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(54) Title: METHODS FOR IDENTIFYING COMPOUNDS THAT DIRECTLY BIND TO INSECT TRANSIENT RECEPTOR POTENTIAL CHANNELS

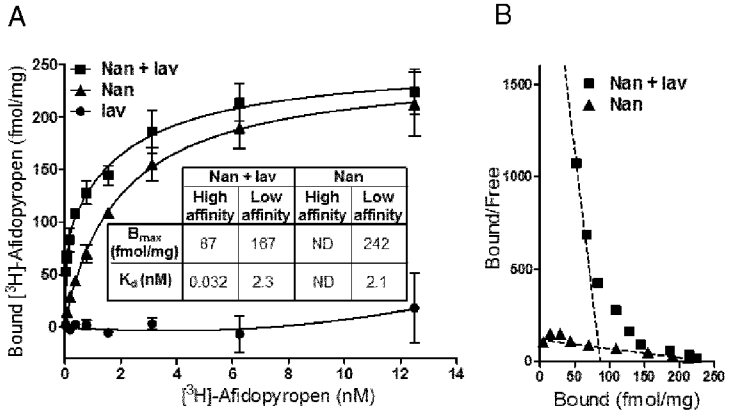


Figure 8. [3H]-Afidopyropen binds to Nan protein, and binding affinity is increased in the presence of lav. (A) Saturation binding of [3H]-afidopyropen to membranes obtained from CHO cells expressing fruit fly Nan and lav, either alone or together. Binding isotherms were fit into two-sites binding model (averages ± S.D. of 3 repetitions). No specific binding to lav was detected. Membranes obtained from both Nan-lav co-expressing cells, and from the cells expressing Nan alone demonstrated specific binding with comparable number of total binding sites at concentration of radioligand approaching saturation. Co-expression of lav together with Nan revealed the presence of high affinity binding sites, which were not detectable in Nan alone-expressing membranes (table insert). (B) Scatchard transformation of the binding isoterms illustrates presence of high affinity sites in the membranes co-expressing Nan and lav, but not Nan alone.

(57) Abstract: The present invention relates to a screening method for determining whether or not a candidate compound directly binds to an insect transient receptor potential V (TRPV) channel. The present invention further provides a method of identifying a compound that directly binds to a Nanchung protein, TRP and/or TRPV protein and/or channel using a binding assay. The present invention further provides a method of classifying an insecticide compound by its mode of action using the binding assay and/or a functional assays.

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— *with sequence listing part of description (Rule 5.2(a))*

METHODS FOR IDENTIFYING COMPOUNDS THAT DIRECTLY BIND TO INSECT TRANSIENT RECEPTOR POTENTIAL CHANNELS

CROSS-REFERENCE TO RELATED APPLICATION

The present patent document claims the benefit of the filing date under 35 U.S.C. §119(e) of Provisional U.S. Patent Application Serial No. 62/182,037, filed June 19, 2015, which is hereby incorporated by reference in its entirety.

SUBMISSION OF SEQUENCE LISTING

The Sequence Listing associated with this application is filed in electronic format *via* EFS-Web and hereby incorporated by reference into the specification in its entirety. The name of the text file containing the Sequence Listing is PF78630_SEQLIST. The size of the text file is 619 KB, and the text file was created on June 18, 2015.

BACKGROUND

The present invention generally relates to methods for determining agents that bind directly to one or more Nanchung proteins, transient receptor potential (TRP) protein complexes and/or channels and/or transient receptor potential V (TRPV) protein complexes and/or channels. The present invention also relates to compositions and methods of insect control as well as mode of action classification for an insecticide composition comprising a compound capable of binding directly to the one or more Nanchung proteins, transient receptor potential (TRP) protein complexes and/or channels and/or transient receptor potential V (TRPV) protein complexes and/or channels. The present invention further relates to compositions and methods of insect control, as well as mode of action classification for an insecticide composition comprising a compound capable of directly binding to the one or more Nanchung proteins, transient receptor potential (TRP) protein complexes and/or channels and/or transient receptor potential V (TRPV) protein complexes and/or channels. The present invention even further relates to compositions and methods of insect control as well as mode of action classification for an insecticide composition comprising a compound capable of directly binding to the one or more Nanchung proteins, transient receptor potential (TRP) protein complexes and/or channels and/or transient receptor potential V (TRPV) protein complexes and/or channels wherein the compound is also capable of modulating the one or more TRP and/or TRPV channels.

Almost all field crops, plants, and commercial farming areas are susceptible to attacks by plant insect pests. Plant insect pests are a major factor in the loss of the world's commercially

important agricultural crops resulting both, in economic hardship to farmers and nutritional deprivation for local populations in many parts of the world. In other words, insect pests cause great loses and damages to human agriculture, food supply, post-harvest storage, horticulture, animal health and public health.

While advances have been made in the control of these insects, these insects have been able to adopt and evade the control measures, resulting in resistant insect populations. As a result, there remains a need for better understanding of the mechanisms that underlie feeding and other behaviors of insect pests. Such knowledge would allow for the design of agents and strategies for intervening or preventing attacks on field crops, plants, and commercial farming areas by the insect pests.

Broad spectrum chemical pesticides and insecticides have been used extensively to control or eradicate plant insect pests of agricultural importance. There is, however, substantial interest in identifying and/or developing effective alternative insecticides. As such, effective methods for screening of the new insecticides would be desirable.

What are needed, then, are new methods that can be employed in screening for agents that modulate insect behavior, bind directly to one or more Nanchung proteins, transient receptor potential (TRP) and/or transient receptor potential V (TRPV) protein complexes and/or channels and in some cases, screening for agents that can act as insecticides.

BRIEF SUMMARY OF THE INVENTION

In one embodiment, the present invention relates to a method for determining whether or not a candidate compound binds directly to one or more Nanchung proteins, transient receptor potential (TRP) and/or transient receptor potential V (TRPV) protein complexes and/or channels. The method may include providing one or more Nanchung proteins, transient receptor potential (TRP) and/or transient receptor potential V (TRPV) proteins, protein complexes and/or channels that may be located in a cell, derived from a cell, produced by a cell or produced in a cell-free system, contacting the one or more Nanchung proteins, TRP , and/or TRPV proteins, protein complexes and/or channels with a candidate compound, and assaying to determine the binding affinity of a candidate compound to the one or more Nanchung proteins, TRP , and/or TRPV proteins, protein complexes and/or channels, wherein the binding affinity of the candidate compound is indicative of the candidate compounds ability to directly bind to one or more Nanchung proteins, TRP , and/or TRPV proteins, protein complexes and/or channels.

For example, in certain embodiments, the binding assay step may include at least one of the following steps: (1) contacting the one or more Nanchung proteins, TRP, and/or TRPV

proteins, protein complexes and/or channels with a compound, wherein the compound may be labeled or unlabeled; (2) measuring the concentration of the compound which is bound to the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels; (3) calculating the equilibrium dissociation constant (K_d) for the one or more compounds; (4) wherein the K_d may be determined using one or more of the following methods: (I)(a) maximum binding (B_{max}) and (b) the concentration of labeled compound needed to reach 50% of maximum binding, (II) fluorescence polarization assay, (III) surface plasmon resonance, (IV) isothermal calorimetry, (V) Schild analysis; (5) contacting the one or more Nanchung proteins, TRP , and/or TRPV proteins, protein complexes and/or channels with a labeled compound having high affinity to the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels; (6) contacting the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels with a candidate compound in the presence of the labeled compound of step 1; (7) increasing the amount of the candidate compound available to contact the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels until binding of the labeled compound is near 0%; (8) calculating the equilibrium inhibition constant (K_i) and/or the equilibrium dissociation constant (K_d) for competition assay using one or more of the following methods: (I) (a) determining amount of bound labeled compound in the absence of the candidate compound and (b) determining concentration of the candidate compound that is required to reduce the amount of bound labeled compound by 50%, (II) fluorescent polarization assay, and/or (III) Schild analysis; (9) comparing the inhibition constant of the candidate compounds to other candidate compounds; (10) comparing the inhibition constant of the candidate compounds to the disassociation constant of the labeled compound.

In a second embodiment, the present invention relates to a method for determining the mode of action classification for the candidate compound according to the Insecticide Resistance Action Committee (IRAC) using one or more of the following: binding assay and/or functional assay. For example, in certain embodiments, a functional assay may be used to determine whether a candidate compound acts as a modulator of the one or more TRP and/or TRPV channels, and a binding assay may be used to determine if the candidate compound binds directly to the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes, and/or channels and more particularly, to the same site on the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes, and/or channels.

The functional assay may include at least one of the following steps: (1) detecting calcium ion mobilization in the first cell in response to the candidate compound, (2) detecting a membrane potential in the first cell in response to the candidate compound, (3) comparing

calcium ion mobilization in the first cell in the absence of the candidate compound with calcium ion mobilization in the first cell in the presence of the candidate compound, (4) comparing a membrane potential in the first cell in the absence of the candidate compound with a membrane potential in the first cell in the presence of the candidate compound, (5) comparing calcium ion mobilization in the first cell in the presence of the candidate compound with calcium ion mobilization reference level indicative of no modulation of the TPRV channel, and/or (6) comparing a membrane potential in the first cell in the presence of the candidate compound with a membrane potential reference level indicative of no modulation of the TPRV channel. Preferably, the candidate compound may modulate the calcium ion mobilization or the membrane potential in the first cell by at least 20% relative to the reference level. The candidate compound may be a modulator that inhibits the activity of the insect TRPV channel. Alternatively, the candidate compound may be a modulator that activates the insect TRPV channel. The candidate compound may be a modulator that inhibits insect feeding behavior.

The binding assay may include at least one of the following steps: (1) contacting the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels with a compound, wherein the compound may be labeled or unlabled; (2) measuring the concentration of the compound which is bound to the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels; (3) calculating the equilibrium disassociation constant (K_d) for the one or more compounds; (4) wherein the K_d may be determined using one or more of the following methods: (I)(a) maximum binding (B_{max}) and (b) the concentration of labeled compound needed to reach 50% of maximum binding, (II) fluorescence polarization assay, (III) surface plasmon resonance, (IV) isothermal calorimetry, (V) Schild analysis; (5) contacting the one or more Nanchung proteins, TRP , and/or TRPV proteins, protein complexes and/or channels with a labeled compound having high affinity to the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels; (6) contacting the one or more one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels with a candidate compound in the presence of the labeled compound of step 1; (7) increasing the amount of the candidate compound available to contact the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels until binding of the labeled compound is near 0%; (8) calculating the equilibrium inhibition constant (K_i) and/or the equilibrium dissociation constant (K_d) for competition assay using one or more of the following methods: (I) (a) determining amount of bound labeled compound in the absence of the candidate compound and (b) determining concentration of the candidate compound that is required to reduce the amount of bound labeled compound by 50%, (II) fluorescent polarization assay, and/or (III) Schild analysis; (9)

comparing the inhibition constant of the candidate compounds to other candidate compounds; (10) comparing the inhibition constant of the candidate compounds to the disassociation constant of the labeled compound.

In the methods set forth herein, the one or more TRP channels, and/or TRPV channels may comprise one or more TRP proteins and/or one or more TRPV proteins in a complex. In the methods set forth herein, the one or more insect TRP channels, and/or TRPV channels may comprise one or more Nanchung proteins, Inactive proteins, TRP proteins, TRPV proteins, Nanchung and Inactive protein complexes, Nanchung and TRPV protein complexes, and/or Nanchung and TRP protein complexes. For clarity, the TRP and/or TRPV channels may also comprise a Nanchung protein and any other TRP channel proteins found in cellular membranes, inserted in artificial membranes and/or a cell-free system. It is to be understood that the Nanchung, TRP and/or TRPV proteins and/or protein complexes may be found in cellular membranes, in solution, or in a cell-free system. It is too be understood that the TRP and/or TRPV channels may be contained within one or more cellular membranes, one or more pieces of cellular membranes, produced in a cellular system, produced in a cell-free system, and/or from cultured cells in a petri dish, or from cells or tissues derived from experimental animals or experimental insects. For purposes of determining whether a candidate compound directly binds to the insect TRP and/or TRPV channels, the TRP and/or TRPV channels may comprise one or more Nanchung, TRP and/or TRPV protein complexes.

It is to be understood that Nanchung and Inactive proteins are both insect TRPV proteins. However, Nanchung may also form a complex with TRP proteins. The ratio of the Nanchung to Inactive proteins co-expressed in the TRP and/or TRPV complex is, preferably, about 3:1 to about 1:3, more preferably about 1:1. The ratio of the Nanchung to TRP proteins co-expressed in the TRP and/or TRPV complex is, preferably, about 3:1 to about 1:3, more preferably about 1:1. The candidate compound may be a small organic molecule, small inorganic molecule, polysaccharides, peptides, proteins, nucleic acids, an extract made from biological materials, and any combination thereof.

The method may further include one or more of these additional steps: providing one or more mammalian TRP channels; contacting the one or more mammalian TRP and/or TRPV channels with a labeled compound and/or a candidate compound, wherein the labeled compound may be the candidate compound or a separate labeled compound; assaying to determine binding affinity of the labeled compound and/or the candidate compound to the one or more mammalian TRP and/or TRPV channels, wherein little to no binding affinity to the one or more mammalian TRP and/or TRPV channel identifies the candidate compound as a selectively binding to the one

or more Nanchung proteins, insect TRP channels and/or TRPV channels. The insect may be an agricultural/horticultural pest or a disease vector or a parasite.

In another embodiment, the methods set forth above may use one or more of the following compounds as the labeled compound: afidopyropen, pymetrozine, and/or N-deacetylated form of pyrifluquinazon.

In yet another embodiment, the present invention relates to a candidate compound selected by the methods described above. The candidate compound may be a modulator that inhibits or increases the activity of the insect TRPV channel. The candidate compound may be a modulator that inhibits a feeding behavior of an insect. Even further, the candidate compound may modulate and/or bind directly to the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels, and in particular to the same site on the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels. The candidate compound may further modulate and/or bind directly to one or more insect Nanchung proteins, insect TRP and/or insect TRPV proteins, protein complexes and/or channels, and in particular to the same site on the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels. The candidate compound may further modulate and/or bind directly to one or more arthropod Nanchung proteins, arthropod TRP and/or arthropod TRPV proteins, protein complexes and/or channels, and in particular to the same site on the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels. The candidate compound may further modulate and/or bind directly to one or more Mollusk Nanchung proteins, Mollusk TRP and/or Mollusk TRPV proteins, protein complexes and/or channels, and in particular to the same site on the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels. The candidate compound may further modulate and/or bind directly to one or more Nematode Nanchung proteins, Nematode TRP and/or Nematode TRPV protein complexes and/or channels, and in particular to the same site on the one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels. The candidate compound may further modulate and/or bind directly to one or more pest Nanchung proteins, pest TRP and/or TRPV proteins protein complexes and/or channels. The candidate compound may further be unable to modulate and/or bind directly to one or more Mammalian Nanchung proteins, Mammalian TRP and/or Mammalian TRPV protein complexes and/or channels and/or other non-target/non-pest species.

In another embodiment, the present invention relates to a composition containing the candidate compound identified by one or more of the methods set forth herein.

In another embodiment, the present invention relates to a method of insect control that includes applying to an insect or to an insects habitat, feeding source, and/or

environment/habitat a composition comprising the candidate compound selected by one or more of the methods described herein or a compound selected by one or more of the methods described above. The compound may be an inhibitor of an insect TRP and/or TRPV channel. The compound may be an activator of an insect TRP and/or TRPV channel. The compound may bind directly to the insect Nanchung protein, TRP and/or TRPV channel. The insect may be an agricultural/horticultural pest or a disease vector or a parasite.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts molecular structures of afidopyropen, pymetrozine (PM), pyrifluquinazon (PFQ) and its N-deacetylated form (dPFQ).

Figure 2 depicts the effects of afidopyorpen and pymetrozine (PM) in American grasshoppers (*Schistocerca Americana)*

Figures 3 depict activation of Ca^{2+} mobilization by afidopyropen, pymetrozine (PM), and N-deacetylated form of pyrifluquinazon (dPFQ) in mammalian cells co-expressing Nan and Iav, but not in parental hamster cells (cells are cells prior to infection with the genes or proteins of interest), nor in cells expressing Nanchung or Inactive alone.

Figure 4 depicts graphs demonstrating that afidopyropen, pymetrozine (PM), and N-deacetylated form of pyrifluquinazon (dPFQ) evoke membrane depolarization response in mammalian cells co-expressing Nanchung and Inactive, but not in parental hamster cells, nor in cells expressing Nanchung or Inactive alone.

Figure 4a depicts graphs demonstrating that N-deacetylated form of pyrifluquinazon (dPFQ) evokes current in frog oocytes co-expressing Nanchung and Inactive, but not in oocytes expressing Nanchung or Inactive alone.

Figure 5 depicts dose response relationships of calcium responses evoked by afidopyropen, pymetrozine (PM), and N-deacetylated form of pyrifluquinazon (dPFQ) in cells co-expressing Nanchung and Inactive.

Figure 6 depicts afidopyropen not activating mammalian TRRV4 channel.

Figure 7 depicts specific binding of [^{3}H]-afidopyropen to membranes co-expressing Nan and Iav.

Figure 8A depicts [^{3}H]-afidopyropen saturation binding to Nan protein and increased binding affinity in the presence of Iav

Figure 8B depicts Scatchard transformation of the saturation binding identified in Figure 8A.

Figure 9A. Both pymetrozine (PM) and N-deacetylated form of pyrifluquinazon (dPFQ) compete with [^{3}H]-afidopyropen for binding to Nan + Iav membranes.

Figure 9B. Both pymetrozine (PM) and N-deacetylated form of pyrifluquinazon (dPFQ) compete with [^{3}H]-afidopyropen from binding to Nan only membranes.

[SN1][SL2]Figures 10-36 correspond to SEQ ID NOS: 1-27, respectively, and provide the nucleotide sequences of a Nanchung (Nan) gene from different species having the accession number specified in the Figure.

Figures 37-63 correspond to SEQ ID NOS: 54-80, respectively, and provide the amino acid sequences of a Nanchung (Nan) protein having the accession numbers specified in the Figure.

Figures 64-89 correspond to SEQ ID NOS: 28-53, respectively, and provide the nucleotide sequences of an Inactive (Iav) gene from different species having the accession numbers specified in the Figure.

Figures 90-115 correspond to SEQ ID NOS: 81-106, respectively, and provide the amino acid sequence of an Inactive (Iav) protein from different species having the accession numbers specified in the Figure.

Figure 116 depicts a sequence alignment of the Nan proteins (SEQ ID NOS 59, 60, 63, 58, 57, 56, 54, 74, 73, 75, 66, 70, 110, 68, and 111, residues 1-448 and 560-900 of SEQ ID NO: 64, and SEQ ID NOS 76, 79, 62, 77, 72, 78, 71, 80, 65, and 61, all respectively, in order of appearance).

Figure 117 depicts sequence alignment of the Iav proteins (SEQ ID NOS 84 and 85, residues 1-916, 954-1102, and 1167-1216 of SEQ ID NO: 86, and SEQ ID NOS 83, 82, 81, 101, 104, 100, 99, 92, 98, 93, 90, 89, 94, 95, 88, 102, 112, 103, 105, 106, 96, 87, and 91, all respectively, in order of appearance).

Figure 118 depicts an alignment tree for Nan proteins.

Figure 119 depicts an alignment tree for Iav proteins.

detailed description of the DRAWINGS AND THE PRESENTLY PREFERRED EMBODIMENTS

I. General Considerations

The transient receptor potential (TRP) channels constitute a large and important class of channels involved in modulating cellular homeostasis. The present invention provides methods and compositions that identify or include one or more compounds that bind to and/or modulate at least one TRP family member, including, but not limited to a TRPV channel in an insect.

Specifically, the present invention provides methods for identifying candidate compounds capable of directly binding to one or more insect Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels and/or modulating one or more insect TRP and/or TRPV channel. Modulating an insect TRP and/or TRPV channel may modulate calcium homeostasis, sodium homeostasis, intracellular calcium levels, membrane polarization (resting membrane potential), and/or cation levels in a cell. Compounds that can modulate one or more insect TRP and/or TRPV channels are useful in many aspects including, but not limited to, insect control. Knowing that a compound binds directly to an insect TRP and/or TRPV channel is critical for insect management planning and preventing the development of resistant insect populations.

The present invention further identifies afidopyropen, PM, and/or dPFQ as compounds having high affinity to Nanchung protein, TRP, and/or TRPV proteins, protein complexes, and/or channels, such that one or more of the compounds above may be used in the methods presented herein as a labeled compound for purposes of the competition binding assay set forth herein.

The present invention also provides compositions comprising the candidate compounds identified herein for use as insecticides for treating pests. The present invention further comprises classifying the candidate compounds identified herein by their mode of action.

Without being bound by theory, the modulation of an insect TRP and/or TRPV elicits a signaling pathway that brings forth sensory neuron modulation which may increase or decrease feeding behavior of an insect, and such modulation (e.g., activation) of an insect TRP and/or TRPV channel in an insect may lead to a decrease in feeding behavior of such insect leading to the insect's death by starvation. Thus, again without being bound by theory, it is believed that compounds that modulate (e.g., activate) an insect TRP and/or TRPV channel may be used as insecticides.

TRP channels have been classified into at least seven groups: TRPC (canonical), TRPV (vanilloid), TRPM (melastatin), TRPP (polycystins), TRPML (mucolipins), TRPA (ankyrin), and TRPN (no mechanosensor potential C), which is not found in humans.

The TRPC group can be divided into 4 subfamilies (TRPC1, TRPC4,5, TRPC3,6,7 and TRPC2) based on sequence homology and functional similarities.

Currently, the mammalian TRPV family has 6 members. TRPV5 and TRPV6 are more closely related to each other than to TRPV1, TRPV2, TRPV3, or TRPV4. TRPA1 is most closely related to TRPV3, and is more closely related to TRPV1 and TRPV2 than to TRPV5 and TRPV6. The insects have only two members of TRPV family: Nanchung (Nan), and Inactive (Iav), which are most closely related to mammalian TRPV5 and TRPV6. The TRPV is

expressed in a great number of organisms, including, e.g., insects (*Drosophila*, *Tribolium*, *Pediculus*, *Culex*, and *Anopheles*), crustaceans (*Daphnia pulex*) nematodes (*Caenorhabditis elegans*), molluscs (*Aplysia californica, Lottia gigantea*) and mammals (humans, mice, rats, monkeys and chimpanzee.

Mollusks, nemotodes, Arthropod, and more particularly insect, TRPV channels are represented by Nanchung and/or Inactive proteins (or homologues of thereof). Nanchung and Inactive proteins form a complex (Nesterov et al. 2015), and are implicated in insect hearing (Matsuura et al., 2009). However, Nanchung may form a complex with other TRP proteins

The TRPM family has 8 members. Constituents include the following: the founding member TRPM1 (Melastatin or LTRPC1), TRPM3 (KIAA1616 or LTRPC3), TRPM7 (TRP-PLIK, ChaK(1), LTRPC7), TRPM6 (ChaK2), TRPM2 (TRPC7 or LTRPC2), TRPM8 (Trp-p8 or CMR1), TRPM5 (Mtr1 or LTRPC5), and TRPM4 (FLJ20041 or LTRPC4).

The sole mammalian member of the TRPA family is TRPA1, whereas insects contain at least four members of this family: TRPA1, Painless, Pyrexia, and Waterwitch.

The TRPML family consists of the mucolipins, which include TRPML1 (mucolipins 1), TRPML2 (mucolipins 2), and TRPML3 (mucolipin3).

The TRPP family consists of two groups of channels: those predicted to have six transmembrane domains and those that have 11. TRPP2 (PKD2), TRPP3 (PKD2L1), TRPP5 (PKD2L2) are all predicted to have six transmembrane domains. TRPP1 (PKD1, PC1), PKD-REJ and PKD-1L1 are all thought to have 11 transmembrane domains. Insects have only one member of TRPP family, which is absent in some species.

The inventors have discovered that afidopyropen binds directly to the Nanchung protein alone or in complex with other TRP and/or TRPV proteins. Furthermore, the inventors have developed methods of identifying additional compounds that bind directly to the insect Nanchung protein, TRPV protein complex or related insect TRP protein complex having a Nanchung protein incorporated in its complex. Even further the inventors have identified that afidopyropen is a compound that is useful for identifying candidate compounds capable of binding directly to the insect Nanchung protein, TRPV protein complex or related insect TRP protein complex having a Nanchung protein incorporated in its complex. Identification of such compounds may lead to the identification of suitable chemical compounds that can function as insecticides and be useful in a pest management program.

Even further the inventors discovered that some compounds have increased binding affinity when both the Nanchung protein and the Inactive protein were present in the protein complex. Accordingly, it may be beneficial to identify compounds that directly bind to one or more TRP and or TRPV protein complexes comprising one or more Nanchung proteins.

Additionally, it may be beneficial to identify compounds that bind directly to one or more TRP protein complexes comprising one or more Nanchung proteins and one or more Inactive proteins. It may also be beneficial to identify compounds that bind directly to one or more Nanchung proteins, and/or TRP and/or TRPV protein complexes and or channels. It may be beneficial to use the identified compounds as insecticides. It may be further beneficial to identify compound that directly bind to one or more Nanchung proteins, and/or TRP and/or TRPV proteins, protein complexes and/or channels and that may be found to modulate the TRP and/or TRPV channels of pest species while not binding directly to and/or modulating the one or more Nanchung proteins, and/or TRP and/or TRPV proteins, protein complexes and/or channels of mammalians and/or other non-pest species.

II. Definitions:

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art. Although any methods, devices, and materials similar or equivalent to those described herein can be used in the practice or testing of the presently disclosed subject matter, representative methods, devices, and materials are now described.

The terms "a," "an," and "the" refer to "one or more" when used in this application, including the claims. Thus, for example, reference to "a cell" (e.g., "a mammalian cell") includes a plurality of such cells (e.g., a plurality of mammalian cells in culture).

As used herein, the term "about," when referring to a value or to an amount of mass, weight, time, volume, concentration or percentage is meant to encompass variations of in some embodiments ±20%, in some embodiments ±10%, in some embodiments ±5%, in some embodiments ±1%, in some embodiments ±0.5%, and in some embodiments ±0.1% from the specified amount, as such variations are appropriate to perform the disclosed method.

The terms "insect," "insect pest," or "plant insect pest" refer to any one of the numerous usually small arthropod animals of the class Insecta that are known to associate with plants and which, as a result of that association, causes a detrimental effect on the plant's health and vigor. The term plant as used herein encompasses whole plants and parts of plants such as roots, stems, leaves and seed, as well as cells and tissues within the plants or plant parts. The terms "insect," "insect pest," or "plant insect pest" are used interchangeably throughout the instant application.

The terms "pests" and/or "pest species" refer to any one of numerous usually small arthropod animals of the class Insecta that are known to associate with plants and which, as a result of that association, causes a detrimental effect on the plant's health and vigor. Additionally, the terms refer to include mollusk, nematodes, other arthropod classes that are known to associate with

plants and which, as a result of that association, causes a detrimental effect on the plant's health and vigor. The terms further includes arthropods, gastropods and nematodes including but not limited to: insects from the order of **Lepidoptera**, for example *Achroia grisella*, *Acleris* spp. such as *A. fimbriana, A. gloverana, A. variana; Acrolepiopsis assectella, Acronicta major, Adoxophyes* spp. such as *A. cyrtosema, A. orana; Aedia leucomelas, Agrotis* spp. such as *A. exclamationis, A. fucosa, A. ipsilon, A. orthogoma, A. segetum, A. subterranea; Alabama argillacea, Aleurodicus dispersus, Alsophila pometaria, Ampelophaga rubiginosa, Amyelois transitella, Anacampsis sarcitella, Anagasta kuehniella, Anarsia lineatella, Anisota senatoria, Antheraea pernyi, Anticarsia (=Thermesia)* spp. such as *A. gemmatalis; Apamea spp , Aproaerema modicella, Archips* spp. such as *A. argyrospila, A. fuscocupreanus, A. rosana, A. xyloseanus; Argyresthia conjugella, Argyroploce* spp., *Argyrotaenia* spp. such as *A. velutinana; Athetis mindara, Austroasca viridigrisea, Autographa gamma, Autographa nigrisigna, Barathra brassicae, Bedellia* spp., *Bonagota salubricola, Borbo cinnara, Bucculatrix thurberiella, Bupalus piniarius, Busseola* spp., *Cacoecia* spp. such as *C. murinana, C. podana; Cactoblastis cactorum, Cadra cautella, Calingo braziliensis, Caloptilis theivora, Capua reticulana, Carposina* spp. such as *C. niponensis, C. sasakii; Cephus spp, Chaetocnema aridula, Cheimatobia brumata, Chilo* spp. such as *C. Indicus, C. suppressalis, C. partellus; Choreutis pariana, Choristoneura* spp. such as *C. conflictana, C. fumiferana, C. longicellana, C. murinana, C. occidentalis, C. rosaceana; Chrysodeixis (=Pseudoplusia) spp. such as C. eriosoma, C. includens; Cirphis unipuncta, Clysia ambiguella, Cnaphalocerus* spp., *Cnaphalocrocis medinalis, Cnephasia* spp., *Cochylis hospes, Coleophora* spp., *Colias eurytheme, Conopomorpha* spp., *Conotrachelus* spp., *Copitarsia* spp., *Corcyra cephalonica, Crambus caliginosellus, Crambus teterrellus, Crocidosema (=Epinotia) aporema, Cydalima (=Diaphania) perspectalis, Cydia (=Carpocapsa)* spp. such as *C. pomonella, C. latiferreana; Dalaca noctuides, Datana integerrima, Dasychira pinicola, Dendrolimus* spp. such as *D. pini, D. spectabilis, D. sibiricus; Desmia funeralis, Diaphania* spp. such as *D. nitidalis, D. hyalinata; Diatraea grandiosella, Diatraea saccharalis, Diphthera festiva, Earias* spp. such as *E. insulana, E. vittella; Ecdytolopha aurantianu, Egira (=Xylomyges) curialis, Elasmopalpus lignosellus, Eldana saccharina, Endopiza viteana, Ennomos subsignaria, Eoreuma loftini, Ephestia* spp. such as *E. cautella, E. elutella, E. kuehniella; Epinotia aporema, Epiphyas postvittana, Erannis tiliaria, Erionota thrax, Etiella* spp., *Eulia* spp., *Eupoecilia ambiguella, Euproctis chrysorrhoea, Euxoa* spp., *Evetria bouliana, Faronta albilinea, Feltia* spp. such as *F. subterranean; Galleria mellonella, Gracillaria* spp., *Grapholita* spp. such as *G. funebrana, G. molesta, G. inopinata; Halysidota* spp., *Harrisina americana, Hedylepta* spp., *Helicoverpa* spp. such as *H. armigera (=Heliothis armigera), H. zea (=Heliothis zea); Heliothis* spp. such as *H. assulta, H. subflexa, H. virescens; Hellula* spp. such as *H. undalis, H. rogatalis; Helocoverpa*

gelotopoeon, Hemileuca oliviae, Herpetogramma licarsisalis, Hibernia defoliaria, Hofmannophila pseudospretella, Homoeosoma electellum, Homona magnanima, Hypena scabra, Hyphantria cunea, Hyponomeuta padella, Hyponomeuta malinellus, Kakivoria flavofasciata, Keiferia lycopersicella, Lambdina fiscellaria fiscellaria, Lambdina fiscellaria lugubrosa, Lamprosema indicata, Laspeyresia molesta, Leguminivora glycinivorella, Lerodea eufala, Leucinodes orbonalis, Leucoma salicis, Leucoptera spp. such as *L. coffeella, L. scitella; Leuminivora lycinivorella, Lithocolletis blancardella, Lithophane antennata, Llattia octo (=Amyna axis), Lobesia botrana, Lophocampa* spp., *Loxagrotis albicosta, Loxostege* spp. such as *L. sticticalis, L. cereralis; Lymantria* spp. such as *L. dispar, L. monacha; Lyonetia clerkella, Lyonetia prunifoliella, Malacosoma* spp. such as *M. americanum, M. californicum, M. constrictum, M. neustria; Mamestra* spp. such as *M. brassicae, M. configurata; Mamstra brassicae, Manduca* spp. such as *M. quinquemaculata, M. sexta; Marasmia spp, Marmara* spp., *Maruca testulalis, Megalopyge lanata, Melanchra picta, Melanitis leda, Mocis* spp. such as *M. lapites, M. repanda; Mocis latipes, Monochroa fragariae, Mythimna separata, Nemapogon cloacella, Neoleucinodes elegantalis, Nepytia* spp., *Nymphula* spp., *Oiketicus* spp., *Omiodes indicata, Omphisa anastomosalis, Operophtera brumata, Orgyia pseudotsugata, Oria* spp., *Orthaga thyrisalis, Ostrinia* spp. such as *O. nubilalis; Oulema oryzae, Paleacrita vernata, Panolis flammea, Parnara* spp., *Papaipema nebris, Papilio cresphontes, Paramyelois transitella, Paranthrene regalis, Paysandisia archon, Pectinophora* spp. such as *P. gossypiella; Peridroma saucia, Perileucoptera* spp., such as *P. coffeella; Phalera bucephala, Phryganidia californica, Phthorimaea* spp. such as *P. operculella; Phyllocnistis citrella, Phyllonorycter* spp. such as *P. blancardella, P. crataegella, P. issikii, P. ringoniella; Pieris* spp. such as *P. brassicae, P. rapae, P. napi; Pilocrocis tripunctata, Plathypena scabra, Platynota* spp. such as *P. flavedana, P. idaeusalis, P. stultana; Platyptilia carduidactyla, Plebejus argus, Plodia interpunctella, Plusia spp, Plutella maculipennis, Plutella xylostella, Pontia protodica, Prays* spp., *Prodenia* spp., *Proxenus lepigone, Pseudaletia* spp. such as *P. sequax, P. unipuncta; Pyrausta nubilalis, Rachiplusia nu, Richia albicosta, Rhizobius ventralis, Rhyacionia frustrana, Sabulodes aegrotata, Schizura concinna, Schoenobius* spp., *Schreckensteinia festaliella, Scirpophaga* spp. such as *S. incertulas, S. innotata; Scotia segetum, Sesamia spp.* such as *S. inferens, Seudyra subflava, Sitotroga cerealella, Sparganothis pilleriana, Spilonota lechriaspis, S. ocellana, Spodoptera (=Lamphygma)* spp. such as *S. eridania, S. exigua, S. frugiperda, S. latisfascia, S. littoralis, S. litura, S. omithogalli; Stigmella* spp., *Stomopteryx subsecivella, Strymon bazochii, Sylepta derogata, Synanthedon* spp. such as S. exitiosa, *Tecia solanivora, Telehin licus. Thaumatopoea pityocampa, Thaumatotibia (=Cryptophlebia) leucotreta, Thaumetopoea pityocampa, Thecla* spp., *Theresimima ampelophaga, Thyrinteina* spp, *Tildenia inconspicuella, Tinea* spp. such as *T.*

cloacella, T. pellionella; Tineola bisselliella, Tortrix spp. such as *T. viridana; Trichophaga tapetzella, Trichoplusia* spp. such as *T. ni; Tuta (=Scrobipalpula) absoluta, Udea* spp. such as *U. rubigalis, U. rubigalis; Virachola* spp, *Yponomeuta padella, and Zeiraphera canadensis*;insects from the order of **Coleoptera**, for example *Acalymma vittatum, Acanthoscehdes obtectus, Adoretus* spp., *Agelastica alni, Agrilus* spp. such as *A. anxius, A. planipennis, A. sinuatus; Agriotes* spp. such as *A. fuscicollis, A. lineatus, A. obscurus; Alphitobius diaperinus, Amphimallus solstitialis, Anisandrus dispar, Anisoplia austriaca, Anobium punctatum, Anomala corpulenta, Anomala rufocuprea, Anoplophora* spp. such as *A. glabripennis; Anthonomus* spp. such as *A. eugenii, A. grandis, A. pomorum; Anthrenus* spp., *Aphthona euphoridae, Apion* spp., *Apogonia* spp., *Athous haemorrhoidalis, Atomaria* spp. such as *A. linearis; Attagenus* spp., *Aulacophora femoralis, Blastophagus piniperda, Blitophaga undata, Bruchidius obtectus, Bruchus* spp. such as *B. lentis, B. pisorum, B. rufimanus; Byctiscus betulae, Callidiellum rufipenne, Callopistria floridensis, Callosobruchus chinensis, Cameraria ohridella, Cassida nebulosa, Cerotoma trifurcata, Cetonia aurata, Ceuthorhynchus* spp. such as *C. assimilis, C. napi; Chaetocnema tibialis, Cleonus mendicus, Conoderus* spp. such as *C. vespertinus; Conotrachelus nenuphar, Cosmopolites* spp., *Costelytra zealandica, Crioceris asparagi, Cryptolestes ferrugineus, Cryptorhynchus lapathi, Ctenicera* spp. such as *C. destructor; Curculio* spp., *Cylindrocopturus* spp., *Cyclocephala spp, Dactylispa balyi, Dectes texanus, Dermestes* spp., *Diabrotica* spp. such as *D. undecimpunctata, D. speciosa, D. longicornis, D. semipunctata, D. virgifera; Diaprepes abbreviates, Dichocrocis* spp., *Dicladispa armigera, Diloboderus abderus, Diocalandra frumenti (Diocalandra stigmaticollis), Enaphalodes rufulus, Epilachna* spp. such as *E. varivestis, E. vigintioctomaculata; Epitrix* spp. such as *E. hirtipennis, E. similaris; Eutheola humilis, Eutinobothrus brasiliensis, Faustinus cubae, Gibbium psylloides, Gnathocerus cornutus, Hellula undalis, Heteronychus arator, Hylamorpha elegans, Hylobius abietis, Hylotrupes bajulus, Hypera* spp. such as *H. brunneipennis, H. postica; Hypomeces squamosus, Hypothenemus* spp., *Ips typographus, Lachnosterna consanguinea, Lasioderma serricorne, Latheticus oryzae, Lathridius* spp., *Lema* spp. such as *L. bilineata, L. melanopus; Leptinotarsa* spp. such as *L. decemlineata; Leptispa pygmaea, Limonius californicus, Lissorhoptrus oryzophilus, Lixus* spp., *Luperodes* spp., *Lyctus* spp. such as *L. bruneus; Liogenys fuscus* , *Macrodactylus* spp. such as *M. subspinosus; Maladera matrida, Megaplatypus mutates, Megascelis* spp., *Melanotus communis, Meligethes* spp. such as *M. aeneus; Melolontha* spp. such as *M. hippocastani, M. melolontha; Metamasius hemipterus, Microtheca spp, Migdolus* spp. such as *M. fryanus, Monochamus* spp. such as *M. alternatus; Naupactus xanthographus, Niptus hololeucus, Oberia brevis, Oemona hirta, Oryctes rhinoceros, Oryzaephilus surinamensis, Oryzaphagus oryzae, Otiorrhynchus sulcatus, Otiorrhynchus ovatus, Otiorrhynchus sulcatus, Oulema melanopus, Oulema oryzae, Oxycetonia*

jucunda, Phaedon spp. such as *P. brassicae, P. cochleariae; Phoracantha recurva, Phyllobius pyri, Phyllopertha horticola, Phyllophaga* spp. such as *P. helleri; Phyllotreta* spp. such as *P. chrysocephala, P. nemorum, P. striolata, P. vittula; Phyllopertha horticola, Popillia japonica, Premnotrypes* spp., *Psacothea hilaris, Psylliodes chrysocephala, Prostephanus truncates, Psylliodes* spp., *Ptinus* spp., *Pulga saltona, Rhizopertha dominica, Rhynchophorus* spp. such as *R. billineatus, R. ferrugineus, R. palmarum, R. phoenicis, R. vulneratus; Saperda candida, Scolytus schevyrewi, Scyphophorus acupunctatus, Sitona lineatus, Sitophilus* spp. such as *S. granaria, S. oryzae, S. zeamais; Sphenophorus* spp. such as *S. levis; Stegobium paniceum, Sternechus* spp. such as *S. subsignatus; Strophomorphus ctenotus, Symphyletes* spp., *Tanymecus* spp., *Tenebrio molitor, Tenebrioides mauretanicus, Tribolium* spp. such as *T. castaneum; Trogoderma* spp., *Tychius* spp., *Xylotrechus* spp. such as *X. pyrrhoderus; and, Zabrus* spp. *such as Z. tenebrioides;* insects from the order of **Diptera** for example *Aedes* spp. such as *A. aegypti, A. albopictus, A. vexans; Anastrepha ludens, Anopheles* spp. such as *A. albimanus, A. crucians, A. freeborni, A. gambiae, A. leucosphyrus, A. maculipennis, A. minimus, A. quadrimaculatus, A. sinensis; Bactrocera invadens, Bibio hortulanus, Calliphora erythrocephala, Calliphora vicina, Ceratitis capitata, Chrysomyia* spp. such as *C. bezziana, C. hominivorax, C. macellaria; Chrysops atlanticus, Chrysops discalis, Chrysops silacea, Cochliomyia* spp. such as *C. hominivorax; Contarinia* spp. such as *C. sorghicola; Cordylobia anthropophaga, Culex* spp. such as *C. nigripalpus, C. pipiens, C. quinquefasciatus, C. tarsalis, C. tritaeniorhynchus; Culicoides furens, Culiseta inornata, Culiseta melanura, Cuterebra* spp., *Dacus cucurbitae, Dacus oleae, Dasineura brassicae, Dasineura oxycoccana, Delia* spp. such as *D. antique, D. coarctata, D. platura, D. radicum; Dermatobia hominis, Drosophila* spp. such as *D. suzukii, Fannia* spp. such as *F. canicularis; Gastraphilus* spp. such as *G. intestinalis; Geomyza tipunctata, Glossina* spp. such as *G. fuscipes, G. morsitans, G. palpalis, G. tachinoides; Haematobia irritans, Haplodiplosis equestris, Hippelates* spp., Hylemyia spp. such as *H. platura; Hypoderma* spp. such as *H. lineata; Hyppobosca* spp., *Hydrellia philippina, Leptoconops torrens, Liriomyza* spp. such as *L. sativae, L. trifolii; Lucilia* spp. such as *L. caprina, L. cuprina, L. sericata; Lycoria pectoralis, Mansonia titillanus, Mayetiola* spp. such as *M. destructor; Musca* spp. such as *M. autumnalis, M. domestica; Muscina stabulans, Oestrus* spp. such as *O. ovis; Opomyza florum, Oscinella* spp. such as *O. frit; Orseolia oryzae, Pegomya hysocyami, Phlebotomus argentipes, Phorbia* spp. such as *P. antiqua, P. brassicae, P. coarctata; Phytomyza gymnostoma, Prosimulium mixtum, Psila rosae, Psorophora columbiae, Psorophora discolor, Rhagoletis* spp. such as *R. cerasi, R. cingulate, R. indifferens, R. mendax, R. pomonella; Rivellia quadrifasciata, Sarcophaga* spp. such as *S. haemorrhoidalis; Simulium vittatum, Sitodiplosis mosellana, Stomoxys* spp. such as *S. calcitrans; Tabanus* spp. such as *T. atratus, T. bovinus, T. lineola, T. similis; Tannia spp., Thecodiplosis*

japonensis, Tipula oleracea, Tipula paludosa, and *Wohlfahrtia* spp.*;* insects from the order of **Thysanoptera** for example, *Baliothrips biformis, Dichromothrips corbetti, Dichromothrips* ssp., *Echinothrips americanus, Enneothrips flavens, Frankliniella* spp. such as *F. fusca, F. occidentalis, F. tritici; Heliothrips* spp., *Hercinothrips femoralis, Kakothrips* spp., *Microcephalothrips abdominalis, Neohydatothrips samayunkur, Pezothrips kellyanus, Rhipiphorothrips cruentatus, Scirtothrips* spp. such as *S. citri, S. dorsalis, S. perseae; Stenchaetothrips spp, Taeniothrips cardamoni, Taeniothrips inconsequens, Thrips* spp. such as *T. imagines, T. hawaiiensis, T. oryzae, T. palmi, T. parvispinus, T. tabaci;* insects from the order of **Hemiptera** for example, *Acizzia jamatonica, Acrosternum* spp. such as *A. hilare;* Acyrthosipon spp. such as *A. onobrychis, A. pisum; Adelges laricis, Adelges tsugae, Adelphocoris* spp., such as *A. rapidus, A. superbus; Aeneolamia* spp., *Agonoscena* spp., *Aulacorthum solani, Aleurocanthus woglumi, Aleurodes* spp., *Aleurodicus disperses, Aleurolobus barodensis, Aleurothrixus* spp., *Amrasca* spp., *Anasa tristis, Antestiopsis* spp., *Anuraphis cardui, Aonidiella* spp., *Aphanostigma piri, Aphidula nasturtii, Aphis* spp. such as *A. craccivora, A. fabae, A. forbesi, A. gossypii, A. grossulariae, A. maidiradicis, A. pomi, A. sambuci, A. schneideri, A. spiraecola; Arboridia apicalis, Arilus critatus, Aspidiella* spp., *Aspidiotus* spp., *Atanus* spp., *Aulacaspis yasumatsui, Aulacorthum solani, Bactericera cockerelli (Paratrioza cockerelli), Bemisia* spp. such as *B. argentifolii, B. tabaci (Aleurodes tabaci); Blissus* spp. such as *B. leucopterus; Brachycaudus* spp. such as *B. cardui, B. helichrysi, B. persicae, B. prunicola; Brachycolus* spp., *Brachycorynella asparagi, Brevicoryne brassicae, Cacopsylla* spp. such as *C. fulguralis, C. pyricola (Psylla piri); Calligypona marginata, Calocoris* spp., *Campylomma livida, Capitophorus horni, Carneocephala fulgida, Cavelerius* spp., *Ceraplastes* spp., *Ceratovacuna lanigera, Ceroplastes ceriferus, Cerosipha gossypii, Chaetosiphon fragaefolii, Chionaspis tegalensis, Chlorita onukii, Chromaphis juglandicola, Chrysomphalus ficus, Cicadulina mbila, Cimex* spp. such as *C. hemipterus, C. lectularius; Coccomytilus halli, Coccus* spp. such as *C. hesperidum, C. pseudomagnoliarum*; *Corythucha arcuata, Creontiades dilutus, Cryptomyzus ribis, Chrysomphalus aonidum, Cryptomyzus ribis, Ctenarytaina spatulata, Cyrtopeltis notatus, Dalbulus* spp., *Dasynus piperis, Dialeurodes* spp. such as *D. citrifolii; Dalbulus maidis, Diaphorina* spp. such as *D. citri; Diaspis* spp. such as *D. bromeliae; Dichelops furcatus, Diconocoris hewetti, Doralis* spp., *Dreyfusia nordmannianae, Dreyfusia piceae, Drosicha* spp., *Dysaphis* spp. such as *D. plantaginea, D. pyri, D. radicola; Dysaulacorthum pseudosolani, Dysdercus* spp. such as *D. cingulatus, D. intermedius; Dysmicoccus* spp., *Edessa spp, Geocoris spp, Empoasca* spp. such as *E. fabae, E. solana; Epidiaspis leperii, Eriosoma* spp. such as *E. lanigerum, E. pyricola; Erythroneura* spp., *Eurygaster* spp. such as *E. integriceps; Euscelis bilobatus, Euschistus* spp. such as *E. heros, E. impictiventris, E. servus; Fiorinia theae, Geococcus coffeae, Glycaspis brimblecombei, Halyomorpha* spp. such as *H. halys; Heliopeltis*

spp., *Homalodisca vitripennis (=H. coagulata), Horcias nobilellus, Hyalopterus pruni, Hyperomyzus lactucae, Icerya* spp. such as *I. purchase; Idiocerus* spp., *Idioscopus* spp., *Laodelphax striatellus, Lecanium* spp., *Lecanoideus floccissimus, Lepidosaphes* spp. such as *L. ulmi; Leptocorisa* spp., *Leptoglossus phyllopus, Lipaphis erysimi, Lygus* spp. such as *L. hesperus, L. lineolaris, L. pratensis; Maconellicoccus hirsutus, Marchalina hellenica, Macropes excavatus, Macrosiphum* spp. such as *M. rosae, M. avenae, M. euphorbiae; Macrosteles quadrilineatus, Mahanarva fimbriolata, Megacopta cribraria, Megoura viciae, Melanaphis pyrarius, Melanaphis sacchari, Melanocallis (=Tinocallis) caryaefoliae, Metcafiella* spp., *Metopolophium dirhodum, Monellia costalis, Monelliopsis pecanis, Myzocallis coryli, Murgantia spp, Myzus* spp. such as *M. ascalonicus, M. cerasi, M. nicotianae, M. persicae, M. varians; Nasonovia ribis-nigri, Neotoxoptera formosana, Neomegalotomus spp, Nephotettix* spp. such as *N. malayanus, N. nigropictus, N. parvus, N. virescens; Nezara* spp. such as *N. viridula; Nilaparvata lugens, Nysius huttoni, Oebalus* spp. such as *O. pugnax; Oncometopia* spp., *Orthezia praelonga, Oxycaraenus hyalinipennis, Parabemisia myricae, Parlatoria* spp., *Parthenolecanium* spp. such as *P. corni, P. persicae; Pemphigus* spp. such as *P. bursarius, P. populivenae; Peregrinus maidis, Perkinsiella saccharicida, Phenacoccus* spp. such as *P. aceris, P. gossypii; Phloeomyzus passerinii, Phorodon humuli, Phylloxera* spp. such as *P. devastatrix, Piesma quadrata, Piezodorus* spp. such as *P. guildinii; Pinnaspis aspidistrae, Planococcus* spp. such as *P. citri, P. ficus; Prosapia bicincta, Protopulvinaria pyriformis, Psallus seriatus, Pseudacysta persea, Pseudaulacaspis pentagona, Pseudococcus* spp. such as *P. comstocki; Psylla* spp. such as *P. mali; Pteromalus* spp., *Pulvinaria amygdali, Pyrilla* spp., *Quadraspidiotus* spp., such as *Q. perniciosus; Quesada gigas, Rastrococcus* spp., *Reduvius senilis, Rhizoecus americanus, Rhodnius* spp., *Rhopalomyzus ascalonicus, Rhopalosiphum* spp. such as *R. pseudobrassicas, R. insertum, R. maidis, R. padi; Sagatodes* spp., *Sahlbergella singularis, Saissetia* spp., *Sappaphis mala, Sappaphis mali, Scaptocoris spp, Scaphoides titanus, Schizaphis graminum, Schizoneura lanuginosa, Scotinophora* spp., *Selenaspidus articulatus, Sitobion avenae, Sogata* spp., *Sogatella furcifera, Solubea insularis, Spissistilus festinus (=Stictocephala festina); Stephanitis nashi, Stephanitis pyrioides, Stephanitis takeyai, Tenalaphara malayensis, Tetraleurodes perseae, Therioaphis maculate, Thyanta* spp. such as *T. accerra, T. perditor; Tibraca* spp., *Tomaspis* spp., *Toxoptera* spp. such as *T. aurantii; Trialeurodes* spp. such as *T. abutilonea, T. ricini, T. vaporariorum; Triatoma* spp., *Trioza* spp., *Typhlocyba* spp., *Unaspis* spp. such as *U. citri, U. yanonensis; and Viteus vitifolii;* insects from the order **Hymenoptera** for example *Acanthomyops interjectus, Athalia rosae, Atta spp such as A. capiguara, A. cephalotes, A. cephalotes, A. laevigata, A. robusta, A. sexdens, A. texana, Bombus spp., Brachymyrmex* spp., *Camponotus spp such as C. floridanus, C. pennsylvanicus, C. modoc; Cardiocondyla nuda, Chalibion sp, Crematogaster spp.,*

