70					75					80	

Tyr Thr Tyr Val Phe Ile Ile Cys Asn Ser Ile Met Cys Phe Gly Phe
 85 90 95
 Ile Trp His Leu Ser Leu Gly Val Leu Tyr Ala Glu Leu Asn Asp Asn
 100 105 110
 Leu Arg Phe Glu Ser Gly Phe Gln Thr Ala Phe Leu Arg Lys Gln Gln
 115 120 125
 Arg Ile Arg Val Gln Lys Ser Met Ala Leu Phe Lys Glu Ile Ser Ser
 130 135 140
 Val Val Thr Ser Leu Gln Asp Ile Phe Asn Val His Leu Phe Leu Ser
 145 150 155 160
 Ala Leu Leu Thr Leu Leu Gln Val Leu Val Val Trp Tyr Lys Met Ile
 165 170 175
 Ile Asp Leu Gly Phe Ser Asp Phe Arg Ile Trp Ser Phe Ser Leu Lys
 180 185 190
 Asn Leu Ile Gln Thr Leu Leu Pro Val Leu Ala Ile Gln Glu Ala Ala
 195 200 205
 Asn Gln Phe Lys Gln Thr Arg Glu Arg Ala Leu Asp Ile Phe Leu Val
 210 215 220
 Gly Lys Ser Lys His Trp Met Lys Ser Val Glu Ile Phe Val Thr His
 225 230 235 240
 Leu Asn Leu Ser Glu Phe Arg Val Asn Leu Leu Gly Leu Phe Asn Val
 245 250 255
 Ser Asn Glu Leu Phe Leu Ile Ile Val Ser Ala Met Phe Cys Tyr Leu
 260 265 270
 Val Phe Val Thr Gln Cys Val Ile Val Tyr Arg Arg Arg Tyr Val Ile
 275 280 285

<210> 89
 <211> 678
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(678)
 <223> Partial coding region GR97D.1

<400> 89
 cgg cga gga aaa ctc cat acc caa ctg gtc acg att tgt ctt tac gcg 48
 Arg Arg Gly Lys Leu His Thr Gln Leu Val Thr Ile Cys Leu Tyr Ala
 1 5 10 15

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acc gtt ttc ctt aac ata ctt tac ggc gtt tat ctc ggc cgc ttt tcc	96
Thr Val Phe Leu Asn Ile Leu Tyr Gly Val Tyr Leu Gly Arg Phe Ser	
20 25 30	
ttc agg cgc aag aag ttt gtg ttt tcc aaa ggg ctc act atc tat agc	144
Phe Arg Arg Lys Lys Phe Val Phe Ser Lys Gly Leu Thr Ile Tyr Ser	
35 40 45	
tta ttt gtg gcc acg ttc ttt gcg ctg ttt tac atc tgg aat att tat	192
Leu Phe Val Ala Thr Phe Phe Ala Leu Phe Tyr Ile Trp Asn Ile Tyr	
50 55 60	
aat gaa att tcc act ggt cag atc aat ctt cgc gat aca att gga ata	240
Asn Glu Ile Ser Thr Gly Gln Ile Asn Leu Arg Asp Thr Ile Gly Ile	
65 70 75 80	
tat tgt tat atg aac gtc tgc gtt tgc cta ttc aac tat gtg acc caa	288
Tyr Cys Tyr Met Asn Val Cys Val Cys Leu Phe Asn Tyr Val Thr Gln	
85 90 95	
tgg gaa aaa aca ctg caa ata att cgg ttt cag aat agt gtg cct ctt	336
Trp Glu Lys Thr Leu Gln Ile Ile Arg Phe Gln Asn Ser Val Pro Leu	
100 105 110	
ttc aag gtc ctc gat tca ctg gac att tcg gcg atg att gtg tgg cgg	384
Phe Lys Val Leu Asp Ser Leu Asp Ile Ser Ala Met Ile Val Trp Arg	
115 120 125	
gca ttt ata tat ggc ttg ctc aag atc gtg ttc tgt ccc ctt atc acc	432
Ala Phe Ile Tyr Gly Leu Leu Lys Ile Val Phe Cys Pro Leu Ile Thr	
130 135 140	
tat ata acg ctg att cta tat cat aga cgc tcc att tcg gaa agt caa	480
Tyr Ile Thr Leu Ile Leu Tyr His Arg Arg Ser Ile Ser Glu Ser Gln	
145 150 155 160	
tgg acg agt gta acg acc acg aag acc atg ttg cca ctg att gtt tcc	528
Trp Thr Ser Val Thr Thr Thr Lys Thr Met Leu Pro Leu Ile Val Ser	
165 170 175	
aat cag ata aat aat tgc ttc ttc ggc ggc ctg gta ctt gca aat ttg	576
Asn Gln Ile Asn Asn Cys Phe Phe Gly Gly Leu Val Leu Ala Asn Leu	
180 185 190	
ata ttt gcc gcg gtg aat cgt aag ctg cac ggc att gtc aag gag gcc	624
Ile Phe Ala Ala Val Asn Arg Lys Leu His Gly Ile Val Lys Glu Ala	
195 200 205	
aat atg ctg cag tca cct gtc cag atg aat ctc cat aag ccc tac tac	672
Asn Met Leu Gln Ser Pro Val Gln Met Asn Leu His Lys Pro Tyr Tyr	
210 215 220	
cgg atg	678
Arg Met	
225	