Dasymutilla occidentalis, Diprion spp., Dolichovespula maculata, Dorymyrmex spp, *Dryocosmus kuriphilus, Formica spp, Hoplocampa* spp. such as *H. minuta, H. testudinea; Iridomyrmex humilis,* Lasius spp. such as *L. niger, Linepithema humile, Liometopum spp, Leptocybe invasa, Monomorium spp such as M. pharaonis, Monomorium, Nylandria fulva, Pachycondyla chinensis, Paratrechina longicornis, Paravespula spp such as P. germanica, P. pennsylvanica, P. vulgaris; Pheidole spp such as P. megacephala; Pogonomyrmex spp such as P. barbatus, P. californicus, Polistes rubiginosa, Prenolepis impairs, Pseudomyrmex gracilis, Schelipron spp, Sirex cyaneus, Solenopsis spp such as S. geminata, S.invicta, S. molesta, S. richteri, S. xyloni, Sphecius speciosus, Sphex spp, Tapinoma spp such as T. melanocephalum, T. sessile; Tetramorium spp such as T. caespitum, T. bicarinatum,* Vespa spp. such as *V. crabro; Vespula spp such as V. squamosal; Wasmannia auropunctata*, *Xylocopa* sp.; insects from the order **Orthoptera** for example *Acheta domesticus, Calliptamus italicus, Chortoicetes terminifera, Ceuthophilus spp, Diastrammena asynamora, Dociostaurus maroccanus, Gryllotalpa spp such as G. africana, G. gryllotalpa; Gryllus spp, Hieroglyphus daganensis, Kraussaria angulifera, Locusta* spp. such as *L. migratoria, L. pardalina; Melanoplus spp such as M. bivittatus, M. femurrubrum, M. mexicanus, M. sanguinipes, M. spretus; Nomadacris septemfasciata, Oedaleus senegalensis, Scapteriscus spp, Schistocerca spp such as S. americana, S. gregaria, Stemopelmatus spp, Tachycines asynamorus, and Zonozerus variegatus;* pests from the Class **Arachnida** for example **Acari,** e.g. of the families Argasidae, Ixodidae and Sarcoptidae, such as Amblyomma spp. (e.g. *A. americanum, A. variegatum, A. maculatum*), Argas spp. such as *A. persicu*), *Boophilus* spp. such as *B. annulatus, B. decoloratus, B. microplus, Dermacentor spp such as D.silvarum, D. andersoni, D. variabilis, Hyalomma* spp. such as *H. truncatum, Ixodes* spp. such as *I. ricinus, I. rubicundus, I. scapularis, I. holocyclus, I. pacificus, Rhipicephalus sanguineus, Ornithodorus* spp. such as *O. moubata, O. hermsi, O. turicata*), *Ornithonyssus bacoti, Otobius megnini, Dermanyssus gallinae, Psoroptes* spp such as *P. ovis, Rhipicephalus* spp such as *R. sanguineus, R. appendiculatus, Rhipicephalus evertsi), Rhizoglyphus spp; Sarcoptes* spp. such as*S. Scabiei*; and Family **Eriophyidae** including *Aceria spp such as A. sheldoni*, *A. anthocoptes*, *Acallitus* spp; *Aculops* spp. such as *A. lycopersici*, *A. pelekassi*; *Aculus* spp such as *A. schlechtendali; Colomerus vitis, Epitrimerus pyri, Phyllocoptruta oleivora; Eriophytes ribis* and *Eriophyes* spp such as *Eriophyes sheldoni*; Family **Tarsonemidae** including *Hemitarsonemus spp., Phytonemus pallidus and Polyphagotarsonemus latus, Stenotarsonemus spp. Steneotarsonemus spinki*; Family **Tenuipalpidae** including Brevipalpus spp. such as *B. phoenicis*; Family **Tetranychidae** including *Eotetranychus spp.*, *Eutetranychus spp.*, *Oligonychus spp., Petrobia latens*, *Tetranychus spp such as T. cinnabarinus, T. evansi, T. kanzawai, T, pacificus, T. phaseulus, T. telarius* and *T. urticae*; *Bryobia praetiosa*; *Panonychus* spp. such as *P. ulmi*, *P. citri*;, *Metatetranychus spp.* and *Oligonychus* spp. such as *O.*

pratensis, O. perseae), *Vasates lycopersici*; *Raoiella indica, Family* **Carpoglyphidae** including *Carpoglyphus spp; Penthaleidae* spp such as *Halotydeus destructor* ; Family **Demodicidae** with species such a *Demodex* spp; Family **Trombicidea** including *Trombicula spp*:; Family **Macronyssidae** including *Ornothonyssus* spp; Family **Pyemotidae** including *Pyemotes tritici*; *Tyrophagus putrescentiae*; Family Acaridae including *Acarus siro*; Family **Araneida** including *Latrodectus mactans*, *Tegenaria agrestis, Chiracanthium sp, Lycosa sp Achaearanea tepidariorum* and *Loxosceles reclusa*; pests from the Phylum **Nematoda,** for example, plant parasitic nematodes such as root-knot nematodes, *Meloidogyne* spp. such as *M. hapla, M. incognita, M. javanica;* cyst-forming nematodes, *Globodera* spp. such as *G. rostochiensis; Heterodera* spp. such as *H. avenae, H. glycines, H. schachtii, H. trifolii;* Seed gall nematodes, *Anguina* spp.; Stem and foliar nematodes, *Aphelenchoides* spp. such as *A. besseyi;* Sting nematodes, *Belonolaimus* spp. such as *B. longicaudatus;* Pine nematodes, *Bursaphelenchus* spp. such as *B. lignicolus, B. xylophilus;* Ring nematodes, *Criconema* spp.*; Criconemella* spp. such as *C. xenoplax* and *C. ornata;* and, *Criconemoides* spp. such as *Criconemoides informis; Mesocriconema* spp.*;* Stem and bulb nematodes, *Ditylenchus* spp. such as *D. destructor, D. dipsaci;* Awl nematodes, *Dolichodorus* spp.*;* Spiral nematodes, *Heliocotylenchus multicinctus;* Sheath and sheathoid nematodes, *Hemicycliophora* spp. and *Hemicriconemoides* spp.*; Hirshmanniella* spp.*;* Lance nematodes, *Hoploaimus* spp.*;* False rootknot nematodes, *Nacobbus* spp.*;* Needle nematodes, *Longidorus* spp. such as *L. elongatus;* Lesion nematodes, *Pratylenchus* spp. such as *P. brachyurus, P. neglectus, P. penetrans, P. curvitatus, P. goodeyi;* Burrowing nematodes, *Radopholus* spp. such as *R. similis; Rhadopholus* spp.*; Rhodopholus* spp.*;* Reniform nematodes, *Rotylenchus* spp. such as *R. robustus, R. reniformis; Scutellonema* spp.*;* Stubby-root nematode, *Trichodorus* spp. such as *T. obtusus, T. primitivus; Paratrichodorus* spp. such as *P. minor;* Stunt nematodes, *Tylenchorhynchus* spp. such as *T. claytoni, T. dubius;* Citrus nematodes, *Tylenchulus* spp. such as *T. semipenetrans;* Dagger nematodes, *Xiphinema* spp.*;* and other plant parasitic nematode species; insects from the order **Isoptera** for example *Calotermes flavicollis, Coptotermes spp such as C. formosanus, C. gestroi, C. acinaciformis; Cornitermes cumulans, Cryptotermes spp such as C. brevis, C. cavifrons; Globitermes sulfureus, Heterotermes spp such as H. aureus, H. longiceps, H. tenuis; Leucotermes flavipes, Odontotermes spp., Incisitermes spp such as I. minor, I. Snyder*; *Marginitermes hubbardi, Mastotermes spp such as M. darwiniensis Neocapritermes spp such as N. opacus, N. parvus; Neotermes spp, Procornitermes spp, Zootermopsis spp such as Z. angusticollis, Z. nevadensis, Reticulitermes* spp. such as *R. hesperus, R. tibialis, R. speratus, R. flavipes, R. grassei, R. lucifugus, R. santonensis, R. virginicus; Termes natalensis;* insects from the order **Blattaria** for example *Blatta spp such as B. orientalis, B. lateralis; Blattella spp such as B. asahinae, B. germanica; Leucophaea maderae, Panchlora nivea,*

Periplaneta spp such as P. americana, P. australasiae, P. brunnea, P. fuligginosa, P. japonica; Supella longipalpa, **Parcoblatta pennsylvanica, Eurycotis floridana,** *Pycnoscelus surinamensis;* insects from the order **Siphonoptera** for example *Cediopsylla simples, Ceratophyllus spp., Ctenocephalides spp such as C. felis, C. canis, Xenopsylla cheopis, Pulex irritans, Trichodectes canis, Tunga penetrans,* and *Nosopsyllus fasciatus;* insects from the order **Thysanura** for example *Lepisma saccharina, Ctenolepisma urbana,* and *Thermobia domestica;* pests from the class **Chilopoda** for example *Geophilus spp.,* Scutigera spp. such as *Scutigera coleoptrata*; pests from the class **Diplopoda** for example *Blaniulus guttulatus, Julus spp , Narceus spp.*; pests from the class **Symphyla** for example *Scutigerella immaculata;* insects from the order **Dermaptera**, for example *Forficula auricularia;* insects from the order **Collembola**, for example *Onychiurus* spp. such as *Onychiurus armatus;* pests from the order **Isopoda** for example, *Armadillidium vulgare, Oniscus asellus, Porcellio scaber;* insects from the order **Phthiraptera**, for example *Damalinia spp.*, Pediculus spp. such as *Pediculus humanus capitis, Pediculus humanus corporis, Pediculus humanus humanus; Pthirus pubis*, Haematopinus spp. such as *Haematopinus eurysternus, Haematopinus suis*; Linognathus spp. such as *Linognathus vituli; Bovicola bovis, Menopon gallinae, Menacanthus stramineus* and *Solenopotes capillatus, Trichodectes spp.*. Examples of further pest species which may be controlled by the compounds and/or compositions identified herein include: from the Phylum **Mollusca**, class **Bivalvia,** for example, *Dreissena spp.*; class **Gastropoda**, for example, *Arion spp., Biomphalaria spp., Bulinus spp., Deroceras spp., Galba spp., Lymnaea spp., Oncomelania spp., Pomacea canaliclata, Succinea spp.;* from the class of the ***helminths***, for example, *Ancylostoma duodenale, Ancylostoma ceylanicum, Acylostoma braziliensis, Ancylostoma spp., Ascaris lubricoides, Ascaris spp., Brugia malayi, Brugia timori, Bunostomum spp., Chabertia spp., Clonorchis spp., Cooperia spp., Dicrocoelium spp., Dictyocaulus filaria, Diphyllobothrium latum, Dracunculus medinensis, Echinococcus granulosus, Echinococcus multilocularis, Enterobius vermicularis, Faciola spp.,* Haemonchus spp. such as *Haemonchus contortus; Heterakis spp., Hymenolepis nana, Hyostrongulus spp., Loa Loa, Nematodirus spp., Oesophagostomum spp., Opisthorchis spp., Onchocerca volvulus, Ostertagia spp., Paragonimus spp., Schistosomen spp., Strongyloides fuelleborni, Strongyloides stercora lis, Stronyloides spp., Taenia saginata, Taenia solium, Trichinella spiralis, Trichinella nativa, Trichinella britovi, Trichinella nelsoni, Trichinella pseudopsiralis, Trichostrongulus spp., Trichuris trichuria, Wuchereria bancrofti.*

The terms “non-pest” and/or “non-target” species refers to all other animals that would not be classified as “pests” and/or “pest species” as defined above.

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base that is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides, conservatively modified variants thereof, complementary sequences, and degenerate codon substitutions that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides.

The terms "nucleic acid" or "nucleic acid molecule" can also be used interchangeably with gene, open reading frame (ORF), cDNA, and mRNA encoded by a gene, nucleic acid molecule, nucleic acid fragment, nucleic acid segment, or polynucleotide.

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, "gene" refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. "Genes" also include non-expressed DNA segments that, for example, form recognition sequences for other proteins. "Genes" can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

The term "gene delivery" or "gene transfer" refers to methods or systems for reliably introducing foreign DNA into target cells and include injection, transduction, transfection, transformation and electroporation. Such methods can result in transient or long term expression of genes.

The term "transduction" refers to the delivery of a DNA molecule to a recipient cell either *in vivo* or *in vitro*, via a replication-defective viral vector, such as, e.g., adenoviral vector.

The term "transfection" is used to refer to the uptake of foreign DNA by a mammalian cell. A cell has been "transfected" when exogenous DNA has been introduced across the cell plasma membrane. Transfection can be used to introduce one or more exogenous DNA moieties, such as a plasmid vector and other nucleic acid molecules, into suitable cells. The term refers to both stable and transient uptake of the genetic material.

The term "transformation" and/or "transfection" refers to a process for introducing heterologous DNA into a cell. Transformed cells are understood to encompass not only the end product of a transformation/transfection process, but also transgenic progeny thereof.

The term "injection" refers to a process for introducing heterologous DNA or RNA into a cell using a syringe and a needle.

The term "vector" refers to any genetic element, such as a plasmid, phage, transposon, cosmid, chromosome, virus, virion, etc., which is capable of replication when associated with the proper control elements, such as a helper virus, and which can transfer gene sequences between cells. Thus, the term includes cloning and expression vehicles, as well as replication-defective viral vectors.

The terms "expression vector" and "expression cassette" refer to a nucleic acid molecule capable of directing expression of a particular nucleotide sequence in an appropriate host cell, typically comprising a promoter operatively linked to the nucleotide sequence of interest which is operatively linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually encodes a polypeptide(s) of interest but can also encode a functional RNA of interest, for example antisense RNA or a non-translated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest can be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette can also be one that is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. Typically, however, the expression cassette is heterologous with respect to the host; i.e., the particular DNA sequence of the expression cassette does not occur naturally in the host cell and was introduced into the host cell or an ancestor of the host cell by a transformation event. The expression of the nucleotide sequence in the expression cassette can be under the control of a constitutive promoter or of an inducible promoter that initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism such as a plant, the promoter can also be specific to a particular tissue, organ, or stage of development.

The term "adenovirus" refers to a vector derived from an adenovirus serotype. Adenoviruses are double-stranded DNA viruses capable of infecting broad range of mammalian cells, both dividing and non-dividing. The adenovirus DNA is linear of approximately 36,000 bp. The most widely used adenoviral vectors for gene delivery are the replication-deficient vectors, in which the E1 and E3 regions of the adenoviral genome are deleted. E1-deleted viruses are propagated in complementing cells, such as HEK-293, which provide E1-encoded proteins in trans. E1/E3-deleted adenoviruses can accommodate up to 7.5 kb of foreign DNA. The classical method of incorporating foreign DNA into adenovirus genome involves homologous recombination in mammalian cells. More efficient method, as described in the present examples involves homologous recombination in *Escherichia coli* between a large plasmid containing most of the adenovirus genome and a small shuttle plasmid. The shuttle plasmid contains the expression cassette flanked by sequences homologous to the region to be

targeted in the viral genome. The recombinant Ad genome is then linearized by restriction digestion and used to transfect E1-complementing mammalian cells to produce viral particles (Douglas JT., Methods Mol Biol. 2004; V246:3-14) To produce adenoviruses containing toxic gene, special adenoviral vectors have been developed where expression of foreign gene is suppressed during virus production. One of these systems, named, SpeAd Ad-teto system is offered by, for example, Welgen, Inc.

The term "tetracycline-controlled transactivator" (tTA) refers to a fusion protein used to control nucleic acid expression in the presence or absence of doxyclycline, tetracycline and related compounds. The tTA includes a Tet repressor (TetR) fused to any domain capable of activating transcription. The tTA may include a TetR fused to a C-terminal portion of adenovirus.

The term "operably linked" refers to two nucleic acid sequences that are related physically or functionally. For example, a promoter or regulatory DNA sequence is said to be "operably linked to" a DNA sequence that encodes an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence will affect the expression level of the coding or structural DNA sequence. A promoter is also said to be operably linked to a nucleotide sequence if when an RNA polymerase binds to the promoter under conditions sufficient for transcription, the nucleotide sequence is transcribed.

The term "isolated," when applied to a nucleic acid or polypeptide, denotes that the nucleic acid or polypeptide is essentially free of other cellular components with which it is associated in the natural state. It can be in a homogeneous state although it can be in either a dry or aqueous solution. Homogeneity and whether a molecule is isolated can be determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A polypeptide that is the predominant species present in a preparation is substantially isolated. The term "isolated" denotes that a nucleic acid or polypeptide gives rise to essentially one band in an electrophoretic gel. Particularly, it means that the nucleic acid or polypeptide is in some embodiments at least about 50% pure, in some embodiments at least about 85% pure, and in some embodiments at least about 99% pure.

The terms "label" and "labeled" refer to the attachment of a moiety, capable of detection by spectroscopic, radiologic, or other methods, to a molecule. Thus, the terms "label" or "labeled" refer to incorporation or attachment, optionally covalently or non-covalently, of a detectable marker into a molecule, such as a biomolecule. Various methods of labeling biomolecules are known in the art and can be used. Examples of labels for biomolecules include, but are not limited to, the following: radioisotopes, fluorescent labels, heavy atoms, enzymatic labels or reporter genes, chemiluminescent groups, and biotinyl groups. In some

embodiments, labels are attached by spacer arms of various lengths to reduce potential steric hindrance. Fluorescent probe that can be utilized include, but are not limited to fluorescein isothiocyanate; fluorescein dichlorotriazine and fluorinated analogs of fluorescein; naphthofluorescein carboxylic acid and its succinimidyl ester; carboxyrhodamine 6G; pyridyloxazole derivatives; Cy2, 3, 3.5, 5, 5.5, and 7; phycoerythrin; phycoerythrin-Cy conjugates; fluorescent species of succinimidyl esters, carboxylic acids, isothiocyanates, sulfonyl chlorides, and dansyl chlorides, including propionic acid succinimidyl esters, and pentanoic acid succinimidyl esters; succinimidyl esters of carboxytetramethylrhodamine; rhodamine Red-X succinimidyl ester; Texas Red sulfonyl chloride; Texas Red-X succinimidyl ester; Texas Red-X sodium tetrafluorophenol ester; Red-X; Texas Red dyes; tetramethylrhodamine; lissamine rhodamine B; tetramethylrhodamine; tetramethylrhodamine isothiocyanate; naphthofluoresceins; coumarin derivatives (e.g., hydroxycoumarin, aminocoumarin, and methoxycoumarin); pyrenes; pyridyloxazole derivatives; dapoxyl dyes; Cascade Blue and Yellow dyes; benzofuran isothiocyanates; sodium tetrafluorophenols; 4,4-difluoro-4-bora-3a,4a-diaza-s-indacene; Alexa fluors (e.g., 350, 430, 488, 532, 546, 555, 568, 594, 633, 647, 660, 680, 700, and 750); isotope of hydrogen (e.g., tritium isotope, 3H), isotope of carbon (e.g., 14C) green fluorescent protein; yellow fluorescent protein or red fluorescent protein. The peak excitation and emission wavelengths will vary for these compounds and selection of a particular fluorescent probe for a particular application can be made in part based on excitation and/or emission wavelengths.

As used herein, the terms "candidate compound" or "test compound" refer to the collection of compounds that are to be screened for their ability to bind to Nanchung proteins, Nanchung and TRP protein complexes, Nanchung and Iav protein complexes, and/or modulate insect TRPV channels and/or insect TRP channels expressing a Nanchung protein. The candidate compounds may encompass numerous classes of chemical molecules, e.g., small organic or inorganic molecules, polysaccharides, biological macromolecules, e.g., peptides, proteins, peptide analogs and derivatives, peptidomimetics, nucleic acids, nucleic acid analogs and derivatives, an extract made from biological materials such as bacteria, plants, fungi, or animal cells or tissues, naturally occurring or synthetic compositions, or combinations thereof. Generally, the candidate compounds can have a molecular weight of about 50 to 500,000, but is not limited thereto.

As used herein, the term "small molecule" refers to a compound that is "natural product-like," however, the term "small molecule" is not limited to a "natural product-like" compound. Rather, a small molecule is typically characterized in that it contains several carbon-carbon bonds, and has a molecular weight more than about 50, but less than about 5000 Daltons (5 kD). Preferably the small molecule has a molecular weight of less than 3 kD, still more

preferably less than 2 kD, and most preferably less than 1 kD. In some cases it is preferred that a small molecule have a molecular mass equal to or less than 700 Daltons.

In some embodiments, the candidate compound may be a synthetic molecule. The term "synthetic molecule" refers to a molecule that does not occur in nature.

In certain embodiments, the candidate compound may be a naturally-occurring molecule. Such a naturally-occurring molecule may be used in a purified or unpurified form, i.e., as obtained from the biological source. The term "naturally occurring" refers to an entity (e.g., a cell, biomolecule, etc.) that is found in nature as distinct from being artificially produced by man. For example, a polypeptide or nucleotide sequence that is present in an organism in its natural state, which has not been intentionally modified or isolated by man in the laboratory, is naturally occurring. As such, a polypeptide or nucleotide sequence is considered "non-naturally occurring" if it is encoded by or present within a recombinant molecule, even if the amino acid or nucleic acid sequence is identical to an amino acid or nucleic acid sequence found in nature.

Depending upon the particular embodiment being practiced, the candidate compounds may be provided free in solution, or may be attached to a carrier, or a solid support, e.g., beads. A number of suitable solid supports may be employed for immobilization of the candidate compounds. Examples of suitable solid supports include agarose, cellulose, dextran (commercially available as, i.e., Sephadex, Sepharose) carboxymethyl cellulose, polystyrene, polyethylene glycol (PEG), filter paper, nitrocellulose, ion exchange resins, plastic films, polyaminemethylvinylether maleic acid copolymer, glass beads, amino acid copolymer, ethylene-maleic acid copolymer, nylon, silk, etc. Additionally, for the methods described herein, the candidate compounds may be screened individually, or in groups. Group screening is particularly useful where hit rates for effective candidate compounds are expected to be low such that one would not expect more than one positive result for a given group.

There are millions of possible candidate compounds. Methods for developing small molecule, polymeric and genome based libraries are known and described, for example, in Ding, et al. J. Am. Chem. Soc. 124: 1594-1596 (2002) and Lynn, et al., J. Am. Chem. Soc. 123: 8155-8156 (2001). A number of small molecule libraries are known in the art and commercially available. Commercially available compound libraries can be obtained from, e.g., ArQule, Pharmacopia, graffinity, Panvera, Vitas-M Lab, Biomol International and Oxford. These libraries can be screened using the screening methods described herein. Chemical compound libraries such as those from of 10,000 compounds and 86,000 compounds from NIH Roadmap, Molecular Libraries Screening Centers Network (MLSCN) can also be used. A comprehensive list of compound libraries can be found at www.broad.harvard.edu/chembio/platform/screening/compound_libraries/index.htm. A

chemical library or compound library is a collection of stored chemicals usually used ultimately in high-throughput screening or industrial manufacture. The chemical library can consist in simple terms of a series of stored chemicals. Each chemical has associated information stored in some kind of database with information such as the chemical structure, purity, quantity, and physiochemical characteristics of the compound.

The term "modulate" refers to an increase, decrease, or other alteration of any, or all, chemical and/or biological activities and/or properties of a biomolecule, such as the TRPV (e.g., insect TRPV) channel of the present invention. The term "modulation" as used herein thus refers to both upregulation (i.e., activation or stimulation) and downregulation (i.e., inhibition or suppression) of such an activity or property. As would be understood by one of ordinary skill in the art, a modulation of a chemical and/or biological activity and/or property of a biomolecule, such as TRPV channel, can result from an increase or decrease in the expression of the biomolecule in a cell. Accordingly, the terms "modulate" and grammatical variants thereof are intended to encompass both direct modulation (e.g., inhibition of a chemical and/or biological activity and/or property of a polypeptide via binding of an inhibitor to the polypeptide) as well as indirect modulation (e.g., upregulation or downregulation of expression of a protein, such as a TRPV channel or inhibition or stimulation of a biomolecule that acts together with a biomolecule of the presently disclosed subject matter to produce a biological effect).

The terms "polypeptide," "protein," and "peptide," which are used interchangeably herein, refer to a polymer of the 20 protein amino acids, or amino acid analogs, regardless of its size or function. Although "protein" is often used in reference to relatively large polypeptides, and "peptide" is often used in reference to small polypeptides, usage of these terms in the art overlaps and varies. The term "polypeptide" as used herein refers to peptides, polypeptides, and proteins, unless otherwise noted. The terms "protein," "polypeptide," and "peptide" are used interchangeably herein when referring to a gene product. Thus, exemplary polypeptides include gene products, naturally occurring proteins, homologs, orthologs, paralogs, fragments and other equivalents, variants, and analogs of the foregoing.

The term TRP channel refers to a channel and/or a protein complex formed from one or more of the following: Nanchung proteins, TRP proteins and/or Inactive protein. It is to be understood that the TRPV channel and/or TRPV protein complex is a type of TRP channel and/or TRP protein complex. Nanchung proteins and Inactive proteins are a type of TRPV proteins which are a type of TRP proteins. TRP proteins may be found in insect cellular membranes; mammalian cellular membranes; derived from a free cell system; produced by a cell culture; and/or produced by cells, including but not limited to a frog egg, insect cell, and/or mammalian cell, that have been genetically modified (including either or both DNA and/or

RNA) to include the genes coding for one or more of the Nanchung proteins, TRP proteins and/or the Inactive proteins. It is to be understood that the TRP proteins disclosed herein may be mammalian TRP proteins and/or arthropod TRP proteins and/or Nematode TRP proteins and/or Mollusk TRP proteins. It is to be further understood that Nanchung and Inactive proteins may be found in arthropods, including, but not limited to insects, as well as Mollusks and/or Nematodes. It is to be understood that TRP and/or TRPV channels may be formed from one or more TRP and/or TRPV protein complexes; from two or more TRP and/or TRPV protein complexes; from three or more TRP and/or TRPV protein complexes, and/or from four or more TRP and/or TRPV protein complexes.

The term "binding affinity" refers to the ability of compounds to form a bond with a receptor. For purposes of this invention, an equilibrium constant is used to determine the binding affinity of one or more compounds with the one or more Nanchung proteins, TRP channels and or TRPV channels. A dissociation constant (Kd) is a specific type of equilibrium constant measured in a labeled compound saturation binding assay. It is the molar concentration of labeled compound that binds to half the receptor sites at equilibrium. The lower the dissociation constant the higher the binding affinity of the candidate compound for the Nanchung protein, a Nanchung TRP protein complex, and or a Nanchung Inactive protein complex. An inhibition constant (Ki) is a specific type of equilibrium constant that is measured using competition binding of an unlabeled compound with a labeled compound. It is the molar concentration of the competing unlabeled compound that would occupy 50% of the receptors at equilibrium, if no labeled compound was present. It can be calculated using the Cheng and Prusoff equation: $K_i=IC_{50}/(1+[L]/K_d)$ where IC_{50} is the molar concentration of competing unlabeled compound which reduces the specific binding of a labeled compound by 50%. In this equation [L] is the molar concentration of a labeled compound in the assay; K_d is equilibrium dissociation constant for a labeled compound. In addition to saturation binding assay, equilibrium dissociation constant, Kd can be measured in multiple ways, including but not limited to:

1. Using the association and dissociation rates constants where Kd=Koff/Kon
2. Using a fluorescence polarization assay
3. Using surface plasmon resonance
4. Using isothermal calorimetry
5. Using Schild analysis

Surface plasmon resonance and isothermal calorimetry do not require labeled compound to measure K_d. In addition, for the competition assay, K_i and/or K_d (for competition

assay) may be calculated using one or more of the following: Cheng and Prusoff equation, fluorescence polarization, and/or Schild analysis. It is to be understood that the K_d and K_i values calculated for a compound should be similar, but due to experimental error the values may have less than a two-fold difference between the two values or less than a three-fold difference between the two-values depending upon the extent of the experimental error.

The term "species specific binding" for purposes of this application refers to preferential binding of a compound to insect TRP and/or TRPV proteins versus vertebrate TRP and/or TRPV proteins.

The term "high affinity" and/or "high binding affinity" refers to a compound whose equilibrium dissociation constant (K_d) and/or equilibrium inhibition constant (K_i) is calculated as being less than or equal to $3x10^{-7}$ M, less than or equal to $3x10^{-8}$ M, and/or less than or equal to $30x10^{-12}$ M. The lower the K_d or K_i the higher the binding affinity for the compound.

The term "mode of action" refers to the classification of a compound and/or a composition according to the Insecticide Resistance Action Committee (IRAC) into the appropriate group based on the compound and/or composition (a) exhibiting the same function as other insecticides in that group and (b) binding directly to the same site on particular proteins, protein complexes and/or protein channels as other compounds and/or compositions in that group.

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III. Screening Methods

The inventors have discovered that insect TRP and/or TRPV channels may be used to identify compounds that block insect feeding behavior and thus be useful as insecticides. As such, in one embodiment, the present invention relates to a method for determining whether or not a candidate compound is a modulator of an insect TRP and/or TRPV channel. It is to be understood herein that insect TRP channels comprise one or more Nanchung proteins in a complex with one or more TRP proteins such that they form an ion channel. It is to be further understood that insect TRPV channels comprise one or more Nanchung proteins in a complex with one or more TRPV proteins, including but not limited to Inactive proteins, such that they form an ion channel. The inventors have further discovered methods of identifying compounds that bind directly to one or more Nanchung proteins, TRP protein complexes and/or TRPV protein complexes. Furthermore the inventors have determined that a compound, afidopyropen, binds directly to one or more Nanchung proteins, TRP and/or TRPV protein complexes and/or channels and that acts as a modulator of one or more TRP and/or TRPV protein channels. It is to be understood that Arthropod, Mollusk and/or Nematode TRP and/or TRPV channels comprise

one or more Nanchung proteins in a complex with one or more TRP and/or TRPV proteins such that they form an ion channel.

The methods identified herein includes providing one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or channels; contacting the first cell with a candidate compound; and assaying for modulation of the insect TRP and/or TRPV channel, wherein the modulation of the insect TRP and/or TRPV channel identifies the candidate compound as a modulator of the insect TRP and/or TRPV channel. Modulation of the TRP and/or TRPV channel may be assayed using conventional *in vitro* and *in vivo* methods well known to the skilled artisan. For example, in certain embodiments, the assaying step may include (1) detecting calcium ion mobilization in the first cell in response to the candidate compound, (2) detecting a membrane potential in the first cell in response to the candidate compound, (3) comparing calcium ion mobilization in the first cell in the absence of the candidate compound with calcium ion mobilization in the first cell in the presence of the candidate compound. For example, calcium response may be measured by assessment of the uptake of Ca^{2+} or by using fluorescent dyes, such as Fluo-4 or Fura-2 or fluorescent proteins, such as Cameleon , (4) comparing a membrane potential in the first cell in the absence of the candidate compound with a membrane potential in the first cell in the presence of the candidate compound, (5) comparing calcium ion mobilization in the first cell in the presence of the candidate compound with calcium ion mobilization reference level indicative of no modulation of the TPRV channel, and/or (6) comparing a membrane potential in the first cell in the presence of the candidate compound with a membrane potential reference level indicative of no modulation of the TPRV channel, (7) comparing ion currents in the first cell in the absence of the candidate compound with a ion currents in the first cell in the presence of the candidate compound using standard electrophysiology methods, such as voltage clamp or patch clamp. It is to be understood that this same assay could be run on TRP and/or TRPV channels from vertebrate, arthropod, mollusks, nematodes or any other organisms. Such a test would allow one to determine whether or not the candidate compound worked as a modulator is those systems and thus, help one determine the potential environmental impact of using the candidate compound as an insecticide.

Preferably, the candidate compound may modulate the calcium ion mobilization or the membrane potential, or ion currents in the first cell by at least 10% relative to the reference level; more preferably at least 20% relative to the reference level; more preferably at least 30% relative to the reference level; more preferably at least 40% relative to the reference level; more preferably at least 50% relative to the reference level; more preferably at least 60% relative to the reference level; more preferably at least 70% relative to the reference level; more preferably

at least 75% relative to the reference level; more preferably at least 80% relative to the reference level; more preferably at least 85% relative to the reference level; more preferably at least 90% relative to the reference level; and more preferably at least 95% relative to the reference level.

In addition, activation of TRPV channel may be assayed using a variety of other conventional assays that measure changes in ion fluxes including, but not limited to, patch clamp techniques, measurement of whole cell currents, radiolabeled ion flux assays, and fluorescence assays using voltage sensitive dyes (Zheng at al., 2004).

Modulation of an insect TRPV channel may also be assessed using a variety of other *in vitro* and *in vivo* assays to determine functional, chemical, and physical effects, e.g., measuring the binding of the insect TRPV to other molecules, including peptides, small organic molecules, and lipids; measuring insect TRPV protein and/or mRNA levels, or measuring other aspects of insect TRPV polypeptides, e.g., transcription levels, or physiological changes.

The inventors have further determined that it is beneficial to identify compounds that bind directly to one or more Nanchung proteins and/or TRP and/or TRPV protein complexes and/or channels and thus be useful as insecticides. As such, in one embodiment, the present invention relates to a method for determining whether or not a candidate compound directly binds in a species specific manner to one or more Nanchung proteins and/or TRP and/or TRPV protein complexes and/or channels. There are two variations of binding assays, a saturation assay and a competition assay. The saturation assay may include at least one of the following steps: (1) contacting the one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels with a compound, wherein the compound may be labeled or unlabeled; (2) measuring the concentration of the labeled compound and/or unlabeled compound which is bound to the one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels; (3) calculating the equilibrium disassociation constant (K_d) for the one or more labeled compounds and/or unlabeled compound (4) wherein the K_d may be determined using a (a) maximum binding (B_{max}) and (b) the concentration of the compound needed to reach 50% of maximum binding.

The competition assay may include one or more of the following steps: (1) contacting the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels with a compound, wherein the compound may be labeled or unlabeled; (2) measuring the concentration of the compound which is bound to the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels; (3) calculating the equilibrium disassociation constant (K_d) for the one or more compounds; (4) wherein the K_d may be determined using one or more of the following methods: (I)(a) maximum binding (B_{max}) and (b) the concentration of labeled compound needed to reach 50% of maximum binding, (II)

fluorescence polarization assay, (III) surface plasmon resonance, (IV) isothermal calorimetry, (V) Schild analysis; (5) contacting the one or more Nanchung proteins, TRP , and/or TRPV proteins, protein complexes and/or channels with a labeled compound having high affinity to the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels; (6) contacting the one or more one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels with a candidate compound in the presence of the labeled compound of step 1; (7) increasing the amount of the candidate compound available to contact the one or more Nanchung proteins, TRP, and/or TRPV proteins, protein complexes and/or channels until binding of the labeled compound is near 0%; (8) calculating the equilibrium inhibition constant (K_i) and/or the equilibrium dissociation constant (K_d) for competition assay using one or more of the following methods: (I) (a) determining amount of bound labeled compound in the absence of the candidate compound and (b) determining concentration of the candidate compound that is required to reduce the amount of bound labeled compound by 50%, (II) fluorescent polarization assay, and/or (III) Schild analysis; (9) comparing the inhibition constant of the candidate compounds to other candidate compounds; (10) comparing the inhibition constant of the candidate compounds to the disassociation constant of the labeled compound.

Binding to a one or more Nanchung proteins, TRP protein complexes and/or channels and/or TRPV protein complexes and/or channels may be assessed using a variety of *in vitro* and *in vivo* assays to determine whether the candidate compound binds directly to the one or more Nanchung proteins, TRP protein complexes and/or channels and/or TRPV protein complexes and/or channels. Identification of molecular targets of insecticides is essential for assessing their spectra, health and environmental impacts, as well as for insect resistance management. Pymetrozine (PM) and pyrifluquinazon (PFQ) are two structurally-related commercial insecticides (chemical structures are shown on Figure 1) which act by disrupting coordination and feeding of plant-sucking insects such as aphids and whiteflies (Casida and Durkin, 2013; Maienfisch, 2012). Pyrifluquinazon can spontaneously de-acetylate in aqueous solutions. The de-acetylated form of pyrifluquinazon (dPFQ) was shown to be significantly more potent than the parent compound, suggesting that pyrifluquinazon is a pro-drug, which is activated through de-acetylation (Nesterov et al., 2015). dPFQ was, therefore, used in the present invention, however it is to be understood that pyrifluquinazon may be used as well.

Afidopyropen is a new insecticide compound with a previously unknown mode of action. Although afidopyropen and Pymetrozine have significantly different chemical structures (Figure 1), they have similar spectrum of insects they are toxic to, and produce similar

behavioral symptoms, including feeding inhibition in aphids (Leichter et al., 2013). However, whether afidopyropen and Pymetrozine bind to the same location and thus would be classified as having the same mode of action was unknown.

TRP and/or TRPV (Transient Receptor Potential) proteins form hetero- and homotetrameric cation channels in various cell types (Venkatachalam and Montell, 2007). Pymetrozine and pyrifluquinazon disturbed *Drosophila* coordination and hearing by overstimulating, and ultimately silencing TRPV channels in chordotonal organs (Nesterov et al., 2015) , which are serially arranged stretch receptors (Kavlie and Albert, 2013) which sense relative position of body parts in insects (Kamikouchi et al., 2009; Sun et al., 2009). While Pymetrozine and pyrifluquinazon were found to bind to the Nanchung protein alone, the modulation effect of the Pymetrozine and pyrifluquinazon required simultaneous presence of two TRPV proteins, Nanchung (Nan) and Inactive (Iav), which co-occur in chordotonal neurons and form functional ion channels. (Nesterov et al., 2015, *PCT/US2014/071489,* which is hereby incorporated by reference in its entirety.)

The current invention shows that afidopyropen, Pymetrozine and de-acetylated pyrifluquinazon, modulate TRP channels directly, by directly binding to the same site on these protein channels. Furthermore, the current invention identifies methods of determining whether or not a candidate compound binds directly to the same site on these proteins, protein complexes and/or protein channels. Determining the binding location and affinities for candidate compounds assists with the classification of a compounds mode of action and allows for better insect management and control that may result in decreased risk of developing resistant insect populations.

The current invention also found that there was increased binding affinity of Pymetrozine, de-acetylated pyrifluquinazon, and afidopyropen in the presence of both the Nanchung protein and the Inactive protein. The current invention also found that afidopyropen exhibited modulation activity only in the presence of both Nanchung and Inactive proteins, protein complexes and/or channels. The current invention also found that afidopyropen exhibited modulation activity in the presence of both Nanchung and TRP proteins, protein complexes and/or channels. Furthermore the current invention identified afidopyropen as having a high binding affinity to the Nanchung protein, a Nanchung-TRP protein complex, a Nanchung-TRP protein channel, a Nanchung-TRPV protein complex, Nanchung-TRPV protein channel, a Nanchung-Inactive protein complex, and a Nanchung-Inactive protein channel. Accordingly, the current invention identifies a labeled compound having a high binding affinity to one or more Nanchung proteins, TRP and/or TRPV proteins, protein complexes and/or protein channels, such

as afidopyropen, pymetrozine and/or de-acetylated pyrifluquinazon, may be used to calculate the binding affinity of a candidate compound using the competition assay as described herein.

As noted previously, the candidate compound may be a small organic molecule, small inorganic molecule, polysaccharides, peptides, proteins, nucleic acids, an extract made from biological materials such as bacteria, plants, fungi, animal cells, animal tissues, and any combination thereof.

Generally, a candidate compound can be tested at any concentration that can modulate the activity of a TRP and/or TRPV channel, and/or exhibit binding to TRP and/or TRPV proteins. In some embodiments, the candidate compound may be tested at a concentration in the range of about 0.01 nM to about 1000 mM. In certain other embodiments, the compound may be tested in the range of about 100 μM to about 1000 μM. In certain further embodiments, the candidate compound may be tested at greater than 0.05 mM, 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM, 1 mM, 1.1 mM, 1.2 mM, 1.3 mM, 1.4 mM, 1.5 mM, 1.6 mM, 1.7 mM, 1.8 mM, 1.0 mM, or 2 mM. Other ranges and concentrations of the candidate compound may also be suitable.

In some embodiments, the candidate compound may be tested at two or more different concentrations. Preferably the highest concentration tested is at least 2×, at least 3×, at least 4×, at least 5×, at least 6×, at least 7×, at least 8×, at least 9×, at least 10×, at least 15×, at least 20×, at least 25×, at least 50×, at least 75×, at least 100×, at least 200×, at least 250× higher than the lowest concentration employed. For example, the candidate compound may be tested at 0.1 mM, 0.5 mM, and 1 mM, where the highest concentration is at least 10X the concentration of the lowest concentration employed.

Generally, the one or more Nanchung proteins, TRP and/or TRPV protein complexes and/or channels may be contacted with a candidate compound for any suitable length of time before measuring the binding affinity and/or activity of the insect TRP and/or TRPV channel and/or proteins. For example, the insect TRPV channel may be contacted with a candidate compound for at least 5 seconds, at least 10 seconds, at least 15 seconds, at least 30 seconds, at least 45 seconds, at least 1 minute, at least 2 minutes, at least 3 minutes, at least 4 minutes, at least 5 minutes, at least 10 minutes, at least 15 minutes, at least 30 minutes, at least 60 minutes, at least 2 hours, at least 3 hours or more before activity and/or binding of the insect TRP and/or TRPV is measured. In some embodiments, activity may be measured at the instant when the insect TRPV is contacted with a candidate compound.

In some embodiments, activity of insect TRPV channel may be measured over a period of time as well as binding of the candidate compound to the one or more Nanchung

proteins, TRP and/or TRPV protein complexes and/or channels. For example, activity may be measured for a period of at least 5 seconds, at least 10 seconds, at least 15 seconds, at least 30 seconds, at least 45 seconds, at least 1 minute, at least 2 minutes, at least 3 minutes, at least 4 minutes, at least 5 minutes, at least 10 minutes, at least 15 minutes, at least 30 minutes, at least 60 minutes, at least 2 hours, at least 3 hours, at least 4 hours or more. The measurement period can start before the one or more Nanchung proteins, TRP and/or TRPV protein complexes and/or channels is contacted with a candidate compound, at the instant when the one or more Nanchung proteins, TRP and/or TRPV protein complexes and/or channels is first contacted with a candidate compound or start after a period of time after the one or more Nanchung proteins, TRP and/or TRPV protein complexes and/or channels is first contacted with a candidate compound. The one or more Nanchung proteins, TRP and/or TRPV protein complexes and/or channels may be continuously contacted with the candidate compound while activity and/or binding is measured.

In some embodiments, the candidate compound has an effective concentration EC50 of less than or equal to 500 nM, less than or equal to 250 nM, less than or equal to 100 nM, less than or equal to 50 nM, less than or equal to 10 nM, less than or equal to 1 nM, less than or equal to 0.1 nM, less than or equal to 0.01 nM, or less than or equal to 0.001 nM for activating and/or binding an insect-specific TRPV channel.

In some embodiments, the candidate compound has an IC50 of less than or equal to 500 nM, less than or equal to 250 nM, less than or equal to 100 nM, less than or equal to 50 nM, less than or equal to 10 nM, less than or equal to 1 nM, less than or equal to 0.1 nM, less than or equal to 0.01 nM, or less than or equal to 0.001 nM for inhibiting and/or binding an insect-specific TRPV channel.

In certain embodiments, the candidate compound is a modulator that inhibits the activity of the TRP and/or TRPV channel.

In certain other embodiments, the candidate compound is a modulator that activates the TRP and/or TRPV channel of insects and/or other pests.

Preferably, the candidate compound is a modulator that inhibits an insect feeding behavior.

In certain embodiments the candidate compound binds directly to the Nanchung protein

In certain other embodiments the candidate compound binds directly to a complex consisting of the one or more Nanchung proteins and one or more TRP proteins.

Preferably the candidate compound binds directly to the one or more Nanchung and Inactive protein complexes.

In certain embodiments, to determine whether a candidate compound preferentially modulates and/or binds to the insect-specific TRPV and/or TRP channel relative to a mammalian-specific TRPV and/or TRP channel, the method may further include providing a second cell expressing a mammalian TRPV and/or TRP channel. The second cell may be contacted with the candidate compound and modulation of and/or binding to the mammalian TRPV and/or TRP channel may be assayed by the methods known in the art, which were also described herein. Following the assaying steps the modulation of and/or binding to the insect TRPV and/or TRP channel may be compared with the modulation of and/or binding to the mammalian TRPV and/or TRP channel and the candidate compound that displays an increased modulation of and/or binding to the insect-specific TRPV and/or TRP channel relative to the mammalian TRPV and/or TRP channel identifies the candidate compound as a selective modulator of and/or binder of the insect TRPV and/or TRP channel. It is to be understood that this method may be employed to determine preferential binding between other species and/or binding to pest species and not to non-pest species as well.

By the term "preferential modulation" is meant that activity or other property of insect-specific TRPV and/or TRP channel is modulated by at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 100%, or more relative to a reference level or the mammalian-specific TRPV and/or TRP channel.

By the term "preferential binding" is meant that the equilibrium binding constant (K_d or K_i) of the insect-specific TRPV and/or TRP channel is decreased by at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 100%, or more relative to a reference level or the mammalian-specific TRPV and/or TRP channel.

In certain other embodiments, non-selective modulators and/or binders of the TRPV and/or TRP channel may be identified. The term "non-selective" in connection with a modulator and/or binder of the TRPV and/or TRP proteins, protein complexes and/or channels means that a compound can modulate and/or bind directly to one or more TRPV and/or TRP proteins, protein complexes and/or channels in different organisms, e.g., a compound may modulate both, arthropod, such as insect, and mammalian TRPV and/or TRP protein complexes and/or channels.

In certain other embodiments, the candidate compound is an insect-specific TRP channel modulator and/or binder and does not modulate the activity of and/or bind to the mammalian-specific TRP, e.g., the tested compound has no significant effect on the mammalian-specific TRPV channel.

In certain embodiments, the one or more Nanchung protein, TRPV and/or TRP protein complex and/or channel is in a biological cell. In some embodiments, the mammalian TRPV and/or TRP channel is in a biological cell. The term "biological cell" or "cell" as used herein has its commonly understood meaning. Inside a cell, the Nanchung protein, TRPV and/or TRP channel may be expressed from an endogenous gene in the cell or from at least one vector that is transfected into the cell. It is to be understood that either the cultured cell, or a cell obtained directly from animal, such as frog oocyte, or whole tissue may be used as a source of the Nanchung, TRP and/or TRPV proteins and/or channels. Preferably, the TRPV channel proteins, Nanchung and Inactive proteins are co-expressed in the cell. The Nanchung and Inactive proteins may be co-expressed at varying rations, preferably, the ratio of the Nanchung to Inactive proteins co-expressed in the first cell is about 3:1 to about 1:3, more preferably about 1:1. It is to be understood that the Nanchung protein may be combined with other TRP channel proteins and that binding to the Nanchung protein in this scenario will have similar effects for purposes of the candidate compound acting as an insecticide. The Nanchung and TRP proteins may be co-expressed at varying rations, preferably, the ratio of the Nanchung to TRP proteins co-expressed in the first cell is about 3:1 to about 1:3, more preferably about 1:1.

In certain embodiments, the one or more Nanchung proteins TRPV and/or TRP protein complexes and/or channels are formed in a cell-free system. The term "cell-free system" as used herein means an in vitro system used to study biological reactions that happen within cells while reducing the complex interactions found in a whole cell. Subcellular fractions can be isolated by ultracentrifugation to provide molecular machinery that can be used in reactions in the absence of many of the other cellular components. Cell-free biosystems can be prepared by mixing one or more of the following: ribosomes; and/or DNA and/or RNA encoding for one or more proteins of interest; membranes; as well as a one or more enzymes and/or coenzymes. Cell-free biosystems have several advantages suitable in industrial applications. In vitro biosystems can be easily controlled. Cell-free systems provide an alternative choice for fast protein synthesis and very high product yields are usually accomplished without the formation of by-products or synthesis of cell mass.

In certain embodiments a cell genetically modified to contain the genes coding for one or more of the proteins Nanchung, TRP and/or Inactive may be used to produce the TRP and/or TRPV channel complex for purposes of the methods described herein.

In certain embodiments a nucleic acid coding for one or more of the proteins Nanchung, TRP and/or Inactive may be introduced into frog oocytes or other cells (parental cells) to produce the TRP and/or TRPV channel complex for purposes of the methods described herein.

The insect TRPV and/or TRP protein complex and/or channel used in the screening assay of the present invention may be any insect TRPV and/or TRP protein complex and/or channel or homolog or a conservative variant thereof. For example, the TRPV and/or TRP protein complex and/or channel may be a *Drosophila* TRPV and/or other member of TRP channel superfamily. Other sources of TRPV and/or TRP protein complex and/or channel may also be suitable for use according to the methods of the present invention.

Insect TRP and/or TRPV channels are thought to be associated with one or more Nanchung proteins and may also include one or more Inactive proteins. The mammalian TRP and/or TRPV channels used in the screening assay may be any mammalian TRP or homolog thereof, preferably a TRPV channel similar to an insect TRPV channel.

In some embodiments, the Nanchung nucleic acid sequences may be selected from the group consisting of a) a polynucleotide molecule comprising a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NOS: 1-27 (FIGS. 10-36); b) a polynucleotide molecule having at least about 70% sequence identity to the sequence of SEQ ID NOS: 1-27 (FIGS. 10-36); and c) a fragment of the polynucleotide molecule of a) or b). Such fragments can be a UTR, a core promoter, an intron, an enhancer, a cis-element, or any other regulatory element.

In some embodiments, the Inactive nucleic acid sequences may be selected from the group consisting of a) a polynucleotide molecule comprising a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NOS: 28-53 (FIGS. 64-89); b) a polynucleotide molecule having at least about 70% sequence identity to the sequence of SEQ ID NOS: 28-53 (FIGS. 64-89); and c) a fragment of the polynucleotide molecule of a) or b). Such fragments can be a UTR, a core promoter, an intron, an enhancer, a cis-element, or any other regulatory element.

Human, mouse, rat, or hamster TRPV1, TRPV2, TRPV3, TRPV4, TRPV5 or TRPV6

The disclosed polynucleotides are capable of providing for expression of Nanchung and Inactive proteins in the host cells.

In certain embodiments, the Nanchung protein sequences may be selected from the group consisting of a) a polypeptide comprising an amino acid sequence having a sequence selected from the group consisting of SEQ ID NOS: 54-80 (FIGS. 37-63); b) a polypeptide having at least 70% sequence identity to the SEQ ID NOS: 54-80 (FIGS. 37-63); and c) a fragment or a conservative variant of the polypeptide of a) or b).

In certain embodiments, the Inactive protein sequences may be selected from the group consisting of a) a polypeptide comprising an amino acid sequence having a sequence selected from the group consisting of SEQ ID NOS: 81-106 (FIGS. 90-115); b) a polypeptide

having at least 70% sequence identity to the SEQ ID NOS: 81-106 (FIGS. 90-115); and c) a fragment or a conservative variant of the polypeptide of a) or b).

The sequence alignment of the Nanchung and Inactive proteins is shown in Figures 116 and 117, respectively. The family distribution tree for the Nanchung and Inactive proteins is shown in Figures 118 and 119, respectively.

As used herein, the "percent sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, where the portion of the polynucleotide or a polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, divided by the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Alignment for the purposes of determining the percentage identity can be achieved in various ways that are within the skill in the art, for example, using publicly available computer software such as BLAST. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve optimal alignment over the full length of the sequences being compared.

As used herein, the term a "conservative variant" refers to an amino acid sequence in which a first amino acid is replaced by a second amino acid or amino acid analog having at least one similar biochemical property, which can be, for example, similar size, charge, hydrophobicity or hydrogen bonding capacity. For example, a first hydrophobic amino acid can be conservatively substituted with a second (non-identical) hydrophobic amino acid such as alanine, valine, leucine, or isoleucine, or an analog thereof. Similarly, a first basic amino acid can be conservatively substituted with a second (non-identical) basic amino acid such as arginine or lysine, or an analog thereof. In the same way, a first acidic amino acid can be conservatively substituted with a second (non-identical) acidic amino acid such as aspartic acid or glutamic acid, or an analog thereof or an aromatic amino acid such as phenylalanine can be conservatively substituted with a second aromatic amino acid or amino acid analog, for example tyrosine. In some embodiments, the peptide comprises conservative variant substitution of at least one amino acid, e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acids. Typically, a conservative variant will retain at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or more of the activity of the wild-type peptide sequence.

Exemplary conservative variant substitution include, but are not limited to, replacement of Alanine (A) with D-ala, Gly, Aib, β-Ala, Acp, L-Cys, or D-Cys; Arginine (R)

with D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Be, D-Met, or D-Ile; Asparagine (N) with D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, or D-Gln; Aspartic acid (D) with D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, or D-Gln; Cysteine (C) with D-Cys, S-Me-Cys, Met, D-Met, Thr, or D-Thr; Glutamine (Q) with D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, or D-Asp; Glutamic Acid (E) with D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, or D-Gln; Glycine (G) with Ala, D-Ala, Pro, D-Pro, Aib, β-Ala, or Acp; Isoleucine (I) with D-Ile, Val, D-Val, AdaA, AdaG, Leu, D-Leu, Met, or D-Met; Leucine (L) with D-Leu, Val, D-Val, AdaA, AdaG, Leu, D-Leu, Met, or D-Met; Lysine (K) with D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, or D-Orn; Methionine (M) with D-Met, S-Me-Cys, Be, D-Ile, Leu, D-Leu, Val, or D-Val; Phenylalanine (F) with D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4 or 5-phenylproline, AdaA, AdaG, cis-3, 4 or 5-phenylproline, Bpa, or D-Bpa; Proline (P) with D-Pro, L-I-thioazolidine-4-carboxylic acid, or D- or -L-1-oxazolidine-4-carboxylic acid (U.S. Pat. No. 4,511,390); Serine (S) with D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met (O), D-Met (O), L-Cys, or D-Cys; Threonine (T) with D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met (O), D-Met (O), Val, or D-Val; Tyrosine (Y) with D-Tyr, Phe, D-Phe, L-Dopa, His, or D-His; and Valine (V) with D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met, AdaA, or AdaG.

Conservative variants of the insect or mammalian TRPV channels can be prepared according to methods for altering peptide sequences known in the art, and include those that may be found in references, which compile such methods, e.g., *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor, or *Current Protocols in Molecular Biology*, F. M. Ausubel, et al., eds., John Wiley & Sons, Inc. New York.

Conservative variants of TRPV and/or TRP channel may also be made by alteration of a nucleic acid encoding the TRPV and/or TRP polypeptide.

In certain embodiments, the screening method of the present invention may be a high-throughput screening. High-throughput screening (HTS) refers to a method for scientific experimentation that uses robotics, data processing and control software, liquid handling devices, and sensitive detectors. High-Throughput Screening or HTS allows a researcher to quickly conduct millions of biochemical, genetic or pharmacological tests. HTS is well known in the art, including, for example, U.S. Pat. Nos. 5,976,813; 6,472,144; 6,692,856; 6,824,982; and 7,091,048.

HTS uses automation to run a screen of an assay against a library of candidate compounds. An assay is a test for specific activity: usually inhibition or stimulation of a biochemical or biological mechanism. Specifically, an assay would be screening for inhibition or stimulation of the insect TRPV channel. Typical HTS screening libraries or "decks" can contain from 100,000 to more than 2,000,000 compounds.

The key labware or testing vessel of HTS is the microtiter plate, which is a small container, usually disposable and made of plastic that features a grid of small, open divots called wells. Modern microplates for HTS generally have either 384, 1536, or 3456 wells. These are all multiples of 96, reflecting the original 96 well microplate with 8×12 9 mm spaced wells.

To prepare for an assay, a researcher fills each well of the plate with the appropriate reagents that he or she wishes to conduct the experiment with. After some incubation time has passed to allow the reagent to absorb, bind to, or otherwise react (or fail to react) with the compounds in the wells, measurements are taken across all the plate's wells, either manually or by a machine. Manual measurements are often necessary when the researcher is using microscopy to (for example) seek changes that a computer could not easily determine by itself. Otherwise, a specialized automated analysis machine can run a number of experiments on the wells such as current or voltage measurements, colorimetric measurements, radioactivity counting, etc. In this case, the machine outputs the result of each experiment as a grid of numeric values, with each number mapping to the value obtained from a single well. A high-capacity analysis machine can measure dozens of plates in the space of a few minutes like this, generating thousands of experimental data points very quickly.

IV. Formulations, Applications and Uses

In another aspect, the invention provides a compound selected by the screening assay described herein. It is to be understood that analogs, derivatives, isomers, and pharmaceutically acceptable salts of the compounds selected by the screening assays described herein as well as any formulations including the selected compound are also included herein.

The compound or group of compounds being determined or identified by the method according to the invention can be used in methods of insect control, e.g., by modulating insect feeding behavior. The identified compounds, analogs, derivatives, isomers, and pharmaceutically acceptable salts thereof are also referred to as "active agents" or "active ingredients" herein.

In some embodiments, the compound modulates the feeding behavior of an insect. As used herein, the term "feeding behavior" refers to the process by which organisms, such as insects obtain food. Without being bound by theory, the modulation of an insect TRPV elicits a signaling pathway that brings forth motor neuron modulation which may ~~increase or~~ decrease feeding behavior of an insect, and such modulation of an insect TRPV channel in an insect may lead to a decrease in feeding behavior of such insect leading to the insect's death by starvation. Thus, again without being bound by theory, it is believed that compounds that modulate (e.g., activate or inhibit) an insect TRPV channel may be used as insecticides. This decrease in

feeding behavior can be used to destroy insects in a particular location and thus control such insects. Thus, in some embodiments, the method comprises modulation of TRPV ion channel or family members in the insect with a compound identified by a screening method described herein.

Accordingly, in certain embodiments, the invention provides a method of insect control by modulating feeding behavior in an insect using a compound identified by the screening methods described herein. As used in context of methods of insect control, compounds identified by the screening methods described herein also include analogs, derivatives, isomers and pharmaceutically acceptable salts of such compounds.

In one embodiment, the methods and active agents described herein are applicable to insects that are agricultural or horticultural pest.

Examples of agricultural pests include, but are not limited to,Aphids (including *Aphis fabae*, *Aphis gossypii*, *Aphis pomi*, *Aulacorthum solani*, *Brevicoryne brassicae*, *Dysaphis plantaginea*, *Macrosiphum euphorbiae*, *Macrosiphum euphorbiae*, *Macrosiphum rosae*, *Myzus persicae*, *Nasonovia ribisnigri*); Whiteflies (including *Aleurodes spp.*, *Bemisia spp.*, *Dialeurodes spp.*, *Trialeurodes spp.*); Planthoppers (including *Laodelphax striatellus*, *Nilaparvata lugens*, *Siphanta spp.*, *Sogatella furcifera*); Leafhoppers (including *Amrasca spp.*, *Empoasca spp.*); Scales (including *Aspidiotus spp.*, *Chrysomphalus aonidum*, *Icerya purchase*, *Unaspis citri*); Mealybugs (including *Maconellicoccus spp.*, *Paracoccus spp.*, *Planococcus spp.*); Pollen beetles (including *Carpophilus spp.*, *Meligethes spp.*); Thrips (including *Caliothrips spp.*, *Frankliniella spp.*, *Scirtothrips spp.*, *Thrips spp.*); and Psyllids (including *Bactericera spp.*, *Cacopsylla spp.*, *Diaphorina citri*, *Paratrioza cockerelli*).

For example, vegetable and cole crops are sensitive to infestation by one or more of the following insect pests: aphids, brown plant hopper, alfalfa looper, armyworm, beet armyworm, artichoke plume moth, cabbage budworm, cabbage looper, cabbage webworm, corn earworm, celery leafeater, cross-striped cabbagewon, european corn borer, diamondback moth, green cloverworm, imported cabbageworm, melonworm, omnivorous leafroller, pickleworm, rindworm complex, saltmarsh caterpillar, soybean looper, tobacco budworm, tomato fruitworm, tomato homworrri, tomato pinworm, velvetbean caterpillar, and yellow-striped annyworm.

Likewise, pasture and hay crops such as alfalfa, pasture grasses and silage are often attacked by pests, such as annyworm, beef annyworm, alfalfa caterpillar, European skipper, a variety of loopers and webworms, as well as yellowstriped armyworms.

Fruit and vine crops are often susceptible to attack and defoliation by achema sphinx moth, amorbia, armyworm, citrus cutworm, banana skipper, blackheaded fireworm, blueberry leafroller, cankerworm, cherry fruitworm, citrus cutworm, cranberry girdler, eastern tent

caterpillar, fall webworm, fall webworm, filbert leafroller, filbert webworm, fruit tree leafroller, grape berry moth, grape leaffolder, grapeleaf skeletonizer, green fruitworm, gummosos-batrachedra commosae, gypsy moth, hickory shuckworm, hornworms, loopers, navel orangeworm, obliquebanded leafroller, orrinivorous leafroller, omnivorous looper, orange tortrix, orangedog, oriental fruit moth, pandemis leafroller, peach twig borer, pecan nut casebearer, redbanded leafroller, redhumped caterpillar, roughskinned cutworm, saltmarsh caterpillar, spanworm, tent caterpillar, thecla-thecla basillides, tobacco budworm, tortrix moth, tufted apple budmoth, variegated leafroller, walnut caterpillar, western tent caterpillar, and yellowstriped annyworm.

Field crops such as canola/rape seed, evening primrose, meadow foam, corn (field, sweet, popcorn), cotton, hops, jojoba, peanuts, rice, safflower, small grains (barley, oats, rye, wheat, etc.), sorghum, soybeans, sunflowers, and tobacco are often targets for infestation by insects, including: armyworm, asian and other corn borers, banded sunflower moth, beet annyworm, bollworm, cabbage looper, corn rootworm (including southern and western varieties), cotton leaf perforator, diamondback moth, european corn borer, green cloverworm, headmoth, headworm, imported cabbagewonn, loopers (including Anacamptodes spp.), obliquebanded leafroller, omnivorous leaftier, podworin, podworm, saltmarsh caterpillar, southwestern corn borer, soybean looper, spotted cutworm, sunflower moth, tobacco budworm, tobacco hornworm, velvetbean caterpillar, Bedding plants, flowers, ornamentals, vegetables and container stock are frequently fed upon by a host of insect pests such as armyworm, azalea moth, beet armyworm, diamondback moth, ello moth (hornworm), Florida fern caterpillar, lo moth, loopers, oleander moth, omnivorous leafroller, omnivorous looper, and tobacco Forests, fruit, ornamental, and nut-bearing trees, as well as shrubs and other nursery stock are often susceptible to attack from diverse insects such as bagworm, blackheaded budworm, browntail moth, california oakworm, douglas fir tussock moth, elm spanworm, fall webworm, fruit tree leafroller, greenstriped mapleworm, gypsy moth, Jack pine budworm, mimosa webworm, pine butterfly, redhumped caterpillar, saddleback caterpillar, saddle prominent caterpillar, spring and fall cankerworm, spruce budworm, tent caterpillar, tortrix, and western tussock moth.

Likewise, turf grasses are often attacked by pests such as armyworm, sod webworm, and tropical sod webworm.

It is also envisioned that the methods described herein are also applicable to pest control, wherein the pests are not insects but rather, e.g., nematodes, slugs or snails.

In one embodiment, the methods described herein are also applicable to insects that are parasites. Examples of some insect parasites are Braconid Wasps, family Braconidae;

Ichneumonid Wasps, family Ichneumonidae; Chalcid Wasps, family Chalcidae; Tachinid Flies, family Tachonidae.

In certain other embodiments, the methods described herein may also be applicable to insects that are disease vectors. Vectors are organisms that can introduce a pathogen such as a bacterium or virus into a host organism to cause an infection or disease. Exemplary disease vector include, but are not limited to, mosquitoes, Ticks, Siphonaptera (fleas), Diptera (flies), Phthiraptera (lice) and Hemiptera (true bugs).

Once a compound suitable for insecticidal use is identified, the active ingredient, or formulations comprising them, may be applied directly to the target insects (i.e., larvae, pupae and/or adults), or to the locus of the insects. In one embodiment, the active ingredient or a formulation and/or composition containing the active ingredient is applied directly to the adult insect. In one embodiment, the active agent is applied directly to the larvae and/or pupae of the target insect. In another embodiment, the active ingredient is applied to the locus of the insects.

Because compounds incorporating hydrophobic moieties will penetrate the insect cuticle, active agents can be conjugated with hydrophobic moieties. Hydrophobic moieties include, but are not limited to, lipids and sterols.

In one embodiment, the active ingredient or a formulation including the active ingredient may be applied as a spray. For example, the active ingredient may be applied as an agricultural spray in aerial crop dusting, an environmental spray to control biting insects, or as a topical spray for localized control of biting insects. The active ingredient may be formulated for the purpose for spray application such as an aerosol formulation. Spray application may be accomplished with a spray pump. The active ingredient may be also encapsulated within materials such as starch, flour and gluten in granular formulations.

In certain embodiments, the active ingredient or a formulation including the active ingredient may be applied in conjunction with other insecticides and/or pesticides such as organo-phosphates, synthetic pyrethroids, carbamates, chlorinated hydrocarbons, when used in agricultural and/or environmental insect control.

The active ingredient may be administered in an amount effective to induce the desired response as determined by routine testing. The actual effective amount will of course vary with the specific active ingredient, the target insect and its stage of development, the application technique, the desired effect, and the duration of the effect, and may be readily determined by the practitioner skilled in the art. "An effective amount of active ingredient" refers to the amount of active ingredient that modulates (activates or inhibits) an insect TRPV channel, e.g., modulates feeding behavior of an insect to achieve the desired insect control.

Methods of formulation are well known to one skilled in the art and are also found in Knowles, D A (1998) Chemistry and technology of agricultural formulations. Kluwer Academic, London, which is hereby incorporated by reference in its entirety. One skilled in the art will, of course, recognize that the formulation and mode of application may affect the activity of the active ingredient in a given application. Thus, for agricultural and/or horticultural use the TRPV inhibitors and/or agonists may be formulated as a granular of relatively large particle size (for example, 8/16 or 4/8 US Mesh), as water-soluble or water-dispersible granules, as powdery dusts, as wettable powders, as emulsifiable concentrates, as aqueous emulsions, as solutions, as suspension concentrate, as capsule suspensions, as soluble (liquid) concentrates, as soluble powders, or as any of other known types of agriculturally-useful formulations, depending on the desired mode of application. It is to be understood that the amounts specified in this specification are intended to be approximate only, as if the word "about" were placed in front of the amounts specified.

These formulations may be applied either as water-diluted sprays, or dusts, or granules in the areas in which insect control is desired. The formulations may contain as little as 0.1%, 0.2% or 0.5% to as much as 95% or more by weight of active ingredient, e.g. insect TRPV inhibitor.

"Dusts" are free flowing admixtures of the active ingredient with finely divided solids such as talc, natural clays, kieselguhr, flours such as walnut shell and cottonseed flours, and other organic and inorganic solids which act as dispersants and carriers for the toxicant; these finely divided solids have an average particle size of less than about 50 microns. A typical dust formulation useful herein is one containing 90 parts, 80 parts, 70 parts, 60 parts, 50 parts, 40 parts, 30 parts, 20 parts, preferably 10 parts, or less of the active ingredient, e.g., insect TRPV inhibitor or insect TRPV agonist. In one embodiment, the dust formulation may include 1 part or less of the active ingredient and 99 parts or more of talc.

Wettable powders, useful as formulations, are in the form of finely divided particles that disperse readily in water or other dispersant. The wettable powder is ultimately applied to the locus where insect control is needed either as a dry dust or as an emulsion in water or other liquid. Typical carriers for wettable powders include Fuller's earth, kaolin clays, silicas, and other highly absorbent, readily wet inorganic diluents. Wettable powders typically are prepared to contain about 5-80% of active ingredient, depending on the absorbency of the carrier, and usually also contain a small amount of a wetting, dispersing or emulsifying agent to facilitate dispersion. For example, a useful wettable powder formulation contains 80.0 parts of the active ingredient, 17.9 parts of Palmetto clay, and 1.0 part of sodium lignosulfonate and 0.3 part of

sulfonated aliphatic polyester as wetting agents. Additional wetting agent and/or oil may be added to a tank mix for to facilitate dispersion on the foliage of the plant.

Other useful formulations are emulsifiable concentrates (ECs) which are homogeneous liquid compositions dispersible in water or other dispersant, and may consist entirely of the active ingredient, and a liquid or solid emulsifying agent, or may also contain a liquid carrier, such as xylene, heavy aromatic naphthas, isophorone, or other non-volatile organic solvents. For insecticidal application these concentrates are dispersed in water or other liquid carrier and normally applied as a spray to the area to be treated. The percentage by weight of the essential active ingredient may vary according to the manner in which the composition is to be applied, but in general comprises 0.5 to 95% of active ingredient by weight of the insecticidal composition.

Flowable formulations are similar to ECs, except that the active ingredient is suspended in a liquid carrier, generally water. Flowables, like ECs, may include a small amount of a surfactant, and will typically contain active ingredients in the range of 0.5 to 95%, frequently from 10 to 50%, by weight of the composition. For insecticidal application, flowables may be diluted in water or other liquid vehicle, and are typically applied as a spray.

Typical wetting, dispersing or emulsifying agents used in agricultural and/or horticultural formulations may include, but are not limited to, the alkyl and alkylaryl sulfonates and sulfates and their sodium salts; alkylaryl polyether alcohols; sulfated higher alcohols; polyethylene oxides; sulfonated animal and vegetable oils; sulfonated petroleum oils; fatty acid esters of polyhydric alcohols and the ethylene oxide addition products of such esters; and the addition product of long-chain mercaptans and ethylene oxide. Many other types of useful surface-active agents are available in commerce. Surface-active agents, when used, typically include 1 to 15% by weight of the composition.

Other useful formulations include suspensions of the active ingredient in a relatively non-volatile solvent such as water, corn oil, kerosene, propylene glycol, or other suitable solvents.

In certain embodiments, formulations for insecticidal applications may include simple solutions of the active ingredient in a solvent, in which it is completely soluble at the desired concentration, such as acetone, alkylated naphthalenes, xylene, or other organic solvents.

Granular formulations, wherein the active ingredient is carried on relative coarse particles, are of particular utility for aerial distribution or for penetration of cover crop canopy. Pressurized sprays, typically aerosols wherein the active ingredient is dispersed in finely divided form as a result of vaporization of a low-boiling dispersant solvent carrier may also be used. Water-soluble or water-dispersible granules are free flowing, non-dusty, and readily water-

soluble or water-miscible. In use by the farmer on the field, the granular formulations, emulsifiable concentrates, flowable concentrates, aqueous emulsions, solutions, etc., may be diluted with water to give a concentration of active ingredient in the range of say 0.1% or 0.2% to 1.5% or 2%.

By far the most frequently used are water-miscible formulations for mixing with water then applying as sprays. Water miscible, older formulations include: emulsifiable concentrate, wettable powder, soluble (liquid) concentrate, and soluble powder. Newer, non-powdery formulations with reduced or no hazardous solvents and improved stability include: suspension concentrate, capsule suspensions, and water dispersible granules. Such formulations are preferably solutions and suspension, e.g., aqueous suspension and solutions, ethanolic suspension and solutions, aqueous/ethanolic suspension and solutions, saline solutions, and colloidal suspensions.

Alternatively, a sprayable wax emulsion formulation may be used. The formulation contains the active ingredient, in an amount from about 0.01% to 75% by weight. The aqueous wax emulsions are broadly described in U.S. Pat. No. 6,001,346, which is hereby incorporated by reference in its entirety. The TRPV inhibitors of the methods described herein can have a viscosity appropriate for use in aerial or backpack spray applications.

The biodegradable wax carrier comprises at least about 10% by weight of the formulation. The biodegradable wax carrier is selected from the group consisting of paraffin, beeswax, vegetable based waxes such as soywax (soybean based), and hydrocarbon based waxes such as Gulf Wax Household Paraffin Wax; paraffin wax, avg. m.p. 53C (hexacosane), high molecular weight hydrocarbons), carnauba wax, lanolin, shellac wax, bayberry wax, sugar cane wax, microcrystalline, ozocerite, ceresin, montan, candelilla wax, and combinations thereof.

Formulations may also contain an emulsifier in an amount from about 1% to about 10% by weight. Suitable emulsifiers include lecithin and modified lecithins, mono- and diglycerides, sorbitan monopalmitate, sorbitan monooleate, sorbitan monolaurate, polyoxyethylene-sorbitan monooleate, fatty acids, lipids, etc. The emulsifiers provide or improve emulsification properties of the composition. The emulsifier can be selected from many products which are well known in the art, including, but not limited to, sorbitan monolaurate (anhydrosorbitol stearate, molecular formula $C_{24}H_{46}O_6$), ARLACEL 60, ARMOTAN MS, CRILL 3, CRILL K3, DREWSORB 60, DURTAN 60, EMSORB 2505, GLYCOMUL S, HODAG SMS, IONET S 60, LIPOSORB S, LIPOSORB S-20, MONTANE 60, MS 33, MS33F, NEWCOL 60, NIKKOL SS 30, NISSAN NONION SP 60, NONION SP 60, NONION SP 60R, RIKEMAL S 250, sorbitan c, sorbitan stearate, SORBON 60, SORGEN 50, SPAN 55, AND SPAN 60; other sorbitan fatty acid ester that may be used include sorbitan monopalmitate,

sorbitan monostearate, sorbitan tristearate, sorbitan monooleate, sorbitan sesquioleate, sorbitan trioleate, sorbitan monooleate, sorbitan trioleate.

In certain embodiments, formulations can include a phagostimulant, such as corn oil, molasses, glycerol, or corn syrup, proteinaceous material (protein or hydrolyzed protein), sugars like sucrose, or food-based ingredients such as trimethylamine, putrescine, bacterial or yeast volatiles or metabolites, ammonium acetate, ammonium carbonate or other ammonia-emitting compounds. Acetic acid vapor can be provided by compounds that produce volatilized acetic acid, for example, aqueous acetic acid, glacial acetic acid, glacial (concentrated) acetic acid, or ammonium producing compounds such as but not restricted to ammonium hydroxide, ammonium carbonate, ammonium bicarbonate, ammonium acetate, etc.

In certain embodiments, the active ingredient may be formulated and/or applied with one or more second compounds. For example, various combinations of TRPV inhibitors and TRPV agonists may be used to obtain greater advantage. For example, both a TRPV inhibitor and TRPV agonist may be applied at the same time. As such in one embodiment, a formulation described herein may include both, a TRPV inhibitor and a TRPV agonist. In one embodiment, two or more active agents may be formulated together. In alternative embodiment, two or more active agents formulated together are all either TRPV inhibitors or are all TRPV agonists. Such combinations may provide certain advantages, such as, without limitation, exhibiting synergistic effects for greater control of insects or non-insect pests, reducing rates of application thereby minimizing any impact to the environment and to worker safety, controlling a broader spectrum of insects and non-insect pests, and improving tolerance by non-pest species, such as mammals and fish. Other second compounds include, without limitation, insecticides, pesticides, plant growth regulators, fertilizers, soil conditioners, or other agricultural and horticultural chemicals. The formulation may include such second compounds in an amount from about 0.002% to about 25% by weight of the composition.

In certain embodiments, the formulations of the present invention may contain visual attractants, e.g. food coloring.

A variety of additives may also be incorporated into the formulation. These additives typically change and/or enhance the physical characteristics of the carrier material and are, therefore, suitable for designing compositions having specific requirements as to the release rate and amount of the active ingredient, protection of the wax composition from weather conditions, etc. These additives are, among others, plasticizers, volatility suppressants, antioxidants, lipids, various ultraviolet blockers and absorbers, or antimicrobials, typically added in amounts from about 0.001% to about 10%, more typically between 1-6%, by weight.

Plasticizers, such as glycerin or soy oil affect physical properties of the composition and may extend its resistance to environmental destruction.

Antioxidants, such as vitamin E, BHA (butylated hydroxyanisole), BHT (butylated hydroxytoluene), and other antioxidants which protect the bioactive agent from degradation, may be added in amounts from about 0.1% to about 3%, by weight.

Ultraviolet blockers, such as beta-carotene, lignin or p-aminobenzoic acid protect the bioactive agents from light degradation may be added in amounts from about 1% to about 3%, by weight.

Antimicrobials, such as potassium sorbate, nitrates, nitrites, and propylene oxide, protect the bioactive agents from microbial destruction may be added in amounts from 0.1% to about 2% by weight.

Adjuvants can also be added to the formulation. An "adjuvant" is broadly defined as any substance added to the spray tank, separate from the insecticide formulation that will improve the performance of the insecticide. These may include, but are not limited to: wetter-spreaders, stickers, penetrants, compatibility agents, buffers, and so on.

Other compounds and materials may also be added provided they do not substantially interfere with the activity of active ingredient. Whether or not an additive substantially interferes with the active ingredient's activity can be determined by standard test formats, involving direct comparisons of efficacy of the composition of the active ingredient without an added compound and the composition of the active ingredient with an added compound.

It was discovered that an insect will stop eating after ingesting a TRP and/or TRPV channel activating compound. For example ingesting a TRPV ion gated channel agonist can cause an insect to stop eating. Thus, in one embodiment, the compounds may be formulated with a food source for insects, e.g., formulated with compounds in insect diet. In another embodiment, the compounds may be formulated with sucrose. Without wishing to be bound by theory, the insect will feed on such mixtures and stop eating.

In certain embodiments, the active agent may be applied to feeding locus of insects. This inhibits insect feeding leading to starvation of insects. In one embodiment, the active agent is applied as a spray to locus of insects, e.g., feeding locus. The active agent may be applied to the insect and/or pest (mollusk, nematode and/or arthropod) feeding source, used in bait or traps, and or directly applied to the pest itself.

In one embodiment, the active agent may be applied to insect traps. For example, the trap may be coated with the active agent or trap may be loaded with insect food comprising an active agent.

The nucleic acid sequences of Nanchung and Inactive subunits of the TRPV channel as well as the corresponding amino acid sequences, their origins and accession numbers (if available) are summarized in Table 1 below. Upon co-expression of the Nanchung and Inactive proteins in a cell, a functional TRPV channel may be formed.

Table 1.

SEQ ID NO.	DESCRIPTION	ORGANISM	ACCESSION NO.
1	Nanchung DNA	*Drosophila melanogaster*	NM_140439.3
2	Nanchung DNA	*Drosophila melanogaster*	NM_001274904.1
3	Nanchung DNA	*Musca domestica*	XM_005180432
4	Nanchung DNA	*Ceratitis capitata*	XM_004537685.1
5	Nanchung DNA	*Anopheles gambiae*	XM_320300.4
6	Nanchung DNA	*Aedes aegypti*	XM_001652374.1
7	Nanchung DNA	*Culex quinquefasciatus*	XM_001847084
8	Nanchung DNA	*Tribolium castaneum*	XM_962803.1
9	Nanchung DNA	*Bombyx mori*	XM_004923013.1
10	Nanchung DNA	*Anopheles darlingi*	gi|312376269
11	Nanchung DNA	*Acyrthosiphon pisum*	XM_001947872.2
12	Nanchung DNA	*Dendroctonus ponderosae*	gi|459669722
13	Nanchung DNA	*Harpegnathos saltator*	gi|307201159
14	Nanchung DNA	*Nasonia vitripennis*	XM_001606052.2
15	Nanchung DNA	*Megachile rotundata*	XM_003706124.1
16	Nanchung DNA	*Apis mellifera*	XM_625167.3
17	Nanchung DNA	*Apis florea*	XM_003689958.1
18	Nanchung DNA	*Pediculus humanus corporis*	XM_002427918.1
19	Nanchung DNA	*Danaus plexippus*	gi|357621160
20	Nanchung DNA	*Solenopsis invicta*	gi|322788678

21	Nanchung DNA	*Acromyrmex echinatior*	gi|332030918
22	Nanchung DNA	*Camponotus floridanus*	gi|307175924
23	Nanchung DNA	*Myzus persicae*	In-house
24	Nanchung DNA	*Bemisia tabaci*	In-house
25	Nanchung DNA	*Euschistus heros*	In-house
26	Nanchung DNA	*Nilaparvata lugens*	In-house
27	Nanchung DNA	*Schistocerca americana*	In-house
28	Inactive DNA	*Drosophila melanogaster*	NM_132125.1
29	Inactive DNA	*Musca domestica*	XM_005180960.1
30	Inactive DNA	*Ceratitis capitata*	XM_004529418.1
31	Inactive DNA	*Aedes aegypti*	XM_001659838.1
32	Inactive DNA	*Culex quinquefasciatus*	XM_001864290.1
33	Inactive DNA	*Anopheles gambiae*	XM_310685.5
34	Inactive DNA	*Tribolium castaneum*	TC012368
35	Inactive DNA	*Megachile rotundata*	XM_003704618.1
36	Inactive DNA	*Apis mellifera*	XM_001121881.2
37	Inactive DNA	*Apis florea*	XM_003690679.1
38	Inactive DNA	*Pediculus humanus corporis*	XM_002432337.1
39	Inactive DNA	*Acromyrmex echinatior*	gi|332020355
40	Inactive DNA	*Harpegnathos saltator*	gi|307206889
41	Inactive DNA	*Bombus impatiens*	XM_003485651.1
42	Inactive DNA	*Bombus terrestris*	XM_003396143.1
43	Inactive DNA	*Dendroctonus ponderosae*	gi|478256802
44	Inactive DNA	*Nasonia vitripennis*	XM_001602538.2
45	Inactive DNA	*Camponotus floridanus*	gi|307168683

46	Inactive DNA	*Danaus plexippus*	gi|357618515
47	Inactive DNA	*Bombyx mori*	XM_004925264.1
48	Inactive DNA	*Acyrthosiphon pisum*	XM_001950061.2
49	Inactive DNA	*Solenopsis invicta*	GL767538.1
50	Inactive DNA	*Schistocerca americana, DNA partial*	In-house
51	Inactive DNA	*Myzus persicae*	In-house
52	Inactive DNA	*Bemisia tabaci*	In-house
53	Inactive DNA	*Euschistus heros*	In-house
54	Nanchung PROT	*Drosophila melanogaster*	NP_648696.2
55	Nanchung PROT	*Drosophila melanogaster*	NP_001261833.1
56	Nanchung PROT	*Musca domestica*	XP_005180489.1
57	Nanchung PROT	*Ceratitis capitata*	XP_004537742.1
58	Nanchung PROT	*Anopheles gambiae*	XP_320300.4
59	Nanchung PROT	*Aedes aegypti*	XP_001652424.1
60	Nanchung PROT	*Culex quinquefasciatus*	XP_001847136.1
61	Nanchung PROT	*Tribolium castaneum*	XP_967896.1
62	Nanchung PROT	*Bombyx mori*	XP_004923070.1
63	Nanchung PROT	*Anopheles darlingi*	EFR23411.1
64	Nanchung PROT	*Acyrthosiphon pisum*	XP_001947907.2
65	Nanchung PROT	*Dendroctonus ponderosae*	ERL84850.1
66	Nanchung PROT	*Harpegnathos saltator*	EFN81068.1
67	Nanchung PROT	*Nasonia vitripennis*	XP_001606102.2
68	Nanchung PROT	*Megachile rotundata*	XP_003706172.1
69	Nanchung PROT	*Apis mellifera*	XP_625170.3

70	Nanchung PROT	*Apis florea*	XP_003690006.1
71	Nanchung PROT	*Pediculus humanus corporis*	XP_002427963.1
72	Nanchung PROT	*Danaus plexippus*	EHJ73092.1
73	Nanchung PROT	*Solenopsis invicta*	EFZ14282.1
74	Nanchung PROT	*Acromyrmex echinatior*	EGI70573.1
75	Nanchung PROT	*Camponotus floridanus*	EFN65752.1
76	Nanchung PROT	*Myzus persicae*	In-house
77	Nanchung PROT	*Bemisia tabaci*	In-house
78	Nanchung PROT	*Euschistus heros*	In-house
79	Nanchung PROT	*Nilaparvata lugens*	In-house
80	Nanchung PROT	*Schistocerca americana*	In-house
81	Inactive PROT	*Drosophila melanogaster*	NP_572353.1
82	Inactive PROT	*Musca domestica*	XP_005181017.1
83	Inactive PROT	*Ceratitis capitata*	XP_004529475.1
84	Inactive PROT	*Aedes aegypti*	XP_001659888.1
85	Inactive PROT	*Culex quinquefasciatus*	XP_001864325.1
86	Inactive PROT	*Anopheles gambiae*	XP_310685.5
87	Inactive PROT	*Tribolium castaneum*	EFA10736.1
88	Inactive PROT	*Megachile rotundata*	XP_003704666.1
89	Inactive PROT	*Apis mellifera*	XP_001121881.1
90	Inactive PROT	*Apis florea*	XP_003690727.1
91	Inactive PROT	*Pediculus humanus corporis*	XP_002432382.1
92	Inactive PROT	*Acromyrmex echinatior*	EGI60788.1
93	Inactive PROT	*Harpegnathos saltator*	EFN84766.1
94	Inactive PROT	*Bombus impatiens*	XP_003485699.1

95	Inactive PROT	*Bombus terrestris*	XP_003396191.1
96	Inactive PROT	*Dendroctonus ponderosae*	ERL85467.1
97	Inactive PROT	*Nasonia vitripennis*	XP_001602588.2
98	Inactive PROT	*Camponotus floridanus*	EFN61724.1
99	Inactive PROT	*Danaus plexippus*	EHJ71463.1
100	Inactive PROT	*Bombyx mori*	XP_004925321.1
101	Inactive PROT	*Acyrthosiphon pisum*	XP_001950096.1
102	Inactive PROT	*Solenopsis invicta*	EFZ13594.1
103	Inactive PROT	*Schistocerca americana, DNA partial*	In-house
104	Inactive PROT	*Myzus persicae*	In-house
105	Inactive PROT	*Bemisia tabaci*	In-house
106	Inactive PROT	*Euschistus heros*	In-house

Adenovirions, which include the adenovirus expression vectors of the present invention, can be produced using the following methodology. Adenovirons may be used to generate cells used to express the proteins of interest, for example, Nanchung, Inactive, TRP and/or TRPV proteins.

The methods of creating an adenovirus generally involves the steps of introducing the vector containing the gene of interest (e.g., Nan or Iav) into a producer cell. The vector containing the gene of interest may be introduced into the producer cell using standard transfection techniques known to one of skill in the art (Zoltukhin et al., Gene Therapy, 6:973-985, 1999). The adenovirus produced by producer cells (packaging cells) are used to transduce a cell of interest. The cell of interest produces the desired proteins.

Preferably, the adenovirions are added to the cells at the appropriate multiplicity of infection according to standard transduction methods appropriate for the particular target cells. Titers of adenovirions to administer can vary, depending upon the target cell type and the particular viral vector, and may be determined by those of skill in the art without undue experimentation.

The cell line may be an insect cell line, such as Sf9 (ATCC# CRL-1711) or Schneider 2 (S2) cells (Life Technologies, #R690-07) (if needed, to introduce a gene of interest into an insect cell transfection techniques may be used among others), African clawed frog (Xenopus laevis) oocytes (to introduce a gene of interest injection techniques may be used), or a mammalian cell line, such as mouse, hamster, human cell line, (to introduce a gene of interest into a mammalian cell several techniques may be used, including but not limited to transfection, adenoviruses, retroviruses, and/or electroporation, etc…) or any other cell line that does not normally expresses Nanching and Inactive proteins. One example of a mammalian cell line suitable for use with the vector expression system of the present invention includes Chinese hamster ovary (CHO-K1) cells (ATCC# CCL-61).

In certain embodiments, the cell line co-expresses the Nanchung and Inactive proteins at a ratio of 3:1, 2:1, 1:1, 1:2, and 1:3. Preferably, the cell line co-expresses the Nanchung and Inactive proteins at a ratio of 1:1.

In some embodiments, a cell expressing a recombinant nucleic acid sequence encoding a TRPV channel is a cell that has been transformed with an expression vector comprising a nucleotide sequence encoding an insect TRPV channel such as, but not limited to the TRPV channel proteins discloses herein. Methods for transforming cells that would be known to one of ordinary skill in the art include, but are not limited to, infection using viral vectors, lipofection, electroporation, particle bombardment, and transfection. Detailed procedures for representative methods can be found in Sambrook & Russell, 2001, and references cited therein. Useful expression vectors and methods of introducing such vectors into cells or expression of the encoded polypeptide are also known to one of ordinary skill in the art. For example, a plasmid expression vector can be introduced into a cell by calcium-phosphate mediated transfection, DEAE-Dextran-mediated transfection, lipofection, polybrene- or polylysine-mediated transfection, electroporation, or by conjugation to an antibody, gramicidin S, artificial viral envelopes, or other intracellular carriers. A viral expression vector can be introduced into a cell in an expressible form by infection or transduction, for example, or by encapsulation in a liposome.

When a cell expressing a recombinant nucleic acid sequence encoding an insect TRPV channel gene product has been produced, these cells can then be employed in testing candidate compounds for an ability to modulate ion transport in the cell through the TRP and/or TRPV channel. The exemplary methods for testing ion transport in the cells were described above as well as presented in the Examples sections below. Other applicable methods would be known to those of skill in the art upon consideration of this disclosure.

EXAMPLES

The following Examples provide illustrative embodiments. In light of the present disclosure and the general level of skill in the art, those of skill will appreciate that the following Examples are intended to be exemplary only and that numerous changes, modifications, and alterations can be employed without departing from the scope of the presently disclosed subject matter.

MODULATION EXAMPLES FPR AFIDOPYROPEN

Example I: Afidopyropen and pymetrozine elicit characteristic hind leg extension in grasshoppers.

Injection of pymetrozine (PM), was shown to produce characteristic hind leg extension in locusts (*Locusta migratoria*), a phenomenon which was attributed to silencing mechanosensory neurons in femoral chordotonal organs (Ausborn et al., 2005). In the current invention, the Inventors tested whether afidopyropen targeted insect chordotonal organs in similar fashion, by injecting this compound into American grasshoppers (*Schistocerca americana*), and found than this injection elicited hind leg extension similarly to pymetrozine (Figure 2), which suggested that pymetrozine and afidopyropen may act on the same molecular target.

Example II : Afidopyropen activates *Drosophila* TRPV channels.

Pymetrozine (PM), pyrifluquinazon and N-deacetylated pyrifluquinazon (dPFQ) elicited calcium mobilization and membrane depolarization in CHO cells (hamster cells) co-infected with adenoviruses expressing insect TRPV channels, Nan and Iav (Nesterov et al., 2013; Nesterov et al., 2015). Using the same approach, the inventors found afidopyropen evoked similar responses in cells co-infected with adenoviruses expressing insect TRPV channels, Nan and Iav. Two different assays were used in these studies: one (Figure 3) monitored calcium mobilization with calcium probe , fluo-4 (Marshall et al., 2013); whereas another one, (Figure 4), measured agonist-induced depolarization of plasma with florescent voltage indicator (Zheng et al., 2004). In both assays, afidopyropen, pymetrozine and N-deacetylated pyrifluquinazon triggered calcium mobilization and membrane depolarization responses only in cells co-infected with Nan and Iav viruses, but not in parental cells (e.g. the hamster cells that weren't infected with Nan and/or Iav), nor in cells expressing Nan and/or Iav alone. In the calcium mobilization assay, dose-dependence curves (Figure 5) yielded the half-maximal effective concentrations (EC_{50}) of 1.0 nM, 64 nM, and 51 nM for afidopyropen, N-deacetylated pyrifluquinazon, and pymetrozine, respectively.

Example III : N-deacetylated pyrifluquinazon activates TRPV channels from pea aphid

To determine whether activation of TRPV channels from other insect species also requires simultaneous presence of Nan and Iav subunits atwo-electrode voltage clamp electrophysiology was used to measure channel opening in *Xenopus laevis* (frog) oocytes injected with Nan and Iav mRNA from pea aphid, *Acyrthosiphon pisum.* Current-voltage tests were performed, where currents were measured over a range of holding potentials. N-deacetylated pyrifluquinazon evoked both inward and outward current responses only in oocytes expressing both Nan and Iav (Figure 4a), but neither Nan no Iav alone.

Example IV: Afidopyropen does not activate mammalian TRPV4 channel.

To gain insight into receptor species specificity of afidopyropen effects, CHO cells (hamster cells) were transduced with the adenovirus expressing mouse TRPV channel, mTRPV4. As shown on Figure 6, the TRPV4 agonist GSK1016790A (Thorneloe et al., 2008), evoked strong calcium response in these cells, whereas afidopyropen failed to activate mTRPV4-expressing cell. GSK1016790A is a known strong agonist of the TRPV4 channel. Accordingly, the inventors found that afidopyropen was a species-specific insecticide, in that it was a modulator of insect TRPV channels but did not modulate the mammalian TRPV4 channel. TRPV4 channel is one of the closest orthologues of the insect TRPV channel. It was chosen to be used based on sequence similarity and the availability of a known agonist.

DIRECT BINDING EXAMPLES

Example V: Afidopyropen directly binds insect TRPV channel

Specific binding of tritium-labeled afidopyropen to membranes prepared from Nan and Iav co-expressing cells exhibited a linear relationship to increasing amounts of membranes, whereas binding to parental cell membranes remained low regardless of the amount of membranes used (Figure 7). Saturation binding (Figure 8) to Nan-Iav membranes revealed the presence of 2 binding sites: one of very high affinity (K_d = 0.032 nM, B_{max} = 87 fmol/mg of membrane proteins), and one of lower affinity (K_d = 2.3 nM, B_{max} = 167 fmol/mg of membrane proteins). In membranes prepared from Nan-only cells, only lower affinity sites were detected (K_d = 2.1 nM, B_{max} = 242 fmol/mg of membrane proteins),whereas no specific binding was observed in membranes prepared from Iav-only cells. From this data, the inventors found that the Nan protein forms the major binding

interface for afidopyropen, whereas the presence of Iav may act as a facilitator to increase binding affinity.

Example VI: Pymetrozine and N-deacetylated form of pyrifluquinazon compete with [^{3}H]-Afidopyropen for binding.

To assess the ability of pymetrozine and N-deacetylated form of pyrifluquinazon to displace [^{3}H]-Afidopyropen from Nan-Iav complexes (Figure 9A), the experiment was performed at low concentration of [^{3}H]- Afidopyropen (0.05 nM), i.e., under conditions where binding of [^{3}H]- Afidopyropen to Nan-only membranes was negligible (Figure 8). Both pymetrozine, N-deacetylated pyrifluquinazon and unlabeled Afidopyropen, completely displaced [^{3}H]- Afidopyropen from the high affinity sites with simple kinetics (Hill values ≈ -1), indicating that all three compounds tested share the same binding site. Noteworthy, for unlabeled Afidopyropen, K_i value of 60 pM measured in displacement assay (Figure 9A) came close to K_d value of 32 pM obtained for [^{3}H]- Afidopyropen in saturating binding experiments (Figure 8), with less than a two-fold difference, which illustrates close similarity for these two values. N-deacetylated pyrifluquinazon and pymetrozine exhibited significantly lower binding affinities than that of Afidopyropen, with K_i values of 9 nM and 50 nM for N-deacetylated pyrifluquinazon and pymetrozine, respectively, which correlates with lower potencies of these compounds in the functional assay (Figure 5). Based on this data, the inventors found that afidopyropen directly binds to the same site as pymetrozine and dPFQ, which means these three compounds have the same mode of action.

Displacement of [^{3}H]- Afidopyropen from Nan-only expressing membranes (Figure 9B) with unlabeled Afidopyropen yielded K_i value of 3.1 nM, which is close to the K_d value of 2.1 nM calculated from saturation binding with [^{3}H]- Afidopyropen (Figure 8). Although pymetrozine and N-deacetylated pyrifluquinazon clearly displaced [^{3}H]-afidopyropen from Nan-only sites, poor solubility of these compounds at high concentrations, prevented competition binding curves from reaching the bottom plateaus, hampering accurate determination of their K_i values. Nevertheless, all three compounds clearly exhibited the same potency ranking (Afidopyropen >_N-deacetylated pyrifluquinazon≥pymetrozine) for low affinity Nan-only sites as for high affinity Nan-Iav complexes. It appears, therefore, that co-expression of Iav protein increases binding affinities for all 3 insecticides, despite significant structural differences between Afidopyropen on one hand, and pymetrozine and N-deacetylated pyrifluquinazon on the other hand (Figure 1). The inventors found that the presence of Inactive protein increased binding affinity for N-deacetylated pyrifluquinazon and pymetrozine, in addition to afidopyropen.

In summary, using the combination of functional and binding assays in the examples above, the inventors demonstrated the following: i) the insect TRPV channel is a direct molecular target of the candidate insecticide, Afidopyropen; ii) Afidopyropen binding site in TRPV protein is shared with two commercial insecticides, pymetrozine and N-deacetylated pyrifluquinazon indicating the same mode of action of all three compounds; iii)binding affinities of all three compounds were measured; iv) Nanchung protein forms the main binding interface for all three compounds, whereas presence of Inactive protein increases binding affinity.(v) new methods were developed which can be used for identifying candidate compounds that may be used as insecticides which act by directly targeting insect TRPV channels (vi) afidopyropen may be used in these methods to assist in the identification of new candidate compounds having same mode of action.

Pymetrozine and GSK10116790A were obtained from Sigma, pyrifluquinazon from ChemService Inc., (West Chester, PA), N-deacetylated pyrifluquinazon from Wako Pure Chemical Industries, LTD (Richmond, VA), and Afidopyropen was synthesized at BASF. Tritium labeled Afidopyropen (19 Ci/mmol) was custom-made by RC TRITEC AG (Teufen, Germany).

Leg extension assay

American grasshoppers (*Schistocerca americana*) were obtained from Dr. Hojun Song (University of Central Florida). Test compounds (10 mM in 100% DMSO), or vehicle (100% DMSO) were applied by injection through the abdominal intersegmental cuticle (3 µl per animal), using Hamilton syringe. The effects of compounds were assessed 40-60 minutes post-injection.

Heterologous expression of Nan and Iav in CHO-K1 cells

To produce Nan, Iav and mTRPV4 with fused FLAG tag and AcGFP fluorescent protein at their carboxyl termini, complementary DNAs (cDNAs) encoding *Drosophila* Nan (NCBI NM_001274904.1) and Iav (NCBI NM_132125.1) were synthesized by Life Technologies (Grand Island, NY), with the addition of sequences encoding FLAG antibody tags at the C-termini. cDNA for mouse TRPV4 (NCBI NM_001274904.1) containing a C-terminal FLAG epitope sequence was purchased from Origene (Rockville, MD). Insect cDNAs were codon-optimized for expression in mammalian cells. The Nan-FLAG and Iav–FLAG cDNAs were subcloned into the Bgl II and HindIII sites of the modified pAcGFP1-Hyg-N1 vector (Clontech, Kyoto, Japan), which contained a FLAG tag at the C-terminus of the AcGFP moiety (pAcGFP1-Hyg-N1-FLAG). The mTRPV4-FLAG cDNA was PCR amplified using the primers 5'-GGACTTTCCAAAATGTCG-3' (SEQ ID NO:108) and 5'-

CCGGCCGTTTATCACTACAGAATTCGAAGCTTAACCTTATCGTCGTCATCCTTGT A-3' (SEQ ID NO: 109), subsequently digested with BglII and HindIII, and sub-cloned into the pAcGFP1-Hyg-N1-FLAG vector. These cloning procedures added an AcGFP protein flanked by two FLAG epitope tags to the carboxyl termini of each Nan, Iav and mouse TRPV4.