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<210> 90
 <211> 226
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 90
 Arg Arg Gly Lys Leu His Thr Gln Leu Val Thr Ile Cys Leu Tyr Ala
 1 5 10 15
 Thr Val Phe Leu Asn Ile Leu Tyr Gly Val Tyr Leu Gly Arg Phe Ser
 20 25 30
 Phe Arg Arg Lys Lys Phe Val Phe Ser Lys Gly Leu Thr Ile Tyr Ser
 35 40 45
 Leu Phe Val Ala Thr Phe Phe Ala Leu Phe Tyr Ile Trp Asn Ile Tyr
 50 55 60
 Asn Glu Ile Ser Thr Gly Gln Ile Asn Leu Arg Asp Thr Ile Gly Ile
 65 70 75 80
 Tyr Cys Tyr Met Asn Val Cys Val Cys Leu Phe Asn Tyr Val Thr Gln
 85 90 95
 Trp Glu Lys Thr Leu Gln Ile Ile Arg Phe Gln Asn Ser Val Pro Leu
 100 105 110
 Phe Lys Val Leu Asp Ser Leu Asp Ile Ser Ala Met Ile Val Trp Arg
 115 120 125
 Ala Phe Ile Tyr Gly Leu Leu Lys Ile Val Phe Cys Pro Leu Ile Thr
 130 135 140
 Tyr Ile Thr Leu Ile Leu Tyr His Arg Arg Ser Ile Ser Glu Ser Gln
 145 150 155 160
 Trp Thr Ser Val Thr Thr Thr Lys Thr Met Leu Pro Leu Ile Val Ser
 165 170 175
 Asn Gln Ile Asn Asn Cys Phe Phe Gly Gly Leu Val Leu Ala Asn Leu
 180 185 190
 Ile Phe Ala Ala Val Asn Arg Lys Leu His Gly Ile Val Lys Glu Ala
 195 200 205
 Asn Met Leu Gln Ser Pro Val Gln Met Asn Leu His Lys Pro Tyr Tyr
 210 215 220
 Arg Met
 225

<210> 91
 <211> 381
 <212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(381)

<223> Partial coding region GR98B.2

<400> 91

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gga cgc gct gga ccc ttt ttt cac tgg gtg aat caa gta tta acc caa      48
Gly Arg Ala Gly Pro Phe Phe His Trp Val Asn Gln Val Leu Thr Gln
 1              5              10              15

atc att ctt ata atg ctt caa ctc aaa ggc ccc gag tat tgc cta ttc      96
Ile Ile Leu Ile Met Leu Gln Leu Lys Gly Pro Glu Tyr Cys Leu Phe
      20              25              30

gtc cta ctg gtt tat gaa ctg att cta aga acg cgc cat gtc ctt gag     144
Val Leu Leu Val Tyr Glu Leu Ile Leu Arg Thr Arg His Val Leu Glu
      35              40              45

cag cta aag gat gat ctc gaa gac ttc gac tgc gga gcc agg att cag     192
Gln Leu Lys Asp Asp Leu Glu Asp Phe Asp Cys Gly Ala Arg Ile Gln
      50              55              60

gag ctg tgc gtg act tta aag cag aac caa ttg ctc att gga cga ata     240
Glu Leu Cys Val Thr Leu Lys Gln Asn Gln Leu Leu Ile Gly Arg Ile
      65              70              75              80

tgg aga ttg gtg gat gag att gga gca tat ttc aga tgg tcc atg act     288
Trp Arg Leu Val Asp Glu Ile Gly Ala Tyr Phe Arg Trp Ser Met Thr
      85              90              95

ctg ctg ttt ctc tac aat gga ctt acc att ctg cac gtt gtc aac tgg     336
Leu Leu Phe Leu Tyr Asn Gly Leu Thr Ile Leu His Val Val Asn Trp
      100              105              110

gct atc att aga tcc atc gat cca aac gat tgc tgt caa ctc agt         381
Ala Ile Ile Arg Ser Ile Asp Pro Asn Asp Cys Cys Gln Leu Ser
      115              120              125

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<210> 92

<211> 127

<212> PRT

<213> *Drosophila melanogaster*

<400> 92

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Gly Arg Ala Gly Pro Phe Phe His Trp Val Asn Gln Val Leu Thr Gln
 1              5              10              15

Ile Ile Leu Ile Met Leu Gln Leu Lys Gly Pro Glu Tyr Cys Leu Phe
      20              25              30