To produce Nan with fused HA epitopes and mCherry fluorescent protein at its carboxyl terminus, codon-optimized *nan* cDNA was PCR amplified using the primers 5'-GCTGGTTTAGTGAACCGTCAG-3' and 5'-CCGCGGTACCGTCGACTGCAGAATTCGAAGCTTAGCGTAATCTGGAACATCGTA TGGGTAGAAGTTGTTGTTGTCGCTGCACTCGGACTTGGG-3', adding an HA epitope tag to the C-terminus of Nan. The PCR product was digested with XhoI and HindIII, and subcloned into the modified pmCherry-N1 vector (Clontech), which contained an HA tag at the C-terminus of the mCherry moiety. This cloning procedure added mCherry protein flanked by two HA epitope tags to the C-terminus of Nan.

To produce adenoviruses, epitope-tagged Nan and Iav were digested with XhoI and NotI and subcloned to the same sites of the adenovirus shuttle vector pENTCMV1-TetO (Welgen Inc., Worceter, MA). Epitope-tagged mTRPV4 was digested with BglII, blunt-ended with Klenow and digested with XbaI. The fragment was subcloned into PmeI and XbaI sites of the pENTCMV1-TetO. pENTCMV1-TetO vectors containing tagged Nan, Iav or mTRPV4 expression constructs were treated with LR Clonase II (Life Technologies) and ligated to a pAdREP plasmid (Welgen), which contains the remaining adenovirus genome. The pENTCMV1-TetO vector contains two Tet repressor binding sites within a modified CMV promoter, which repress transcription of the gene of interest in cells expressing the Tet repressor. The recombination products were transformed into *Escherichia coli* cells, positive clones were selected, and the cosmid DNA was isolated. The cosmid DNA was digested with Pac I and then transfected into HEK293-TetR cells, which produce the Tet repressor (Postle et al., 1984), preventing expression of TRP channels by the adenovirus packaging cells. Adenoviruses were purified from large-scale cultures and viral titers were calculated as viral particles/mL = Absorption at 260 nm x 1.1x 10^{14}.

<u>Heterologous expression of Nan and Iav in frog (*Xenopus laevis*) oocytes</u>

Nan and Iav coding sequences were RT-PCR amplified from pea aphid (*Acyrthosiphon pisum*) antennal total RNA using the QIAGEN Onestep RT-PCR Kit (cat# 210212) and the primers nan-Ap start 5'-GCCACCATGGGTAACACCGAGAGCAATG-3', nan-Ap stop 5'-TTATTCATTTGCTTTTAGATTAAATGTCCC-3', iav-Ap start 5'-

GCCACCATGGGAAATTCTTGTGCGAG-3' and iav-Ap stop 5'-TCAGAAATCGTCGTTGGG-3', and cloned into the oocyte expression vector pGH19. Linear cDNA templates for transcription were produced by PCR amplification from these constructs using the vector specific primers 5'-GTTGTAAAACGACGGCCAGTGAATTG-3' and 5'-GACACTATAGAATACTCAAGCTAGCCTCGAGG-3'. These primers were designed to include the T7 promoter and the 3'UTR sequence from the Xenopus globin-XI gene found in pGH19 in the PCR product. The PCR conditions were 1 cycle at 95°C for 4 minutes, 35 cycles with 95 °C for 30 seconds, 55 °C for 30 seconds and 65 °C for 4 minutes, and 1 cycle at 68 °C for 6 minutes.

In vitro transcription was performed with the T7 polymerase mMessage mMachine kit (Ambion). *Xenopus laevis* ovaries were obtained from Xenopus1, Inc. (Dexter, MI). The lobes were partially dissected and digested with collagenase type 1 (Alfa Aesar) dissolved in Oocyte Ringers solution (pH 7.5, in mM: NaCl 82.5, KCl 2, MgCl2 1, HEPES 5) until defolliculated. Defolliculated oocytes were washed with and incubated in ND-96^{+} (pH 7.5, in mM: NaCl 96, KCl 2, MgCl2 1, CaCl2 1.8, HEPES 5, Na Pyruvate 2.5 and Gentamycin 50 ug/mL) for two hours before RNA injection. Stage IV and V oocytes were injected with RNA from Nan, Iav or both using a Nanoject automatic injector (3-00-203-X, Drummond Scientific). For one to one expression of each subunit, 0.15 ng of RNA for each subunit was co-injected in 50 nL of RNAse free water (3 ng/uL). For single subunit RNA injections, 30 ng of RNA was injected in 50 nL (600 ng/uL) water to ensure maximal expression of the single subunit. Prior to any measure or comparison steps, oocytes were incubated at 17°C in ND-96^{+} and the media was changed daily. Further testing steps were made 3 days after RNA injection and/or after sufficient protein production by the oocytes.

Calcium imaging and membrane depolarization assays

Titers of adenoviruses which allow for equal expression levels of recombinant TRP channels, and optimal cell responses were established previously (Nesterov et al., 2015).Hamster CHO-K1 cells (ATCC ® CCL-61TM) were infected with adenoviruses expressing AcGFP-Iav, mCherry-Nan, 1:1 mixture of AcGFP-Iav and mCherry-Nan, (4000 viral particles per cell) or AcGFP-mTRPV4 (400 viral particles per cell). The cells were seeded on poly-D-lysine coated 96-well plates (Greiner Bio-One, Frickenhausen, Germany) in 100 µl of media, at a density of 40,000 cells per well. The cells were kept overnight at 37°C, followed by 3 days at 25°C. The medium was changed two days after seeding. Both

Ca^{2+} mobilization and changes of membrane potential were measured using a FLIPR-TETRA instrument (Molecular Devices, Sunnyvale, CA). Ca^{2+} mobilization was measured using fluo-4AM (Life Technologies). The cells were loaded with 50 µl of Hank's buffered salt solution (HBSS) containing 4 µM fluo-4AM, 5mM probenecid, 20 mM $CaCl_2$, and 0.02% pluoronic for 2 hours at 25oC. The dye was then discarded, 50 µl of HBSS were added. The test compounds were dissolved in DMSO and added to the cells in 50 µl HBSS, yielding a final DMSO concentration of 0.2%. Fluorescence was monitored for 10 minutes at 1 second intervals at 470-495nm/515-575nm excitation/emission wavelengths. Changes of membrane potential were measured using a similar procedure, except that the cells were loaded for 2 hours with a proprietary membrane potential dye (Molecular Devices, Cat # R8042) dissolved in HBSS. The dye loading solution was discarded and replaced with 50 ul of 20mM HEPES, 11.1mM Glucose, 125mM NaCl, and 2.5mM KCl, and 20 mM $CaCl_2$. The test compounds dissolved in DMSO were added to the cells in 50 µl of the same solution, yielding a final DMSO concentration of 0.2%. Fluorescence was monitored for 10 minutes at 1 second intervals at 510-545 nm/565-625 nm excitation/emission.

EC_{50} values were calculated using GraphPad Prism (GraphPad Software).

Two-electrode voltage clamping of *Xenopus laevis* oocytes.

Oocytes were placed in a RC-8 recording chamber (Warner Instruments) filled with ND-96 bath solution (in mM: NaCl 96, KCl 2, MgCl2 1, CaCl2 1.8, and HEPES 5, pH 7.5,). Glass microelectrodes filled with 3 M KCl and with resistances between 0.9-1.4 MΩ were used to voltage clamp the oocytes through a Turbo Tec 10-C amplifier (npi) and ITC-16 computer interface (InstruTech) controlled by PatchMaster recording software v.2x73.5 (HEKA). Oocytes were perfused with ND-96 saline at 2 mL/min (gravity fed). N-deacetylated_pyrifluquinazon (dPFQ) was delivered through the same perfusion line directly over the cell by switching out the bath solution with 10 uM dPFQ diluted in ND-96 and 0.1% DMSO. Between voltage steps, oocytes were held at -20 mV. Every 10 seconds, the voltage was stepped to +40 mV and the current, after equilibration, was measured and plotted over time as chart recordings (Figure 4a). Current voltage relationships for single and co-expressed subunits were determined by measuring currents elicited by stepping the voltage from the holding potential of -20 mV to voltages between -100 through +60 mV. Chart recordings and IV tests were exported from Patchmaster and analyzed and plotted with Prism 6 (GraphPad). Chart recording currents were normalized to the initial current for each cell (I/I_0). N-deacetylated pyrifluquinazon evoked both inward and outward current responses only in oocytes expressing both Nan and Iav (Figure 4a), but neither current responses

inward or outward were evoked in oocytes expressing Nan or Iav alone. Accordingly, a method for determining whether or not a candidate compound may be a modulator of an insect TRPV channel may include providing a first cell expressing an insect TRPV channel, wherein that first cell may be a *Xenopus laevis* oocyte; contacting the first cell with a candidate compound, wherein the candidate compound may be dPFQ; and assaying for modulation of the insect TRPV channel, wherein the modulation identifies the candidate compound as the modulator of the insect TRPV channel and further wherein the assaying step comprises at least of one the following steps: comparing the electrical current between the first cell in the absence of the candidate compound with the electrical current in the first cell in the presence of the candidate compound; and/or comparing the electrical current between the first cell in the presence of the candidate compound and having one or more Nanchung proteins and one or more Inactive proteins with the electrical current of the first cell in the presence of the candidate compound and not having one or more Nanchung proteins and/or one or more Inactive proteins.

Membrane preparation

CHO-K1 cells were transduced with adenoviruses expressing AcGFP-tagged Nan and Iav either alone, or as 1:1 mixture (4000 viral particles per cell). The adenovirus-transduced cells were seeded at 10 x 10^6 cells per T175 flask (Greiner) and kept at 37˚C 18 hrs followed by incubation at 25˚C for 72 hrs. The media was changed at 24 hrs and 72 hrs post transduction. The cells were rinsed twice with PBS, and incubated in Versene solution (Life Technologies) for 10 min at room temperature. Detached cells were pelleted at 300 × g for 10 min and resuspended in 8 mL of ice-cold 20 mM Hepes (pH 7.3) containing 1% (wt/vol) protease inhibitors mixture (Halt; Thermo Fisher). After 10 min on ice, the cells were homogenized by sonication. The samples were centrifuged at 300 × g for 10 min, and supernatants were collected and centrifuged for 2 h at 50,000 × g. Membranes were resuspended in 0.5 mL of 50mM HEPES, 100mM NaCl, 1mM $CaCl_2$, 5mM $MgCl_2$, pH 7.4, and stored at −80°C. Protein content was determined using the Bradford Method.

[^{3}H]- Afidopyropen binding assay

Equilibrium binding assays were performed in the binding buffer (50mM HEPES, 100mM NaCl, 1mM $CaCl_2$, 5mM $MgCl_2$, pH 7.4). The reactions were performed in 96-well U-bottom polypropylene plates. 100 µL membranes resuspended in the binding buffer containing Tween-20 (0.0025% final concentration in the assay), were combined with either 200 µl (saturation binding experiments), or 800 µl (ligand displacement experiments) of binding buffer containing [^{3}H]- afidopyropen, dissolved in ethanol, and, where indicated, test

compounds, dissolved in DMSO. The final concentrations of ethanol and DMSO were kept at 0.2% and 0.25% respectfully in both saturation binding and competition experiments. Typically, 60-100 μg of membranes were used per data point. Followed by 3 hours of incubation at room temperature, assay mixes were filtered through Multiscreen HTS+ 96 Hi Flow FC filters (EMD Millipore), pre-wetted with 0.1% polyethyleneimine. Filters were washed three times with 200 μl of ice-cold binding buffer, scintillation cocktail was added and radioactivity was measured using Wallac 1450 Microbeta counter. Non-specific binding was measured in the presence of 500-fold excess of unlabeled Afidopyropen. Typically, ligand depletion accounted for less than 10% of total ligand. In saturation binding studies, at the lowest concentrations of [^{3}H]-afidopyropen, equal to 49 pM and 97.7 pM, ligand depletion was 19% and 14%, respectfully. That was corrected by assuming that concentration of free ligand was equal to total minus bound concentration. Nonlinear regression analysis was performed using GraphPad Prism (GraphPad Software), and K_i values were calculated by Cheng-Prusoff method (Cheng and Prusoff, 1973).

It is therefore intended that the foregoing detailed description be regarded as illustrative rather than limiting, and that it be understood that it is the following claims, including all equivalents, that are intended to define the spirit and scope of this invention.

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CLAIMS

1. A method for determining whether a compound binds directly to one or more Nanchung proteins, comprising:

(a) providing one or more Nanchung proteins;

(b) contacting the one or more Nanchung proteins with one or more compounds; and

(c) determining the binding affinity of the one or more compounds to the one or more Nanchung proteins.

2. The method of claim 1, further comprising one or more TRP proteins, wherein the one or more TRP proteins form a complex with the one or more Nanchung proteins.

3. The method of claim 2, wherein the one or more TRP proteins are one or more TRPV proteins.

4. The method of claim 3, wherein the one or more TRPV proteins is an Inactive protein.

5. The method of claims 1-4, wherein the one or more Nanchung proteins form one or more TRP and/or TRPV channels.

6. The method of claim 5, further wherein the one or more TRP and/or TRPV channels are insect TRP and/or TRPV channels.

7. The method of claims 1-6, wherein the one or more compounds includes at least one candidate compound.

8. The method of claim 7, wherein the candidate compound is a labeled compound.

9. The method of claims 1-7, wherein the one or more compounds includes at least one labeled compound and at least one candidate compound.

10. The method of claim 9, wherein the labeled compound has a high binding affinity to the one or more Nanchung proteins.

11. The method of claim 10, wherein the binding affinity is determined using one or more equilibrium binding constants, including K_d and/or K_i.

12. The method of claims 9-11, wherein the binding affinity of the labeled compound to the one or more Nanchung proteins has an equilibrium dissociation constant (K_d) of less than or equal to $3x10^{-7}$ M

13. The method of claims 9-12, wherein the binding affinity of the labeled compound to the one or more Nanchung proteins has an equilibrium dissociation constant (K_d) of less than or equal to $3x10^{-8}$ M

14. The method of claims 9-13, wherein the binding affinity of the labeled compound to the one or more Nanchung proteins has an equilibrium dissociation constant (K_d) of less than or equal to $30x10^{-12}$ M

15. The method of claims 1-14, wherein at least one of the one or more compounds are labeled with a tritium isotope.

16. The method of claim 15, wherein the labeled compound is afidopyropen.

17. A method for classifying a compound, comprising:

(1) a binding assay step, wherein one or more Nanchung proteins are contacted by one or more candidate compounds and determining the binding affinity for the one or more candidate compounds to the one or more Nanchung proteins,

(2) identifying a mode of action classification for the insecticide compound comprising the compound.

18. The method of claim 17, wherein the method for classifying a candidate compound further comprises:

a modulator assay step, wherein one or more TRP and/or TRPV channels are contacted with one or more candidate compounds and an assay is used to determine whether the one or more candidate compounds acts as a modulator of the one or more TRP and/or TRPV channels.

19. The method of claim 17-18, wherein the binding step comprises one or more of the following steps:

(a) providing one or more of the following: Nanchung proteins, Inactive proteins, TRP and/or TRPV proteins, protein complexes and/or channels;

(b) contacting the one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels with one or more compounds;

(c) measuring the amount of the one or more compounds which are bound to the one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels;

(d) calculating the equilibrium disassociation constant (K_d) for the one or more compounds;

(e) wherein the K_d may be determined using one or more of the following methods: (I)(a) maximum binding (B_{max}) and (b) the concentration of compound needed to reach 50% of maximum binding, (II) measuring association (Kon) and dissociation (Koff) rates of the compound where Kd=Koff/Kon, (III) fluorescence polarization assay, (IV) surface plasmon resonance, (V) isothermal calorimetry, (VI) Schild analysis.

(f) contacting the one or more Nanchung proteins, TRP , and/or TRPV protein complexes and/or channels with a labeled compound having high affinity to the one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels;

(g) contacting the one or more one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels with at least one candidate compound in the presence of the one or more labeled compounds;

(h) increasing the amount of the at least one candidate compound available to contact the one or more Nanchung proteins, TRP, and/or TRPV protein complexes and/or channels until binding of the labeled compound is near 0%;

(i) calculating the equilibrium inhibition constant (K_i) and/or the equilibrium dissociation constant (K_d) for competition assay using one or more of the following methods: (I) (a) determining amount of bound labeled compound in the absence of the candidate compound and (b) determining concentration of the candidate compound that is required to reduce the amount of bound labeled compound by 50%, (II) fluorescent polarization assay, and/or (III) Schild analysis;

(j) comparing the inhibition constant of the candidate compounds to other candidate compounds inhibition constants;

(k) comparing the inhibition constant of the candidate compounds to the disassociation consonant of the labeled compound.

(l) identifying one or more candidate compounds having a high affinity to the one or more Nanchung proteins, Inactive proteins, TRP and/or TRPV proteins, protein complexes and/or channels.

20. The method of any of claims 18, wherein the candidate compound is a modulator that inhibits insect feeding behavior.

21. The method of any of claims 1-20, wherein the candidate compound is selected from the group consisting of small organic molecule, small inorganic molecule, polysaccharides, peptides, proteins, nucleic acids, an extract made from biological materials, and any combination thereof.

22. A method for determining whether a candidate compound binds directly to a mammalian TRP and/or TRPV protein, comprising:

(a) providing one or more mammalian TRP and/or TRPV protein;

(b) contacting the one or more mammalian TRP and/or TRPV proteins with a one or more compounds;

(c) calculating the binding affinity of the one or more compounds to the one or more mammalian TRP and/or TRPV proteins; and

(d) comparing the binding affinity of the one or more compounds to the one or more mammalian TRP and/or TRPV proteins with the binding affinity of the one or more compounds to the insect TRP and/or TRPV protein complexes, wherein an increased binding affinity of the one or more compounds to the insect TRP and/or TRPV protein complexes relative to the mammalian one or more TRP and/or TRPV proteins identifies the one or more compounds as selectively binding to the insect TRP and/or TRPV protein complexes, wherein the binding affinity is determined using one or more equilibrium binding constants, including K_d and/or K_i.

23. The method of claim 22, wherein the one or more compounds includes one or more candidate compounds.

24. The method of claim 23, wherein the one or more compounds includes one or more labeled compounds.

25. The method of claim 24, wherein the labeled compounds, includes one or more candidate compounds.

26. The method of claim 24-25, wherein the one or more labeled compounds are labeled with a tritium isotope.

27. The method of claim 26, wherein the one or more compounds has increased binding affinity to the one or more Nanchung proteins, wherein the the K_i or K_d is 10 times lower relative to the mammalian TRP protein

28. A composition comprising one or more compounds that directly bind to one or more insect TRPand/or TRPV protein complexes.

29. A composition comprising one or more compounds selected by the method of any of claims 1-28.

30. The composition of claims 28-29, wherein the one or more compounds acts as a modulator for one or more insect TRP and/or TRPV channels.

31. The composition of claims 28-30, wherein the one or more compounds act as a modulator that inhibits a feeding behavior of an insect.

32. The composition of any of claims 28-31, wherein the one or more compounds comprises afidopyropen.

33. A method of insect control comprising applying the composition of claims 28-32 to one or more of: an insect, an insect habitat, baits, traps and/or an insect feeding source.

34. The method of claim 33, wherein the compound is an inhibitor of an insect TRP channel.

35. The method of claims 33-34, wherein the compound is an activator of an insect TRP channel.

36. The method of any of claims 33-35, wherein the insect is an agricultural/horticultural pest or a disease vector or a parasite.

37. The method of claim 36, wherein the agricultural pest is selected from the group consisting of Aphids (including *Aphis fabae, Aphis gossypii, Aphis pomi, Aulacorthum solani, Brevicoryne brassicae, Dysaphis plantaginea, Macrosiphum euphorbiae, Macrosiphum euphorbiae, Macrosiphum rosae, Myzus persicae, Nasonovia ribisnigri*); Whiteflies (including *Aleurodes spp., Bemisia spp., Dialeurodes spp., Trialeurodes spp.*); Planthoppers (*including Laodelphax striatellus, Nilaparvata lugens, Siphanta spp., Sogatella furcifera*); Leafhoppers

(including *Amrasca spp., Empoasca spp.*); Scales (including *Aspidiotus spp., Chrysomphalus aonidum, Icerya purchase, Unaspis citri*); Mealybugs (including *Maconellicoccus spp., Paracoccus spp., Planococcus spp.*); Pollen beetles (including *Carpophilus spp., Meligethes spp.*); Thrips (including *Caliothrips spp., Frankliniella spp., Scirtothrips spp., Thrips spp.*); and Psyllids (including *Bactericera spp., Cacopsylla spp., Diaphorina citri, Paratrioza cockerelli*).

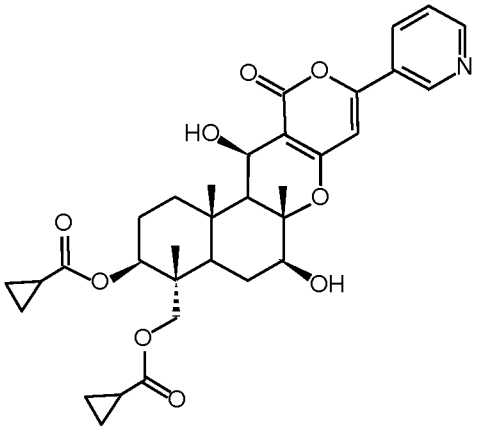
38. A method for determining whether a compound binds directly to the same site on one or more Nanchung proteins, comprising:

(a) providing one or more Nanchung proteins;

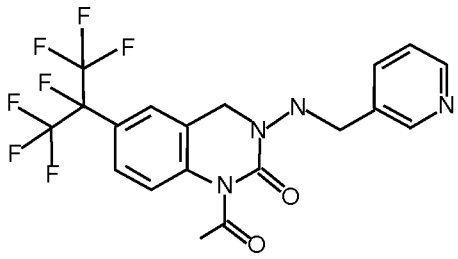
(b) contacting the one or more Nanchung proteins with one or more compounds, wherein the one or more compounds is selected from the group consisting of: afidopyropen, pymetrozine, pyrifluquinazon and/or N-deacetylated_pyrifluquinazon;

(c) contacting the one or more Nanchung proteins with one or more candidate compounds; and

(c) determining the binding affinity of the one or more candidate compounds to the one or more Nanchung proteins.

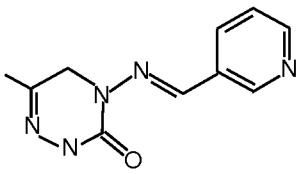


Afidopyropen (AP)
CAS No:915972-17-7

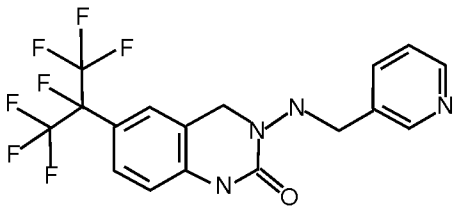


Pyrifluquinazon (PFQ)
CAS No: 337458-27-2

Hydrolysis



Pymetrozine (PM)
CAS No: 123312-89-0



Deacetylated
pyrifluquinazon (dPFQ)
CAS No: 337457-78-0

Figure 1. Chemical structures of test compounds

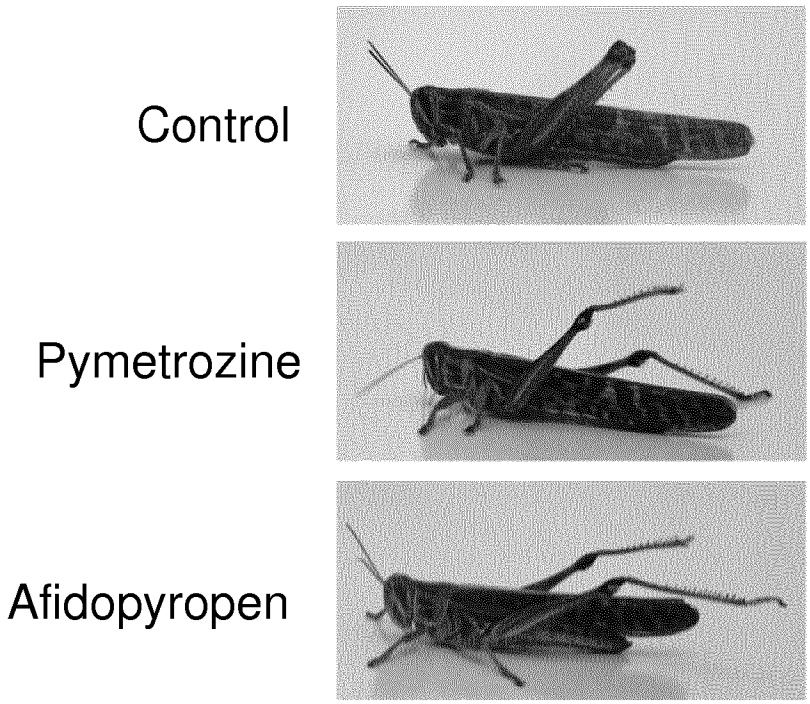


Figure 2. Afidopyropen and pymetrozine cause similar symptoms in American grasshoppers. Injection of either pymetrozine or afidopyropen causes characteristic hind leg extension, a phenomenon which was attributed to interference wit function of femoral chordotonal organs

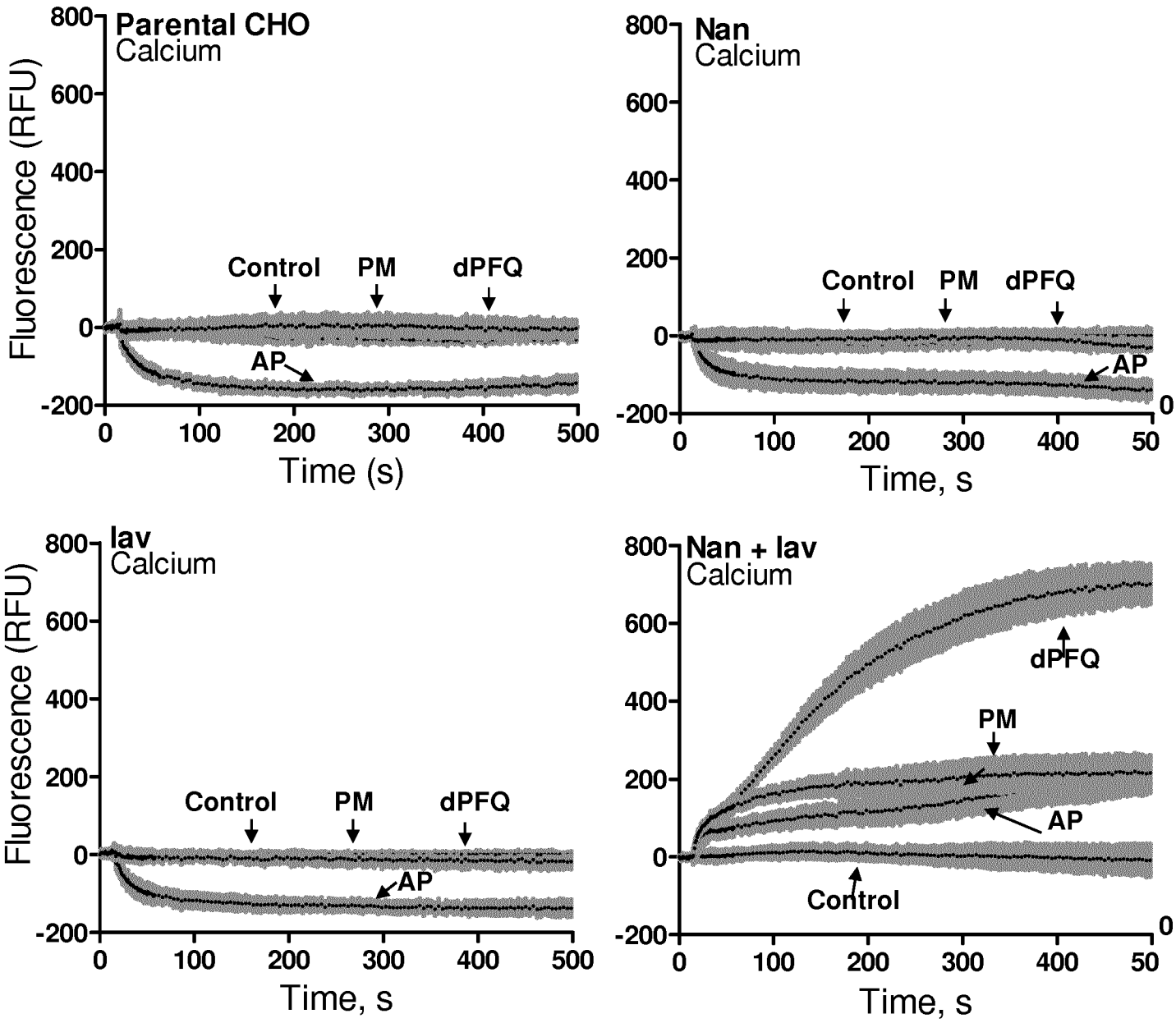


Figure 3. Afidopyropen evokes calcium response in Nan-lav co-expressing cells. Afidopyropen (AP), pymetrozine (PM), and N-deacetylated form of pyrifluquinazon (dPFQ) evoke calcium signals (relative fluorescence units, RFU) in CHO cells co-expressing Nan and lav but not parental cells nor cells expressing Nan or lav alone (averages (lines) ± 1 S.D. (areas) of 4 repetitions. All three insecticides were used at 10 μM. Calcium mobilization was monitored using calcium sensitive fluorescent indicator, fluo-4.

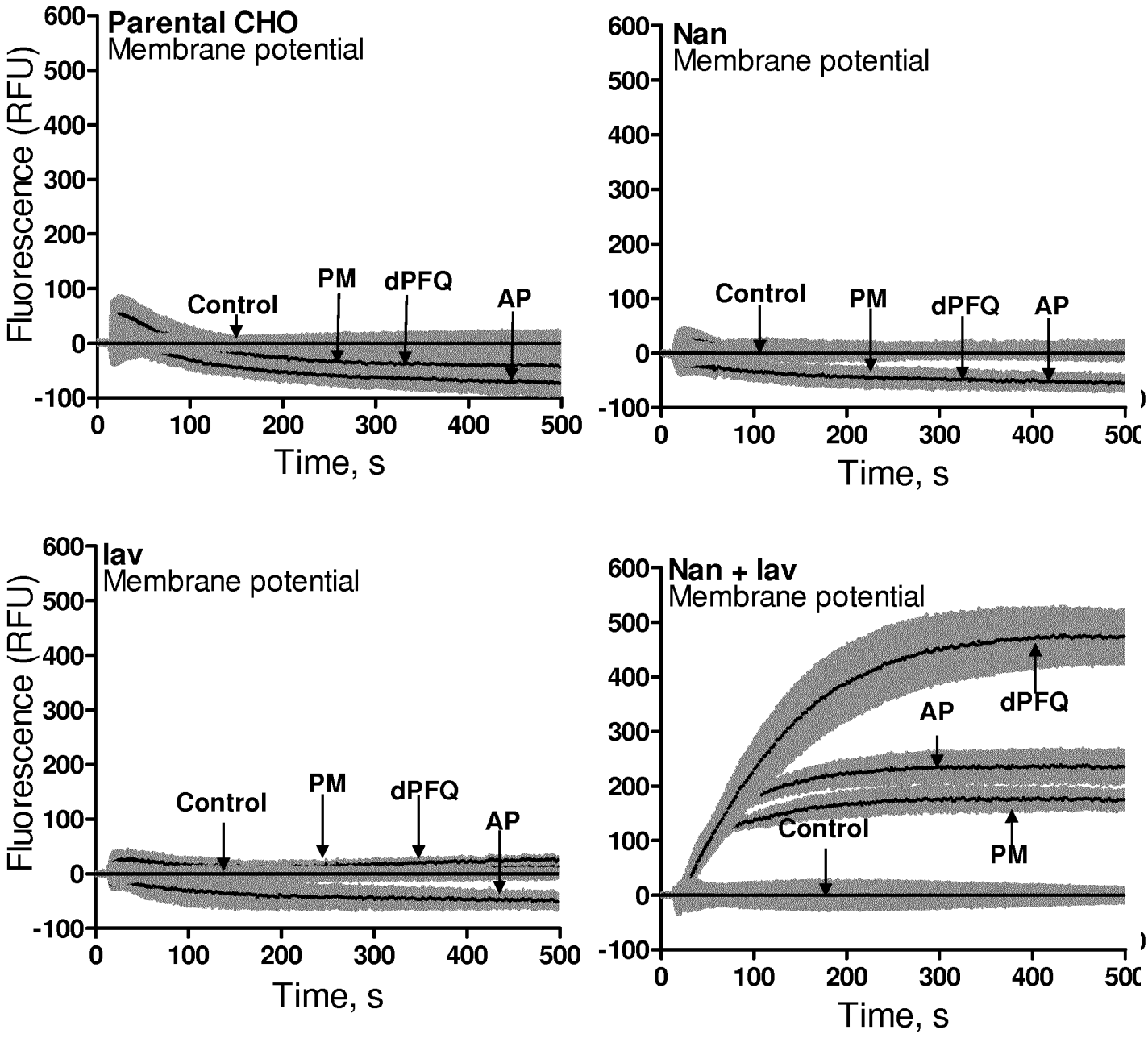


Figure 4. Afidopyropen triggers membrane depolarization in Nan-lav co-expressing cells. Afidopyropen (AP), pymetrozine (PM), and N-deacetylated form of pyrifluquinazon (dPFQ) evoke changes in membrane potential (relative fluorescence units, RFU) in CHO cells co-expressing Nan and lav, but not in parental cells, nor in cells expressing Nan or lav alone (averages (lines) ± 1 S.D. (areas) of 4 repetitions. All three insecticides were used at 10 μM. Membrane depolarization was monitored using proprietary membrane potential indicator (Molecular Devices).

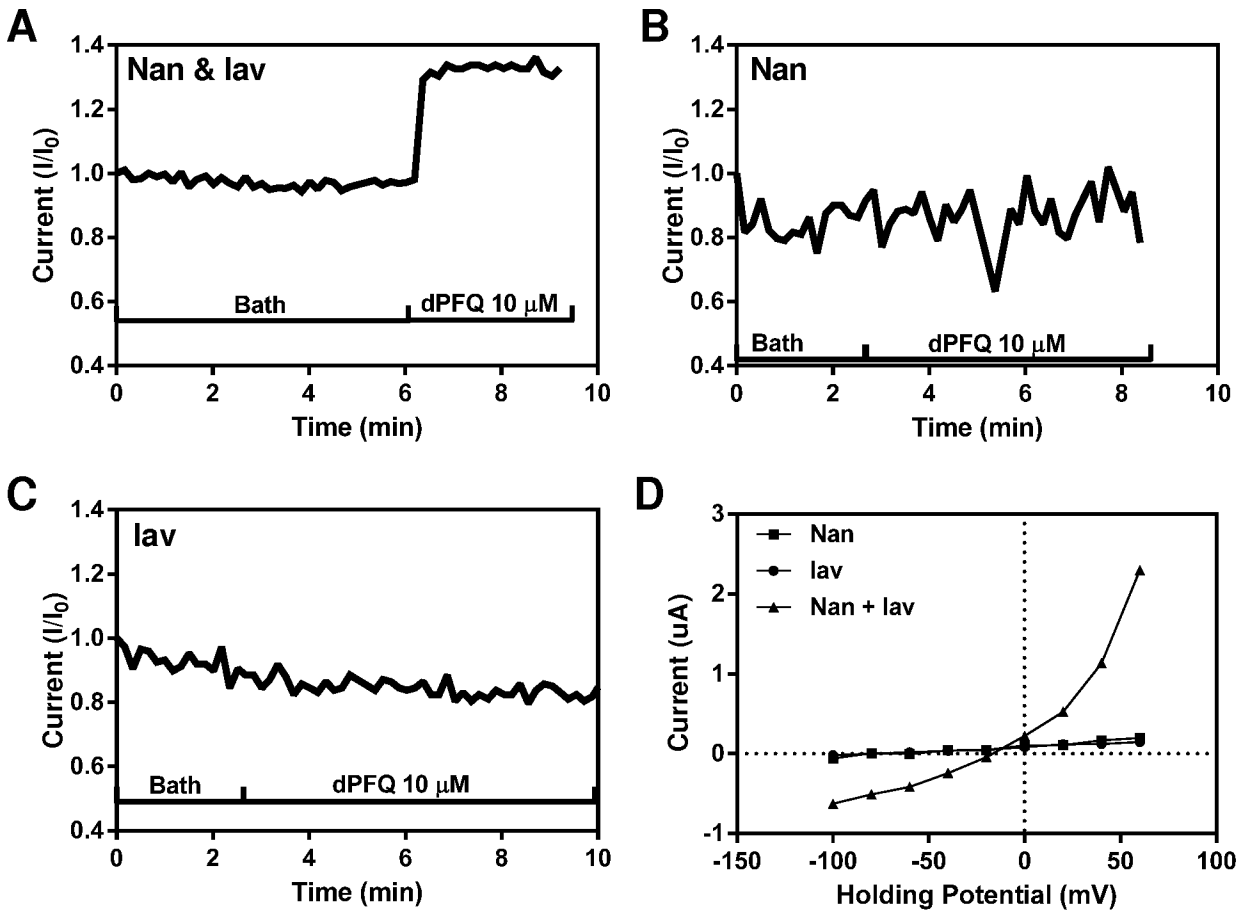


Figure 4a. N-deacetylated form of pyrifluquinazon (dPFQ) stimulates aphid Nan and lav expressed in *Xenopus* oocytes. Two-electrode voltage clamp current recordings from oocytes expressing one or both of the Nan and lav subunits from pea aphid. **(A-C)** Chart recording of current responses to +40 mV from -20 mV. Oocytes were perfused with bath solution (ND-96) and the perfusion bath was switched to dPFQ (10 μM) as indicated for each cell. Current plotted every 10 seconds for cells expressing either **A)** Nan and lav (0.15 ng RNA 1:1), **B)** Nan only (30 ng), or **C)** lav only (30 ng). Chart recording currents normalized to the initial current for each cell (I/I_0). **D)** The current-voltage relationship after application of dPFQ for the cells in A-C. Only the cell expressing both Nan and lav shows inward and outward current responses to dPFQ over the experimental voltage range.

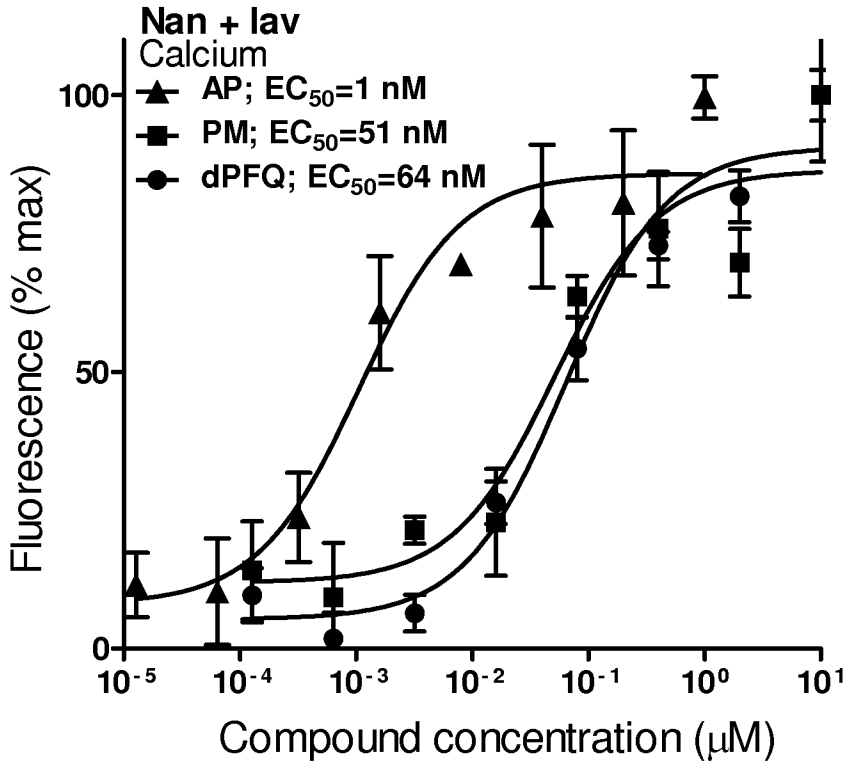


Figure 5. Dose-response relationships of calcium responses evoked by afidopyropen (AP), pymetrozine (PM), and N-deacetylated form of pyrifluquinazon (dPFQ) in cells co-expressing Nan and lav. Calcium mobilization was monitored using calcium sensitive fluorescent indicator, fluo-4 (averages ± 1 S.D.).

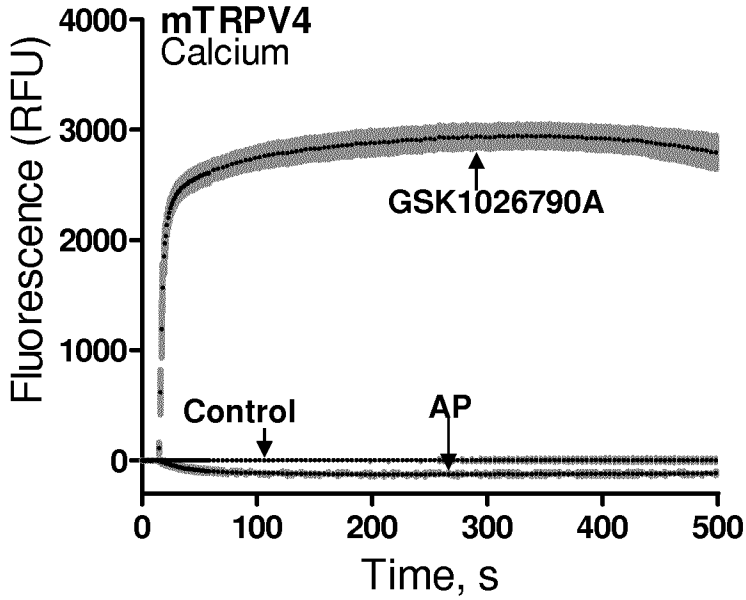


Figure 6. Afidopyropen does not activate mammalian TRRV4 channel. Agonist of TRPV4 channel, GSK1016790A, but not afidopyropen evokes calcium signals (relative fluorescence units, RFU) in CHO cells expressing mouse TRPV4 channel (averages (lines) ± 1 S.D. (areas) of 4 repetitions. Both compounds were used at 10 μM. Calcium mobilization was monitored using calcium sensitive fluorescent indicator, fluo-4.

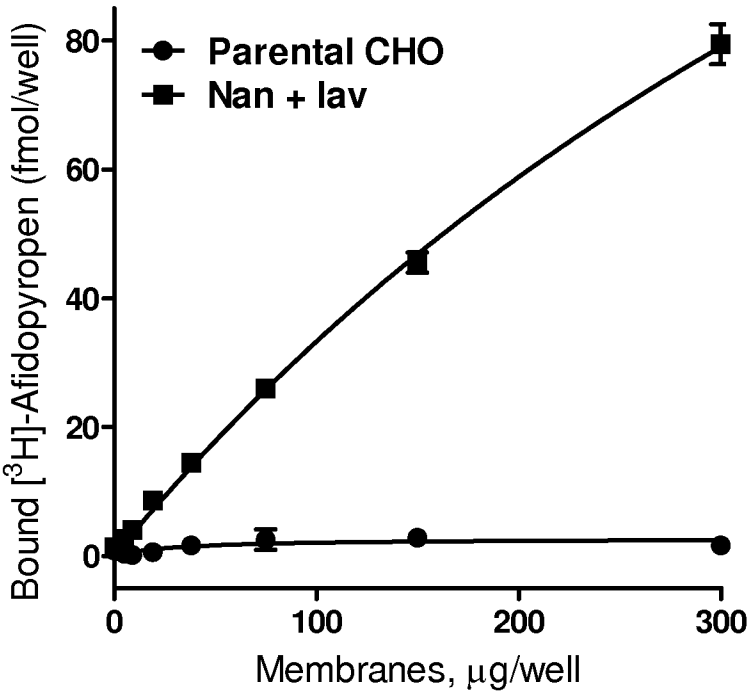


Figure 7. Specific binding of [^{3}H]-afidopyropen to membranes co-expressing Nan and lav.
Binding of [^{3}H]-afidopyropen demonstrates linear relationship to increasing amounts of microsomal membranes obtained from Nan-lav co-expressing CHO cells, but not from the parental cells ± SD (n=3). [^{3}H]-afidopyropen was used at 10 nM.

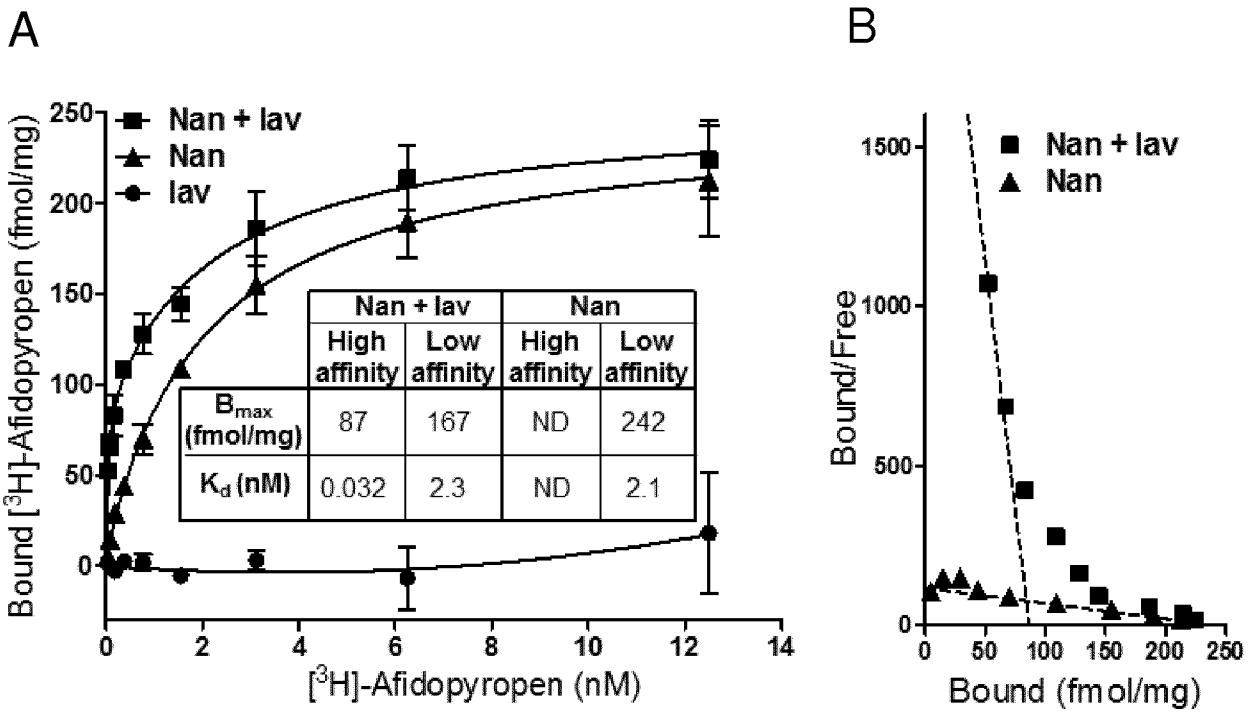


Figure 8. [^{3}H]-Afidopyropen binds to Nan protein, and binding affinity is increased in the presence of Iav. (A) Saturation binding of [^{3}H]-afidopyropen to membranes obtained from CHO cells expressing fruit fly Nan and Iav, either alone or together. Binding isotherms were fit into two-sites binding model (averages ± S.D. of 3 repetitions). No specific binding to Iav was detected. Membranes obtained from both Nan-Iav co-expressing cells, and from the cells expressing Nan alone demonstrated specific binding with comparable number of total binding sites at concentration of radioligand approaching saturation. Co-expression of Iav together with Nan revealed the presence of high affinity binding sites, which were not detectable in Nan alone-expressing membranes (table insert). (B) Scatchard transformation of the binding isoterms illustrates presence of high affinity sites in the membranes co-expressing Nan and Iav, but not Nan alone.

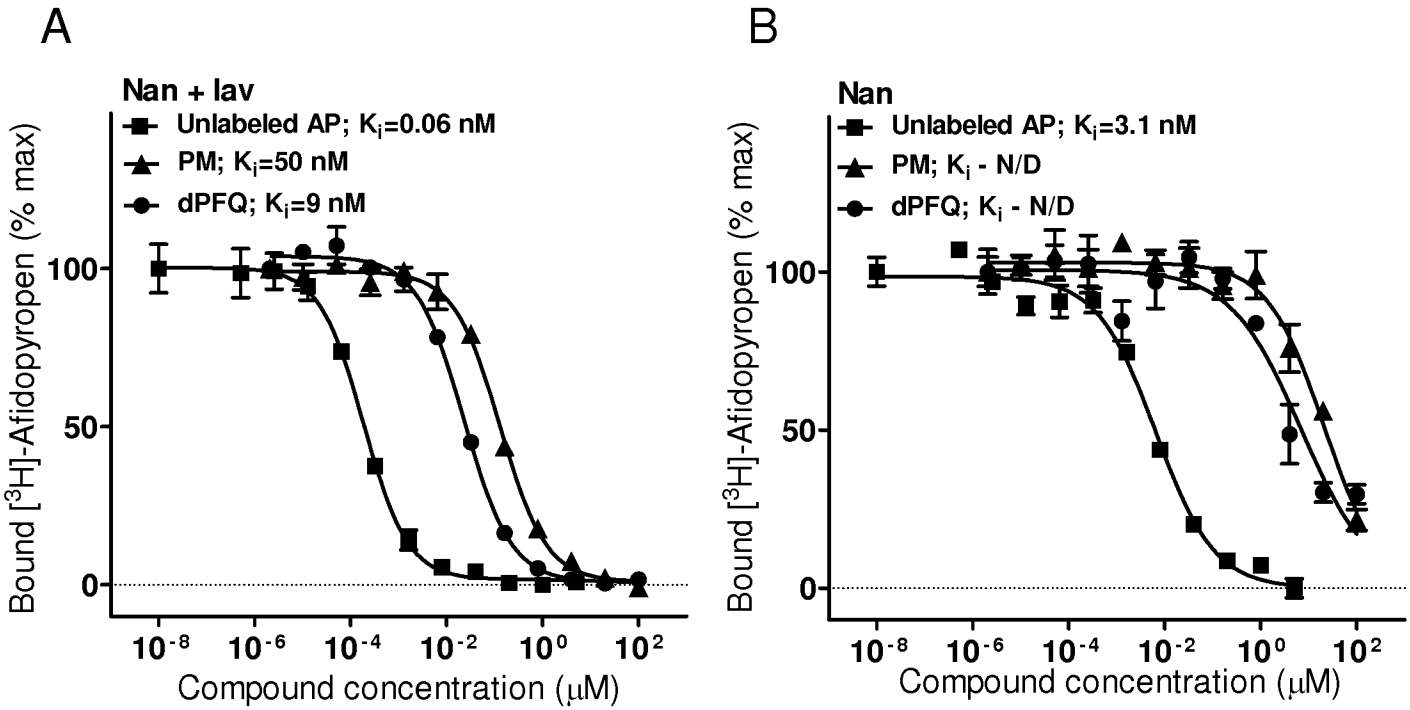


Figure 9. Both pymetrozine and N-deacetylated form of pyrifluquinazon compete with [^{3}H]-afidopyropen for binding. Displacement of [^{3}H]-afidopyropen by PM, dPFQ and unlabeled afidopyropen (AP), ± SD (n=3). K_i values were computed using Cheng and Prussoff algorithm. **(A)** membranes were obtained from CHO cells co-expressing Nan and lav, and low concentration of [^{3}H]-afidopyropen (50 pM), was used to detect binding primarily to Nan-lav complexes. **(B)** membranes were obtained from CHO cells expressing Nan only, and [^{3}H]-afidopyropen was used at concentration 800 pM. Displacement curves for PM and dPFQ did not reach bottom plateaus because of poor solubility of these compounds at concentrations exceeding 100 μM.

Figure 10 - SEQ ID NO: 1
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Figure 11 - SEQ ID NO: 2

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FIGURE 12 - SEQ ID NO: 3

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FIGURE 13 - SEQ ID NO: 4

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TTGCGTAATGTACAAAACCTGACAGCTTTGACGTTGGCGGCGAAATTGGGTCGCGTCGAGATGTTCTTTCACATATT
GAGTATTGAACGCGAGATCTACTGGCAGTTGGGTAGCATAACGTGTGCGGCATATCCACTCTCGATGATCGACACAA
TCGATGTGGAGACGGGTAATATCAATAAGGACTCGGTTTTGAATTTTGTCGTGTTTGGTGACAAACTGGAGCACTTG
GAGCTGCTGGATGGCGTAGTGATCGATTTGTTGAAGACCAAATGGGAGTCCTTCGTCAAGTCGCGTTTCTACAAGCA
GTTTTATATGTTCTCCTTCTATTTTCTCTTCTCATTAATCAGTTTCATCTCGCGACCAGGACCGACTGAAAAGAATG
AGGACGATGATGATGATGATGATGCTGATGCTAGCGTTGAGGCTACCGTAACGCGCGCAGCGAATAGTACGGCTCCG
CTACAACGTGGCGATCAGTGGTTCAAGCGCTTGATCAAGCGTGCTATCGACAAGATGGAATACAAAACCTTTTGGCT
GAACTTCACAGACTACTTTGATGACAACGACGTGGAATCGGTGCCACCGTGGTGGGCGAGCTATGCCGAGTGCCCGC
TTATGAACATGGAATCGGACTTAGCGAAGCTACGCATTGTGGCGGAAATAATTATATTTTTTGGCTCGGTTCTATAT
TTATTCGCCGCGCTGAGAGAGGCACGCTTTCTGGGCTATAAAATGTTTGTCGAAAATATGATGACCGCACCTTCGCG
TGTCATGTTTCTTTTCTCTTGCGCACTGATGATGTCTATACCTTGGCTGAGGGTGTTTTGTCTGACTGAGATCGATG
ACCACGTGGCGGTATTTATTATGCTTACAACAGCACCCTATTTTCTGTTCTTCTGTCGCGGCTTCAAAACTGTCGGT
CCCTTCGTTGTGATGATCTATCGCATGGTCATGGGTGATCTTATACGTTTTGTCTCCATTTATTTGGTTTTTGTAAT
GGGTTTCTCGCAAGCTTACTATATTATTTTTCTCACCTTTGACAATCCCGCTACACCGGAGGAAATCGATGACTCCG
AGTCGAATCCAATGCCCTCACCAATGGAGTCTATCGTTGCAATGTTTCTGATGTCACTCACGAATTTCGGTGACTAT
TTCGGCGGCATGGCCTCGACACAGCATGAATATGAAGCGAAGACACTCTTCTTTCTCTTCATGGTAATCGTCAGTGT
GTTGTTGGTGAACATGTTGATCGCCATGATGGGTAATACCTATCAGAAGATTGCCGAAATACGCAACGAATGGCAAC
GTCAGTGGGCGCGTATAGTTTTGGTGGTGGAGCGCAGTGTACCACCAGCGGAGCGGCTCAAGAACTTCATGCACTAC
AGTCAACCAATGTCGGACGGCAGGCGTGCGTTGGTGTTGCGTTTAAATATGAGCGATGAAGTTAAGGAGGAAATGAA
GGAGGTACAAGAGACCAAACGCATACATCAGCGCTTCTCGAAGAAACGACAAATTGAGCGCGAGGCGAGAGCACAAA
AGAGACAAGAGGAGTATGAGAAATTCTTTGGCAAGAAGCCGTCGGGCAACAGTGATAACAATAATGCCTAA

FIGURE 14 - SEQ ID NO: 5

<> 9
<> 2502
<> DNA
<> Anopheles gambiae
<> XM_320300.4
<> ?
>gi|158300355|ref|XM_320300.4| Anopheles gambiae str. PEST AGAP012241-PA (AgaP_AGAP012241) mRNA, complete cds

ATGGGAAATACCGAGAGCAATGTGACCAGTGGCGTTAAGAAGCAGGCTGGAGTGTCCACCCAGGCGCTGTACAAGTT
CGTCAACCTGAAGGGCGGCGGCCTGCTGGTGGACATGATGAAGCGCGCGATACAGAACAAGCAGTACGCCGAGATTG
ATCATGCGATCAAGACGAAGGTGGAACCGTTTCTGTACAACAAGGGCAAGGGGAAGTACATCCCCGTGTCGGTGCTG
GTGCTGTTACGAAACCGGGAGCGGCCGCGCCACAAGCAGCTGCCCGAGATCCGGGCGATGGAGAACCCGGAGGAGGA
CTTTGACATCGATGCGGTCTGTCCGGAAGTGAGCGAAGCCGAGTACTACCTAAACCCGTCCGGCTATCGGGAGGTGT
GCTGGAACATAAAGGAACGTGGCGCTGTGGGAGAGACAATTCTACACCTTTGCCTACTGAACGCCACTTCCCTGCAT
GCGGATCTAGCCAAACGACTGCTGCGCTTCTATCCCAAGCTCATCAACGACGTGTACATGTGCGACGAGTACTACGG
TGAGAATGTCCTGCATCTCGCAATCGTGAACGAAGATCCTGCCATGGTGAAGTATCTGCTCGATCACAACGCGGACG
TAAACGAGCGCTGCTGCGGTACGTTCATGTGCCCGGAAGACCAGAAAGCCTCCCGCTACGATACGCCCGAAACGGAG
GTCGTCCAGATGGTGCAGGTGACGAACTACGACGGCTACGTGTACTGGGGCGAGTACCCGCTCACCTTTGCCGCCTG
TCTCGGGCAGGAGGAGTGCTACCGGCTGGTGCTGGCCCGCGGCGCCGACCCGGACAACAAAGACTTCAACGGCAACA
CGGTGCTGCACATGCTGGTGATATACGAGAAGATTGCCACGTTCGACATGGGGTACGAGGTGGGTTCGTCGCTTAGC
ATCCGCAACCACCAGAACCTGACGCCGCTGACGCTGGCGGCCAAGCTCGGCCGGGTGGAGATGTTCTTTCACATCAT
GAACATCGAGCGCGAGATCTACTGGCAGCTGGGCAGCATCACGTGCGCGGCCTATCCGCTCGGCCTGATCGACACGA
TCGACGTGGAGACGGGAAACATTAACAAAGATTCCGCCCTCAATCTGGTGGCGTTCGGCGACAAGGACGAGCATCTC
GATCTGCTAGACGGGGTGCTGATCGATCTGCTCAAGACGAAGTGGAACACGTTCGTGAAGGACAAGTTCTATCGGCA
GTTTTTCATGTTCTTCTGCTACTTTTGCGTGTCGCTGGTGAGCTTCACGCTGCGCAATGGACCACCACCGGCGGAGG
ATGACGATGGGAAGGAGAGCGAGGCTGGGGGGAATAAAACGGCAGCTGTCACGAAGGAAGAGCTTCGTCGGCAGCTG
TGGAACGAAACGACGCTAGAGGATGCGCTGGCTGCGCTTGCCGGCAATGGAAGCTTCGCTGGACGGTTGTCGAATCT
GGAGCAGAGCAACGGAAGTAGCGACGCGATGGGTGAGTTTGATCCTGCCGAGATGGACGACGAGGGTCTGTTCTTCA
ACTCCAACTGTCACACGATGGATTACGACGGTGTGGAGGGCAAGGTGCGTCTCATATCGGAGATGATCATACTGGTC
GGTTCGTTTCTGTATCTGCTCGCTGCCTTGCGGGAGTTGAAGTTTCTTGGGCGGAAAATGTTCTTCGAAAATCTTAT
GACAGCACCATCGAGGGTTATGTTTCTGTTTTCCTGCTGCATAATGATGATCGTACCGTTTCTGAAGGTTCTCTGCT
TTACGGAGCTGGAAGATCACGTAGCCGTAACGATCATGCTGACGACGGCGCCCTATTTTTTATTCTTCTGTCGTGGC
TTCAAAACGGTCGGACCGTTCGTGGTGATGATATACCGCATGGTGATGGGCGATCTGTTGCGGTTCGTCGTCATCTA
TCTGGTATTTGTGATGGGCTTCTCGCAGGCGTACTACATTGTGTTTTTGTCCTACAAACCGGACGAGGAAGGCGACC
CAAACCCGATGCCGTCGCCGATCGAGTCGATCGTAGCGATGTTTCTGATGTCGCTGACCAACTTTGGCGATTACTAT
GGCGCACTGGAGAACACCGACCACGAGATGTGCGCAAAGATCTTGTTCGTGCTGTTCATGGTGATCGTTGCCGTGCT
GTTGGTGAACATGTTGATCGCTATGATGGGCAACACGTACCAGAAGATTGCAGAAACGAAGAACGAGTGGCAGCGCC
AGTGGGCCCGCATCGTGCTCGTCGTCGAGCGTGGCGTCCCACCAAAGGAGCGGCTCAAGAACCTGATGTCGTACAGC
CAACCGATGTCGGACGGGCGTCGTGCGCTGGTGCTACGATTAAACATGACGGAAGATAAGGAAGAGATGAAGGAGAT
ACTCGAAATGAAGCGCGTCCACGAGCGGCTCTCTATAAAGCGGCAGATCGAGCGGGATGCACGGGCCGAGCAGCGTC
GGCTGCTGCGCGAGAAGTACTTGAATATGTCTTCATGA

FIGURE 15 - SEQ ID NO: 6

<> 11
<> 2448
<> DNA
<> Aedes aegypti
<> XM_001652374.1
<> ?
>gi|157114791|ref|XM_001652374.1| Aedes aegypti hypothetical protein partial mRNA

ATGGGAAATACCGAGAGCAATGTCACCAGCGGAGTCAAGAAACAGGCCGGAGTGTCCACCCAGGCTCTGTACAAGTT
CGTCAATCTGAAGGGTGGTGGTCTTTTGGTGGACATGATGAAAAGAGCAATCCAAAACAAACAATATGCAGAAATAG
ATCATGCGATCAAAACGAAAGTCGAACCCTTCCTGTACAATAAGGGCAAAGGGAAGTATATCCCAGTGGCCCAGTTG
GTGCTGCTGAGGAATCGAGAACGACCTCGATCCAAGCAGTTGCCAGAGATTCGTGCCTTGGAAAACCCTGAAGAGGA
TTTCGACATTGACGCAGTATGTCCGGACGTGACCGAGGGCGAATACCAGAGGAATCCATCGGGGTACAGGGAGGTGT
GCTGGAACATCAAGGAACGAGGAGCAGTCGGCGAAACTATTCTTCATCTGTGCTTGCTGAACGCAACATCTTTGCAT
GCTGATCTTGCCAAGCGCCTACTACGTTTCTACCCGAAGCTCATCAACGATATCTACATGTGCGATGAGTATTACGG
GGAAAGTGTGCTCCACGTGGCAATTGTCAACGAAGATCCGGCCATGGTTAAGTATTTATTGGACAGTGGTTCCGATG
TAGACGAGAGATGTTGCGGAACGTTCATGTGTCCAGAGGACCAAAAGGCAACGCGATACGATTCTATCGAAACGGAA
ATCATTTGCGTACTTCCCATGACCAACTACGATGGGTATGTGTATTGGGGCGAATATCCGTTGAGTTTTGCCGCTTG
CTTAGGCCAGGAGGAATGCTACCGGTTGGTGTTGGCTCGGGGAGCTGATCCAGATAATCAGGATTCGAACGGAAACA
CCGTTTTGCACATGTTGGTCATCTACGAGAAAATCTCAACATTCGACATGGCGTATGAAGTCGGCTCATCGCTGGAC
ATAAGAAACCTGCAGAATTTGACGCCGTTGACTTTGGCAGCCAAGTTGGGTCGGGTTGAGATGTTTTTCCACATTAT
GAACATCGAACGAGAAATCTACTGGCAGTTGGGAGCTATCACTTGTGCAGCCTATCCGCTTGCTTTGATCGACACGA
TCGACATCGAAACAGGGAACATTAACAAAGATTCAGCATTAAATTTAGTGGTATTCGGCGACAAAGCGGAGCATTTA
GACCTACTAGAAGGTGTACTGATTGATTTGCTCAAGACCAAGTGGAACTCGTTCGTCAAAGACAAGTTCTATCGCCA
ATTCTTCGTGTTCTTTTGGTATTTTTGCGTTTCACTAGTAAGCTTCACTCTGAGAAGGGGACCAATGAATTTGGAGG
AGACGGCAGCCAACCGCACCACAACCAGCATTACTTTGAAAAATTTGACATTTTCTGATTCGACTAACGCAACATTA
CCCACTTTACTGGCTGCGGATGTGAACGAAAAAATCGTTCAATTTATTGCAAACGAAACGTTATTCGATCCGGCAGT
TATGGAAGAAAACACTTTCTTTAATTCTAAATGTGCCACCATGGCATACGACACACTGCAGGATAAGATAAGGTTGG
TTTCGGAGATCATCATTCTCATCGGATCATTCTTGTACCTAGTTGGAGCGTTGAGAGAATTTCGATTCTTGGGACGA
AAAATGTTCTTTGAGAATTTGATGATTTCCCCTTCTCGAGTTATGTTTCTGTTCTCGTGCTGCATAATGATGATCGT
ACCGTTTCTGAAAGTCCTTTGCTTAATCGAGCTTGAGGATCACGTTGCCGTGACGATTATGTTGACTACTGCTCCGT
ACTTTTTGTTCTTCTGTCGTGGTTTCAAAACCGTTGGACCGTTCGTTGTGATGATCTACCGCATGGTGATGGGAGAC
TTGCTGCGATTCGTCGTCATCTATCTGGTGTTCGTGATGGGATTTTCCCAGGCCTACTACATTGTGTTCTTGTCGTT
CAAGGGTGAAGAGGAAGGCGATGAAAACCCGATGCCTTCGCCGATGGAGTCGATAGTGGCGATGTTTTTGATGTCGC
TGACGAATTTCGGCGACTACTACGGTGCACTGGAGAAAACCGAGCACGAGGGATGCGCTAAGGTTCTTTTCGTCATT
TTCATGGTTATTGTGGCCGTCCTGTTGGTCAACTTGCTCATCGCCATGATGGGTAACACCTACACCATGATTGCCGA
AACGAAGAACGAATGGCAACGGCAATGGGCACGAATCGTTCTGGTAGTGGAACGAGGAGTTCCTCCGAGCGAGCGAC
TCAAAAACTTCATGAGCTACAGCCAACCCATGTCGGACGGGAGACGAGCCCTCGTGTTGCGATTGCATATGACGGAC
GAAGACAAGGAAGAGATGAAGGAAATCCTCGAGATGAAACGTGTCCATGAACGCTTGAAGAAGAAACGTCAGGTGGA
ACGAGAATTAAGAGCCGAGCAGCGACGACTAATCATGGAGAAATATGCAAACGTACCTTGA

FIGURE 16 - SEQ ID NO: 7

<> 13
<> 2451
<> DNA
<> Culex quinquefasciatus
<> XM_001847084
<> ?
>gi|170038598|ref|XM_001847084.1| Culex quinquefasciatus TRP channel protein nanchung, mRNA

ATGGGAAATACCGAAAGTAACGTCACCAGTGGCGTCAAGAAGCAGGCCGGAGTGTCCACCCAGGCACTGTACAAGTT
TGTCAACCTGAAAGGTGGCGGCCTGCTGGTGGACATGATGAAGCGGGCGATCCAAAACAAACAGTACGCCGAAATAG
ACCACGCAATAAAGACCAAGGTGGAACCGTTTCTGTACAACAAGGGCAAGGGGAAGTACATTCCGGTGGCACAGTTG
GTGTACCTAAGGAACCGGGAACGGCCACGCCACAAGCAACTGCCGGAAATTCGTGCCCTCGAAAATCCCGAGGAGGA
CTACGATATAGACAAAGAGTGCCCGGATGTGACCGAGGGCGAGTACATGCGGAACCCCGGGGGGTACAGGGAGGTGT
GCTGGAACATCAAGGAACGTGGCGCAGTAGGCGAGACCATTTTGCATTTGTGCCTTCTGAACGCAACTTCACTGCAC
GCAGATCTGGCGAAGCGCCTGCTGCGATTCTACCCTAAACTGATTAACGATGTGTACATGTGCGATGAGTACTACGG
CGAAAGTGTGCTGCATTTGGCGATCGTCAACGAAGATCCGGCCATGGTGAAATACCTGCTGGATGCCGGGTCCGACG
TGAATGAACGGTGCTGCGGGACGTTCATGTGTCCGGAGGATCAAAAAGCATCCCGGTTCGATTCACTGGAAACGGAA
ATAATCTGTGTGATGCCACAAACCAACTACGACGGATACGTCTATTGGGGAGAGTACCCGTTGAGCTTCGCCGCTTG
TTTGGGCCAGGAAGAGTGCTACCGGTTGGTGTTGGCACGGGGAGCCGACCCGGATAACCAGGATTCAAACATGAACA
ACGTTCTACACATGATGGTGATTTACGAAAAGTTAACGACGTTCGACATGGCGTACGAAGTGGGTTCTTCGCTGAGC
ATAAGAAATCTCCAAAATCTAACACCGTTGACGTTGGCCGCCAAGCTGGGTCGCGTCGAAATGTTCTTCCACATCAT
GAACATTGAGCGGGAGATCTACTGGCAATTGGGAAGTATTACGTGTGCCGCCTACCCGCTGGCATTGCTCGATACCA
TCGACATCGAAACCGGCAACATTAGCAAAGATTCCGCGCTGAATCTGGTCGTTTTCGGCGACAAAGACGAGCATTTA
GATCTCCTCGAAGGAGTCCTCATCGATCTCCTGAAAACCAAATGGAACACGTTCGTCAAGGACAAGTTCTACAGCCA
ATTTTTCGTGTTCTTTTGCTATTTTTGTGTGTCACTGATTAGCTTCACACTGCGCGAGGGACCAATGAAGCTAGAGG
ACGGAGAGGCCAACAAAACTACCACGAGTATTCAGCTAAAAAATATGACCCTGGCCGACCTCACCAACGCCAGTACG
CTGTCCTCGCTACTGGTCACCGACGTGAGCGGCAAGATCGTCGGACTCAACGGGAGTGAAACGTTCTTCGACCCGTC
GACGATCGAGTCCGACATGTTCTTCAACTCCAAGTGTCCAACGATGATCTACAAGGGTATCGAGGGGAAAATTCGAC
TGGTTTCGGAAGCAATTATTCTGGTGGGATCATTTCTCTATCTGGTTTCGGCTTTGAGAGAATCTCGCTTTCTTGGG
AGGAAAATGTTTATCGAAAATTTGATGACCGCTCCTTCCAGAGTAATGTTCCTGTTTTCCTGCTGTATCATGATGGT
AGTTCCTTGCCTCAAAGTGCTATGTTTCACCGAGTTGGAAGATCACGTTGCGGTCGTGATTATGCTGACAACTGCGC
CCTACTTCCTGTTCTTCTGTCGCGGCTTCAAAACGGTCGGACCGTTCGTGGTGATGATTTACCGCATGGTGATGGGA
GATCTGCTCCGGTTCGTGGCCATTTACTCGGTGTTCGTGATGGGCTTCTCCCAGGCCTACTACATCGCGTTCCTGTC
GTACAAGGGCGAGGAGGAGGGCGACGAGAATCCGATGCCCTCGCCGATGGAGTCGATCGTGGCCATGTTTCTGATGT
CGTTGACCAACTTTGGCGATTACTACGCCGCGCTCGAGGATACCGCCCACGAGGGTTGCGCAAAGGTACTCTTTGTG
ACATACATGGTAATTGTGGCGGTGCTGTTGGTCAACTTGCTGATCGCTATGATGGGTAATACGTACACCAAGATTGC
CGAGACGAAAAACGAGTGGCAACGGCAGTGGGCTCGCATCGTTCTGGTCGTCGAGCGAGGCGTTCCACCGGCAGAAC
GTCTGAAGAACCTAATGAACTACAGTCAACCCATGTCGGACGGTAGAAGGGCCTTGGTTTTGCGATTGAATATGACG
GAAGAGGATAAGGAAGAGATGAAGGAGATCCTTGACATGAAACGGGTGCACGAACGGCTGTCCAAGAAGCGAGCAGT
TGAGCGGGAAGCACGCGCCGAGCAGAGACGTCTCATTGCGGAGAAATACGCAAACGTACCGTAG

FIGURE 17 - SEQ ID NO: 8

<> 15
<> 2385
<> DNA
<> Tribolium castaneum
<> XM_962803.1
<> ?
>gi|91081968|ref|XM_962803.1| PREDICTED: Tribolium castaneum similar to nanchung CG5842-PA (LOC656262), mRNA

ATGGGTAATACCGAAAGTAACGTTACTAGTGGTGTTAAGAAGCAAGCTGGTGCTTCAGTGCAACCAATTTATAAATT
ATGCGATTTGAAAGGGGGAGGGCTCCTAGTGGAATTAATGAAACGGGCCACACAAAACAAGCAATATGCAGAACTAG
ACCACGCAATAAAAACCAAGGTGGAGCACTTTTTGTACAATAAAGGGGCTGGACGGTATTTCACAATATCGGACTTG
GTTCTTTTGAGGAATAAGGAAAGGTCTCGCCAGAAATGGTTACCACAATTGAAAGCAATGGAAAACCCTGAAGATTT
TGAAATTGATGATGAAGGCCCCGAAATAACAGAAGAACAGTATCAAAAAAATCCGCATTTGTACCGTCACGTTTGCT
GGAAAATCAAGGAACGCGGAGCCGTGGGCGAAAGCATAATGCACTTGTGTTTGCTAAATGCCACTTCCTTGCACGCT
GATATCGCAAAGAGGCTTTTACGCTTTTACCCCAAATTGATTAACGATATTTACATGTCGGATGAATATTACGGAGA
AAACGTTTTGCACATTGCTATCGTAAACGAGGATCCGTCAATGGTAAAATTCCTTCTAGATTCGGGTGTAAATATCC
AAGAACGCTGCTGTGGCAACTTTATGTGTCCCGAAGATCAGAAATCGTCTCGTTATGACTCCTTGGACCACGAGTGG
GTCAACGTTTGCCCGGTCACGAATTACGAAGGCTATGTATACTGGGGCGAATATCCTCTAACTTTCGCCGCGTGTTT
AGGACAGGAAGAGAGCTTTCGCTTGATGCTGTCCAGGGGGGCTGATCCCGATGCTCAAGACACCAACGGGAACACGG
TCCTACACTTGCTTGTCATTTTGCAGAAATTGGAGGCTTTCGATATGGCCTACGAAGTGGGGGCCAAATTATCAATC
CGAAACGTGTTGAGTCTGACTCCACTAACTCTGGCCGCAAAACTTGCCAGAATCGATATGTTTTTCCACATTTTGAA
CTTGGAACGCGAAATTTATTGGCAAATTGGCAGCATCACGTGCGCTGCTTACCCTCTATCGCAGATTGATACAATTG
ACATTGAAACGGGCCAAATAAGCAAAACTTCAGCCCTTAATCTTGTGGTGTTTGGTGACAAAGACGAGCACTTGGAG
TTGATGGACGGTGTTTTGATCGACTTGCTTAATGCGAAATGGAACACTTTTGTCAAGTTTAAATTCTACAAACAGTT
TTTCACGTTTGCGTTCTATTTTTTGATCTCCCTTGTTGCTTTCACGCTACGGCCAGGGCCCCCACACAAGGAGGCCA
AACTGGTGAATGTCACAATAAACGCCACTGTTTCAAATACTTCCAAGTGGGAAAATCTCACTTCTATACCGTTCGGT
AAAACCCCGGATGATGATGACAGCGACATGGAAGAATGGTGGGACAATTTGCAAGAAGAATGTCGCTTGATGCAACT
AGAATCACCCGAATCTAAAATTCGACTCACTGCAGAGGTTTTGATGGTTGTGGGGGCTTTTGCATATCTGGCAGCCG
CAGTTCGCGAGGCTAGGTTTTTAGGGGGGCGCATGTTTTTCGAAAATCTTATGACTGCACCGTCAAGAGTCATGTTT
TTATTTTCTTGTATTTTAATGTTAACGGTGCCATGTTTGAGACTGGCTTGTTTGGATGAGTTTGAAGATATTGTAGC
TGTGGTGATTATGTTGACCACTGCACCGTATTTTCTCTTCTTCTGTCGAGGTTTTAAAACAGTGGGACCCTTCGTTG
TGATGATCTACAGGATGGTGATGGGTGATTTGATAAGATTTGCTTCAATTTATCTAGTGTTTGTCATGGGGTTTTCT
CAAGCTTTTTACATCATTTTTCTCTCGTTTGATAACCCACTAACCCCTGACGACGTTGACGATTCCGCAACTAACCC
CATCTCCACCCCCATCGAGTCAATTATGGCGATGTTTCTGATGTCAATGACCAATTTCGGTGACTATTATGCGGCCT
TCGAAAAAACTGACCATGAATACGAAGCTAAAATGTTGTTTGTTGTATTTATGGTAATCGTTTCAATTTTACTGATC
AACATGTTGATTGCCATGATGGGCAACACTTACCAAAAAATCGCAGAGACAAGAAACGAGTGGCAAAGACAATGGGC
GCGAATTGTTTTGGTTGTTGAAAGGGGGGTGAGTCCCTCTGAGCGTTTGAAACAACTTATGGTTTATTCACAACCTA
TGTCCGATGGAAGAAGGGCTTTAGTGTTGAGATTAAACCAGTCTGACGAGGACAAGGAGGAAATGAAGGAAATTCTA
GAAATGCGGCGCAGGCATGAAAGACACATAAAGAAAAGAAGCGAAAAGTTGAAAGAGAATGCAAAAAAGAATTGA

FIGURE 18 - SEQ ID NO: 9

<> 17
<> 2526
<> DNA
<> Bombyx mori
<> XM_004923013.1
<> ?
>gi|512892990|ref|XM_004923013.1| PREDICTED: Bombyx mori transient receptor potential cation channel subfamily V member 5-like (LOC101740263), mRNA

ATGGGTAACACAGAGAGTAATGTGACGAGCGGTGTGAAGAAGCAAGCTGGGACGTCAGAGCAAAAGCTTTACAAACT
AGTCGATATAAAAGGAGGAGGTCTCCTGGTGGACATGATGAAGCGAGCTCTGCAGAACAAGCAATACGCCGAGATAG
ATCACGCTATCAAGACTAAAGTTGAGCCGTTTTTGTATAATAGAGGGAGGGGTCGATATATACCGATATCCCATCTC
GTCTTGCTCAGGAACAAAGAGAGACCGAGACACAAACTGCTGCCTCCACTCAGAGGCATGGAAAACCCTGACGAGGA
ATTTGACGTGGATAAGGACTGGCCAGTTGTTACTCAAGAGGAATATGACGCTAATCCCTCCGGATACAGGGAACTTT
GTTGGGATGTCAAAGAGAGAGGTGCAGTGGGTGAGACTATTCTGCACTTGTGTCTGCTCAATGCGACTTCGCTCCTA
GCTCATCTCGCTAAAAGACTACTACGCTTTTATCCTAAAATGATTAATGATATTTATATCAGCGATGAATACTATGG
TGAAACTGTATTACATATTACAATAGTCAACGAAGATCCGACAATGGCAAAGTTTCTACTGGACGCGGGTGCGGATT
ACCACGAGCGTTGCTACGGGAACTTCATGTGTCCTGAGGATCAAAAGGCTTCCAGGACGGACTCTTTCGATCACGAA
TGGGTCAACGTCCAGCCTGACACTAATTATAATGGGTACGTCTACTGGGGCGAGTACCCGTTGAGTTTCGCAGCATG
CTTAGGCCAGGAGGAGTGCTACCGTTTGATCTTAGCACGAGGAGCGGATCCTGATAAGCAGGATACTAATGGCAATA
CAGTTCTGCACATGCTAGTCATATACGAGAAGATGAGCACATTCGATATGGCTTACGAAGTGGGCGCGTCCCTAAAC
ATTCGTAACGTACAAAACCTAACTCCCCTAACCCTTGCCGCCAAGCTAGCTCGCACCGAGATGTTCTTTCACATTCT
AAACATCGAAAGGGAGATTTACTGGCAGATCGGCGCCACCACATGCGCCGCCTACCCTTTAGGACAAGTTGATACAA
TAGACACTGAAACAGGACTAATTAGTAAGGATTCAGCTCTGAATTTGGTTGTTTTTGGGGAAAAAGATGAGCATTTA
GGTCTACTAGAAGGTATGCTGATAGACTTATTGAAAACGAAATGGAACACGTTCGTTAAGTTTCGTTTCTACAGGCA
GTTCATATTATTTTCATGTTACTTCTTGGTTTCACTGATCTGCTTCACATTGAGACCAGGACCACCGGACAGAGCAT
TGAATACAACTGTCTTGAACTCAACTATTGGTCCAAACGTTACCGACGCCGAGCTGGTATCGGATGTCGAAAATTGC
ACAATGACCCCGAACGCAGATTTTGATACGAATGCTGTTGAAGTCCTGAACGGTACTAAGTTCGGCGGTTCTCATTG
TGCACGATTCAAAAGTCACCCCAAAGAAAAATCGACTGAAGCACCCAGGGAGAATGACGTTGAAGGTTGGTGGGAAG
ACTTGACAGAGGAATGCAGGTTGATGAACTTGGACACGTGGCAAGCCAAACTAAGGATATCTGCAGAGCTTCTGTTG
TGGATGGGGGCTTTGGCTTATTTCGGAGCTGCGTTACGTGAAGCAAAGTTCCTCGGGATCAAAATGTTTATAGAGAA
TCTGAGCACTGTGCCATCCAGGGTGATGTTCTTGTTTTCGTGTCTGCTGATGTTGATACTGCCAACTTTGAGGTTAT
GGTGCGCTGACGAGGCGGAGGACCATCTCGCTGTCATGATCATGCTCACTACTGCTCCTTACTTCTTGTTCTTTTGC
AGGGGTTTCAAAACAGTGGGTCCATTCGTGGTCATGATATACCGCATGGTGATGGGTGACCTGCTACGTTTCGTTTG
TATATATTTGGTATTCGTTATGGGATTCTCACAAGCGTACTACGTTATATTCTTATCATTCGACAATCCCAACACGC
CTGAAGGCGTTGATGACTCGGTGTCCAACCCAATGCCCTCCCCCATGGAGAGCATCATGGCGATGTTCCTAATGTCT
CTAACGTCGTTCTCAGATTACTATACCGCGTTCGATCGCACCGACCACGAAATAGAGGCAAAGCTCCTCTTCGTGAT
ATATATGATAATAGTAGCGATTCTCCTGGTGAACATGTTGATTGCCATGATGGGGAACACTTACCAGAAGATAGCGG
AGACGAGGAACGAATGGCAGCGGCAGTGGGCCCGGATAGTGCTGGTGGTGGAGCGAGGAGTTCCACCGGCGCAGAGA
TTAAAGCAGCTGATGACGTACAGTCAGCCTATGGCCAATGGAAAGAGAGCTTTAGTCTTGAGAATCAATCAAAAGGA
CGAAGACAAGGAAGAGATGAAAGAGATTTTGGAAATGAAGAGAACTCACGAGCGCATTGTAGCTAAGAGGAAGCAAC
GGGAGGCGCTTAAGCCTGGCGAGATCCCGCCACCCGCCAGAGATTATCCTATTAGGAAATGA

FIGURE 19 - SEQ ID NO: 10

<> 19
<> 2379
<> DNA
<> Anopheles darlingi
<> gi|312376269
<> ?
>(gi|312376269:23843-24241, 24691-25751, 25787-26047, 26365-26638, 26714-26956, 27039-27179) Anopheles darlingi Cont15134, whole genome shotgun sequence

ATGGGAAATACGGAGAGTAATGTGACCAGTGGCGTGAAGAAGCAGGCCGGAGTGTCCACCCAGGCCCTGTACAAGTT
CGTCAACCTGAAGGGCGGTGGGCTGCTGGTGGATATGATGAAACGGGCGATCCAGAACAAGCAGTACGCCGAGATTG
ACCACGCGATCAAGACGAAGGTCGAACCCTTCCTGTACAACAAAGGCAAAGGAAAGTACATCCCGGTGTCGGTGCTG
GTGCTGTTGCGAAACAGTGAGCGACCGAGGCACAAGCAGCTGCCCGAAATCCGAGCGTTGGAGAACCCGGAGGAGGA
CTTTGATATCGATGCAGTCTGCCCGGAAGTGAGCGAAGCGGAGTACTACCTCAACCCATCCGGGTACCGGGAGGTGT
GCTGGAACGTCAAGGAACGTGGAGCAGTCGGTGAGACGATTCTGCATCTTTGCCTGCTCAACGCTACGTCACTACAT
GCCGATCTGGCGAAGCGGCTTCTACGCTTCTATCCAAAGCTCATCAACGACGTGTACATGTGCGACGAGTACTACGG
CGAGAGTGTTCTCCATCTGGCCATCGTAAACGAGGATCCCGCGATGGTGAAATACCTGCTCGATCACAACTCGGACG
TAAACGAGCGCTGCTGCGGGACGTTCATGTGCCCGGAGGATCAAAAGGCTTCCCGCTACGATACTCCCGAGACGGAA
GTCGTCCAGATGGTGCAGCTCACGAACTACGATGGGTACGTGTATTGGGGCGAGTATCCCCTTACATTTGCCGCCTG
TCTAGGACAAGAAGAGTGCTACCGGCTGGTGTTGGCCCGCGGTGCCGACCCGGACAACAAGGACTTTAACGGCAACA
CGGTACTGCATATGCTGGTGATATACGAGAAGATTACCACGTTCGATATGGGCTACGAGGTAGGATCATCGTTAAGC
ATACGGAATCACCAGAATCTAACGCCGCTAACGTTGGCGGCGAAGCTTGGCCGCGTCGAGATGTTCTTCCACATTAT
GAACATTGAGCGAGAGATTTACTGGCAGCTGGGTAGCATTACCTGTGCCGCCTATCCGCTCGTCCTGATCGACACGA
TCGACGTAGAAACCGGTAACATCAGCAAAGACTCGGCCCTGAATTTGGTCGTGTTTGGTGACAAAGATGAGCATCTG
GATCTACTGGACGGTGTGCTGATCGATCTGCTCAAGACGAAGTGGAACACGTTCGTGAAGGACAAATTCTATCGACA
GTTCTTCATGTTTTTCTGCTACTTCTGTGTTTCGCTGATCGGCTTCACGCTACGCAATGGACCACCACCGCCCGAGG
AAGACGACGAAAATCGTGCCGGTGGTGGCAGTGGCAACAAAACGTCCTCAGCTTCGAAGCAGGATCTTCGGCAACGA
TTATGGAACCGAACGGTAACATTAGAGGACGCGGACAATGTAAGCAGCCTTTTAAGTGACATTATGGGGATTGATGC
GCTTGGCAAACTGGCCGAGCAGCTTCTTAACGGAAGCGAAGGATCGGGTGCATTCAAACCCGAAACGGTCGAAGAGG
AAGAGGATGGGCTGTTCTTCAACTCCAAGTGTCACACCATGGATTATGATGGCGTTGAGGGAAAGGTACGATTCGTG
GCCGAAGTCATCATACTGATCGGTTCCTTCCTCTATCTCCTGTCGGCGTTGCGCGAGCTAAAGTTTCTTGGCCGGAA
GATGTTCTTCGAAAATTTGGTAAGCCGTGGCTTCAAGACGGTCGGTCCTTTCGTGGTGATGATCTACCGTATGGTGA
TGGGTGATCTGCTGCGGTTCGTCGTCATCTATCTGGTGTTTGTGATGGGTTTCTCGCAGGCGTACTATATCGTGTTT
CTCTCCTACAAACCGGAGGAGGACGGTGACGCCAATCCGATGCCATCGCCCATCGAATCGATCGTCGCCATGTTTCT
GATGTCGCTGACCAACTTTGGGGATTACTATGGAGCGCTCGAAAACACGGATCACGAGATGTGCGCCAAGATCCTGT
TCGTGCTCTTTATGGTGATTGTGGCGGTGCTGTTGGTGAACATGCTGATCGCTATGATGGGTAACACCTACCAGAAG
ATCGCCGAAACCAAGAACGAATGGCAACGCCAGTGGGCACGCATCGTGCTGGTGGTAGAACGTGGTGTGCCACCGAA
GGAGCGGCTCAAAAATCTCATGTCCTACAGTCAACCGATGTCGGATGGTCGGCGAGCACTGGTGCTCCGGTTAAACA
TGACGGACGAAGACAAAGAGGAAATGAAGGAGATCCTCGAGATGAAACGTGTTCACGAGCGGCTGTCGAAGAAGCGG
CAGGTCGAGCGGGATGCCCGGGCCGAGCAGCGACGTTTGCTGCGCGAAAAATATCTCAACATGACGTAG

FIGURE 20 - SEQ ID NO: 11

<> 21
<> 2703
<> DNA
<> Acyrthosiphon pisum
<> XM_001947872.2
<> ?
>gi|328706725|ref|XM_001947872.2| PREDICTED: Acyrthosiphon pisum transient receptor potential cation channel subfamily V member 6-like (LOC100160148), mRNA

ATGGGTAACACCGAGAGCAATGTGGCCAGTGGTGTCAAGAAGCAAGTCGACACCTCGTCACTGCAGATATACAACCT
TGTCGACCTGAAAGGTTGTGGTCTTCTCGTGGATTTGATGAAGAAAGCCGTGCAGACGAAAAATTTTACCGAGCTGG
ACAACGCGATCAAAACCCAAGTGGAACCCATGCTGTACAACAAAGGTGAAGGTAGAATGATACCTATCGCCAAACTC
GTGTTGCTGAGAAATCGCGACCGTTCCCGGGCAAGATGGCTTCCACCGCTAAAGAACATGGAAGACACCAATGATTA
CGACATAGAAAAAGACATTCCCACCATTGAAGAACTGGAAAAGCTGGGGGGAAGTGCAGTACAGGGAAGTGTGCTGGG
ATCTGAAGGAAAGAGGCACCGTCGGCGAAACGGCGTTACATCTATGTTTGCTGAACGCTACGTCAATACACGCAGAC
TTGGCCAAAAGGCTGTTGCATTTCTATCCAAAGCTCGTAAATGACATTTACATGATTGACGAGTATTACGGAGAGAG
CGTTTTGCACATGGCCATCGTCAACGAAGATCCGGCCATGGTGAAGGTACTGATGGACAGCGGGGCTAACCTCAACG
AACGGTGTTTCGGGAACTTCATGAGCACTGAAGATCAAAAGGCTTCTAGATCGGATTCGCTCGACCACGAATGGGTG
AACCTATGTCCCGACACCAATTATGAAGGGTACGTGTATTGGGGCGAATATCCACTGTCATTTGCAGCGTGTCTCGG
CCAAGAGGAGAGCTACCGTTTGATGTTGGCGAGAGGCGCTGACCCAAATAACCAGGACACCAACGGCAACACGGTTC
TGCATATGCTTGTAATTTACGAAAAAATTTCGACGTTCGACATGGCCTACGAAATTGGGGCGGAACTCAACATTAGG
AACGTGCAAAATTTGACGCCACTCACACTGGCCGCGAAACTGGCTCGGATCCAAATGTTCTTTCACATACTCAAAAT
CGAACGGGAAATTTATTGGCAAATCGGCAGTATCACTTGTGCTGCGTACCCCCTGACCCAAATCGACACCATCGACA
ATGACACCGGGCAGATCAGCAGAAACTCGGCGCTCAACTTGGTTGTATTTGGCGAAAGTCCGGAACACTTGGAGATG
ATGGACGGTGTGTTGGTGGATCTGTTAAATGCCAAATGGAACGCTTTCGTGAAATTCCGGTTCTATAGGCAGTTCAT
CTTGTTCGCCTTTTACTTTTCCATATCTATGGTATGCTTCGTGCTGCGTCCCGGACCGCCACCCACTGGTCTTAAGC
CACCATTAATCAACTACACTTCCACGTCGACCACGGTGGCCACCACGCCGTTTGACTTCATGGACAACGAGTCGATG
TTGCCCGACATGTACGACGAGATGATGATCGGCGGTGGCGGTCCGACCGAGTTCGAGACGGTGCAGGTGACCACGGA
AATGGCGACGACCAGCGACAACGCGACGACGACCAACAACGGTAGCGGTATCGGAACGCCACTGATCTACGAGGACG
GCGGCGGTGGAGGTGGTGGAGGTGGTACCGTGAGCTTGCACGGGAAGAGTTCGGGTTCGGACAGGGGCAAACACAGG
AGCACGTGGAGTCCGGCCAACCATACGTTCAAGACCAACTACACGTACAACTACAACAAATCAAGAAAATTTTGGTG
GAACAAGAGACAAAAGGTATGCAGATTAATGGCTGTGCACTCGACTGACGATTTAATCAGAATGGGATCGGAAGTGG
GAATGTTTATGGGAGCATTCCTCTATCTTCTGGCCGCGGTCAGAGAAGCTGGTTTTTTGGGCACACAGATGTTCATT
GAAAACTTGGCCATAGCACCGGCAAGAGTGATGTTTCTGTTCTCGTGCCTGCTCATGATGACCATACCGCCGCTGAG
ACTGACATGCTATGACAAAGCCGAAGACATAATAGCCGTAATCATTATGTTGACCACTTGTCCGTACTTTTTGTTCT
TCTGCAGGGGTTTCAAAACCGTCGGGCCATTCGTGGTGATGATCTATAGGATGGTGATGGGAGACTTGTTGAGGTTC
GTTTCCATTTACATGGTGTTCGTGATGGGTTTCTCGCAAGCTTATTACGTGATTTTCCTGTCTTACGACAATCCGCT
GACGCCAGAGGGTATCGATGACTCGGTACTGAACCCGATGCCCACGCCGACCGAGTCCATCATGGCGATGTTCCTTA
TGTCCGTCAACACGTTCACAGACTACTACACGGCGTTTGACAAGACTAGTCACACGTTGGTCGCAAAGTTTTGCTTT
ATAGTTTTCATGGTAATCGTGGCCATATTGCTGGTGAACATGTTGATCGCCATGATGGGCAACACTTATCAAAAGAT
TGCCGAGACCAGAAACGAATGGCAGAGACAATGGGCTCGGATCGTACTGGTGGTAGAGAGAGGTGTCAGTCCGTCGC
AAAGGCTCATAAAGCTCATGTACTACTCGCAACCGATGTCAGATGGCCGGAGGGCGTTGGTGTTGCGACTCAATCAG
ACGGATGAAGACAAGGAGCAAATGAAAGAGATATTGGAAATGAAACGCATTCACAATCGCTATGTAGAAAGAATGCG
CGCCAGAGACCTGAGCAGCAAACTATCGTCTTCGTGCGGAAAAAATGCAAACAATGGGACATTTAATCTAAAAGCAA
ATGAATAA

FIGURE 21 – SEQ ID NO: 12

<> 23
<> 2124
<> DNA
<> Dendroctonus ponderosae
<> gi|459669722
<> ?
>(gi|459669722:185092-185182, 185261-185343, 185427-185522, 185961-186048, 186740-186916, 186972-187161, 188137-188290, 188952-189102, 190036-190139, 190195-190330, 190603-190754, 192662-192816, 192876-192985, 193039-193220, 193273-193527) Dendroctonus ponderosae unplaced genomic scaffold Seq_983944, whole genome shotgun sequence

ATGGGTAATACCGAGAGTAATGTTACTAGTGGCGTCAAAAAACAGGCGGGAGCCGCCATGCAGCCGATATATAAACT
TTGTGATTTGAAAGGGGGCGGTCTGCTGGTGGAACTTATGAAAAGGGCAGCCCAGAATAAGCAGTACGCGGAAATAG
ATCACGCCATCAAAACTAAGGTGGAACATTTTCTGTACAATAAAGGTGCCGGGCGTTATATCCCAATATCTCAAATG
GTGCTTTTAAGGAACAAGGAACGCGGGAAGCATAAACTGCTGCCCCAACTTAGAGGAATGGAAAATCCTGAGGATTT
TGAAGTCGATGATGAAGGACCCGAAATAACTGAAGAAGAGTACAATAAAGATCCATCATTATATCGGCATGTTTGTT
GGAAGCTGAGAGAAAGAGGAGCGGTTGGAGAAACAATTTTACATCTTTGTTTATTGAATGCCACTTCTCTACATGCA
GACATCGCCAAGAGGCTATTGAGGTTCTATCCCAAATTGATCAACGATATTTACATATCAGATGAATACTATGGTGA
AAATGTTCTACATATCGCCATAGTTAACGAGGATCCTTCCATGGTAAAGTTTCTTCTTGCCGCAAATGTGAACTTTC
AGGAAAGATGTTTCGGTAATTTCATGTGTCCAGAAGATCAGAAATCATCGAGAACTGATTCTCTAGATCACGAATGG
GTGAATGTTTATCACGAAACAAATTATGATGGATATGTGTACTGGGGTGAATATCCATTGTCATTTGCTGCATGTTT
AGGTCAAGAAGAAAGTTTTCGATTAATTTTGGCAAAGGGTGCCAATTTAGATGCACAAGACACTAATGGAAACACTG
TCCTGCATTTATTAGTTATTTATTCCAAAGTGGAAGCTTTCGATATGGCATATGAATTAGGTGCTCACCTTTCAATA
AGGAACATTCTGAAAATGACACCTTTAACGCTGGCCGCCAAGCTAGCAAGAATGGATATATTTTTCCATATTTTAAA
GCTAGAGAGGGAAATATACTGGCAGATAGGAAGCATTACATGTGCCGCCTATCCTCTATCTCAGATTGATACGATAG
ATGTTAAGACTGGACAAATCAGTAAAATGTCAGCGCTGAATCTGGTAGTATTTGGTGATAAAGATGAACATTTAGAA
CTGCTCGATGGAGTATTAGTTGATCTATTAAATGCCAAGTGGAATACGTTTGTGAAATCTAAATTTTACCGGCAATT
TTTTACTTTTGCGTTTTATTTCACCGTATCGCTTGTGGATACCAGCAATGATGATTATGATGTTGAGGAATGGTGGG
ATAATTTACGAGAGGAATGTCGATTAATGAATTTAGACACGACTGAGTCACTAGTGAGATTTACTGCTGAACTTGGA
ATCACGTTTGGTGCATTTCTTTATTTGGCGGCCGCAATGACTGCTCCTTCGAGAGTTATGTTCTTGTTTTCCTGCAT
TTTGGTTTTTGGAGTAATTCCTAGCCTGCGCTTGGTATGCATGGATGAAGTTGAAGATATAATCGCAGTAGTAGTTA
TGCTAACGACGGCTCCATATTTCCTATTTTTCTGTAGAGGCTTTAAAACAGTAGGTCCGTTTGTGGTAATGATCTAT
CGCATGGTTCTAGGCGACTTGCTACGTTTCGCAACTATATACATGGTTTTTGTCATGGGATTTTCTCAAGCATACTA
CATAATTTTCTTGTCTTTTGATAACCCATTGACACCAGAAGACGTCGATGACTCGGCTACGAATCCAATGTCAACTC
CATCCGAATCCATTATGGCAATGTTTTTAATGTCCATGACCAACTTCGGAGATTATTACACAGCATTTGCTAGGACC
GAGCACGAATATGAGGCTAAAATTCTTTTCGTAATATTTATGGCCATTGTGGCAATTTTGTTAATTAATATGTTAAT
CGCTATGATGGGTAACACATACCAAAAGATAGCGGAAACGCGTAACGAATGGCAGCGACAGTGGGCTCGCATTGTTT
TGGTCGTAGAAAGAGGTGTTAGCCCACCTGAACGGCTCAAGCAATTGAATGTTTATTCACAACCAATGAGCGATGGC
AAAAGAGCTCTCGTTTTAAGGCTCAACCAGTCGGTAAGATATTAG

FIGURE 22 - SEQ ID NO: 13

<> 25
<> 2718
<> DNA
<> Harpegnathos saltator
<> gi|307201159
<> ?
>(gi|307201159:26763-26853, 32620-32798, 32877-32964, 33380-33556, 33655-33844, 34113-34266, 34456-34710, 34779-34861, 34958-35470, 36042-36207, 36369-36630, 38038-38219, 38530-38646, 38749-38874, 38961-39095) Harpegnathos saltator unplaced genomic scaffold scaffold1583, whole genome shotgun sequence