Val Leu Leu Val Tyr Glu Leu Ile Leu Arg Thr Arg His Val Leu Glu
      35              40              45

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Gln Leu Lys Asp Asp Leu Glu Asp Phe Asp Cys Gly Ala Arg Ile Gln
 50 55 60
 Glu Leu Cys Val Thr Leu Lys Gln Asn Gln Leu Leu Ile Gly Arg Ile
 65 70 75 80
 Trp Arg Leu Val Asp Glu Ile Gly Ala Tyr Phe Arg Trp Ser Met Thr
 85 90 95
 Leu Leu Phe Leu Tyr Asn Gly Leu Thr Ile Leu His Val Val Asn Trp
 100 105 110
 Ala Ile Ile Arg Ser Ile Asp Pro Asn Asp Cys Cys Gln Leu Ser
 115 120 125

<210> 93
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Positive
 control primer for preparing cDNA

<400> 93
 cggatcccta tgtcaaggtg

20

<210> 94
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Positive
 control primer for preparing cDNA

<400> 94
 gaagagcttc gtgctgggtct

20

We claim:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - a) an isolated nucleic acid molecule that encodes the amino acid sequence of a
5 *Drosophila* Gustatory Receptor protein;
 - b) an isolated nucleic acid molecule that encodes a protein fragment of at least 6 amino acids of a *Drosophila* Gustatory Receptor protein; and
 - c) an isolated nucleic acid molecule which hybridizes to a nucleic acid molecule comprising a nucleotide sequence encoding a *Drosophila* Gustatory Receptor protein under
10 conditions of sufficient stringency to produce a clear signal.
2. The isolated nucleic acid molecule of claim 1 wherein the nucleic acid comprises at least one exon-intron boundary located in a position selected from the group consisting of:
 - a) the nucleotides encoding the amino acids which comprise the third extracellular
15 loop of a *Drosophila* Gustatory Receptor protein; and
 - b) the nucleotides encoding the amino acids which comprise the seventh transmembrane domain of a *Drosophila* Gustatory Receptor protein.
3. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule is
20 selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90 and 91.
4. The isolated nucleic acid molecule of any one of claims 1-3, wherein said nucleic
25 acid molecule is operably linked to one or more expression control elements.
5. A vector comprising an isolated nucleic acid molecule of any one of claims 1-3.

6. A host cell transformed to contain the nucleic acid molecule of any one of claims 1-3.

7. A host cell comprising a vector of claim 5.

5

8. A host cell of claim 7, wherein said host is selected from the group consisting of prokaryotic hosts and eukaryotic hosts.

9. A method for producing a protein or protein fragment comprising the step of
10 culturing a host cell transformed with the nucleic acid molecule of any one of claims 1-3 under conditions in which the protein or protein fragment encoded by said nucleic acid molecule is expressed.

10. The method of claim 9, wherein said host cell is selected from the group
15 consisting of prokaryotic hosts and eukaryotic hosts.

11. An isolated protein or protein fragment produced by the method of claim 10.

12. An isolated protein or protein fragment selected from the group consisting of:
20 a) an isolated protein comprising one of the amino acid sequences depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92;
b) an isolated protein fragment comprising at least six amino acids of any of the sequences depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34,
25 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92;

c) an isolated protein comprising conservative amino acid substitutions of any of the sequences depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34,

36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92; and

d) naturally occurring amino acid sequence variants of any of the sequences depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44,
 5 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90 and 92.

13. The isolated protein or protein fragment of claim 12 wherein the protein or protein fragment of a *Drosophila* Gustatory Receptor protein has at least one of the following conserved amino acids selected from the group consisting of:

- 10 a) Serine in the amino terminal domain;
- b) Phenylalanine in the first transmembrane domain;
- c) Arginine in the first extracellular loop;
- d) Leucine in the fourth transmembrane domain;
- e) Leucine in the third transmembrane domain;
- 15 f) Glycine in the fifth transmembrane domain;
- g) Tyrosine in the fifth transmembrane domain;
- h) Leucine in the third extracellular loop;
- i) Phenylalanine in the third extracellular loop;
- j) Alanine in the seventh transmembrane domain;
- 20 k) Glycine in the seventh transmembrane domain;
- l) Leucine in the seventh transmembrane domain;
- m) Aspartate in the seventh transmembrane domain;
- n) Alanine in the seventh transmembrane domain;
- o) Threonine in the seventh transmembrane domain;
- 25 p) Tyrosine in the seventh transmembrane domain;
- q) Valine in the seventh transmembrane domain;
- r) Glutamine in the carboxy terminal domain; and
- s) Phenylalanine in the carboxy terminal domain.

14. An isolated antibody that binds to a polypeptide of claim 11, 12 or 13.

15. The antibody of claim 14 wherein said antibody is a monoclonal or polyclonal antibody.

5

16. A method of identifying an agent which modulates the expression of a protein or protein fragment of claim 11, 12 or 13 comprising the steps of:

a) exposing cells which express the protein or protein fragment to the agent; and

10 b) determining whether the agent modulates expression of said protein or protein fragment, thereby identifying an agent which modulates the expression of a protein or protein fragment of claim 11, 12 or 13.