ATGGGCAATACCGAGAGCAACGTCACGAGCGGCGTGAAAAAGCAGACGGACACGTCGTCCATCATGCTTTATAAGTT
GGTCGATCTGAAAGGCGGTGGGTTGTTCGTAGACATGATGAAGAGAGCAGCGCAAACTAAGCAGTTCGCAGAGTTGG
ATCACGCGGTGAGAACAAAGGTCGAGCCCTACCTGTACAACAAAGGAAAGGGCAAGTGGATACCCGTGGACAAACTG
GTTCTTCTAAGAAACAAAGATCGTCCGCGACATAAAATGCTGGCACCTTTGAAAGCCATGGAAAATCCGGCGGATTA
CGACATAGATAAGGACATGGGTGATGAAGATGTTGACGAGACTAAAATAGACAAAAGCAAATACAGACTGGTCTGCT
GGAGCCTGAGCGAGAGAGGCGCTGTCGGTGAAACTATCCTGCACTTGTGCATGTTAAATGCCACTGCTCTCCACGCG
GATCTGGCGAAACGATTGCTACGCTTCTATCCGAATCTCATAAACGACATTTACATAAGCGACGAATACTACGGAGA
GAACGTGCTGCACATCGCGATCGTAAACGAGGACCCAGCGATGGTGAAGTATCTTCTAGACAGCGGTGCGGATGTTC
ACGAGAGGTGCTTCGGTAACTTCATGTGTCCGGAGGATCAGAAAGCGTCAAGGGTTGATAGTCTGGACCACGAGTGG
GTGTGCGTTGCACCGGAGACCAATTACAGCGGATACGTGTACTGGGGAGAATACCCGTTGAGCTTCGCCGCGTGTCT
GGGCCAGGAGGAGTGCTACAGGCTTATGCTCGCCAGAGGCGCGGATCCTGACAAGCAGGACACCAACGGCAACACGG
TTTTGCACATGTTGGTGATATATGAGAAGCTGACTACGTTCGACATGGCGTACGAAGTGGGAGCCTCGTTGGCCATA
AGAAACGTCCAACACCTGACTCCGCTGACGTTGTCAGCAAAGCTGGCCAAGATCGAGATGTTCTTTCACATTCTGAA
CATCGAGAGAGAGATATACTGGCAGATCGGTAGCATAACTTGCGCAGCTTACCCGTTGTCGCAAATAGACACGATCG
ATATTAACATCGGGACTATCAACAAGAACTCCGCCCTGAATTTGGTTGTTTTTGGGGAAAAAGACGAGCATCTAGAA
TTGATGGACGGTATGTTAGTCGACCTTCTGAACGCCAAGTGGAACACTTTCGTTAAGTCTCGATTCTACCGTCAATT
CTTCCTCTTCTGCTTCTACTTCGTGCTGTCGCTGATCAGCTTCACTCTTCGCCCGGGCCCGTTGCCGCAGGAGACCG
AAAATGCGAACGATACGAGAACGAATTCATCGAACGCAACGGCGATGGAGATTCTTAGGTTGTTCCAAAGCTCGGAC
CTGTCGAACCTCGTCACGAACAGCCTCGCCGCGGCTTTTGCCTCGAACCTCAAATCGTCCTTAAACGTGACGCAAGA
ATCGTTGGAGAAGATCCAGCTGCAAGTGACGTCGAACATTACATCGGCCCTGAAGAATATTTTGCCTTCGCTGAGCG
ACAACGAGGGCATCCTGAGTGCCCCTGACGAAGCCGCCATTCGTACGCTGTGGTATACCAGTAGTCCGTACAATGAG
TCAGATTACTTGACAGATGCTTACAACGAGAATGTCACGAGCGATGCGAATTCGACCGCGGGGACGATCATCGGCAG
CATCGAGGTGTCGAAGTCCAACGATAAGGACAATTGGTGGGAAGATCTGACGGAAGAATGCAGGCTGATGCAGCTAA
CGACGATAAGTGCGAAGATCCGGCTGACTGCGGAAGTGCTGATGGAAATCGCCGCGGTGCTCTACATTTTAGCCGCA
CTGCGGGAGGCGAGGTTTTTGGGGCTCAACATGTTCGTCGAGAATCTAATGACAGCGCCGTCGCGCGTCATGTTTCT
CTTCTCGTGCTGCATCTTACTCTCGTTTCCATTTCTGAGATTAGCCTGCGCCGACGAAGTCGAAGACATGTTGGCGG
TCGTGGTGATGCTGACAACGGCACCGTATTTCTTATTCTTCTGCAGAGGCTTCAAGACGGTCGGTCCGTTCGTCGTG
ATGATTTACAGGATGATCATGGGCGACCTCCTCAGATTCGTGTCCATCTATCTGGTCTTCGTCATGGGCTTCTCTCA
AGCGTACTACATTATATTTCTGTCGTTCGACAACCCGAATACCCCGGAAGGCGTCGACGATTCGGTATCGAACCCGA
TGCCGTCGCCGATGGAGAGCATCATGGCGATGTTCCTGATGAGCATGACGAACTTCGGCGACTACTACGGCGCGTTC
GAGCGAACCGAACACGAGTCCGAGGCTAAGCTGCTGTTTGTGTTGTACATGGCGATCGTGGCGATCCTGCTCGTAAA
CATGCTAATTGCTATGATGGGCAACACTTACCAGAAGATCGCCGAGACCAGAAATGAATGGCAAAGACAATGGGCGC
GCATAGTTCTGGTCGTGGAGAGAGGAGTCAGCCCCGCCGAGAGGCTGAAGAAGCTCATGGACTACTCTCAGCCGATG
TCCGGCGGCCGTCGAGCGTTGGTCCTCCGGTTGAATCAAAGTGAGGAGGACAAGGAGGAGATGAAGGAAATACTCGA
GATGAAGAGGACCCACGATAGACTGCTGAAGAAGAGGCAAGGGAGAATGTCAAAGGAGAAAGTTCTGGCCGAGAGCG
AAATTATTATTACCCGAAATTGA

FIGURE 23 - SEQ ID NO: 14

<> 27
<> 2756
<> DNA
<> Nasonia vitripennis
<> XM_001606052.2
<> ?
>gi|345488310|ref|XM_001606052.2| PREDICTED: Nasonia vitripennis nanchung, transcript variant 1 (Nan), mRNA

ATGGGTAACGCCGAGAGCAACGTCACCAGCGGCGTGAAAAAACAGACGGATGCAGGTGCGATCGCCCTGTACAAACT
CGTTGATCTCAAAGGTGGTGGTCTGCTGGTGGACATGATGAAGCGGGCCTCGCAAACGAAACAGTACGCTGAGATAG
ATCACGCAATTAGGACAAAAGTCGAGCCGTTTCTGTACAACGGAGGCAAAGGCAAGTGGATACCCATAGCGAAACTG
GTGCTCTTGAGGAATAAAGAAAGGGGGAGACACAAAATGTTACCCGTGCTCAAAGCCATGGAGAAGCCCGAGGACTA
CGATATCGATAAGGACATGGCTAACGACCCGGAGCCGGATGAAAACACAATCGACAAGAGTAAATACAAGCTCGTCT
GTTGGACCCTGAGCGACAGAGGAGCAGTGGGCGAGACGATTCTGCATCTCTGCATGCTCAACGCCACGCAGCTCCAC
GCGGATCTGGCGAAGAGGCTGCTGCGCTTCTATCCGAACCTCATCAACGACATTTACATCGATGACGAATACTACGG
AGAGAACGTCCTGCACATCGCGATAGTGAACGAAGACCCGTCGATGGTGAAATTCCTGCTGGACAGCGGAGCGAACG
TGAACGAGCGTTGCTGCGGCAACTTCATGTGTCCGGAAGATCAAAAGGCTTCTAGGAACGACAGCGTCGAGCATGAA
TGGGTCTGCGTATGCTCGGAAACCAACTACGATGGTTACGTCTACTGGGGCGAGTATCCTTTGAGCTTCGCAGCCTG
TTTGGATCAGGAGGAATGCTACCGGCTGATACTAGCCAAAGGCGCCGATCCAGATAGCCAGGACACGAACGGCAACA
CCGTTCTCCACATGCTCGTCATTTACGAAAAGCTCGAAACCTTCGACATGGCCTACGAGGTCGGTTCTTCCTTGTCG
ATACGAAACGTCCTGCAACTGACACCTTTAACGCTAGCCGCCAAACTCGCGAGGGTGGAGATGTTCTTCCATATTCT
GAACATCGAGCGCGAGATCTACTGGCAGATCGGTAGCATCACCTGCGCGGCTTATCCGCTTTCTCAGATCGACACTA
TCGACGTGGACACCGGAAAGATCAGCAACAACTCGGCGTTGAATTTGGTCGTTTTCGGTGATAAAGAGGAGCATCTC
AAACTGCTGGAAGGCGTGCTGATCGATCTACTGAACGCAAAGTGGAATACTTTCGTCAAGTCCAGGTTCTACCAGCA
GTTCTACCTCTTCTTCTGTTACTTCATCCTCTCGCTGATAAGCTGCACCCTCCGACCTGGTCCCATAACGAAGACCG
ACGCTCCAACCACGACACCACATCCCATGAACGACACGAGCATCGAGTCCATCACTCCGACCTCGGAACCTTTAGAG
CTGCAGACCTTGTCGTCGCTTCTGGCGAAAAACTTGGCCGAACAACTCGTCATGGGTATGAAGATGTACGGCAACGT
CTCCGAGGACTCACTCGCGAGGATAAGTCTCCAGGTGGCTTCAAACATCAGCGGCTCGATCAAGGACATCTGGACGA
GGCAGAACCTCACGAGCAACGACACCGACTACGTCGATATCGCAGGAGGTCTGTACGCGGACGTCAACGAGACCAGC
GCGAGTGATCCCTTCGATTTGAACGCGAGCGATATCGTGATTCTTAAGAAGGGAAAGAAGGAACTCGATGACTGGTG
GGATGACCTAACCGAAGACTGCCGACTCATGCAGATGAACAGTACCTCGGCGAAAATCCGCCTGACGGCCGAGATAT
TCATGGAATTCGGCGCTATACTTTACATATGCGCTGCGCTCCGAGAGGCGAGGTTCCTCGGGCTCAACATGTTCATC
GAGAATCTCATGACGGCTCCGTCGCGCGTCATGTTTCTCTTCTCCTGCTGCATCCTCCTGTCCTTTCCGTTTCTGAG
GATGTCCTGCGCCGACGAGGTCGAGGACATACTCGCTGTAGTGGTGATGCTCACGACCGCGCCCTACTTCCTCTTCT
TCTGCAGAGGCTTCAAGACCGTCGGGCCCTTCGTCGTCATGATCTACAGGATGATCATGGGTGACCTGCTCAGATTC
GTCTCGATCTATCTGGTCTTCGTCATGGGCTTCTCTCAAGCTTACTACATAATCTTCCTGTCGTTCGACAATCCGAT
CACGCCCGAGGGTGTCGACGACAGCAAAGCTAATCCACTACCGTCAGCCATGGAGAGCATCATGGCGATGTTCCTCA
TGAGCATGACGAATTTCGGCGATTACTACGACGCTTTCGAGAACACCGAGCACGAGATGTTGGCCAAGTGTCTCTTC
GTCGTGTATATGGCCATTGTGTCGGTTCTACTGGTGAACATGCTCATCGCTATGATGGGCAATACCTACCAGAAGAT
CGCTGAAACGAGGAACGAGTGGCAGAGACAGTGGGCTAGGATAGTTCTCGTGGTGGAGAGAGGAGTAGCCCCGGCGG
AGAGATTGAAGAAACTGAACGTTTACTCGCAACCGATGTCCGATGGGCGTAAGGCATTGGTACTGAGGTTGAATCAA
ACTGACAAAGATAAGGAGGAGATGAAGGACATCCTGGAAATGAAGAGGATACACATAAAATCGATAAAGAGACGCAA
GGACAAGCTGCAGAAGGCGAAAGAAGACGCTGAAAAGCTCCAGCAGCAGATGGCCGATAAGGACAATAAGGACAAAG
CCGTTATTATACAATGAGAATTTTTCTATGTATATAATAAAGCGCTCTTGTAAATATATTC

FIGURE 24 - SEQ ID NO: 15

<> 29
<> 2712
<> DNA
<> Megachile rotundata
<> XM_003706124.1
<> ?
>gi|383861395|ref|XM_003706124.1| PREDICTED: Megachile rotundata transient receptor potential cation channel subfamily V member 6-like (LOC100883930), mRNA

ATGGGGAACACGGAGAGTAACGTAACTAGCGGCGTGAAGAAACAAACAGACTCCTCTTCTATCTTACTTTACAAGCT
GGTCGATTTAAAAGGTGGTGGTTTATTAGTGGACATGATGAAAAGAGCAACGCAAACTAAACAGTACGCTGAACTAG
ATCACGCTCTAAGAACAAAAGTGGAGCCGTATTTATACAATAAGGGTAAAGGTAAATGGATCCCGATAGAAAAGTTG
GTTCTACTGCGGAATAAAGATCGTCCGAAGCATAAAATGCTTCCACCATTGAGGGCTATGGAGAATCCGGCTGATTA
CGACATAGACAAGGATATGGGCGAGGAAGAAGTGGACGAAACGAAGATAGATAAAAGCAAGTACAGATTGGTCTGCT
GGAGCTTGAGTCAAAGAGGAGCAGTAGGAGAGACGATTATGCATTTATGCATGTTACATGCGACTGCTATTCACACC
GATCTGGCTAAACGTTTACTACGTTTCTATCCTAAGCTCATCAATGACATCTATATCAGTGACGAATACTATGGTGA
AAATGCATTACACATCGCTATAGTGAACGAAGATCCAGCTATGGTAAAGTTCCTTCTAGACAGCGGCGCCGACGTGC
ACGAAAGATGCGTAGGAAATTTTATGTGTCCGGAGGATCAGAAAGCGTCGAGAACAGACAGCGTGGACCACGAATGG
GTTTGCGTGGCTCCCGAAACGAATTACAGCGGATACGTTTACTGGGGTGAATATCCATTAAACTTCGCCGCGTGTTT
AGGCCAAGAAGAGTGCTACAGATTGATACTCGCTAGAGGAGCAGATCCCGACAAGCAAGACACCAATGGAAACACGG
TTCTGCACATGTTGGTGATCTATGAAAAGATGGCCACGTTCGATATGGCGTACGAGGTAGGAGCATCGTTATCGATC
AGAAACGCGCAACATTTGACACCGCTGACGTTATCGGCGAAGCTGGCAAGGATCGAAATGTTTTTTCACATTTTGAA
CATCGAGAGGGAGATTTATTGGCAGATTGGCAGCATTACGTGTGCGGCTTATCCCCTCTCGCAAGTGGACACTATCG
ATGTGAACACTGGTAGCATCAGCCACACTTCCGCCCTGAATCTGGTGGTCTTTGGAGAAAAGGATGAGCACTTGGAA
CTAATGGATGGTACCATGGTTGACCTATTAAACGCGAAGTGGAACACCTTTGTCAAGTCCAGATTTTATCGCCAGTT
CTTCCTATTTTGTTTTTACTTTATTCTTTACTTGATCAGTTTCACTCTTCGACCTGGTCCTTCGGTCACATCGACTG
CTACAACTGCTCCGACTACAGAATCGACCACACCGAAATTGCCAGATCCTCCTCCAAATTTTATTCCAGTTACGAAT
CAAAAAACGTTTCTCGAAGCGAGCCTCTCGTCGTCCTTGGATGAAATTGTGACAAACGCCCTGAATTTAAATTTCCC
TTCGAACGCGACGGCTCGCTTTGACGATCTAAAACTCGATCTCGTAACCCACATAATGTCTAATCTGAAGAACATAT
TGAATGGGAACGAGACCAAAAACGAGCCATTTAACAGCTCCCAACTCGCCAGGTTTGACAAACATTTATTCCGCGAA
AATGACACTGATTATTCTACTAGCATCTTGAACGAGACCGCCGACGTTGATTCCACGACGAAGTTTTCGTTTGACAA
TTCTGTACTGTTTGAGGCTGATAATAAAAGCGATTGGTGGACTGATCTTACCACAGAATGCCGATTAATGCAACTGA
CCACCGCATCCGCGAAGATCCGATTAATCGCAGAAATATTTATGGAAATCGCAGCTATTCTTTACATTCTTGCAGCG
CTAAGAGAGGCCAGGTTTCTAGGTCTCAACATGTTCATCGAAAATCTGATGACTGTACCATCGAGAGTAATGTTTCT
CTTCTCCTGTTGCATACTGCTCTCTTTTCCGTTTCTGAGATTATCCTGTGCTGACGAAGTGGAAGATGTGCTAGCAG
TGGTAGTAATGTTGACTACAGCACCATATTTTTTGTTCTTCTGCAGAGGTTTCAAAACGGTCGGCCCTTTCGTCGTG
ATGATTTATAGAATGATCATGGGCGACCTACTTCGGTTCGTATCCATCTATTTGGTCTTTGTAATTGGATTTTCTCA
AGCTTATTACATCATATTTCTATCTTTTGATAATCCAAACACGCCAGAAGGTGTTGATGATTCAGTGAGCAATCCAA
TGCCATCACCAATAGAAAGCATCATGGCAATGTTTCTAATGAGTATGACGAACTTTGGAGATTACTATGGTGCATTT
GAGAGGACCCGACATGAAATGGAAGCCAAGTTTCTGTTTGTTGTATACATGGCTATTGTTGCTATCTTACTTGTGAA
CATGTTGATTGCTATGATGGGGAATACGTATCAAAAAATTGCAGAAACTAGGAATGAATGGCAGAGACAATGGGCAC
GTATAGTTTTGGTAGTAGAAAGAGGAGTAAGTCCTCAAGAAAGGCTTAAAAAATTGATGGATTATTCTCAACCAATG
TCTGATGGCCGCAGAGCATTGGTGCTCAGATTAAATCAATCGGAAGAAGATAAGGAAGAAATGAAGGAGATTTTGGA
AATGAAGAGGACTCATGAGAGATTATATAAAAAGAGGCAACTTAAAACAACAAAAGAAAAGACTACAATAACAGAGG
AGAATGTTACTTTATAG

FIGURE 25 - SEQ ID NO: 16

<> 31
<> 2664
<> DNA
<> Apis mellifera
<> XM_625167.3
<> ?
>gi|328787658|ref|XM_625167.3| PREDICTED: Apis mellifera nanchung (Nan), mRNA
ATGGGAAATACGGAAAGCAACGTAGCCAGCGGAGTGAAGAAACAGACGGACGCATCGTCCATTTTGCTTTACAAATT
GGTCGACTTGAAAGGTGGTGGCCTATTGGTGGATATGATGAAAAGGGCAACGCAAACTAAACAGTACGCGGAATTGG
ACCATGCCCTGAGAACAAAAGTAGAGCCATATTTATATAACAAGGGTAAAGGTAAATGGATCCCGATCGAGAAATTG
GTTTTGCTGAGAAACAAAGATCGTCCAAAGCACAAAATGCTTCCACCGTTGCGAGCTATGGAAAATCCGGCCGATTA
CGACATAGACAAAGATATGGGCGAAGACGAGGTGGACGAGACGAAAATAGATAAAAGCAAGTACAGATTAGTGTGCT
GGAGCTTGAGCGAGAGAGGAGCGGTCGGTGAAACGATTCTACATTTGTGCATGCTACACGCAACTGCTATTCACATC
GATTTGGCTAAACGTTTGCTACGTTTTTATCCCAAGCTTATCAACGATGTGTACATAAGCGACGAGTATTATGGCGA
GAGCGCGTTACACATCGCGATTGTAAACGAGGACCCGTCAATGGTAAAATTCCTTTTGGATAGCGGTGCGGACGTGC
ACGAGAGATGCATAGGAAACTTTATGTGTCCAGAGGATCAAAAAGCGTCGAGGGCGGACAGTCTTGATCACGAATGG
GTTTGCGTAACTCCGGAAACCAATTACAACGGGTACGTTTACTGGGGCGAGTATCCTTTAAATTTTGCTGCGTGCCT
GGGACAGGAAGAGTGTTACAGATTGATACTCGCAAGGGGAGCCGACCCCGACAAGCAAGATACGAACGGAAATACCG
TTTTACACATGTTGGTCATTTACGAAAAATTGGCCACGTTCGACATGGCGTACGAGGTGGGAGCATCGTTGGCCATC
AGGAATGCCCAACACTTAACGCCCTTGACATTGTCGGCGAAATTGGCGAAGATCGAGATGTTTTTCCACATTTTAAA
CATCGAGCGAGAGATTTATTGGCAGATCGGAAGCATAACGTGCGCAGCTTATCCTCTCTCGCAAGTCGACACCATCG
ATGTCGACACGGGAAGCATTAGTCATAATTCCGCTCTAAATCTGGTCGTATTCGGCGAAAAAGATGAGCATTTGGAA
TTGATGGACGGAATCCTGGTCGATCTGTTGAACGCCAAATGGAACACGTTCGTCAAATTTCGCTTTTACCGCCAATT
TTTCCTCTTTTGCTTCTACTTCGTCCTGTCGTTGATCAGTTTCACCCTTCGACCCGGCCCAGCAACAACATCGTCCG
TATCCAATCCTCAGATCACGTCCACCGAATTGCCCACAATTCCCCCAAAAATGGATCCACCCGTCCACAATTCCGAT
CTCCCCCTCCTCCTTGACAAAATTCTTTCCACCGCTCTCGTCTCGAAAAGGTATCCTTGGAATTTGACGAGAACGCG
TCTCGACAAGCTGAAGCTCGATATCGTGGAGAACTTGACATCCGCTTTGAGCGATATGCTCGGGACATACCGAAACG
AGATCAAATTGTTTAACCGTTCTGACAAAACGTCCATCTACTCGTCTAGAAACGACGCTAAACCGATCGACGAGACT
GTCCTCCGGATAAATTCGACGATCCTGTTCAACGGCGATGGGATATCGTTTACCAGCAAGTACAATTGGTGGAACAA
TCTTACAGAGGAATGCAGACTCATGCATCTAGATACGTTATCGACAAAGATTAGATTGACTGCCGAGGTATTAATGG
AAATTGCGGCCACTCTTTATATTTTTGCAGCATTGCGCGAAGCCAGATTTCTAGGTCTTAATATGTTTATAGAAAAT
CTAATGACCGCACCGTCCAGAGTGATGTTCCTCTTCTCATGCTGTATATTGTTAACCTTCCCGTTTCTAAGATTGAT
CTGCGCCGACGAAATTGAAGATATGTTAGCCGTGGTCGTCATGCTCACCACGGCACCGTATTTTCTATTCTTCTGCA
GAGGTTTCAAAACGGTCGGCCCATTCGTCGTGATGATTTACAGAATGATCATGGGCGATCTGCTACGTTTCGTCTCC
ATTTACTTGGTCTTCGTGATGGGATTTTCCCAAGCATACTACATTATATTTTTATCTTTCGATAATCCAAACACACC
GGAAGGAGTAGACGATTCGATGAGCAATCCGATGCCATCACCAATAGAAAGTATAATGGCGATGTTTCTTATGAGCA
TGACAAACTTTGGAGATTATTATGGTGCTTTTGAAAGAACGCAACACGAGATGGAAGCCAAATTCTTATTTGTAGTT
TACATGGCTATCGTTGCTATATTATTGGTAAATATGTTAATTGCCATGATGGGGAATACATATCAGAAAATTGCAGA
AACGAGAAATGAATGGCAAAGACAATGGGCACGCATAGTTTTAGTAGTTGAAAGAGGAGTGAGCCCTGATGAAAGAC
TTAAAAAATTAATGGATTATTCTCAACCAATGTCTGATGGTCGAAGAGCATTGGTACTTCGATTGAATCAATCGGAA
GAGGACAAAGAAGAAATGAAGGAAATTCTAGAGATGAAAAGAACTCATGATAAATTATACAAAAGAAGACAGAGCAA
AACAATGAAAAAGATTTTAACATCAGAAGATAATGTTATTTTATAA

FIGURE 26 - SEQ ID NO: 17

<> 33
<> 2739
<> DNA
<> Apis florea
<> XM_003689958.1
<> ?
>gi|380011848|ref|XM_003689958.1| PREDICTED: Apis florea transient receptor potential cation channel subfamily V member 5-like (LOC100863041), mRNA

ATGGGAAATACGGAGAGCAACGTGGCCAGCGGTGTGAAGAAACAGACGGACGCGTCGTCCATTTTGCTTTACAAATT
AGTCGACTTGAAAGGAGGTGGTTTATTGGTAGATATGATGAAAAGGGCAACGCAAACTAAACAATACGCGGAATTGG
ATCACGCACTGAGAACAAAAGTAGAACCGTATTTATATAACAAGGGTAAAGGTAAATGGATCCCGATCGAGAAATTG
GTTTTGTTGAGGAACAAGGATCGTCCAAAGCACAAAATGCTTCCACCGTTGCGGGCTATGGAAAATCCGGCCGATTA
CGACATAGACAAAGATACGGGCGAAGATGAAGTGAGGGACGAGACGAGAATAGATAAAAGCAAGTACAGATTAGTAT
GCTGGAGCTTGAGCGAGAGAGGAGCAGTCGGTGAAACAATTTTACATTTGTGTATGCTACATGCAACTGCTATTCAC
ATCGATTTGGCTAAGCGTTTGCTACGTTTTTATCCCAAGCTTATCAACGATGTTTACATAAGCGACGAGTATTATGG
CGAGAGCGCATTACACATCGCAATCGTGAACGAGGATCCGTCAATGGTGAAATTCCTTTTGGATAGCGGTGCGGACG
TGCACGAAAGATGCATAGGAAACTTTATGTGTCCAGAGGATCAAAAAGCGTCGAGAGCGGACAGTCTGGATCACGAA
TGGGTTTGCGTAACTCCGGAAACTAATTACAACGGGTACGTTTACTGGGGCGAGTATCCTTTAAATTTTGCCGCGTG
TTTGGGACAGGAAGAGTGTTACAGATTGATACTCGCGAGGGGGGCTGACCCCGACAAACAAGATACGAACGGGAACA
CCGTTTTACACATGCTGGTCATTTACGAAAAATTGGCGACATTCGATATGGCGTACGAAGTGGGCGCATCGTTAGCG
ATCAGGAATGCTCAACACTTAACGCCCTTGACGTTGTCGGCCAAATTGGCAAAGATCGAAATGTTTTTTCACATTTT
GAACATCGAGCGAGAGATTTATTGGCAGATCGGAAGTATAACGTGCGCAGCTTATCCTCTCTCGCAAGTCGACACCA
TCGATGTCGACACGGGAAGCATTAGCCACAATTCCGCTCTAAATCTGGTCGTGTTCGGCGAAAAAGACGAGCATTTG
GAATTGATGGACGGGATTCTGGTTGATCTGTTGAACGCCAAGTGGAACACATTCGTCAAATTTCGGTTTTATCGTCA
ATTTTTCNCTTTTTGTTTTTACTTTGTCCTGTCGTTGATCAGTTTCACCCTTCGACCTGGCCCAGCGACGACATCAT
CCGTTCCCAACCCCGTCGCTCAAACGCCCCTTACGTCCACCGAATTGTCCACAATTTCCCCAAAAGTGGATCCTCCC
GTCTCGAACGTTACTGTCAATCGAAGCTCGAATGCTTTCCAACACGATTCCAATCTCTCCCTCCTTCTTGATAAAAT
TCTTTCCACTGCAAGCGTAAAATATCCTTGGAACGTGACAAGAACTCGTCTCGATAAGCTGAAGCTCGATATCATCG
AGAATTTGACAACCGCTTTGAACAATCTACTGTCGACACACCGAGACGAGATCGAATTTTTTAACCACTCTTACAAA
ACAACCGAATATTTCCATTCTACGAGAAACGATACCACGCCGATCGATAATTTGAAAATTACGATCAATGAAACTGT
CCTTTCGGTAAATTCGACGATTCTGTTCAACGATGGGATATCGTTTGCCACTGGCAAATACAACTGGTGGAACAATC
TTACAGAAGAATGTAGACTAATGCATGTAGATACGTTATCGACAAAGATTAGATTGACTGCTGAAGTATTAATGGAA
ATTGCGGCCACTCTTTACATTTTTGCAGCATTGCGAGAAGCCAGATTCCTTGGTCTTAATATGTTCATTGAAAATCT
AATGACTGCACCGTCCAGAGTGATGTTTCTCTTTTCCTGCTGTATATTGTTAACCTTCCCATTTTTAAGATTGATTT
GCGCCGACCAAGTTGAAGATATGCTAGCTGTTGTCGTTATGTTAACCACGGCACCGTATTTCTTATTTTTCTGTAGA
GGTTTCAAAACGGTCGGCCCATTCGTCGTGATGATTTACAGAATGATCATGGGCGATCTCCTCCGTTTCGTCTCCAT
TTACTTGGTCTTCGTGATGGGATTTTCCCAAGCATACTATATTATATTTTTATCTTTCGATAATCCAAATACACCGG
AAGGAGTAGATGATTCGATGAGCAATCCAATGCCGTCACCAATAGAAAGTATAATGGCAATGTTTCTTATGAGCATG
ACAAACTTTGGAGATTATTATGGTGCTTTTGAAAGAACGCAACACGAGATAGAAGCCAAGTTTTTATTTGTAGTATA
CATGGCGATCGTTGCTATATTATTGGTAAATATGTTAATTGCCATGATGGGAAATACGTATCAGAAAATTGCAGAAA
CAAGAAATGAATGGCAAAGACAATGGGCACGTATAGTTTTAGTAGTTGAAAGAGGAGTGAGCCCTGAGGAAAGACTT
AAGAAATTAATGGATTATTCTCAACCAATGTCCGATGGTCGAAGAGCATTAGTACTTCGATTGAATCAATCGGAAGA
GGACAAAGAAGAAATGAAAGAAATTCTAGAGATGAAAAGAACTCATGATAAATTATACAAAAAAAGACAGAGCAAAA
TAATGAAAAAGATTTTAACATCAGAGGATAATGTTATTTTATAA

FIGURE 27 - SEQ ID NO: 18

<> 35
<> 2472
<> DNA
<> Pediculus humanus corporis
<> XM_002427918.1
<> ?
>gi|242014576|ref|XM_002427918.1| Pediculus humanus corporis conserved hypothetical protein, mRNA

ATGGGAAATACAGAGAGTAACGTTACGAGTGGTGTAAAAAAACAAGCGGGAACATCCGAACAACCATTGTACAAATT
AGTCGGTTTAAAAGGTGGAGGTCTTTTGGTCGACATGATGAAAAGAGCGACACAAACGAAACAATATGCTGAATTAG
ATCACGCGATCAAAACAAAAATTGAACCTTTTTTATATAACAAAGGAAAAGGAAGATTGATACCCATATCACAGTTG
GTACTTTTAAGAAACTGCGAAAGATCTAGAACAAAATTGCTTCCGCTTCTTAAAAACATGGAAGATCCAGAATCTGA
ATTTGACATGGATCGTGATGGAAATCCTGGAGATTTTCAACCGGCTCCAGATGGCGTACAAGAAGATTTTCACGATT
ACAATAAAAAATATAGAGACGTTTGTTGGGATTTGAAAAAAAGGGGAGCCGTGGGAGAAACATGCCTTCACCTGTGC
ATGCTTAATGCCACGTCAATCCACGCGGATTTAGCTAAAAGATTATTAAAATTTTATCCGAAACTTATAAATGACAT
TTACATGTCGGACGAATATTACGGTGAAAGCGTTCTTCACGTGGCAATAGTAAATGAAGATCCTGCCATGGTTAAAT
ATTTACTCGATAGCGGTTCTAATTTTCACGAACGTTGTTTTGGAAATTTCATGTGTCCAGAAGATCAAAAAGCAACA
AGAACGGATTCTCTCGATCATGAATATGTTAATTTATCAACGGAAACTAATTACGAAGGATACGTTTATTGGGGAGA
ATATCCGTTAAGTTTTGCAGCTTGTTTGGGACAAGAAGAAAGTTATCGTTTGATGCTTGCCAAGGGTGCCAATCCCG
ATAATCAAGATACAAATGGCAACACTGTTTTACACATGCTCGTCATACATAATAAATTGCCCATGTTTGACGTGGCT
TATGAAGTTGGCGCCAATTTATCGTTAAAAAATGCAAAATGTCTAACGCCACTTACACTTGCGGCAAAATTAGCAAG
AGTCGAACTTTTTTTTCATATTTTAAACATAGAAAGAGAAATTTATTGGCAAATAGGGAGCATAACGTGTGCGGCAT
ATCCGTTATCACAAATCGATACGATTGATATCGAAACCGGAAACATAAGTAAAAATTCAGCGTTAAATTTAGTCGTT
TTCGGAGAAAAAGACGAACATTTAGAACTCATGGATGGAGTATTGGTAGATTTATTAGTCGCAAAATGGAACACCTA
CGTTAAATTCAGATTCTACAGGCAATTTATATCTTTTTTTTTCTATTTTCTTATCTCTGTTATCTGTTTTACACTTC
GACCCGGTCCTCCGACAGGAACAACAACAACAACAAACGGTATCGTCGTTTTAAATAATAATAACAACAACATAACG
TCCGTTGTTGATAATTCAAATAACGTTACCACCACCACCGCCACAACTACTGCCACGTCATATTCTTTTCCTGGTCA
CGTGATAGTGACACTTTTATCGTATGATAAATACGAAGATAAAATACGTATAATATCAGAATTAGCGATGGAAATCG
GATCTGTTTTGTATTTGTTAGGAGCATTGAGAGAAGCTAAATTTTTAGGGATTCACATGTTTATTGAAAATTTGATG
ACAGCTCCGTCGAGAGTTTTATTTTTAGGTTCTTGTTGCATAATGCAATTCGTACCTTGGCTCAGGATCACGTGTAA
AGAAGAAACGGAAGATATCGTTGCCGTTATCATTATGTTAACGACGGCTCCATATTTTTTATTTTTTTGCAGAAAAA
TGAACGACCCCGTTTTTCTTTTTCTTTTTTTTTTTAATAAAAAAAATTTTTTTTCTAATTTTTTTTTTTTTTTTTTT
ACAAAGCCAACTTATTATATAATATTCCTTTCGTTTGATAATCCAAAAACTCCCGATGGAGTCGACGATTCTGGAAC
AAATCCAATGCAAAGCCCAGTTGAATCCATAATGGCAATGTTTTTAATGTCTCTGACAAATTTTGGAGAATATTACG
GTGCATTCGAAAAGACTGAACACGAATTTGTTGCAAAGTTAATGTTTGTCGTTTACATGGCTATCGTTGCTATATTA
CTCGTTAACATGTTGATCGCCATGATGGGTAATACGTATCAAAAAATAGCAGAAACGAGAAACGAATGGCAAAGACA
ATGGGCAAGAATTGTTTTGGTTGTTGAAAGAGGTGTGAGTCCTCAAGAAAGGTTAAAAAAATTAATGCTTTATTCTC
AGCCTATGTCTGACGGAAGAAGAGCATTAGTTTTACGATTGCATCAAACGCCAGAAGACAAAGAAGAAATGAAAGAA
ATATTAGATATGAAAAGAATACACAATAGAACGGTTCAAAGGCGAAAAGCTAAAGAAAATAAAAATGTCACGTTTGC
TGGTACCCCTAAAAATGGCATTAAAAATCGTTTGCTCGGTCCCGTTCCCCCATTAAAAAGCATACCGTCAAAACCTA
AAATTTAA

FIGURE 28 - SEQ ID NO: 19

<> 37
<> 1068, partial
<> DNA
<> Danaus plexippus
<> gi|357621160
<> ?
>(gi|357621160:c3951-3760, c3525-3397, c3296-3158, c1274-1085, c586-433, c334-71) Danaus plexippus, whole genome shotgun sequence

ATGCTGGAGTCAGGAGGTGGTTTACTTGTGGACATGATGAAGAGGGCGGTTCAGAATAAGCAGTACGCTGAGATAGA
CCACGCTATCAAGACTAAGGTGGAGCCCTTTCTCTACAATAAGGGCAAGGGCAGGCATATCCCTATATCGCATCTTG
TGCTGTTGAGGAATAAGGAACGAGGGAGGCATAAATTGCTGCCACCGTTACGTGGCATGGAGAATCCTGACGAAGAG
TTTGATGTAGAGAAGGATTGGCCAGTTGTGACCCAGGAAGAATACGAGGCGAATCCCTCGGCTTACAGGGAGCTTTG
CTGGGACCTGAAGGAACGCGGTGCCGTCGGTGAGACAATCCTTCACCTTTGTCTTCTAAACGCTACCTCACTTTTAG
CTGATTTAGCCAAGAGATTGCTTCGTTTTTACCCAAAACTTATAAACGACATTTACATGAGCGACGAGTATTACGGT
GAGAGCGTACTTCATATGACTATTGTAAACGAGGACCCGACTATGGTGAAATTTCTTTTGGATTCCGGAGCTGATTA
TCATGAACGTTGCTTCGGGAACTTCATGTGTCCTGAGGATCAGAAGGCCTCCCGAACAGATTCCTTCGACCACGAGT
GGGTCAACGTCCAGCCGGACACCAACTATGACGGGTACGTATATTGGGGGGAATACCCTTTAAGTTTCGCGGCCTGT
CTCGGTCAGGAGGAGTGCTACAGGCTCATACTGGCAAGAGGAGCGAACCCCGACAAACAGGACACCAATGGCAACAC
CGTACTGCATATGCTGATCATTTATGATAAAATAAGCACATTCGATATGGCGTATGAAGTTGGTGCATCCCTAAACA
TCAGGAACGTTCAGAACCTAACACCGCTCACCCTGGCCGCTAAACTGGCGAGAGTTGAGCTGTTCTTCCATATCCTG
AACATTGAAAGGGAGATCTATTGGCAAATCGGAGCCACCACCTGTGCAGCGTATCCTCTGGGACAAGTTGACACTAT
TGACACCGAGACCGGAAGGATTAGTAAAGATTCGGCGCTGAATTTAGTTGTATTTGGGGTTAGTTAG

FIGURE 29 – SEQ ID NO: 20

<> 39
<> 2583, partial
<> DNA
<> Solenopsis invicta
<> gi|322788678
<> ?
>(gi|322788678:c>387241-387065, c386978-386891, c385583-385407, c384935-384734, c384460-384325, c384092-383838, c383766-383684, c383540-383034, c382274-382109, c381583-381322, c379659-379478, c379232-379116, c378734-378609, c378544-<378440) Solenopsis invicta unplaced genomic scaffold Si_gnG.scaffold05712, whole genome shotgun sequence

GGCGGATTGTTAGTGGATATGATGAAGAGAGCCTCTCAGACCAAGCAGTACGCGGAGTTGGATCACGCGATGAGAAC
GAAGGTCGAGCCGTTTTTGTACAACAAAGGAAAGGGCAAATGGATACCCATAGAAAAATTGGTCCTCCTACGAAATA
AGGATCGTCCGCGACATAAAATGCTACCACCTTTGAAAGCCATGGAAAATCCAGCGGATTACGATATCGATAAGGAT
ATGGGCGATGAGGAAGTCGACGAAGCTAAGATAGATAAAAGCAAATATAGGCTGGTGTGCTGGAATCTGAGCGACAG
AGGTGCCGTCGGCGAAACCATTTTGCATTTGTGCATGTTGAACGCGACAGCCATCCACGCCGATTTGGCGAAACGAC
TGTTGCGTTTCTATCCTCTGCTTATATACGATATTTATTTGTGCGACGAGTATTACGGGGAGAATGTCTTGCACATC
GCTATCGTTAACGAGGACCCGTCGTTGGTCAAGTTTCTTCTGGATAGTGGAGCGGACGATCCGCGCATTATCCACGA
AAGGTGCTTCGGCACCTTCATGTGTCCGGAGGACCAGAAGGCGTCGAGGTTTGACAGTATGGACCACGAGTGGGTGT
GCGTCACACCGGAGACCGATTACAATGGCTATGTGTACTGGGGAGAATATCCGTTGAGTTTCGCCGCATGCCTCGGT
CAGGAAGAGTGCTACAGGCTTATACTAGCCAGAGGCGCGGATCCTGATAAGCAGGACACGAATGGCAACACCGTTTT
GCACATGCTGGCTACGTTCGACATGGCTTATGAGGTAGGAGCTTCTCTCGACATAAGAAACGTTCAACACCTAACTC
CGTTGACCTTAGCAGCAAAGTTGGCCAGGATCGAGATGTTCTTTCACATCCTGAACATCGAAAGAGAGATATACTGG
CAAATCGGTAGTATAACTTGCGCAGCCTACCCTTTATCGCAAATAGATACGATCGATGTTAACACGGGGACAATTAA
CAAAACTTCTGCCCTGAATCTGGTTGTTTTTGGCGACAAAGATGAACATTTAGAGTTGATGGACGGAATGCTAGTCG
ATCTGCTAAACGCCAAGTGGAACACTTTCGTTAAATCTCGATTTTACCGTCAATTCTTCCTCTTCTGCTTCCACTTC
GTGCTGTCGCTGATTAGCTTCACTCTTCGCCCTGGCCCGTCGACCATGGAAACAGATGAAAACGCGAACGATACGTC
GACGAAGACAAATTCTTCAAATATAACAGAGCCCATAATTCTCAAGCCCCTCCAAAGCTCGGATCTGTCGGAACTGG
TTACGAATAGCTTCGTGGCGGCTTTTGCGTCGAATCTCAAGTCATCCTTAAACATGACGCAGGAATCATTGGAGAAA
ATCCAGCTGCAAGTAACATCGAATATCACATCGGCCTTGAAGAGCATTTTGCTCTTGACGTTGAACGAAAACGAGGG
CATTCTGAGTCCTCCTGACGAGGCCACCATCCATACGCCGTGGTATACCGACAGCTCTCCAAATACGTCGGACTATT
TCACAGATCTCTACAATAAAACTGTCGTAGCCGAAAATTCGACTGTCAAGGCAGTTGTCGATGACGTCGCGCAAACC
GATTACTGGTGGGACGATTTCGCCGAGGAGTGTAGACTGATGCAGCTAACAGAAACGAGTGCGAAGATTCGTCTAAC
TGCGGAAACTTTTATGTACATCGCAGCGGTGCTTTATATCTTGGCTGCATTGAGGGAGGCGAGATTTTTAGGTCTCA
ACATGTTCATCGAAAATCTCGCGACGGCGCCATCGCGCGTGATGTTTCTGTTCTCGTGCTGTATCCTGCTGTCGTTC
CCATTTTTGCGATTTGTCTGCGCGGACGAGATCGAAGACATACTGGCGGTCGTGGTGATGCTGACGACCGCGCCGTA
CTTTCTGTTCTTCTGCCGGGGCTTCAAGACGGTCGGGCCGTTCGTCGTGATGATTTACAGGATGATCATGGGCGACC
TCCTCAGATTCGTCTGCATCTACCTTGTCTTCGTTATGGGATTCTCCCAAGCGTACTACATCATATTCCTGTCGTTC
GACAATCCGAACACTCCGGAGGGCACCGACGACTCGATAACGAATCCGATGCCGTCGCCGATGGAGAGCGTCATGGC
GATGTTCCTGATGAGCATGACGAACTTCGGAGATTACTTTGGCGCGTTTGAAAGAACCGAGCACGAGTTCGAGGCCA
AGCTGCTGTTCGTGTTGTACATGGTGATCGTGGCGATCCTGCTCGTAAACATGTTGATCGCCATGATGGGCAACACT
TACCAGAAGATCGCCGAAACCAGGAATGAATGGCAGCGGCAATGGGCGCGGATAGTTTTGGTCGTGGAGAGAGGTGT
CAGTCCCGCTGAAAGGCTGAAAAAATTGACAGACTATTCTCAGCCCATGTCCGACGGCCGTCCTGCGTTGGTTCTTC
GATTACATCAAACTGAGGAGGACAAGGAAGAGATGAAGGAGATACTCGAGATGAAGAGAACCCACGAAAAATTGCTG
AAGAAAAGACAATGCAGGATGTCAAAGGAGAAGATTCTGTCT

FIGURE 30 – SEQ ID NO: 21

<> 41
<> 2586
<> DNA
<> Acromyrmex echinatior
<> gi|332030918
<> ?
>(gi|332030918:309691-309781, 317981-318159, 318242-318329, 319179-319355, 319934-320135, 320432-320567, 320999-321253, 321328-321410, 321580-322092, 322373-322538, 323028-323289, 324761-324942, 325161-325277, 326205-326339) Acromyrmex echinatior unplaced genomic scaffold scaffold115, whole genome shotgun sequence

ATGGGTAATACCGAGAGCAATGTTGCGAGCAGCGTGAAGAAACAAACGGATACGTCGTCCATCCTGCTCTATAAATT
AGTCGACTTGAAGGGTGGCGGATTGTTGGTGGACATGATGAAAAGAGCCACGCAGACTAAGCAGTTTGCAGAGTTGG
ATCACGCGATGAGAACCAAAGTAGAACCGTTTCTGTACAACAAGGGAAAAGGCAAGTGGATACCAGTGGACAAATTA
GTTCTTCTACGAAATAAAGATCGTCCGCGGCATAAAATGCTACCGCCTTTAAAAGCTATGGAAAATCCAGCTGATTA
CGATATCGATAAAGACATGGGCGACGAGGAAGTTGATGAGGCCAAGATCGATAAAAGCAAATATAGACTGGTATGTT
GGAATTTAAGCGACAGAGGTGCTGTTGGCGAAACTATCTTGCATTTGTGCATGTTGCACGCGACCGCCATTCATGCT
GATTTGGCAAAACGACTGTTGCGTTTCTATCCGAAGCTTATAAACGATATTTATCTAAGCGATGAGTACTATGGAGA
GAATGTCTTGCACATCGCTATTGTAAACGAGGATCCATCGATGGTTAAGTTCCTTCTCGACAGCGGAGCAGACGATC
CGTGCATTATCCACGAGAGGTGCTTCGGCAACTTCATGTGCCCAGAAGATCAGAAGGCGTCGAGGTTTGACAATATG
GACCACGAGTGGGTGTGTGTTTCACCGGAAACCAATTACAACGGTTATGTGTACTGGGGAGAATATCCGTTAAGCTT
CGCCGCATGTCTCGGTCAGGAAGAGTGCTACAGGCTTATATTAGCCAGAGGTGCAGATCCTGATAAGCAGGACACGA
ATGGCAATACCGTTATGCATATGCTAGCCACGTTCGACATGGCTTATGAAGTAGGAGCTTCTCTCGGCATAAGAAAC
GTTCAACATCTGACTCCGTTGACTTTGGCTGCAAAGTTGGCCAGGATTGAGATATTCTTTCACATCATGAATATCGA
AAGAGAGATATACTGGCAAATCGGTAGCATAACTTGCGCAGCCTACCCTTTATCGCAAATAGATACGATCGACGTTA
ATACGGGCACAATCAACAATAATTCCGCCCTGAATCTGGTTGTTTTTGGTGATAAAGATGAACATTTAGAGTTAATG
GACGGTGTGTTAGTCGATCTTTTAAATGCCAAGTGGAACACCTTCGTTAAATCCCGATTCTACAATCAATTCTTTCT
TTTCTGCTTCTACTTCGTACTATCGCTGATTAGCTTCACCCTTCGACCTGGCCCATCAACCATAGAAACAGACGAAA
ATGCAAATGATACGTCGACGAGGACAAATTCCTCCAACATAACGGAGCCTATAATTCACAAGACTCTCCAAAGCTCG
GATCTGTCAGAATTGGTTACGAATAGTCTCGTAGCGGCTTTTACCTCGAATTTTAAATCATCCTTAAATATGACGCA
GGAATCGCTAGAAAAGATCCAGCTACAAGTAACGTCAAACATCACGTCAGCCCTGAAGAGCATTTTGCTCTTGACGT
TGAACGAAAATGAGGGCATTCTGAGTCCTCCTGACGAGGCCACCATTCATACGCTGTGGTATACCGATAGCCCTCCA
AACGCGTCGGATTATTTTATGAATACTTACAACAAAACCGACGCGAATTCAACTGTCAAGACAATTATCGACGGCGT
CGCGCGACCAAAATTTAAAAGCAATTATTGGTGGGACGATTTCTCGGAGGAGTGCAGACTCATGCAGCTATCAGAAA
TGAGTGCAAAAATTCGTCTAACTGCGGAAATTTTTATGTTCATCGCAGCGGTGCTCTACATTTTGGCTGCGTTGCGG
GAGGCGAAATTCTTAGGTCTTCATATGTTCATCGAAAATCTCATGACGGTGCCGTCACGCGTGATGTTCCTGATCTC
GTGCTGCATCCTGATGTGGTTCCCGGTTCTGCGATTTACTTGCTCCGACGAGGTCGAAGATATGCTAGCAGTCGTAG
TGATGCTGACGACGGCGCCATACTTTTTATTCTTCTGCCGGGGCTTCAAGACGGTCGGACCGTTCGTCGTGATGATT
TACAGGATGATCATGGGTGATCTCATCAGATTCGTCTCTATCTACCTCGTTTTTGTCATGGGATTCTCTCAAGCATA
TTACATCATATTCCTGTCATTCGACAACCCGAATACTCCAGAGGGCATCGACGACTCTATCACGAATCCGATGCCAT
CGCCGATGGAAAGTGTTATGGCGATGTTCCTGATGAGCATGACGAATTTCGGTGATTACTTTGGCGCGTTTGACAGA
ACCGAGCATGAATTCGAGGCCAAGCTGCTGTTTGTATTGTACATGGCGATTGTGGCAATCTTGCTCGTGAACATGTT
GATCGCTATGATGGGCAACACTTACCAGAAGATCGCTGAAACCAGGAACGAATGGCAACGGCAAGAGGAAGACAAGG
AAGAGATGAAGGAGATACTCGAGATGAAGAGAACCCATGATAGATTGCTGAAGAAAAGACAAAATAGAATGTCAAAG
GAAAAGATTATATTTGAAACAGAACCTATTATTACCAAGAATTGA

FIGURE 31 – SEQ ID NO: 22

<> 43
<> 2715
<> DNA
<> Camponotus floridanus
<> gi|307175924
<> ?
>(gi|307175924:c183397-183307, c179197-179019, c178952-178865, c178703-178527, c177969-177768, c177459-177324, c177108-176854, c176778-176696, c176511-175996, c175760-175595, c175215-174954, c174185-174004, c173751-173635, c173554-173429, c173364-173230) Camponotus floridanus unplaced genomic scaffold scaffold967, whole genome shotgun sequence

ATGGGTAATACAGAGAGTAATGTTACGAGCGGTGTAAAGAAACAAACGGACACATCGTCCATCGTGCTTTATAAATT
AGTCGATTTAAAAGGTGGTGGTTTGTTAGTTGATATGATGAAAAGAGCCACTCAGACAAAGCAGTTTGCGGAATTAG
ACCATGCGATGAGAACGAAAGTCGAGCCCTTTTTATATAACAAGGGGGAAGGCAAATGGATACCTATAGACAAATTG
GTCCTCTTACGAAATAAAGATCGTCCGCGACACAAAATGCTAGCACCGTTAAAAGCTATGGAAAATCCAGCGGATTA
CGATATAGACAAAGATATGGGCGATGAGGAAGTTGATGAAACTAAGATAGATAAAAGCAAATATAGATTAGTGTGCT
GGAATTTGAGTGAGAGAGGTGCTGTCGGCGAAACTATTTTGCATTTATGTATGTTAAACGCTACTGCTCTCCACGCT
GATTTGGCAAAAAGACTATTACGTTTCTATCCGAAGCTTATAAACGATATTTATCTATGCGACGAATATTACGGTGA
AAATGTATTACATATTGCTATTGTGAACGAGGATCCATCGATGGTCAAGTATCTTCTCGACAGCGGCGCGGACGACC
CGCGCATTATCCACGAGAGATGCTTCGGTAATTTTATGTGTCCGGAAGATCAGAAAGCATCGAGGTTTGATAGTCAA
GATCACGAATGGGTGTGCGTCACACCAGAAACCAATTATAACGGATACGTGTATTGGGGAGAGTATCCCTTGAGCTT
TGCCGCATGCCTTGGTCAGGAAGAATGCTACAGACTTATACTTGCCAGAGGTGCGGATCCGGATAAACAGGATACGA
ATGGGAACACCGTTTTACATATGCTGGCTACGTTCGATATGGCCTATGAAGTGGGGGCTTCTCTAGACATAAGAAAC
GTTCAACATCTGACTCCATTGACTTTGGCAGCAAAGCTAGCTAGGATAGAGATGTTCTTTCACATTCTGAATATCGA
GAGAGAGATATACTGGCAAATAGGTAGCATAACTTGCGCAGCCTATCCTTTGTCGCAAATAGATACAATAGACGTTA
ATGCAGGAACAATCAACAATAATTCTGCTCTAAATTTGGTTGTTTTTGGCGAGAAAGATGAACATTTAGAGTTAATG
GACGGCGTCCTAATCGATCTTTTAAATGCCAAGTGGAACACTTTTGTTAAATTCCGATTCTATCGTCAATTCATTCT
CTTCTACTTCTACTTTGTGCTATCGCTGATTAGTTTCACTCTTCGTCCTGGCCCGCAAACAGATGAAAATGCGAATG
ATACATTGACAAACTCATTCAACACGACGAGGGAATCCATGATTCTCAAGTCTCTTCACAGTTCGGATCTATCAGAA
CTGGTTACAAATAGTTTCACAGCAGCTTTTACTTCGAACTTCAAATCATCCTTAAACGTAACGCAAGAGTCATTGGA
GAAGATCCAGCTGCAAGTGACGTCGAATGTTACATCTGCTCTGAGAAGCATTTTGCTTTTAACGTTGAGCAACAATG
AGGATCTTTTGAGTTCCCCTGATGAGGCCGCCATTCATACACTGTGGTATACCGATAATCCTCAAAACGCGTCGGAT
TATTTCATAAATATGTATAATAAAACTGTTACAATTGATACTAACTCAACCGCCAAAACTACCATCGACGATGTCAC
ACTATTAGGAAAATTTAACAATCACGAAAAATGGTGGGATGATCTTACAGAAGAATGCAGACTGATGCAATTGACAA
CAATGAGCGCGAAGATCCGTCTTACTGCGGAAATCGTGATGTATTTTGCGGCAGTGCTCTACATCTTGGCTGCGTTG
CGAGAAGCGAGATTTTTAGGTCTCAACATGTTCATTGAAAATCTCATGACGGCGCCGTCGCGCGTCATGTTTCTGTT
CTCGTGTTGCATCTTAATGTCGTTTCCGGTTCTGAGACTTTCCTGCTCCGATGAGGTCGAAGACGTGCTGGCAGTTG
TAGTGATGCTAACAACGGCGCCATATTTTTTATTCTTCTGCCGAGGTTTCAAGACAGTCGGCCCGTTTGTCGTGATG
ATTTACAGAATGATTACGGGCGATCTCCTCAGATTCGTCTCTATCTATCTCGTCTTCGTGATGGGATTCTCTCAAGC
GTATTATATCATATTTTTGTCGTTTGACAATCCGAATACTCCGGAAGGCGTTGACGATTCGATAACAAATCCTATGC
CATCGCCGATGGAGAGCGTTATGGCAATGTTTCTGATGAGCATGACAAATTTCGGCGATTATTATGCCACGTTTGAC
AGAACCGAGCATGAATTCGAAGCCAAGCTGCTGTTCGTGTTATATATGGCGATCGTGGCAATCCTGCTCGTAAACAT
GTTGATTGCTATGATGGGCAACACTTACCAGAAGATCGCTGAAACCAGAAATGAGTGGCAGAGACAATGGGCGCGCA
TAGTCTTGGTTGTGGAGAGAGGCGTAAGTCCTGCTGAAAGATTAAAAAAATTGATGGACTATTCTCAGCCCATGTCT
GACGGTCGTAAAGCGTTGGTTCTCCGATTAAATCAAACTGAAGAAGACAAGGAAGAAATGAAAGAGATACTTGAAAT
GAAAAGGACGCACGATAAATTAATAAAGAAAAGACAAGACAAAATATTAAAGGAGAAAGCTTTAGCTGAAACAGAAG
CTGTTATTACTAGAAAATAA

FIGURE 32 - SEQ ID NO: 23

<> 45
<> 2014, partial
<> DNA
<> Myzus persicae
<> in-house
<> ?