17. A method of identifying an agent which modulates the activity of a protein or protein fragment of claim 11, 12 or 13 comprising the steps of:

15 a) exposing cells which express the protein or protein fragment to the agent; and

b) determining whether the agent modulates the activity of said protein or protein fragment, thereby identifying an agent which modulates the activity of a protein or protein fragment of claim 11, 12 or 13.

20 18. The method of claim 17, wherein the agent modulates at least one activity of the protein or protein fragment.

19. A method of identifying an agent which modulates the transcription of the nucleic acid molecule of any one of claims 1-3 comprising the steps of:

25 a) exposing cells which transcribe the nucleic acid to the agent; and

b) determining whether the agent modulates transcription of said nucleic acid, thereby identifying an agent which modulates the transcription of the nucleic acid molecule of any one of claims 1-3.

20. A method of identifying binding partners for a protein or protein fragment of either claim 11, 12 or 13 comprising the steps of:

- a) exposing said protein or protein fragment to a potential binding partner; and
- b) determining if the potential binding partner binds to said protein or protein fragment, thereby identifying binding partners for the protein or protein fragment.

21. A method of modulating the expression of a nucleic acid encoding a protein or protein fragment of claim 11, 12 or 13 comprising administering an effective amount of an agent which modulates the expression of a nucleic acid encoding the protein or protein fragment.

22. A method of modulating at least one activity of a protein or protein fragment of claim 11, 12 or 13 comprising the step of administering an effective amount of an agent which modulates at least one activity of the protein or protein fragment.

23. A method of identifying novel gustatory receptor genes comprising the steps of:

- a) selecting candidate gustatory receptor genes by screening a nucleic acid database using an algorithm trained to identify seven transmembrane receptors genes;

- b) screening said selected candidate gustatory receptor genes by identifying nucleic acid sequences with conserved amino acid residues and intron-exon boundaries common to gustatory receptors, and having open reading frames of sufficient size so as to encode a seven transmembrane receptor; and

- c) identifying the novel gustatory receptor genes and measuring the expression of gustatory receptor genes wherein the detection of expression confirms said candidate gustatory gene as an gustatory gene.

24. A method of identifying novel gustatory receptor genes comprising the steps of:

- a) selecting candidate gustatory receptor genes by screening a nucleic acid database

for nucleic acid sequences with sufficient homology to at least one known gustatory receptor gene;

b) screening said selected candidate gustatory receptor genes by identifying nucleic acids with conserved amino acid residues and intron-exon boundaries common to gustatory
5 receptors, and having open reading frames of sufficient size so as to encode a seven transmembrane receptor; and

c) identifying the novel gustatory receptor genes and measuring the expression of gustatory receptor genes wherein the detection of expression confirms said candidate gustatory gene as an gustatory gene.

10

25. A transgenic insect modified to contain a nucleic acid molecule of any of claims 1-3.

15

26. The transgenic insect of claim 25, wherein the nucleic acid molecule contains a mutation that alters expression of the encoded protein.