CGCGATCAAAACACAAGTGGAACCCATGCTGTACAACAAGGGTGAAGGCAGAATGATACCGATTGCCAAACTCGTGT
TACTGAGAAATCGCGACCGTTCCCGGGCAAGATGGCTTCCACCGTTAAAGAACATGGAAGACGCCAATGAATACGAT
ATCGAAAAAGACATTCCCACCATCGAAGAACTGGAAAAGCTGGGGGAAGTGCAGTNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNTGGCAAGAGGAGCCGATCCAAATAACCAGGATACCAACGGCAATACAGTTCTGCA
CATGCTCGTAATTTACGAAAAAATCTCGACGTTCGACATGGCCTACGAAATCGGGGCGGAGCTCAACATTAGGAACG
TGCAAAATTTGACACCACTCACGCTGGCCGCGAAACTGGCTCGGATCCAAATGTTCTTTCACATACTCAAAATCGAA
CGGGAAATTTATTGGCAAATCGGCAGTATCACTTGTGCCGCGTACCCCCTGNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACACTTGGAGATGATGG
ACGGTGTGTTGGTGGATCTGCTAAATGCTAAATGGAACGCTTTCGTGAAATTCCGGTTCTATAGGCAGTTCATCTTG
TTCGCGTTTTACTTTTCCATATCCATGGTGTGCTTCGTTTTGCGTCCCGGGCCGCCACCCACTGGTCTTAAGCCGCC
ATTAATCAACTACACTTCGACGTCGACCACGGTGGCCACCACGCCGTTTGACTTCATGGACAACGAGTCGATGTTGC
CCGACAACGTCATGTACGACGAAATGATGATCGGCGGTGGCGGTCCGACCGAATTCGAAACGCCGGTGGTAACCACG
GAGATGGCGACGGTCAATGACAACGCCACAACCAACAACGGTACCGGTATCATCCGTACGCCACTGATCTACGAGGA
CGGTGCTGGAGGTGGTGGTGGAAGTGGTACCGTAAGCTTGCACGGTAAGAGTTCCGGTTCGGACAGGGGCAAACACA
GGAGCACGTGGAATCCCGCCAACCATACGTTCAAGACCAACTACACGTACAACTACAACAAATCGAGAAAATTTTGG
TGGAACAAGAGACAAAAGGTGTGCAGATTAATGGCAGTGCATTCGACTGATGATCTAATCAGAATGGGGTCGGAAGT
GGGAATGTTTGTGGGAGCCTTCCTCTATCTACTGGCCGCAGTCAGAGAAGCTGGATTTTTGGGCTCCCAGATGTTCA
TTGAAAACCTGGCCATAGCACCGGCAAGAGTGATGTTTCTGTTCTCGTGCCTGCTCATGATGACCATACCACCACTG
AGACTGACGTGCTATGACAAAGCCGAAGACATAATAGCCGTAATCATCATGTTGACCACTTGTCCGTACTTTTTGTT
CTTCTGCAGGGGTTNNNNNNNNNNNNNNNNNNNNTGGTGATGATCTACAGGTTGGTGATGGGAGACTTGCTGAGAT
TCGTTTCCATTTACATGGTGTTCGTGATGGGGTTCTCGCAAGCTTATTACGTGATTTTCCTATCTTACGACAACCCG
CTGACACCAGAGGGCATTGACGATTCCGTGCTGAACCCGATGCCCACGCCGACCGAGTCCATCATGGCGATGTTCCT
TATGTCCGTCAATACGTTCACAGATTACTACACGGCGTTCGACAAGACTAGTCACACGTTGGTCGCAAAGTTTTGCT
TTATAGTTTTCATGGTGATCGTGGCCATATTGCCGGTGAACATGTTAATCGCCATGATGGGGGACACTTATCAAAAG
ATCGCCGAGACCAGAAACGAATGGCAGAGACAATGGGCTCGGATCGTACTGGTGGTAGAGAGAGGTGTCAGCCCGTC
ACAGAGGCTCAAAAAGCTCATGTACTACTCGCAACCGATGTCAGATGGTCGGAGGGCGTTGGTGTTGCGACTCAATC
AGACGGATGAAGACAAGGAGCAAATGAAAGAGATATTGGAAATGAAACGCATTCACAATCGCTATGTTGAAAGAATG
CGCGCAAGAGACCTGAGCAGCAAACTATCGTCTTCGTGCGGAAAAAATGCAAACGATGGGACAATTAATTTAAAAGC
AAATAAATA

FIGURE 33 – SEQ ID NO: 24

<> 47
<> 1661, partial
<> DNA
<> Bemisia tabaci
<> in-house
<> ?

GATCCTGAGAAAATTGATCCGAAGAAATGCCGAGAGGTATGCTGGGATTTGATGGAACGTGGAGCGGTGGGTGAAAC
TATTCTCCATCTGTGCCTCCTCAACGCCACATCCATCCATGCAGACTTGGCCAAGCGACTCCTCCGCTTTTATCCGA
AACTTATCAACGATATATACATGTGCGACGAATATTACGGTGAAAGTGTGCTACATATTGCCATAGTGAACGAAGAT
CCAGCGATGGTGAAGTTCCTTTTAGACAGTGGCGCTGACTACCACGAGCGTTGTACCGGGAACTTCATGTGTCCTGA
GGATCAGAAGGCTACAAGGCAGGACACAGTTGAGCATGAATGGGTGAATCTGTCGCCACTCACCAACTACGAGGGAT
ACGTGTACTGGGGTGAGTACCCACTTAGTTTTGCGGCTTGTCTGGGCCAAGAAGAGTGCTTCCGACTCATGCTCGCG
CGAGGAGCAAATCCCGATAATCAAGACACAAATGGAAATACCGTTCTTCATATGCTCGTCATCTATGAGAAACTCGA
AACATTTGACATGGCATACGAAGTTGGCGCCAACATTTCTGTTCGGAATGTCCAGAATTTGACTCCTCTCACTTTGG
CAGCAAAACTCGCGAGAATTGAGATGTTCTTCCACATTTTAAACATCGAACGCGAAATCTATTGGCAAATTGGCAGT
ATTGCATGTGCAGCTTATCCTCTAGGGCAAATCGACACAATTGACATCGAAACAGGACACATCAGCAAAAATTCGGC
TCTTAATCTTGTGGTCTTTGGGGACAAAGACGAACATCTGGAGTTGATGGATGGCGTTTTGGTGGACCTTTTGAACG
CCAAGTGGAACGCTTTTGTCAAATTGAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNN

FIGURE 34 - SEQ ID NO: 25

<> 49
<> 2428, partial
<> DNA
<> Euschistus heros
<> in-house
<> ?

CTCAGGTTCTACCCCAAGCTCATCAATGACGTCTACATGTCCGATGAATACTATGGTGAAAGTGTCCTGCATATTGC
CATAGTCAACGAAGATCCTGCGATGGTGAAATTCCTACTAGACAGCGGTGTCAATGTCAATGAACGCTGTTTTGGCA
ACTTTATGTGTCCTGAGGACCAGAAGGCATCGAGGACTGATTCACTCGATCATGAATGGGTCAACTTGCAATCATTT
ACTACTTATGAGGGGTATGTATATTGGGGTGAGTACCCACTATCCTTTGCGGCCTGCCTTGGACAGGAAGAAYGCTA
CAGATTGATGCTTGCACGAGGAGCTAATCCTGACAATCAGGATACCAACGGAAATACCGTTCTTCATATGCTAGTCA
TATACTGTAAAATACAAACTTTCGACATGGCCTATGAAGTTGGTGGAGACCTATCAATAAGAAATGTCCAATATCTA
ACACCATTGACATTGGCAGCTAAATTAGCTAGGATTGAACTATTCTTCCACATATTAAATATTGAAAGAGAAATATA
CTGGCAGATTGGCAGCATAACTTGTGCAGCTTACCCACTTTCACAAATCGATACTATTGATATTGTGACTGGAAACA
TCAGCAAAAATTCTGCTTTAAATCTTGTCGTTTTTGGCGAAAAGGATGAACATTTGGAACTTATGGATGGTGTCCTG
ATCGACCTTTTAAACGCAAAATGGAATGCCTTTGTAAAATTTAGGTTTTATAGACAGTTTTTCTTATTTCTCTTTTA
CTTCTTGATTTCGCTTATTTGTTTCACTCTACGACCTGGACCTCCACCAGTTAAACCAATATCAAGTTTCAACAGTA
CCAAACCCAGCGGAAATAACATTACTGCTGAATTGTCGCCAGAAAGCAATGCAACTACTGTTCCAAAATGGATTTAC
AAAACAGAAATTAAAAAGTATGATCCCGAAGACAACAGTAGTCAAAACAGCAGACTTAATGTAATATTACGTGAAGT
CATTTTGACATCTTTGAAAGTTGAAGATATTGATAAAGTAGTTTCTTTTTCAAATGCAGAGCCGCAAGACAATTCCA
GGGAAGATGCAGATGGATTGGTTTGCAATGGCGATTCTGTTCATTCCTGTTTAGGAAATGGATCTGATGTTGTTGCT
GTATTTGGAAAAGGCAAGAGCCCAAAAGTACCAAAACCTGGAGCCTCCGCCGATGATTTTGATTATGACGACACTTG
GTGGGAAGAATTTGGACAATGCAGATTACTTCAGGTCACTTCCTACATTGAAATGACCCGCCTTATATCAGAAGTCT
TGTTGGACATCGGAGCTTTGCTATACATATTAGCAGCATTGAGAGAAGCGAGATTTCTAGGATGGAGCATGTTTGTG
GAGAATTTGATGACTGCTCCTTCAAGAGTTATGTTTTTGTTTTCATGCTGTTTGATGCTAACGATGCCATTTTTAAG
ATTTACCTGCAATGAAGAAATAGAAGACATGATGGCAGTTATTATAATGCTCACCACTGCTCCTTATTTTCTGTTTT
TCTGCAGAGGTTTCAAGACCGTTGGTCCATTTGTTGTGATGATATATAGGATGATAATGGGAGACTTGTTGAGATTT
GCTACAATATATCTTGTCTTTGTGATGGGGTTTGCTCAAGCATATTATATCATTTTCCTGTCATTTGATAACCCACT
GACACCCGAAGGAGTGGATGATTCTGTAAGTAATCCTATTCCGAACCCAATGGAAGCAGTCATGGCAATGTTTTTTA
TGTCAATGACAAGTTTTGGCGATTACTATCCAGCTTTAGAAAGGACAGCTCATGAATTCTGTGCTAAGCTTTGTTTT
GTGATATACATGGCAATAGTAGCAATTCTACTGGTTAATATGTTAATTGCTATGATGGGAAATACTTATCAAAAAAT
AGCTGAAACAAGAAATGAATGGCAGAGACAGTGGGCCAGAATAGTATTAGTGGTTGAAAGAGGAGTAAGTCCATCAG
AGAGGTTAACTAAACTAATGTGGTACTCACAGCCTATGTCAGATGGAAGAAGAGCGCTGGTACTGAGGCTAAACCAA
TCGGAGGAAGATAAAGAGGAAATGAAAGAAATTCTAGAGATGAAAAGAATTCACAACAGAATGGTACAAAAAAGGAA
AGAAAGGGAAAAGTCGATGAACAAAAGCCCAAATTTGATCAATTTAAACAGTCCGGCTGAAAATGTTAAAAATACAA
ATCCTTTCAGTTAATTCAGTTAACAGAACAAAGTGAATTAAACACAACAGAATAATCTTCTTATGAAACTATGATAT
CAGCCCCTGAAGTCTTTGTATCAAATCAAGCACCCTGTGAGCAGATGGGCAATAAACAAAAAATATGTTTTCTATGG
ACTAGCCCCAAAATAGATCTATTGATTTCAATGAAACTTGC

FIGURE 35 - SEQ ID NO: 26

<> 51
<> 2205, partial
<> DNA
<> Nilaparvata lugens
<> in-house
<> ?

CTGCATATGGCCATTGTGAATGAGGACCCAGGCATGGTGAAGTTCCTGCTGAACTCGGGAGCCGACTTCCACGAACG
CTGCTTCGGCAACTTCATGTGTCCCGAGGACCAGAAGGCATCCCGCTCCGATTCCTTCGATCACGAATGGGTCAATC
TCTGGCCTGTCACCAACTACGAGGGTTATGTGTACTGGGGCGAATACCCGCTATCTTTTGCTGCGTGTTTGGGTCAG
GAGGAATGCTATCGGCTCATGCTAGCCAGGGGGGCCAACCCCGACAACCAGGACACTAATGGCAACACTGTTCTTCA
CATGCTTGTCATATACGAGAAAATGGGAACGTTTGACACAGCTTACGAGCTGGGTGCCAACGTATCGGTGAGGAACA
TTCAGAACTTGACACCTCTGACACTGGCAGCCAAGCTGGCCAGAATTGAAATGTTCTTCCACATAATGAACATCGAA
CGAGAAATTTACTGGCAAATTGGTAGTATTACTTGTGCGGCCTATCCCTTGATGCTRATCGATACAATAGATATTGA
AACAGGGRATATTAGCAAAGATTCGGCTCTCAATCTTGTCGTATTTGGGGACAAAGATGAGCATTTGGATTTGATGG
AAGGCGTGCTGGTAGATTTGCTCCATGCCAAATGGAATGCATTTGTCAAGTTCAGGTTTTACCGCCAGTTCATAATG
TTCTTCCAGTACTTTCTGATATCGTGCGTGTGCTTCATACTGCGGCCTGGTCCCCCCGAAGCGCACGACGGTATGAA
CATCACCGCCAATGCTACACTCAACCTGAGCTTCGGGGTGCTYGAAGTCCGACCTGARGCGTTGCAAGCGYTGCTCT
AYMGGCTCGAGAAGCTGTCACTGCCCCAGTCGGGTGATCTGGAAAGGTTCATTCTGGAATCTCTRGCTGATGAGAAG
TCAATTTCAGAAGCTGCATTAGAGAACGATGAGAATCGGGRACCAGGCTGGAACAATAGTGTRTTTTCAACGTATGA
AACGCTGGCTCGTGATACGGGCTACCAAACTGATGAGAGTCCRCATGACGGATTGTCGAGTAGTATGGATTAYGCCG
AGGTGGCCGAGCGATTGACCAAACTGATGATTGATGTCAAYCTGACTGAGAGGAGTGGAGCTGTCAATGAGATTATA
CTGAAAGCTTTGCCTAGTCTTGAGGAGAAAGAGGATGGTTTGGAGGAGTGGTGGAGCGGAATAGCCGGTGACTGTAT
CCTGTTGCAGGTGAATGACCTCTACGACTTGGCACGCCTGTGCGCCGAGGTGGCGCTTGAAATTGGCGCCTTTCTCT
ACCTGCTGGCAGCACTGCGCGAGGCCCGCTTCCTCGGACTCAAAATGATGATCGAGAATCTGATGACGGCGCCGTCG
CGTGTGATGTTCCTGTTCTCATGCTGCCTGATGATGACGATGCCCTTCTTCCGCTTCACCTGCCAGGACGAGACCGA
GGACATCCTGGCCGTTGTCATCATGCTCACAACGGGGCCTTACTTCCTCTTCTTTTGCAGAGGGTTCAAAACAGTGG
GACCTTTCGTAGTGATGATTTACAGAATGGTAATGGGTGATCTTCTGAGATTCGTGTCTATTTACATGGTGTTTGTG
ATGGGATTTTCACAAGCGTATTACATAATTTTCTTGACGTACGACAACCCGACTACACCAGAAGGTACGGACGACAC
TACGTCGAATCCACTGCCCAGTCCAATTGAAGCCATTATGGCCATGTTCTTCATGTCACTCACCAACTTTGGAGATT
ACTACTCTGCGTTCGAGAACACTGAACATGAAATCGAAGCTAAGGCTTTCTTTGTGATTTACATGGTGATTGTGGCG
ATTCTTCTAATCAACATGTTGATCGCTATGATGGGTAACACTTACCAGAAGATTGCTGAAACAAAGAACGAATGGCA
AAGACAATGGGCCAGAATAGTTCTGGTTGTGGAGAGAGGTGTTAGTCCTAAGGAACGCTTGAAAAAGCTCATGTCCT
ATTCACAGCCTATGTCCGATGGAGGGAGGGCTCTGGTTCTCAGGCTGAACATGACGGAAGAAGACAAGGAAGAAATG
AAAGAAATCCTGGAAATGAAACGTGTACGTGATAAAATTGTCATGAAGCGCAAAAAAGGCTTGAAATTGTTGGGGAC
TACAACTCCTAGTCCAAAGAGGATGAAAGGCCGAGAAACTCCTATTTAA

FIGURE 36 - SEQ ID NO: 27

<> 53
<> 487, partial
<> DNA
<> schistocerca americana
<> in-house
<> ?
CTGCATATGGCCATTGTGAATGAGGACCCGGCCATGGTGAAGTTCCTGCTGGACAGTGGTGCCAACGTGCACGAGCG
CTGCTTCGGCACGTTCATGAGCCCGGAGGATCAGAAGGCCCAGCGCTCAGACTCCCTGGACCACGAGTGGGTCAACG
TCAACTCGGACACAAACTATGAAGGCTACGTGTACTGGGGGGAATACCCGCTGAGCTTCGCTGCCTGCCTGGGACAG
GAGGAGTGCTATCGGCTGGTGCTCGCCAAGGGTGCCAACCCAGATAGCCAAGACACCAACGGAAACACGACACTGCA
CATGCTCGTCATCCACAGGAAGATGACCCAGTTCGACATGGCTTATGAAGTTGGCTCTTCACTCGACATTAAGAATA
ACCTCAACCTCACACCTCTCACGTTAGCCGCTAAGCTGGCACGAATAGAGATGTTTTTCCATATCTTAAACATAGAA
AGAGAGATCTACTGGCAAATAGGTT

FIGURE 37 – SEQ ID NO: 28

<> 2
<> 833
<> PRT
<> Drosophila melanogaster
<> NP_648696.2
<> ?
>gi|45550616|ref|NP_648696.2| nanchung, isoform A [Drosophila melanogaster
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAEIDHAIKTKVEPFLYNKGAGRYFPISKL
VLLRNRDRPRTRQLPEIRALENPDDDFNIHDYCPEVSEAEYISNPTAYRFVCWDLNMRGAVGETILHLCLLNASSLH
ADLAKRLLKFYPKLILDIYMSDEYYGESVLHIAIVNEDPAMVKYLLDANADVQERCCGAFMSAEDTKFSRTDSPDHE
YVALCPMTNYDGYVYWGEYPLSFAACLSQEECFRLVLARGADPDFQDTNGNTVLHMLVIYEKIEMFDVGYEVGTNIH
IKNIQNLTPLTLAAKLGRVEMFFHVMSIEREIYWQLGSITCAAYPLLMIDTINEETGNINKDSVLNFVVFGDKLEHL
ELLDGVVIDLLKTKWDTFCKSRFYKQFYMFALYFLISLFSFILRPGPDAKDEDEDGANSTTAKSDLYRQNGSDSYHL
HSKRATMTTEYKTFWLNFTEYYDPSEVEVLPAWWESYAQCPLMNLESDLAKLRIMAELLNFVGAILYLLVALREARF
LGLKMFIENLMTAPSRVMFLFSCALMMTIPWLRVSCLTEIDDHVTVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMV
MGDLLRFVSIYLVFVMGFSQAFYIIFLTFDNPSSPEDQDAESNPMPSPMESIVAMFLMSLTNFGDYYGAMVSTQHEY
EAKILFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEWQRQWARIVLVVERSVPPAERLKNFMQYSQSMSDGRRAL
VLRLNMTEEKEEMKEVQEMKRIHQRFAKKRQMEREARALRRQQEYEKFFGTAPKSECSDNNNF

FIGURE 38 – SEQ ID NO: 29

<> 4
<> 834
<> PRT
<> Drosophila melanogaster
<> NP_001261833.1
<> ?
]>gi|442632275|ref|NP_001261833.1| nanchung, isoform B [Drosophila melanogaster]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAEIDHAIKTKVEPFLYNKGAGRYFPISKL
VLLRNRDRPRTRQLPEIRALENPDDDFNIHDYCPEVSEAEYISNPTAYRFVCWDLNMRGAVGETILHLCLLNASSLH
ADLAKRLLKFYPKLILDIYMSDEYYGESVLHIAIVNEDPAMVKYLLDANADVQERCCGAFMSAEDTKFSRTDSPDHE
YVALCPMTNYDGYVYWGEYPLSFAACLSQEECFRLVLARGADPDFQDTNGNTVLHMLVIYEKIEMFDVGYEVGTNIH
IKNIQNLTPLTLAAKLGRVEMFFHVMSIEREIYWQLGSITCAAYPLLMIDTINEETGNINKDSVLNFVVFGDKLEHL
ELLDGVVIDLLKTKWDTFCKSRFYKQFYMFALYFLISLFSFILRPGPDAKDEDEDGANSTTAKSDLYRQNGSDSYHL
HSKRATMTTEYKTFWLNFTEYYDPSEVEVLPAWWESYAQCPLMNLESDLAKLRIMAELLNFVGAILYLLVALREARF
LGLKMFIENLMTAPSRVMFLFSCALMMTIPWLRVSCLTEIDDHVTVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMV
MGDLLRFVSIYLVFVMGFSQAFYIIFLTFDNPSSPEDQDAESNPMPSPMESIVAMFLMSLTNFGDYYGAMVSTQHEY
EAKILFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEWQRQWARIVLVVERSVPPAERLKNFMQYSQSMSDGRRAL
VLRLNMTEEEKEEMKEVQEMKRIHQRFAKKRQMEREARALRRQQEYEKFFGTAPKSECSDNNNF

FIGURE 39 - SEQ ID NO: 30

<> 6
<> 838
<> PRT
<> Musca domestica
<> XP_005180489.1
<> ?
>gi|557761542|ref|XP_005180489.1| PREDICTED: transient receptor potential cation channel subfamily V member 5-like [Musca domestica]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAEIDHAIKTKVEPFLYNKGAGRYFPISKM
VLLRNKERARTKQLPEIRALENPDEDFNIHDYCSEVSEAEYISNPSAYRFVCWNLNERGAVGETILHLCLLNASSLH
ADLAKRLLKFYPKLIMDIYLSDEYYGESVLHIAIVNEDPAMVKYLLDANADVQERCCGAFMSAEDQKASRYDSPEHE
YVGVHPMTNYDGYVYWGEYPLSFAACLSQEECFRLVLARGADPDSQDTNGNTVLHMLVIYEKIDMFDVAYEVGTNIH
IRNVQNLTPLTLAAKLARVEMFFHILSIEREIYWQLGSITCAAYPLSKIDTIDVKTGNINKDSVLNFVVFGDKLEHL
ELLDGVVIDLLKTKWETFVKSRFYKQFYMFSFYFLFSLVSFISRPGPKIEDEDEEGDANDSAGKGNDSTTNARLLYA
TPASRVTGIEKLPYKTFWLNFSEYIDDDANAENMPSWWASYEECPLMDMETNLAKFRIVSEIVIFFGAILYLLSALR
EAKFLGYKMFVENLMTAPSRVMFLFSCCLMMTIPWLRLSCLTELDDHVAVMIMLTTAPYFLFFCRGFKTVGPFVVMI
YRMVMGDLIRFVSIYLVFVMGFSQAYYIIFLTFDNPATPEEIDDTGTNPMPSPMESVVAMFLMSLTNFGDYYGAMGS
TQHEYEAKILFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEWQRQWARIVLVVERSVPPAERLKNFMQYSQPMSD
GRRALVLRLNMSDEDKEEMKEVQEMKRIHQRFSKKRQMEREARAKKRQEEYEKFFGATPTSDNENNNF

FIGURE 40 - SEQ ID NO: 31

<> 8
<> 844
<> PRT
<> Ceratitis capitata
<> XP_004537742.1
<> ?
>gi|499014264|ref|XP_004537742.1| PREDICTED: transient receptor potential cation channel subfamily V member 5-like [Ceratitis capitata]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAEIDHAIKTKVEPFLYNKGAGRYFPISKL
VLLRNKERARTKQLPEIRAMENPDEDFNIHDHCTEVSEAEYISNPSAYRYVCWNLNERGAVGETILHLCLLNASSLH
ADLAKRLLKFYPKLILDVYMCDEYYGESVLHIAIVNEDPAMVKYLLDAGADVQERCCGAFMSAEDQKASRYDSPDHE
YVGVQPMTNYDGYVYWGEYPMSFAACLSQEDCFRLVLARGADPNLQDTNGNTSLHMLVIYEKIEMFDVAYEVGTNIH
LRNVQNLTALTLAAKLGRVEMFFHILSIEREIYWQLGSITCAAYPLSMIDTIDVETGNINKDSVLNFVVFGDKLEHL
ELLDGVVIDLLKTKWESFVKSRFYKQFYMFSFYFLFSLISFISRPGPTEKNEDDDDDDDADASVEATVTRAANSTAP
LQRGDQWFKRLIKRAIDKMEYKTFWLNFTDYFDDNDVESVPPWWASYAECPLMNMESDLAKLRIVAEIIIFFGSVLY
LFAALREARFLGYKMFVENMMTAPSRVMFLFSCALMMSIPWLRVFCLTEIDDHVAVFIMLTTAPYFLFFCRGFKTVG
PFVVMIYRMVMGDLIRFVSIYLVFVMGFSQAYYIIFLTFDNPATPEEIDDSESNPMPSPMESIVAMFLMSLTNFGDY
FGGMASTQHEYEAKTLFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEWQRQWARIVLVVERSVPPAERLKNFMHY
SQPMSDGRRALVLRLNMSDEVKEEMKEVQETKRIHQRFSKKRQIEREARAQKRQEEYEKFFGKKPSGNSDNNNA

FIGURE 41 – SEQ ID NO: 32

<> 10
<> 833
<> PRT
<> Anopheles gambiae
<> XP_320300.4
<> ?
>gi|158300356|ref|XP_320300.4| AGAP012241-PA [Anopheles gambiae str. PEST]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAEIDHAIKTKVEPFLYNKGKGKYIPVSVL
VLLRNRERPRHKQLPEIRAMENPEEDFDIDAVCPEVSEAEYYLNPSGYREVCWNIKERGAVGETILHLCLLNATSLH
ADLAKRLLRFYPKLINDVYMCDEYYGENVLHLAIVNEDPAMVKYLLDHNADVNERCCGTFMCPEDQKASRYDTPETE
VVQMVQVTNYDGYVYWGEYPLTFAACLGQEECYRLVLARGADPDNKDFNGNTVLHMLVIYEKIATFDMGYEVGSSLS
IRNHQNLTPLTLAAKLGRVEMFFHIMNIEREIYWQLGSITCAAYPLGLIDTIDVETGNINKDSALNLVAFGDKDEHL
DLLDGVLIDLLKTKWNTFVKDKFYRQFFMFFCYFCVSLVSFTLRNGPPPAEDDDGKESEAGGNKTAAVTKEELRRQL
WNETTLEDALAALAGNGSFAGRLSNLEQSNGSSDAMGEFDPAEMDDEGLFFNSNCHTMDYDGVEGKVRLISEMIILV
GSFLYLLAALRELKFLGRKMFFENLMTAPSRVMFLFSCCIMMIVPFLKVLCFTELEDHVAVTIMLTTAPYFLFFCRG
FKTVGPFVVMIYRMVMGDLLRFVVIYLVFVMGFSQAYYIVFLSYKPDEEGDPNPMPSPIESIVAMFLMSLTNFGDYY
GALENTDHEMCAKILFVLFMVIVAVLLVNMLIAMMGNTYQKIAETKNEWQRQWARIVLVVERGVPPKERLKNLMSYS
QPMSDGRRALVLRLNMTEDKEEMKEILEMKRVHERLSIKRQIERDARAEQRRLLREKYLNMSS

FIGURE 42 – SEQ ID NO: 33

<> 12
<> 815
<> PRT
<> Aedes aegypti
<> XP_001652424.1
<> ?
>gi|157114792|ref|XP_001652424.1| hypothetical protein AaeL_AAEL001123 [Aedes aegypti]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAEIDHAIKTKVEPFLYNKGKGKYIPVAQL
VLLRNRERPRSKQLPEIRALENPEEDFDIDAVCPDVTEGEYQRNPSGYREVCWNIKERGAVGETILHLCLLNATSLH
ADLAKRLLRFYPKLINDIYMCDEYYGESVLHVAIVNEDPAMVKYLLDSGSDVDERCCGTFMCPEDQKATRYDSIETE
IICVLPMTNYDGYVYWGEYPLSFAACLGQEECYRLVLARGADPDNQDSNGNTVLHMLVIYEKISTFDMAYEVGSSLD
IRNLQNLTPLTLAAKLGRVEMFFHIMNIEREIYWQLGAITCAAYPLALIDTIDIETGNINKDSALNLVVFGDKAEHL
DLLEGVLIDLLKTKWNSFVKDKFYRQFFVFFWYFCVSLVSFTLRRGPMNLEETAANRTTTSITLKNLTFSDSTNATL
PTLLAADVNEKIVQFIANETLFDPAVMEENTFFNSKCATMAYDTLQDKIRLVSEIIILIGSFLYLVGALREFRFLGR
KMFFENLMISPSRVMFLFSCCIMMIVPFLKVLCLIELEDHVAVTIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGD
LLRFVVIYLVFVMGFSQAYYIVFLSFKGEEEGDENPMPSPMESIVAMFLMSLTNFGDYYGALEKTEHEGCAKVLFVI
FMVIVAVLLVNLLIAMMGNTYTMIAETKNEWQRQWARIVLVVERGVPPSERLKNFMSYSQPMSDGRRALVLRLHMTD
EDKEEMKEILEMKRVHERLKKKRQVERELRAEQRRLIMEKYANVP

FIGURE 43 – SEQ ID NO: 34

<> 14
<> 816
<> PRT
<> Culex quinquefasciatus
<> XP_001847136.1
<> ?
>gi|170038599|ref|XP_001847136.1| TRP channel protein nanchung [Culex quinquefasciatus]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAEIDHAIKTKVEPFLYNKGKGKYIPVAQL
VYLRNRERPRHKQLPEIRALENPEEDYDIDKECPDVTEGEYMRNPGGYREVCWNIKERGAVGETILHLCLLNATSLH
ADLAKRLLRFYPKLINDVYMCDEYYGESVLHLAIVNEDPAMVKYLLDAGSDVNERCCGTFMCPEDQKASRFDSLETE
IICVMPQTNYDGYVYWGEYPLSFAACLGQEECYRLVLARGADPDNQDSNMNNVLHMMVIYEKLTTFDMAYEVGSSLS
IRNLQNLTPLTLAAKLGRVEMFFHIMNIEREIYWQLGSITCAAYPLALLDTIDIETGNISKDSALNLVVFGDKDEHL
DLLEGVLIDLLKTKWNTFVKDKFYSQFFVFFCYFCVSLISFTLREGPMKLEDGEANKTTTSIQLKNMTLADLTNAST
LSSLLVTDVSGKIVGLNGSETFFDPSTIESDMFFNSKCPTMIYKGIEGKIRLVSEAIILVGSFLYLVSALRESRFLG
RKMFIENLMTAPSRVMFLFSCCIMMVVPCLKVLCFTELEDHVAVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMG
DLLRFVAIYSVFVMGFSQAYYIAFLSYKGEEEGDENPMPSPMESIVAMFLMSLTNFGDYYAALEDTAHEGCAKVLFV
TYMVIVAVLLVNLLIAMMGNTYTKIAETKNEWQRQWARIVLVVERGVPPAERLKNLMNYSQPMSDGRRALVLRLNMT
EEDKEEMKEILDMKRVHERLSKKRAVEREARAEQRRLIAEKYANVP

FIGURE 44 – SEQ ID NO: 35

<> 16
<> 695
<> PRT
<> Tribolium castaneum
<> XP_967896.1
<> ?
>gi|91081969|ref|XP_967896.1| PREDICTED: similar to nanchung CG5842-PA [Tribolium castaneum]
MGNTESNVTSGVKKQAGASVQPIYKLCDLKGGGLLVELMKRATQNKQYAELDHAIKTKVEHFLYNKGAGRYFTISDL
VLLRNKERSRQKWLPQLKAMENPEDFEIDDEGPEITEEQYQKNPHLYRHVCWKIKERGAVGESIMHLCLLNATSLHA
DIAKRLLRFYPKLINDIYMSDEYYGENVLHIAIVNEDPSMVKFLLDSGVNIQERCCGNFMCPEDQKSSRYDSLDHEW
VNVCPVTNYEGYVYWGEYPLTFAACLGQEESFRLMLSRGADPDAQDTNGNTVLHLLVILQKLEAFDMAYEVGAKLSI
RNVLSLTPLTLAAKLARIDMFFHILNLEREIYWQIGSITCAAYPLSQIDTIDIETGQISKTSALNLVVFGDKDEHLE
LMDGVLIDLLNAKWNTFVKFKFYKQFFTFAFYFLISLVAFTLRPGPPHKEAKLVNVTINATVSNTSKWENLTSIPFG
KTPDDDDSDMEEWWDNLQEECRLMQLESPESKIRLTAEVLMVVGAFAYLAAAVREARFLGGRMFFENLMTAPSRVMF
LFSCILMLTVPCLRLACLDEFEDIVAVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLIRFASIYLVFVMGFS
QAFYIIFLSFDNPLTPDDVDDSATNPISTPIESIMAMFLMSMTNFGDYYAAFEKTDHEYEAKMLFVVFMVIVSILLI
NM

FIGURE 45 - SEQ ID NO: 36

<> 18
<> 841
<> PRT
<> Bombyx mori
<> XP_004923070.1
<> ?
>gi|512892991|ref|XP_004923070.1| PREDICTED: transient receptor potential cation channel subfamily V member 5-like [Bombyx mori]
MGNTESNVTSGVKKQAGTSEQKLYKLVDIKGGGLLVDMMKRALQNKQYAEIDHAIKTKVEPFLYNRGRGRYIPISHL
VLLRNKERPRHKLLPPLRGMENPDEEFDVDKDWPVVTQEEYDANPSGYRELCWDVKERGAVGETILHLCLLNATSLL
AHLAKRLLRFYPKMINDIYISDEYYGETVLHITIVNEDPTMAKFLLDAGADYHERCYGNFMCPEDQKASRTDSFDHE
WVNVQPDTNYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVLHMLVIYEKMSTFDMAYEVGASLN
IRNVQNLTPLTLAAKLARTEMFFHILNIEREIYWQIGATTCAAYPLGQVDTIDTETGLISKDSALNLVVFGEKDEHL
GLLEGMLIDLLKTKWNTFVKFRFYRQFILFSCYFLVSLICFTLRPGPPDRALNTTVLNSTIGPNVTDAELVSDVENC
TMTPNADFDTNAVEVLNGTKFGGSHCARFKSHPKEKSTEAPRENDVEGWWEDLTEECRLMNLDTWQAKLRISAELLL
WMGALAYFGAALREAKFLGIKMFIENLSTVPSRVMFLFSCLLMLILPTLRLWCADEAEDHLAVMIMLTTAPYFLFFC
RGFKTVGPFVVMIYRMVMGDLLRFVCIYLVFVMGFSQAYYVIFLSFDNPNTPEGVDDSVSNPMPSPMESIMAMFLMS
LTSFSDYYTAFDRTDHEIEAKLLFVIYMIIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVPPAQR
LKQLMTYSQPMANGKRALVLRINQKDEDKEEMKEILEMKRTHERIVAKRKQREALKPGEIPPPARDYPIRK

FIGURE 46 - SEQ ID NO: 37

<> 20
<> 792
<> PRT
<> Anopheles darlingi
<> EFR23411.1
<> ?
>gi|312376272|gb|EFR23411.1| hypothetical protein AND_12928 [Anopheles darlingi]
MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAEIDHAIKTKVEPFLYNKGKGKYIPVSVL
VLLRNSERPRHKQLPEIRALENPEEDFDIDAVCPEVSEAEYYLNPSGYREVCWNVKERGAVGETILHLCLLNATSLH
ADLAKRLLRFYPKLINDVYMCDEYYGESVLHLAIVNEDPAMVKYLLDHNSDVNERCCGTFMCPEDQKASRYDTPETE
VVQMVQLTNYDGYVYWGEYPLTFAACLGQEECYRLVLARGADPDNKDFNGNTVLHMLVIYEKITTFDMGYEVGSSLS
IRNHQNLTPLTLAAKLGRVEMFFHIMNIEREIYWQLGSITCAAYPLVLIDTIDVETGNISKDSALNLVVFGDKDEHL
DLLDGVLIDLLKTKWNTFVKDKFYRQFFMFFCYFCVSLIGFTLRNGPPPPEEDDENRAGGGSGNKTSSASKQDLRQR
LWNRTVTLEDADNVSSLLSDIMGIDALGKLAEQLLNGSEGSGAFKPETVEEEEDGLFFNSKCHTMDYDGVEGKVRFV
AEVIILIGSFLYLLSALRELKFLGRKMFFENLVSRGFKTVGPFVVMIYRMVMGDLLRFVVIYLVFVMGFSQAYYIVF
LSYKPEEDGDANPMPSPIESIVAMFLMSLTNFGDYYGALENTDHEMCAKILFVLFMVIVAVLLVNMLIAMMGNTYQK
IAETKNEWQRQWARIVLVVERGVPPKERLKNLMSYSQPMSDGRRALVLRLNMTDEDKEEMKEILEMKRVHERLSKKR
QVERDARAEQRRLLREKYLNMT

FIGURE 47 – SEQ ID NO: 38

<> 22
<> 900
<> PRT
<> Acyrthosiphon pisum
<> XP_001947907.2
<> ?
>gi|328706726|ref|XP_001947907.2| PREDICTED: transient receptor potential cation channel subfamily V member 6-like [Acyrthosiphon pisum]
MGNTESNVASGVKKQVDTSSLQIYNLVDLKGCGLLVDLMKKAVQTKNFTELDNAIKTQVEPMLYNKGEGRMIPIAKL
VLLRNRDRSRARWLPPLKNMEDTNDYDIEKDIPTIEELEKLGEVQYREVCWDLKERGTVGETALHLCLLNATSIHAD
LAKRLLHFYPKLVNDIYMIDEYYGESVLHMAIVNEDPAMVKVLMDSGANLNERCFGNFMSTEDQKASRSDSLDHEWV
NLCPDTNYEGYVYWGEYPLSFAACLGQEESYRLMLARGADPNNQDTNGNTVLHMLVIYEKISTFDMAYEIGAELNIR
NVQNLTPLTLAAKLARIQMFFHILKIEREIYWQIGSITCAAYPLTQIDTIDNDTGQISRNSALNLVVFGESPEHLEM
MDGVLVDLLNAKWNAFVKFRFYRQFILFAFYFSISMVCFVLRPGPPPTGLKPPLINYTSTSTTVATTPFDFMDNESM
LPDMYDEMMIGGGGPTEFETVQVTTEMATTSDNATTTNNGSGIGTPLIYEDGGGGGGGGGTVSLHGKSSGSDRGKHR
STWSPANHTFKTNYTYNYNKSRKFWWNKRQKVCRLMAVHSTDDLIRMGSEVGMFMGAFLYLLAAVREAGFLGTQMFI
ENLAIAPARVMFLFSCLLMMTIPPLRLTCYDKAEDIIAVIIMLTTCPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRF
VSIYMVFVMGFSQAYYVIFLSYDNPLTPEGIDDSVLNPMPTPTESIMAMFLMSVNTFTDYYTAFDKTSHTLVAKFCF
IVFMVIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPSQRLIKLMYYSQPMSDGRRALVLRLNQ
TDEDKEQMKEILEMKRIHNRYVERMRARDLSSKLSSSCGKNANNGTFNLKANE

FIGURE 48 – SEQ ID NO: 39

<> 24
<> 707
<> PRT
<> Dendroctonus ponderosae
<> ERL84850.1
<> ?
>gi|546673192|gb|ERL84850.1| hypothetical protein D910_02274 [Dendroctonus ponderosae]
MGNTESNVTSGVKKQAGAAMQPIYKLCDLKGGGLLVELMKRAAQNKQYAEIDHAIKTKVEHFLYNKGAGRYIPISQM
VLLRNKERGKHKLLPQLRGMENPEDFEVDDEGPEITEEEYNKDPSLYRHVCWKLRERGAVGETILHLCLLNATSLHA
DIAKRLLRFYPKLINDIYISDEYYGENVLHIAIVNEDPSMVKFLLAANVNFQERCFGNFMCPEDQKSSRTDSLDHEW
VNVYHETNYDGYVYWGEYPLSFAACLGQEESFRLILAKGANLDAQDTNGNTVLHLLVIYSKVEAFDMAYELGAHLSI
RNILKMTPLTLAAKLARMDIFFHILKLEREIYWQIGSITCAAYPLSQIDTIDVKTGQISKMSALNLVVFGDKDEHLE
LLDGVLVDLLNAKWNTFVKSKFYRQFFTFAFYFTVSLVDTSNDDYDVEEWWDNLREECRLMNLDTTESLVRFTAELG
ITFGAFLYLAAAMTAPSRVMFLFSCILVFGVIPSLRLVCMDEVEDIIAVVVMLTTAPYFLFFCRGFKTVGPFVVMIY
RMVLGDLLRFATIYMVFVMGFSQAYYIIFLSFDNPLTPEDVDDSATNPMSTPSESIMAMFLMSMTNFGDYYTAFART
EHEYEAKILFVIFMAIVAILLINMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPPERLKQLNVYSQPMSDG
KRALVLRLNQSVRY

FIGURE 49 – SEQ ID NO: 40

<> 26
<> 905
<> PRT
<> Harpegnathos saltator
<> EFN81068.1
<> ?
>gi|307201162|gb|EFN81068.1| Transient receptor potential cation channel subfamily V member 6 [Harpegnathos saltator]
MGNTESNVTSGVKKQTDTSSIMLYKLVDLKGGGLFVDMMKRAAQTKQFAELDHAVRTKVEPYLYNKGKGKWIPVDKL
VLLRNKDRPRHKMLAPLKAMENPADYDIDKDMGDEDVDETKIDKSKYRLVCWSLSERGAVGETILHLCMLNATALHA
DLAKRLLRFYPNLINDIYISDEYYGENVLHIAIVNEDPAMVKYLLDSGADVHERCFGNFMCPEDQKASRVDSLDHEW
VCVAPETNYSGYVYWGEYPLSFAACLGQEECYRLMLARGADPDKQDTNGNTVLHMLVIYEKLTTFDMAYEVGASLAI
RNVQHLTPLTLSAKLAKIEMFFHILNIEREIYWQIGSITCAAYPLSQIDTIDINIGTINKNSALNLVVFGEKDEHLE
LMDGMLVDLLNAKWNTFVKSRFYRQFFLFCFYFVLSLISFTLRPGPLPQETENANDTRTNSSNATAMEILRLFQSSD
LSNLVTNSLAAAFASNLKSSLNVTQESLEKIQLQVTSNITSALKNILPSLSDNEGILSAPDEAAIRTLWYTSSPYNE
SDYLTDAYNENVTSDANSTAGTIIGSIEVSKSNDKDNWWEDLTEECRLMQLTTISAKIRLTAEVLMEIAAVLYILAA
LREARFLGLNMFVENLMTAPSRVMFLFSCCILLSFPFLRLACADEVEDMLAVVVMLTTAPYFLFFCRGFKTVGPFVV
MIYRMIMGDLLRFVSIYLVFVMGFSQAYYIIFLSFDNPNTPEGVDDSVSNPMPSPMESIMAMFLMSMTNFGDYYGAF
ERTEHESEAKLLFVLYMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPAERLKKLMDYSQPM
SGGRRALVLRLNQSEEDKEEMKEILEMKRTHDRLLKKRQGRMSKEKVLAESEIIITRN

FIGURE 50 – SEQ ID NO: 41

<> 28
<> 903
<> PRT
<> Nasonia vitripennis
<> XP_001606102.2
<> ?
>gi|345488311|ref|XP_001606102.2| PREDICTED: transient receptor potential cation channel subfamily V member 5 isoform 1 [Nasonia vitripennis]
MGNAESNVTSGVKKQTDAGAIALYKLVDLKGGGLLVDMMKRASQTKQYAEIDHAIRTKVEPFLYNGGKGKWIPIAKL
VLLRNKERGRHKMLPVLKAMEKPEDYDIDKDMANDPEPDENTIDKSKYKLVCWTLSDRGAVGETILHLCMLNATQLH
ADLAKRLLRFYPNLINDIYIDDEYYGENVLHIAIVNEDPSMVKFLLDSGANVNERCCGNFMCPEDQKASRNDSVEHE
WVCVCSETNYDGYVYWGEYPLSFAACLDQEECYRLILAKGADPDSQDTNGNTVLHMLVIYEKLETFDMAYEVGSSLS
IRNVLQLTPLTLAAKLARVEMFFHILNIEREIYWQIGSITCAAYPLSQIDTIDVDTGKISNNSALNLVVFGDKEEHL
KLLEGVLIDLLNAKWNTFVKSRFYQQFYLFFCYFILSLISCTLRPGPITKTDAPTTTPHPMNDTSIESITPTSEPLE
LQTLSSLLAKNLAEQLVMGMKMYGNVSEDSLARISLQVASNISGSIKDIWTRQNLTSNDTDYVDIAGGLYADVNETS
ASDPFDLNASDIVILKKGKKELDDWWDDLTEDCRLMQMNSTSAKIRLTAEIFMEFGAILYICAALREARFLGLNMFI
ENLMTAPSRVMFLFSCCILLSFPFLRMSCADEVEDILAVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRF
VSIYLVFVMGFSQAYYIIFLSFDNPITPEGVDDSKANPLPSAMESIMAMFLMSMTNFGDYYDAFENTEHEMLAKCLF
VVYMAIVSVLLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVAPAERLKKLNVYSQPMSDGRKALVLRLNQ
TDKDKEEMKDILEMKRIHIKSIKRRKDKLQKAKEDAEKLQQQMADKDNKDKAVIIQ