Figure 1

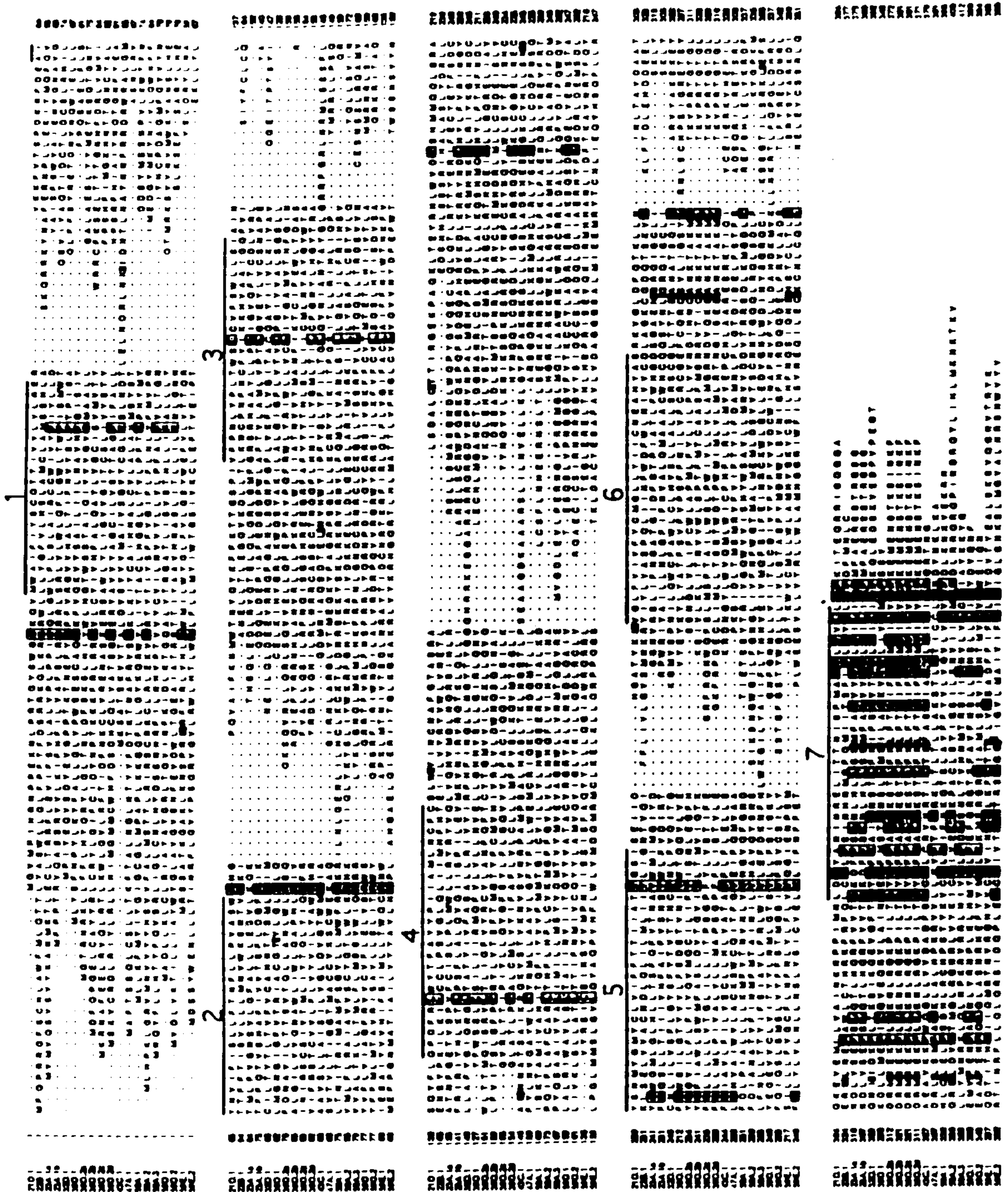


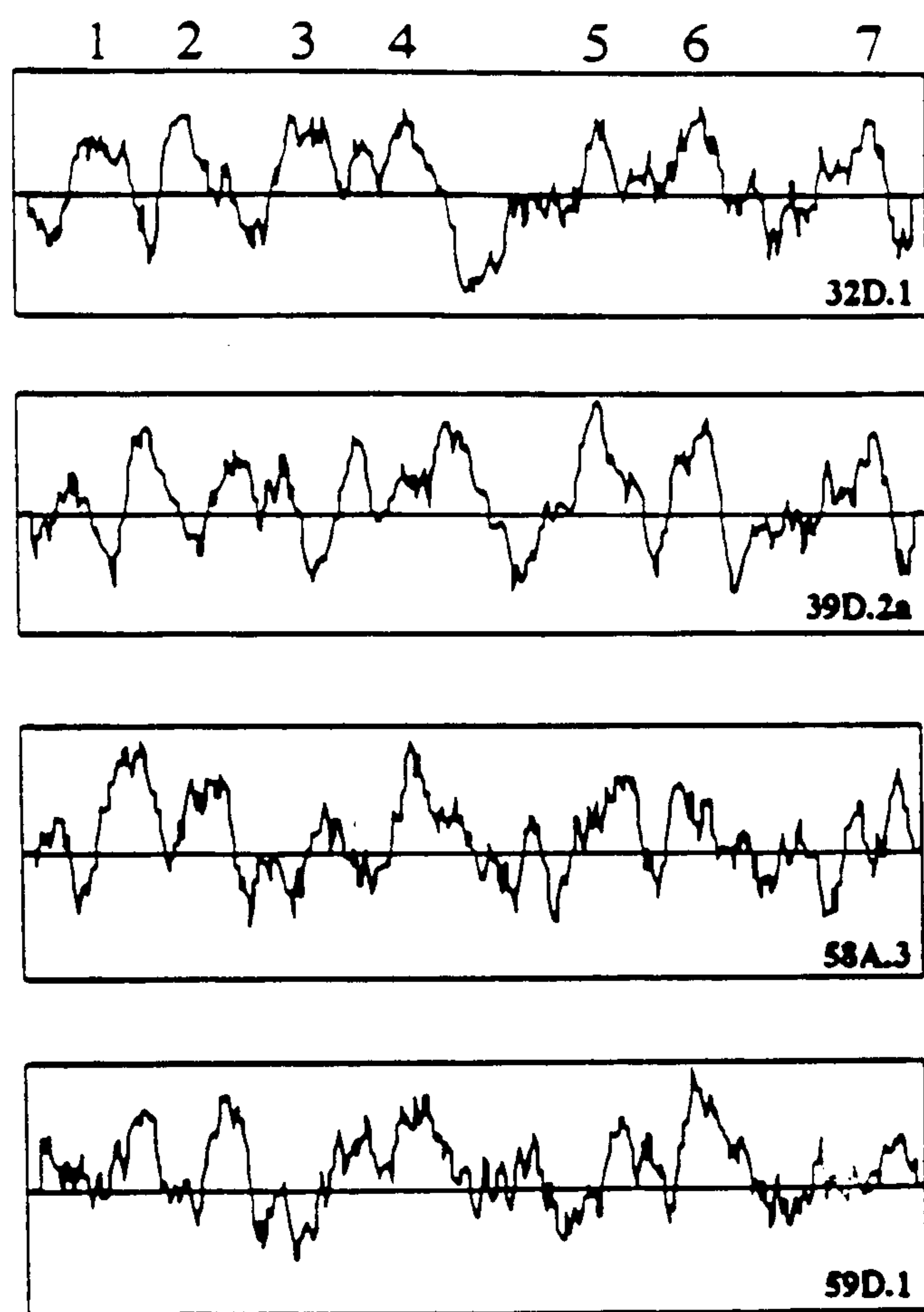
Figure 2

Figure 3

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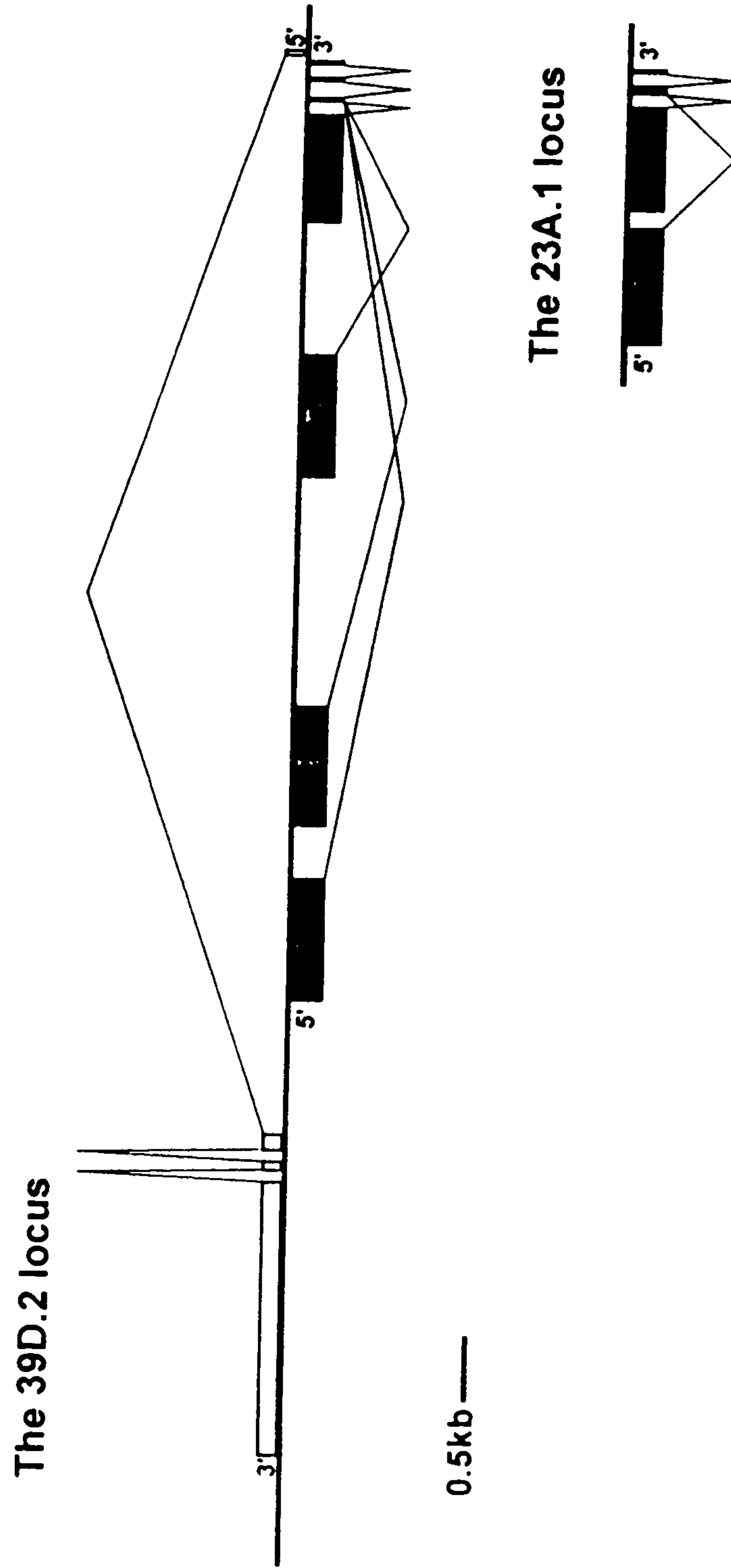


FIG. 4

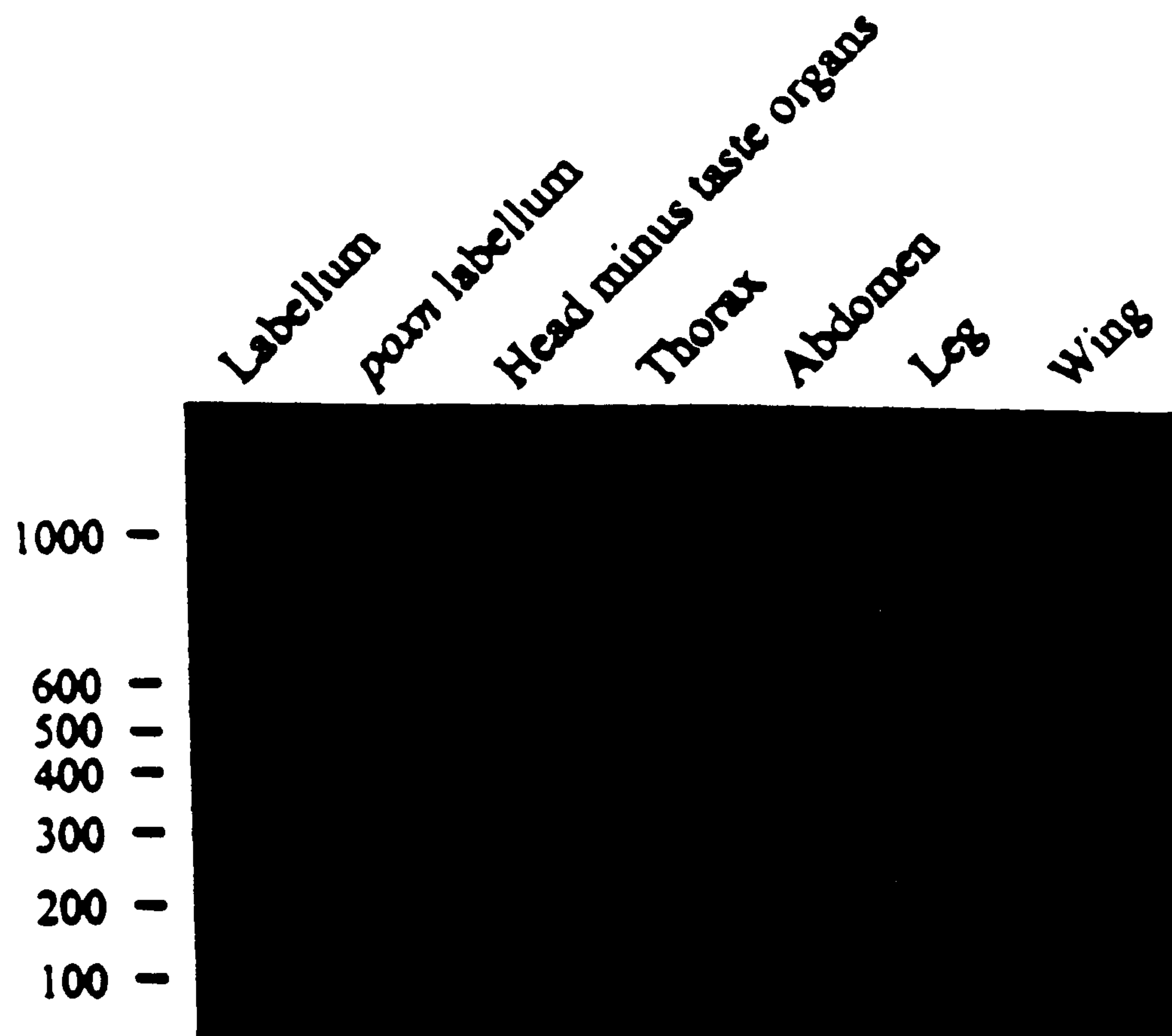
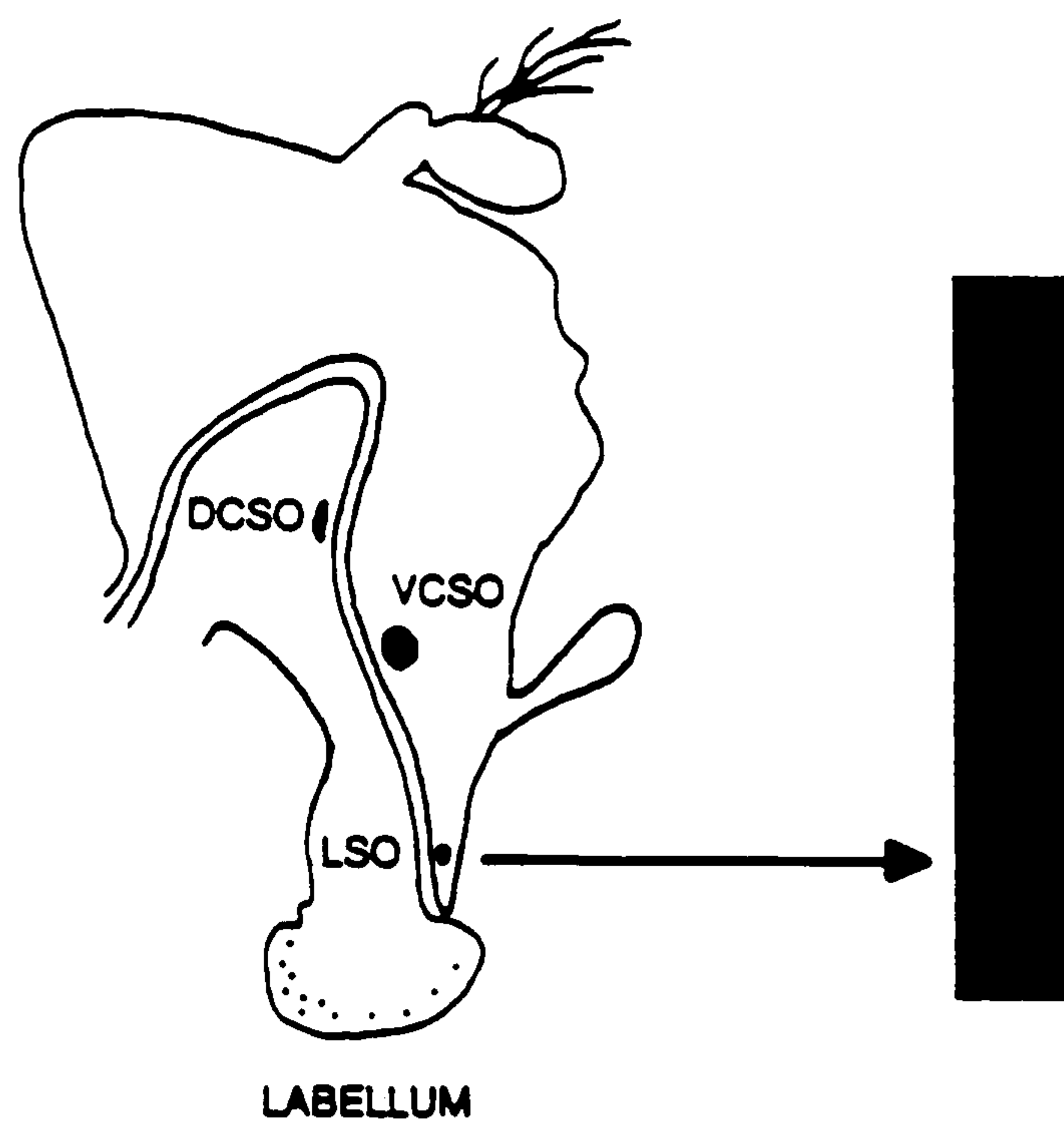
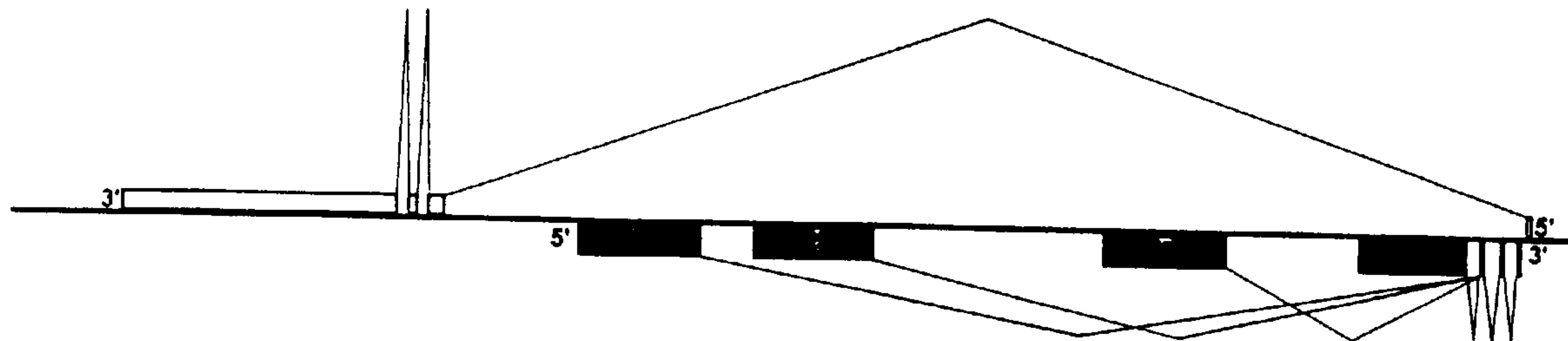


FIG. 5



The 39D.2 locus



0.5kb —

The 23A.1 locus