FIGURE 51 - SEQ ID NO: 42

<> 30
<> 903
<> PRT
<> Megachile rotundata
<> XP_003706172.1
<> ?
>gi|383861396|ref|XP_003706172.1| PREDICTED: transient receptor potential cation channel subfamily V member 6-like [Megachile rotundata]
MGNTESNVTSGVKKQTDSSSILLYKLVDLKGGGLLVDMMKRATQTKQYAELDHALRTKVEPYLYNKGKGKWIPIEKL
VLLRNKDRPKHKMLPPLRAMENPADYDIDKDMGEEEVDETKIDKSKYRLVCWSLSQRGAVGETIMHLCMLHATAIHT
DLAKRLLRFYPKLINDIYISDEYYGENALHIAIVNEDPAMVKFLLDSGADVHERCVGNFMCPEDQKASRTDSVDHEW
VCVAPETNYSGYVYWGEYPLNFAACLGQEECYRLILARGADPDKQDTNGNTVLHMLVIYEKMATFDMAYEVGASLSI
RNAQHLTPLTLSAKLARIEMFFHILNIEREIYWQIGSITCAAYPLSQVDTIDVNTGSISHTSALNLVVFGEKDEHLE
LMDGTMVDLLNAKWNTFVKSRFYRQFFLFCFYFILYLISFTLRPGPSVTSTATTAPTTESTTPKLPDPPPNFIPVTN
QKTFLEASLSSSLDEIVTNALNLNFPSNATARFDDLKLDLVTHIMSNLKNILNGNETKNEPFNSSQLARFDKHLFRE
NDTDYSTSILNETADVDSTTKFSFDNSVLFEADNKSDWWTDLTTECRLMQLTTASAKIRLIAEIFMEIAAILYILAA
LREARFLGLNMFIENLMTVPSRVMFLFSCCILLSFPFLRLSCADEVEDVLAVVVMLTTAPYFLFFCRGFKTVGPFVV
MIYRMIMGDLLRFVSIYLVFVIGFSQAYYIIFLSFDNPNTPEGVDDSVSNPMPSPIESIMAMFLMSMTNFGDYYGAF
ERTRHEMEAKFLFVVYMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPQERLKKLMDYSQPM
SDGRRALVLRLNQSEEDKEEMKEILEMKRTHERLYKKRQLKTTKEKTTITEENVTL

FIGURE 52 - SEQ ID NO: 43

<> 32
<> 887
<> PRT
<> Apis mellifera
<> XP_625170.3
<> ?
>gi|328787659|ref|XP_625170.3| PREDICTED: transient receptor potential cation channel subfamily V member 6 [Apis mellifera]
MGNTESNVASGVKKQTDASSILLYKLVDLKGGGLLVDMMKRATQTKQYAELDHALRTKVEPYLYNKGKGKWIPIEKL
VLLRNKDRPKHKMLPPLRAMENPADYDIDKDMGEDEVDETKIDKSKYRLVCWSLSERGAVGETILHLCMLHATAIHI
DLAKRLLRFYPKLINDVYISDEYYGESALHIAIVNEDPSMVKFLLDSGADVHERCIGNFMCPEDQKASRADSLDHEW
VCVTPETNYNGYVYWGEYPLNFAACLGQEECYRLILARGADPDKQDTNGNTVLHMLVIYEKLATFDMAYEVGASLAI
RNAQHLTPLTLSAKLAKIEMFFHILNIEREIYWQIGSITCAAYPLSQVDTIDVDTGSISHNSALNLVVFGEKDEHLE
LMDGILVDLLNAKWNTFVKFRFYRQFFLFCFYFVLSLISFTLRPGPATTSSVSNPQITSTELPTIPPKMDPPVHNSD
LPLLLDKILSTALVSKRYPWNLTRTRLDKLKLDIVENLTSALSDMLGTYRNEIKLFNRSDKTSIYSSRNDAKPIDET
VLRINSTILFNGDGISFTSKYNWWNNLTEECRLMHLDTLSTKIRLTAEVLMEIAATLYIFAALREARFLGLNMFIEN
LMTAPSRVMFLFSCCILLTFPFLRLICADEIEDMLAVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVS
IYLVFVMGFSQAYYIIFLSFDNPNTPEGVDDSMSNPMPSPIESIMAMFLMSMTNFGDYYGAFERTQHEMEAKFLFVV
YMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPDERLKKLMDYSQPMSDGRRALVLRLNQSE
EDKEEMKEILEMKRTHDKLYKRRQSKTMKKILTSEDNVIL

FIGURE 53 - SEQ ID NO: 44

<> 34
<> 912
<> PRT
<> Apis florea
<> XP_003690006.1
<> ?
>gi|380011849|ref|XP_003690006.1| PREDICTED: LOW QUALITY PROTEIN: transient receptor potential cation channel subfamily V member 5-like [Apis florea]
MGNTESNVASGVKKQTDASSILLYKLVDLKGGGLLVDMMKRATQTKQYAELDHALRTKVEPYLYNKGKGKWIPIEKL
VLLRNKDRPKHKMLPPLRAMENPADYDIDKDTGEDEVRDETRIDKSKYRLVCWSLSERGAVGETILHLCMLHATAIH
IDLAKRLLRFYPKLINDVYISDEYYGESALHIAIVNEDPSMVKFLLDSGADVHERCIGNFMCPEDQKASRADSLDHE
WVCVTPETNYNGYVYWGEYPLNFAACLGQEECYRLILARGADPDKQDTNGNTVLHMLVIYEKLATFDMAYEVGASLA
IRNAQHLTPLTLSAKLAKIEMFFHILNIEREIYWQIGSITCAAYPLSQVDTIDVDTGSISHNSALNLVVFGEKDEHL
ELMDGILVDLLNAKWNTFVKFRFYRQFFXFCFYFVLSLISFTLRPGPATTSSVPNPVAQTPLTSTELSTISPKVDPP
VSNVTVNRSSNAFQHDSNLSLLLDKILSTASVKYPWNVTRTRLDKLKLDIIENLTTALNNLLSTHRDEIEFFNHSYK
TTEYFHSTRNDTTPIDNLKITINETVLSVNSTILFNDGISFATGKYNWWNNLTEECRLMHVDTLSTKIRLTAEVLME
IAATLYIFAALREARFLGLNMFIENLMTAPSRVMFLFSCCILLTFPFLRLICADQVEDMLAVVVMLTTAPYFLFFCR
GFKTVGPFVVMIYRMIMGDLLRFVSIYLVFVMGFSQAYYIIFLSFDNPNTPEGVDDSMSNPMPSPIESIMAMFLMSM
TNFGDYYGAFERTQHEIEAKFLFVVYMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPEERL
KKLMDYSQPMSDGRRALVLRLNQSEEDKEEMKEILEMKRTHDKLYKKRQSKIMKKILTSEDNVIL

FIGURE 54 - SEQ ID NO: 45

<> 36
<> 823
<> PRT
<> Pediculus humanus corporis
<> XP_002427963.1
<> ?
>gi|242014577|ref|XP_002427963.1| conserved hypothetical protein [Pediculus humanus corporis]
MGNTESNVTSGVKKQAGTSEQPLYKLVGLKGGGLLVDMMKRATQTKQYAELDHAIKTKIEPFLYNKGKGRLIPISQL
VLLRNCERSRTKLLPLLKNMEDPESEFDMDRDGNPGDFQPAPDGVQEDFHDYNKKYRDVCWDLKKRGAVGETCLHLC
MLNATSIHADLAKRLLKFYPKLINDIYMSDEYYGESVLHVAIVNEDPAMVKYLLDSGSNFHERCFGNFMCPEDQKAT
RTDSLDHEYVNLSTETNYEGYVYWGEYPLSFAACLGQEESYRLMLAKGANPDNQDTNGNTVLHMLVIHNKLPMFDVA
YEVGANLSLKNAKCLTPLTLAAKLARVELFFHILNIEREIYWQIGSITCAAYPLSQIDTIDIETGNISKNSALNLVV
FGEKDEHLELMDGVLVDLLVAKWNTYVKFRFYRQFISFFFYFLISVICFTLRPGPPTGTTTTTNGIVVLNNNNNNIT
SVVDNSNNVTTTTATTTATSYSFPGHVIVTLLSYDKYEDKIRIISELAMEIGSVLYLLGALREAKFLGIHMFIENLM
TAPSRVLFLGSCCIMQFVPWLRITCKEETEDIVAVIIMLTTAPYFLFFCRKMNDPVFLFLFFLIKKIFFLIFFFFF
TKPTYYIIFLSFDNPKTPDGVDDSGTNPMQSPVESIMAMFLMSLTNFGEYYGAFEKTEHEFVAKLMFVVYMAIVAIL
LVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPQERLKKLMLYSQPMSDGRRALVLRLHQTPEDKEEMKE
ILDMKRIHNRTVQRRKAKENKNVTFAGTPKNGIKNRLLGPVPPLKSIPSKPKI

FIGURE 55 – SEQ ID NO: 46

<> 38
<> 356, partial
<> PRT
<> Danaus plexippus
<> EHJ73092.1
<> ?
>gi|357621161|gb|EHJ73092.1| hypothetical protein KGM_12483 [Danaus plexippus]
MLESGGGLLVDMMKRAVQNKQYAEIDHAIKTKVEPFLYNKGKGRHIPISHLVLLRNKERGRHKLLPPLRGMENPDEE
FDVEKDWPVVTQEEYEANPSAYRELCWDLKERGAVGETILHLCLLNATSLLADLAKRLLRFYPKLINDIYMSDEYYG
ESVLHMTIVNEDPTMVKFLLDSGADYHERCFGNFMCPEDQKASRTDSFDHEWVNVQPDTNYDGYVYWGEYPLSFAAC
LGQEECYRLILARGANPDKQDTNGNTVLHMLIIYDKISTFDMAYEVGASLNIRNVQNLTPLTLAAKLARVELFFHIL
NIEREIYWQIGATTCAAYPLGQVDTIDTETGRISKDSALNLVVFGVS

FIGURE 56 – SEQ ID NO: 47

<> 40
<> 861, partial
<> PRT
<> Solenopsis invicta
<> EFZ14282.1
<> ?
>gi|322788689|gb|EFZ14282.1| hypothetical protein SINV_03089 [Solenopsis invicta]
GGLLVDMMKRASQTKQYAELDHAMRTKVEPFLYNKGKGKWIPIEKLVLLRNKDRPRHKMLPPLKAMENPA
DYDIDKDMGDEEVDEAKIDKSKYRLVCWNLSDRGAVGETILHLCMLNATAIHADLAKRLLRFYPLLIYDI
YLCDEYYGENVLHIAIVNEDPSLVKFLLDSGADDPRIIHERCFGTFMCPEDQKASRFDSMDHEWVCVTPE
TDYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVLHMLATFDMAYEVGASLDIRNVQH
LTPLTLAAKLARIEMFFHILNIEREIYWQIGSITCAAYPLSQIDTIDVNTGTINKTSALNLVVFGDKDEH
LELMDGMLVDLLNAKWNTFVKSRFYRQFFLFCFHFVLSLISFTLRPGPSTMETDENANDTSTKTNSSNIT
EPIILKPLQSSDLSELVTNSFVAAFASNLKSSLNMTQESLEKIQLQVTSNITSALKSILLLTLNENEGIL
SPPDEATIHTPWYTDSSPNTSDYFTDLYNKTVVAENSTVKAVVDDVAQTDYWWDDFAEECRLMQLTETSA
KIRLTAETFMYIAAVLYILAALREARFLGLNMFIENLATAPSRVMFLFSCCILLSFPFLRFVCADEIEDI
LAVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVCIYLVFVMGFSQAYYIIFLSFDNPNTPE
GTDDSITNPMPSPMESVMAMFLMSMTNFGDYFGAFERTEHEFEAKLLFVLYMVIVAILLVNMLIAMMGNT
YQKIAETRNEWQRQWARIVLVVERGVSPAERLKKLTDYSQPMSDGRPALVLRLHQTEEDKEEMKEILEMK
RTHEKLLKKRQCRMSKEKILS

FIGURE 57 - SEQ ID NO: 48

<> 42
<> 861
<> PRT
<> Acromyrmex echinatior
<> EGI70573.1
<> ?
>gi|332030947|gb|EGI70573.1| Transient receptor potential cation channel subfamily V member 6 [Acromyrmex echinatior]
MGNTESNVASSVKKQTDTSSILLYKLVDLKGGGLLVDMMKRATQTKQFAELDHAMRTKVEPFLYNKGKGKWIPVDKL
VLLRNKDRPRHKMLPPLKAMENPADYDIDKDMGDEEVDEAKIDKSKYRLVCWNLSDRGAVGETILHLCMLHATAIHA
DLAKRLLRFYPKLINDIYLSDEYYGENVLHIAIVNEDPSMVKFLLDSGADDPCIIHERCFGNFMCPEDQKASRFDNM
DHEWVCVSPETNYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVMHMLATFDMAYEVGASLGIRN
VQHLTPLTLAAKLARIEIFFHIMNIEREIYWQIGSITCAAYPLSQIDTIDVNTGTINNNSALNLVVFGDKDEHLELM
DGVLVDLLNAKWNTFVKSRFYNQFFLFCFYFVLSLISFTLRPGPSTIETDENANDTSTRTNSSNITEPIIHKTLQSS
DLSELVTNSLVAAFTSNFKSSLNMTQESLEKIQLQVTSNITSALKSILLLTLNENEGILSPPDEATIHTLWYTDSPP
NASDYFMNTYNKTDANSTVKTIIDGVARPKFKSNYWWDDFSEECRLMQLSEMSAKIRLTAEIFMFIAAVLYILAALR
EAKFLGLHMFIENLMTVPSRVMFLISCCILMWFPVLRFTCSDEVEDMLAVVVMLTTAPYFLFFCRGFKTVGPFVVMI
YRMIMGDLIRFVSIYLVFVMGFSQAYYIIFLSFDNPNTPEGIDDSITNPMPSPMESVMAMFLMSMTNFGDYFGAFDR
TEHEFEAKLLFVLYMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQEEDKEEMKEILEMKRTHDRLLKKRQNRMSK
EKIIFETEPIITKN

FIGURE 58 - SEQ ID NO: 49

<> 44
<> 904
<> PRT
<> Camponotus floridanus
<> EFN65752.1
<> ?
>gi|307175942|gb|EFN65752.1| Transient receptor potential cation channel subfamily V member 5 [Camponotus floridanus]
MGNTESNVTSGVKKQTDTSSIVLYKLVDLKGGGLLVDMMKRATQTKQFAELDHAMRTKVEPFLYNKGEGKWIPIDKL
VLLRNKDRPRHKMLAPLKAMENPADYDIDKDMGDEEVDETKIDKSKYRLVCWNLSERGAVGETILHLCMLNATALHA
DLAKRLLRFYPKLINDIYLCDEYYGENVLHIAIVNEDPSMVKYLLDSGADDPRIIHERCFGNFMCPEDQKASRFDSQ
DHEWVCVTPETNYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVLHMLATFDMAYEVGASLDIRN
VQHLTPLTLAAKLARIEMFFHILNIEREIYWQIGSITCAAYPLSQIDTIDVNAGTINNNSALNLVVFGEKDEHLELM
DGVLIDLLNAKWNTFVKFRFYRQFILFYFYFVLSLISFTLRPGPQTDENANDTLTNSFNTTRESMILKSLHSSDLSE
LVTNSFTAAFTSNFKSSLNVTQESLEKIQLQVTSNVTSALRSILLLTLSNNEDLLSSPDEAAIHTLWYTDNPQNASD
YFINMYNKTVTIDTNSTAKTTIDDVTLLGKFNNHEKWWDDLTEECRLMQLTTMSAKIRLTAEIVMYFAAVLYILAAL
REARFLGLNMFIENLMTAPSRVMFLFSCCILMSFPVLRLSCSDEVEDVLAVVVMLTTAPYFLFFCRGFKTVGPFVVM
IYRMITGDLLRFVSIYLVFVMGFSQAYYIIFLSFDNPNTPEGVDDSITNPMPSPMESVMAMFLMSMTNFGDYYATFD
RTEHEFEAKLLFVLYMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPAERLKKLMDYSQPMS
DGRKALVLRLNQTEEDKEEMKEILEMKRTHDKLIKKRQDKILKEKALAETEAVITRK

FIGURE 59 - SEQ ID NO: 50

<> 46
<> 668, partial
<> PRT
<> Myzus persicae
<> in-house
<> ?
AIKTQVEPMLYNKGEGRMIPIAKLVLLRNRDRSRARWLPPLKNMEDANEYDIEKDIPTIEELEKLGEVQXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXARGADPNNQDTNGNTVLH
MLVIYEKISTFDMAYEIGAELNIRNVQNLTPLTLAAKLARIQMFFHILKIEREIYWQIGSITCAAYPLXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXHLEMMDGVLVDLLNAKWNAFVKFRFYRQFILFAFYFSISMVCFVLRPGPPPTGLKPP
LINYTSTSTTVATTPFDFMDNESMLPDNVMYDEMMIGGGGPTEFETPVVTTEMATVNDNATTNNGTGIIRTPLIYED
GAGGGGGSGTVSLHGKSSGSDRGKHRSTWNPANHTFKTNYTYNYNKSRKFWWNKRQKVCRLMAVHSTDDLIRMGSEV
GMFVGAFLYLLAAVREAGFLGSQMFIENLAIAPARVMFLFSCLLMMTIPPLRLTCYDKAEDIIAVIIMLTTCPYFLF
FCRGXXXXXXXXVMIYRLVMGDLLRFVSIYMVFVMGFSQAYYVIFLSYDNPLTPEGIDDSVLNPMPTPTESIMAMFL
MSVNTFTDYYTAFDKTSHTLVAKFCFIVFMVIVAILPVNMLIAMMGDTYQKIAETRNEWQRQWARIVLVVERGVSPS
QRLKKLMYYSQPMSDGRRALVLRLNQTDEDKEQMKEILEMKRIHNRYVERMRARDLSSKLSSSCGKNANDGTINLKA
NK

FIGURE 60 - SEQ ID NO: 51

<> 48
<> 553, partial
<> PRT
<> Bemisia tabaci
<> in-house
<> ?
DPEKIDPKKCREVCWDLMERGAVGETILHLCLLNATSIHADLAKRLLRFYPKLINDIYMCDEYYGESVLHIAIVNED
PAMVKFLLDSGADYHERCTGNFMCPEDQKATRQDTVEHEWVNLSPLTNYEGYVYWGEYPLSFAACLGQEECFRLMLA
RGANPDNQDTNGNTVLHMLVIYEKLETFDMAYEVGANISVRNVQNLTPLTLAAKLARIEMFFHILNIEREIYWQIGS
IACAAYPLGQIDTIDIETGHISKNSALNLVVFGDKDEHLELMDGVLVDLLNAKWNAFVKLRXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XX

FIGURE 61 – SEQ ID NO: 52

<> 50
<> 748, partial
<> PRT
<> Euschistus heros
<> in-house
<> ?
LRFYPKLINDVYMSDEYYGESVLHIAIVNEDPAMVKFLLDSGVNVNERCFGNFMCPEDQKASRTDSLDHEWVNLQSF
TTYEGYVYWGEYPLSFAACLGQEEXYRLMLARGANPDNQDTNGNTVLHMLVIYCKIQTFDMAYEVGGDLSIRNVQYL
TPLTLAAKLARIELFFHILNIEREIYWQIGSITCAAYPLSQIDTIDIVTGNISKNSALNLVVFGEKDEHLELMDGVL
IDLLNAKWNAFVKFRFYRQFFLFLFYFLISLICFTLRPGPPPVKPISSFNSTKPSGNNITAELSPESNATTVPKWIY
KTEIKKYDPEDNSSQNSRLNVILREVILTSLKVEDIDKVVSFSNAEPQDNSREDADGLVCNGDSVHSCLGNGSDVVA
VFGKGKSPKVPKPGASADDFDYDDTWWEEFGQCRLLQVTSYIEMTRLISEVLLDIGALLYILAALREARFLGWSMFV
ENLMTAPSRVMFLFSCCLMLTMPFLRFTCNEEIEDMMAVIIMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRF
ATIYLVFVMGFAQAYYIIFLSFDNPLTPEGVDDSVSNPIPNPMEAVMAMFFMSMTSFGDYYPALERTAHEFCAKLCF
VIYMAIVAILLVNMLIAMMGNTYQKIAETRNEWQRQWARIVLVVERGVSPSERLTKLMWYSQPMSDGRRALVLRLNQ
SEEDKEEMKEILEMKRIHNRMVQKRKEREKSMNKSPNLINLNSPAENVKNTNPFS

FIGURE 62 – SEQ ID NO: 53

<> 52
<> 734, partial
<> PRT
<> Nilaparvata lugens
<> in-house
<> ?
LHMAIVNEDPGMVKFLLNSGADFHERCFGNFMCPEDQKASRSDSFDHEWVNLWPVTNYEGYVYWGEYPLSFAACLGQ
EECYRLMLARGANPDNQDTNGNTVLHMLVIYEKMGTFDTAYELGANVSVRNIQNLTPLTLAAKLARIEMFFHIMNIE
REIYWQIGSITCAAYPLMLIDTIDIETGXISKDSALNLVVFGDKDEHLDLMEGVLVDLLHAKWNAFVKFRFYRQFIM
FFQYFLISCVCFILRPGPPEAHDGMNITANATLNLSFGVLEVRPEALQALLYRLEKLSLPQSGDLERFILESLADEK
SISEAALENDENRXPGWNNSVFSTYETLARDTGYQTDESPHDGLSSSMDYAEVAERLTKLMIDVNLTERSGAVNEII
LKALPSLEEKEDGLEEWWSGIAGDCILLQVNDLYDLARLCAEVALEIGAFLYLLAALREARFLGLKMMIENLMTAPS
RVMFLFSCCLMMTMPFFRFTCQDETEDILAVVIMLTTGPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVSIYMVFV
MGFSQAYYIIFLTYDNPTTPEGTDDTTSNPLPSPIEAIMAMFFMSLTNFGDYYSAFENTEHEIEAKAFFVIYMVIVA
ILLINMLIAMMGNTYQKIAETKNEWQRQWARIVLVVERGVSPKERLKKLMSYSQPMSDGGRALVLRLNMTEEDKEEM
KEILEMKRVRDKIVMKRKKGLKLLGTTTPSPKRMKGRETPI

FIGURE 63 - SEQ ID NO: 54

<> 54
<> 162, partial
<> PRT
<> schistocerca americana
<> in-house
<> ?
LHMAIVNEDPAMVKFLLDSGANVHERCFGTFMSPEDQKAQRSDSLDHEWVNVNSDTNYEGYVYWGEYPLSFAACLGQ
EECYRLVLAKGANPDSQDTNGNTTLHMLVIHRKMTQFDMAYEVGSSLDIKNNLNLTPLTLAAKLARIEMFFHILNIE
REIYWQIG

FIGURE 64 - SEQ ID NO: 28

<> 1
<> 3372
<> DNA
<> Drosophila melanogaster
<> NM_132125.1
<> ?
>gi|24640230|ref|NM_132125.1| Drosophila melanogaster inactive (iav), mRNA
ATGAAGTTCCTCCTGAAGAAATGCCTGCGCAAGAAGGCGCCCGAGATGAAACCCGGGGCCATCCTGGATGCCGTCAT
CTCGCAATCATCGGCCACCGCGTGCAAGTGCCTGCTGTACAAACTGGCGGATTACAAAAGAGGTGGTGATCTCATCG
ATGCCATCAACTCGGGCGGACTGATTGCCGTGGAGCAGCTGATCCGGGAGCAGTTTGGCGTCTTCATGTACAACGAT
GGCAAGGGCCAGGTGATAAACCGTGCTGAGTTTCTGCGCTGGAAGTACCGCGACCACACCGAGGTGACCATACCCAT
TGAGGCATCCCTGTCCATCCACGATCCGCTGGGCAAATGGGAGGACCACAAGGCCTGCTGGCAGATGCAGTACCGCG
GCGCCCTGGGCGAGAGTCTGCTCCATGTGCTCATCATCTGCGATTCCAAGGTGCACACCAAGTTGGCGCGCGTGCTG
CTCCGCGTGTTCCCCAATCTGGCGCTGGATGTGATGGAGGGCGAGGAGTATCTGGGTGCTAGTGCCCTGCACCTGTC
GATTGCCTACAGCAACAATGAGCTGGTGGCGGATCTGATCGAGGCCGGAGCGGATATCCATCAGCGAGCGATTGGTA
GCTTCTTTCTGCCACGTGACCAACAGCGAGCGAATCCGGCCAAGAGCACCGACTACGAGGGACTGGCCTACATGGGT
GAATATCCGCTGGCTTGGGCCGCCTGCTGTGCCAACGAGAGTGTCTACAACCTGCTGGTGGACTGCGGATCCGATCC
GGATGCCCAGGACTCCTTCGGCAATATGATCCTGCACATGGTGGTCGTGTGCGACAAACTGGACATGTTCGGCTATG
CCCTGCGACATCCCAAGACGCCGGCCAAGAATGGCATTGTCAACCAGACGGGACTGACTCCACTCACTCTGGCCTGC
AAGCTGGGACGGGCGGAGGTCTTTCGTGAAATGTTGGAGCTGTCCGCCCGCGAGTTTTGGCGCTACAGTAACATCAC
CTGTTCCGGCTATCCACTGAATGCACTGGACACTCTTCTGCCGGACGGAAGGACTAATTGGAATTCCGCCTTGTTCA
TCATTCTGAACGGCACCAAGCCGGAGCATCTGGACATGTTGGACGGCGGCATTATCCAGCGCCTGCTGGAGGAGAAG
TGGAAGACCTTTGCGCAGAACCAGTTTCTGAAGCGTCTGCTCATCCTGTCCACCCATCTGCTATGCCTGTCCGTATC
GGTGTATTTGCGTCCAGCGCACGATGGTGAAGCCGAGGATGAGGACTCCGAGGGATCGGATGCCTCGGCAGCCGCTC
TGCTGGACATACAGTCGGATGAGGGCGACAGTGGTGGTGGTGACTACAATGCCCAGACGGTGGCCCGTTACTGCGCC
GAGTTTGCCACCCTGGTGGGAGTTTTAAGCTATGTGATCTTCCAGCAAGGCGACGAGATAAAGAACCAGGGTTTGTC
CGCCTTTCTCAAGCAGCTGTCCCATGCGCCGGCTAAGGCCATCTTCCTGTTCTCCAACTTGCTGATCCTGGCGTGCA
TTCCATTTCGTTTGATTGGCGACACCGATACCGAGGAGGCCATCCTGATTTTCGCTGTGCCGGGCTCCTGGTTTCTC
CTAATGTTCTTTGCTGGTGCCATTCGGCTGACGGGTCCGTTTGTGACCATGATCTATTCCATGATCACGGGCGACAT
GTTCACCTTCGGCATCATCTACTGCATCGTCCTGTGCGGATTCTCGCAGGCCTTCTACTTCCTCTACAAGGGACATC
CCCAGGTGCAGTCCACCATGTTCAATACCTACACCAGCACTTGGATGGCCCTGTTCCAAACCACACTGGGTGATTAT
AACTATCCCGATCTCAATCAGACCACATATCCCAATCTCTCCAAGACCGTGTTTGTCATCTTTATGATCTTCGTACC
CATCCTGTTGCTCAACATGTTGATTGCCATGATGGGCAACACCTATGTGACTGTGATCGAGCAGTCGGAGAAGGAAT
GGATGAAGCAGTGGGCCAAGATTGTCGTCACCCTGGAGCGCGCTGTTCCGCAGGCGGATGCCAAGGGCTATCTGGAG
GCATACTCCATCCCGCTGGGTCCGTCCGATGACTCCGGTTTCGAAGTGCGCGGCGTGATGGTCATCAAGAGCAAGAG
CAAGACGAGGGCCAAGCAGCGAAAAGGAGCCGTCTCCAACTGGAAGCGCGTGGGTCGTGTGACGCTAACGGCGCTCA
AGAAACGCGGAATGACCGGCGAGGAGATGCGTCGCCTTATGTGGGGCCGTGCCTCCATCTCCAGTCCCGTGAAAGTG
ACGAAGCAGAAGCTTAAGGATCCCTACAATCTGCACACGGACTCCGACTTCACCAACGCCATGGACATGCTGACCTT
CGCTAGCAACCCGGCTTCCTCCAATGGCGTCACCCTGCGATCGGTAACAGCGCCTCCGCCCGCACCGCCAGCACCGG
ATCCCTTCAGGGAGCTGATCATGATGTCGGACCAGCGACCGGAGACCCATGATCCCCACTACTTTGCCGGCCTGCAG
CAGCTGGCCAATAAGGCTTTCGATTTGGTGGAGCAAACGATGAAGACACAGCCGCAAGCGCCGGTGGCCAAGAAGGT
GGATCCACTGCCAGTGGCTTCGGTGGCCAAAGCATCTCCAGCCGCTCCTGCAACACAAGCTACTGCTACTGCTGCTG
CTGCTTCCGATCTAATGGCCATGCCACTGCCCATTTCGAACTTGAGCAATCTTTTCCAAGACCCCAAGGACATTGTC
GATCCCAAAAAGCTGGAGGAGTTCATGGCCATGCTGGCCGAGGTGGAAACCGAGGAGAGCGACAGCGGCGGACCCAT
TCTCGGCAAGCTATCGCTGGCCAAACGGACACACAATGCCCTATCCAAGGCGGAAATTCGACGGGATCAGCAGGGAT
TCGAGGGTCACAGCCATGGACAGTTTCAGCCCATGTCCTCGGTGTGGGCACCACCTGGCCTGGATGTGGACACGGGC
TTCCACTTCGATGAAGCCGTCGCGGAGGAGGTGCTGACCATCGAACAGGAAGCCGAAGTGGAGACCGAGGACGGCAA
TGGTGGACAGGACAGCGAGGATATACCCACGGCGGAGGAGGTGCACGCCACTATGAAGCAGTTTCACCTGCGCAAGT
GCCAGCCAGCACAGGATGAGGCCGCTCGTCGCGCCAAAAGTGCTCGTGTTCGTCGCCGAAACAAAGTTTCGCCGGAG
CAAAGCGATGATCCGGACGAGCGCAGCCAGCGGGGACGTTCCGCTTACACGCGGCGAACGCAATCGCCGCCCGATCC
GCTGGAACCATGGAGCACCCGCGAACTGCAGGACATCAACAAGATCCTGGCCAGAAAGTGA

FIGURE 65 - SEQ ID NO: 29

<> 3
<> 3387
<> DNA
<> Musca domestica
<> XM_005180960.1
<> ?
>gi|557762605|ref|XM_005180960.1| PREDICTED: Musca domestica uncharacterized LOC101887788 (LOC101887788), mRNA

ATGAGGCTGTTCATGAAAAAGTGTTTGAGAAAAAAGCCTCAGGAATTGAAACCTGGAGCGATTTTAGATGCTGTCAT
TTCACAGTCATCGGCAACAGCTAGCAAATGTTTGCTCTACAAGTTGGCGGACTACAAACGGGGAGGCGACCTCATTG
ATGCCATCAACACCGGAGGGCTGGTGGCGGTGGAACAACTGATTCGCGAACAATTTGGCATATTCATGTATAACGAT
GGCAAGGGTCAGGTCATTAATCGTGCCGAATTCTTGCGTTGGAAATATCGTGACCACACCGAAGTGACCATACCCAT
AGAAGCCTCTTTATCCATACACGATCCATTGGGTAAATGGAAGGATCACAGTGCCTGTTGGCAGATGCAGTATCGTG
GCGCCTTGGGAGAGAGTCTGCTGCACGTCTTGATTATTTGCGATTCCAAAATGCATACCAAATTGGCGCGTATCTTG
TTGAGGGTGTTTCCTCGCCTGGCATTGGATGTCATCGAGGGCGAGGAGTATTTGGGTGCAAGTGCATTGCATTTGGC
CATAGCTTATAGCAATAATGAGTTGGTTGCCGATTTAATTGAGGCAGGAGCTGACATCAATCAGAGAGCCATTGGAA
GTTTCTTTTTGCCCAAGGATCAACAGAGAGCCAATCCGGCAAAGAGTACAGATTACGAGGGTTTGGCTTATATGGGC
GAATATCCATTGTCATGGGCTGCCTGCTGCGCCAATGAAAGTGTCTATAATCTGTTGATTGATCATGATGCCGATCC
CGATGCCCAGGATAGTTTTGGAAACATGATCCTGCACATGGTGGTGGTGTGTGATAAGTTGGACATGTTTGGATATG
CTCTACGCCACCCCAAGACTCCGGCCAAAAATGGAATTGTTAATCATTCTGGTCTGACACCTCTAACATTGGCTTGC
AAATTGGGTCGGGCTGAGGTGTTCAGGGAAATGTTGGAACTATCGGCCAGAGAATTTTGGCGTTATAGTAACATTAC
CTGTTCGGGTTATCCTTTGAATGCTTTGGACACGCTGCTACCAGATGGGAGGACCAATTGGAATTCGGCCTTGTTTA
TTATTTTGAACGGTACCAAGGAGGAACATTTGGATATGTTAGATGGTGGGATTATACAGCGTCTGCTGGAGGAGAAA
TGGAAGACCTTTGCCCAGAATCAATTTCTAAAGCGTTTGCTGATTTTGGTGGTGCATTTGTTGTGCCTCTCAACGTC
GGTGTATCTGAGGCCAGCCCATGATGGCGATGATGACGAAGAAGATGAAACGGCTCAGGCTAATGCAGGACTACAGA
CCAATGATCCAGAAAACGAAGAATATGATATTCAAACAATAGTGAGATATTGTGCTGAGCTGTGTACCATTGCGGGG
GTCCTTAGTTTCCTGATTTTCCAACAAGGCGATGAAATAAAGAATCAGGGATTGTCAGCCTTCCTCAAACAACTGTC
CCATGCTCCAGCTAAGGTAATATTCTTGGTCTCGAATCTGATGATTTTGGCCTGCATACCCTTTCGCCTAATGGGTG
ACACGGACACAGAAGAGGCCATACTTATATTTGCTGTGCCGGGAAGTTGGTTCTTGCTGATGTTCTTTGCGGGTGCA
ATTCGTTTGACCGGTCCCTTCGTAACCATGATCTACTCCATGATAACAGGTGACATGTTTACGTTTGGCATTATTTA
CTCCATTGTTCTGTGTGGCTTTTCCCAGGCGTTTTATTTCCTTTACAAAGGACATCCCCAATTGCAGTCGACTATGT
TTGATACCTTTCCCAGCACCTGGATGGCCCTGTTTCAAACCACTTTGGGAGATTACAATTATCCCGATTTGAATCAA
ACAACCTACCCGAACTTGTCGAAAACCGTTTTCGTTATTTTCATGATTTTCGTTCCCATTCTGTTGCTGAACATGTT
GATCGCCATGATGGGCAACACCTACGCCCATGTCATTGAACAATCCGAAAAGGAATGGATGAAACAGTGGGCCAAGA
TTGTGGTCACACTGGAAAGGGCAGTTCCCCAAGCGGATGCAAAAAATTATCTGGAAGCCTATTCCATACCCTTGGGT
CCTTCGGATGATTCCGGATTTGAGGTTAGGGGAGTAATGGTCATTAAGAGCAAAAGTAAGACAAGAGCCAAACAACG
CAAGGGAGCAGTATCGAATTGGAAGAGAGTGGGCCGTGTAACGCTCAATGCCTTGAAGAAACGTGGTATGACGGGTG
AGGAGATGCGTCGTCTTATGTGGGGCCGAGCATCCATATCGAGTCCCATTAAAGTGGCCAAGAAGAAACTGAAGGAT
CCCTACAATCTAAATCAAGAGCCTGGGGGTCAATCCAATTTGACCAGTGCCATGGACATGCTTAATTTTGCCAATGA
CCCAGCCTCCAGCTCGGGATTGGCTTTTAGAACTTCTGGTACTCAGGACCCCAAGGAGAAGAAGGATGTGCCACACA
TTCCCGCACCAGATCCCCTGCGTGATTTGGTTCTGTTAGCCGAAGAGAAGCCGGAAGTACACGATCCACAATTCTAT
TCAGCATTGATTCAGTTGGCCAACAAGGCCTATGATTTGGTGAAGAAAACCCTGGAAACCCAACATCAGCCACAAGT
TGAGGAGCCGATACCACTCACAGAGGCCACCAGTTTGAAGGACGTCACACTGACAAAACAACCCGATCCCGTTGCTG
CTGATGCTGGACTCCTTGGCGACATGGCCATGGGTGCCAATCTTACCAATCTCTTTCAAGACCCCAAAGATATTGTG
GACCCAAAGAAACTCGAACAATTTCTGAAAATGGTAGCTGATGTTGAGACCGAGGAAAGTGATGGAGGTGGTCCAAT
TTTGGGAAAACTTTCATTGGCCCGCAGGACACGCAATGCCCTATTTAAGGTACCCATACCCAAGAGTACTCTTGGCG
ACAGTTCGGATAAGTTAATTAATTCGGTGTGGGACAAGGTGCCAGCCGACAATGATGAGGACAGTATTCCGGCCTTT
GATTTCCAAGAAGCTCTGGCTGAACATGTCCTGACAGTGGAACAAGAGGCCGATGTGGAGACCGAAGATGCAAACGA
TGATTCGGGTGAGACCATGGACGATATACCCACAGCGGAGGAAGTACACGCTACCATGAAGCAATTTCATTTGCGTA
AGCGTCAATATCAGCAGGACGATGCAGCACGTCGTGCTAAGACGGCTCGAATAAGGCGCAAGAATAAAGTTGCTCCA
GATTATGCTGGGAGTGAAGAGCAATATGGACGTGGCCGTTCGGCACCCATGAAAAAGAAACATGATGAGGATGAAAT
GTCACCTCCTGATCCCTTGGAACCATGGAGTACTCGGGAATTGCAAAATATTAATAAAATCCTGGCAAAAAAGTAA

FIGURE 66 - SEQ ID NO: 30

<> 5
<> 3435
<> DNA
<> Ceratitis capitata
<> XM_004529418.1
<> ?
>gi|498980909|ref|XM_004529418.1| PREDICTED: Ceratitis capitata uncharacterized LOC101456642 (LOC101456642), mRNA

ATGAAATTCTTTTTGAAAAAATGTCTACGCAAAAAACCGGAGGAGATGAAACCAGGCGCCATACTGGACGCCGTCAT
TTCGCAATCCTCACCAATGGCCAACAAATGTCTACTCTACAAGCTGGCCGACTACATGCGCGGCGGTGACCTCATCG
ACGCACTGAACACTGGCGGCCTGGTCGCCGTGGAACAACTGATACGCGAGCAGTTCGGCATATTTATGTATAACGAT
GGCAAGGGACAGGTGATTAATCGTGCCGAGTTTTTACGCTGGAAATATCGCGATCACACTGAAGTTACTATACCGAT
TGAGGCTTCGCTCTCACGTCACGATCCGCTGGGCAAGTGGGAGGATCATAAAGCCTGTTGGCAAATGCAATTTCGTG
GGGCACTCGGTGAGAGTTTACTGCACGTGCTCATCATTTGCGATTCGAAAATACACACAAAGCTAGCGCGGGTACTG
ATACGAGTCTTTCCGAATCTGGCACAAGATGTGATGGAGGGTGAGGAGTATTTGGGTGCTAGTGCGTTGCATTTGGC
GATTGCTTATAGCAATAATGAGCTTGTGGCCGATTTGATTGAAGCAGGCGCTGATATAAATCAGCGTGCTATTGGCA
GTTTCTTTCTGCCGCGTGACCAGCAACGTCGAAATCCAGCCAAGTCGACGGACTATGAAGGATTGGCGTATCTGGGC
GAGTATCCGTTGGCATGGGCGGCATGTTGCGCCAATGAAAGTGTGTACAATTTGCTGGTGGACTGTGGTGCAGACCC
AGATGCACAAGACTCGTTTGGTAATATGATACTGCATATGGTGGTGGTGTGCGATAAATTGGATATGTTCGGTTATG
CTCTTCGCCATCCAAAAACGCCAGCCAAAAATGGTATCGCCAACCACAGTGGACTCACACCGCTGACACTTTCTTGC
AAACTGGGACGCGCTGAAGTTTTTCGTGAGATGTTGGAGCTTTCCGCACGTGAGTTTTGGCGTTACAGCAACATCAC
CTGCTCGGGTTATCCGCTCAACGCTTTAGATACTTTGCTGCCAGATGGACGCACAAATTGGAACTCGGCGCTGTTTA
TCATCTTGAATGGCACCAAAGAGGAACATTTGGATATGTTGGACGGCGGCATCATACAACGTTTACTGGAAGAGAAA
TGGAAAACCTTTGCTCAAAATCAATTCCTCAAACGTCTACTGATCCTAGTCATACACTTGGTTTTCCTCTCCATCTC
AGTTTATATGCGTCCCGCGCGTGTTGCAGACGATGATGATGAAGATGAGATAGATGCGTCTTCGAAAGACACTAAAG
CTCTTGAGCTTGCCACGGAATTGGATGAAGATGAGTACGATGTGCAGACTATTGTGCGCTACTGCGCAGAGTTTGGC
ACTATAGTGGGCGTATTGAGTTACGTTATCTTTCAGCAGGGAGATGAGATCAAAAATCAAGGTTTGCCAGCGTTCTT
AAAGCAGTTGACTCACGCTCCAGCCAAAGCTATCTTTCTAGTCTCTAATCTGCTAATTCTCGCCTGTATACCCTGTC
GACTCATGGGTGATACGGACGCCGAGGAGGCTATACTCATCTTTGCCGTGCCTGGCAGTTGGTTTCTGCTAATGTTT
TTTGCCGGCGCCATACGTCTGACGGGTCCTTTCGTTACTATGATATACTCCATGATTACAGGCGATATGTTCACGTT
TGGCATTATTTATTGTATCGTACTATGCGGCTTCTCGCAAGCTTTCTACTTTCTCTACAAGGGGCATCCACAAATAC
AGTCGACTATGTTCAATACCTTTCCCAGTACTTGGATGGCTTTGTTTCAAACCACACTCGGAGACTATAATTATCCC
GACTTGAACAATACAACATATCCGAACCTCTCGAAGACTGTATTCGTTATATTTATGATTTTCGTGCCGATTTTATT
GTTGAACATGTTAATCGCTATGATGGGCAACACCTACGCGCAAGTTATCGAAAGATCGGAGAAAGAGTGGATGAAAC
AGTGGGCAAAGATCGTGGTGACCTTGGAACGCGCTGTACCACAAGCTGATGCTAAGAACTATCTAGAGGCCTATTCA
ATACCACTCGGACCAATAGATGACTCCGGATATGAGGTGCGCGGTGTAATGGTTATCAAGAGCAAGGCGAAGACCAG
AGCTAAACAGCGTAAGGGTGCAGTTTCTAATTGGAAGCGCGTTGGTCGGGTCACATTGAATGCGTTGAAAAAGCGCG
GCATGACCGGCGAGCAAATGCGTCGTTTAATGTGGGGACGTGCATCCATATCAAGTCCGATTAAGATTACAAAAAAG
AAGTTGAAAGATCCCTACAATTTGAATCCACAAAATGATCTCACAAGCGCTATGGATATGTTGACCTTTGCCAATGA
TCCCGCAGCAAGCGCTGGTCTACAACTACGCTCCTCACTCATGGACTCCGGTGCCGAGGGCAAAGCAGCAAAAGTGC
AGGAGGAAAATCAGCAACCCGCACCAGATCCACTGCGCGACTTAATTTTCCTCGCCGATCGTCGTCCGGAAATGCAT
GATCCTCAGTATTTTGTTGGCCTACAGCAATTGGCAAATCAGGCATTGGATTTGGTAGAACAAACAATGGGCATCCA
TCCACCACCCACTCCCGCAACTGATGCTTTACTTCTATCAGCAGCTGCTGCTACAACAACTATCGGTGCAGTGACAA
TGCAAACAGCCACAACTGTTGCCGCACCGAGCGCAGATTTAATTACCCCATTGGGCGCGAATTTAACAACGCTCTTT
CAAGATAACAAAGATGTCGTGGATCCGCAAAAGCTTCAAGAATTCTTGAAAATGTTGGCCGAGATCGAGACCGAGGA
GAGTGATGGCGGTGGTAGACCAATTTTGGGCAAGTTATCGCTTTCTCGACGTACAAAGAGCGCTCTTTCGAAGGCTC
AGATTAAGAAAGATACGGTCGGTGGTAGTCCTGATAAATTGATCCCATCGGTTTGGTCACATAATTTACCGCAACCA
GATGAGGAACCGGAATTCAACTTCGAGGCTGCACTAGCCGAGGAACACACACTCACCATTGAACAGGAGGCTGAGGT
GGAGACCGAAACCGGCAACGAGCGTGAGGATAGCGAAGATTGTCCGACGGTAGAGGAGGTGCATGCAACAATGAAAC
AATTCCACCTGCGTAAGCGGCAATATCAACAGGACGACGCAGCACGACGAGCGAAAAGTGCACGCATCAAGCGCAAA
AATAGAATTTCACCGGAACAATCCCATGAGTGTGATGACGGCAGCAGCGGCGGCGGCGGAGGTAAGTCAACACACCC
ACGCGGCGCTTCAGCGCCAGGCCGTAAGCACACGGTGAGCGAACGCTTGTCGCCGCCGGATCCTCTGGAGCCGTGGA
GTACGCGCGAATTGCAAAATATCAACAAAATATTAGCGCGCAAGTGA

FIGURE 67 - SEQ ID NO: 31

<> 7
<> 3363
<> DNA
<> Aedes aegypti
<> XM_001659838.1
<> ?
>gi|157121230|ref|XM_001659838.1| Aedes aegypti hypothetical protein partial mRNA

ATGGTCCAATTCGACTGGCGGCGTATGTGTCGCAAGAAGCGAAAGGTTCCTCAGGGCGGTGCTATCCTGGATCAAGT
GATTTCCCAGTCGGCCAATGCTTCTAATCAGTGCTTGCTGTATAAGATGGCTAATTACAAACGGGGTGGAGATTTGA
TCGATGCGTTCCAGGTCGGAGGGCAGAAGGCCGTGGAGCAGTTGATTCGGGAGCAGTTTGGAGTTTTTATGTACAAC
AATGGCCGCGGACAGATCATCAATAGGGCCGAGTATCTACGGTGGAAGTACATGGATAATCATGAGGTCGTCATCCC
GATTGAGGCGTCGTTGTCTCCGCATGATCCTTTGGGCAAATGGGTCGATCATAAGGCCTGCTGGCAGATGCAGTATC
GTGGATTGCTGGGCGAGAGTTTGCTGCACGTGTTGATCATCTGCGATACGAAGATTCACACGAAGTTGGCCCGCATC
CTGCTGCGCGTGTTCCCCGAGCTGTCGATCGACGTGATGGAAGGCGAGGAGTACCTGGGCGCTAGTGCACTCCACTT
GGCGATCGCGTACAGCAACAACGAGTTGGTGGGCGATCTGATCGATGCCGGAGCGGACGTGTCCCAGCGCGCCATCG
GACGGTTCTTCCTTCCACGGGATCAGCAGGGCTTGAAGCCGGCCAAGAACACCGACTACGAGGGGTTGGCCTACTTG
GGCGAGTATCCGCTGGCGTGGGCCGCCTGCTGCGCCAATGAGTCCGTCTATAACCTGCTGCTGGAATGCGGGGCGGA
TCCGAACGCGCAGGACAGCTTCGGGAACATGATTCTGCACATGGTCGTCGTCTGCGATAAGCTGGATATGTTCGGGT
ATGCCCTTCGTCATCCGAAGCTTCCCTGTAAAAATGGGATCGTCAATGAGTCCGGACTCACGCCGTTGACCTTGGCC
TGTCGATTGGGTCGTGATGAAGTGTTCCGTGAGATGTTGGAGTTGTCGGCGAGGGAGTTTTGGCGGTACAGTAACAT
CACCTGTTCCGGATATCCGTTGAACGCATTGGACACGTTGATGCCCGACGGAACTACCAATTGGAATTCGGCGCTGT
TTATCATCCTCAACGGAACCAAGGAAGAGCATTTGAACATGCTGGACGGTGGCATCGTGGAACGTCTGCTGGACGAG
AAGTGGAAGACGTTCGCTCGGAACCAGTTCATCAAGCGACTGCTGATCCTCGCTCTGCATCTGTTCTGCTTGTCGTG
TTCGGTCTACTTGAGACCGGTGCGAGTTTTCAAGGAGGAGAGTGAAGAGGGAAGCGATGGAGGAGATGGAGCGGGTA
CAGCTGCTCCGGACGGTGTCGATGATGATGAGGACATTGATTTGACGACCTGGTTCCGGTATGGATTCGAGATCGCA
ACCGTGATGGGAGTACTGAGCTACGTGGTTCTTCAACAGGGTGATGAGATCAAGAATCAGGGATTGATCTCGTTTAT
AAAGTCACTTGGAAATGCTCCGGCGAAAGCTATCTTCCTGATCTCCAATCTGATGATCTTGGCTTGCATCCCGTTCC
GAATGATGGGTGACGTTGAACACGAGGAGGCCATTCTGTTGTTCGCAGTCCCAGGATCATGGTTCCTGCTGATGTTC
TTTGCTGGCGCCATCGGCTTAACAGGTCCCTTCGTCACCATGATCTTCTCTATGATCACGGGTGACATGTTCACCTT
CGGCATCATCTACATGATCGTTCTGTTCGGATTTTCCCAGGCGTTCTACTTCCTGTACAAAGGTCATCCGGAAGCGG
AGGATTCTCCATTTGGGAGCTACTTCGGCACTTGGATGGGCCTGTTCCAGACAACCCTCGGCGATTACGATTACGCC
GACTTGAATCTTACGACCTACCCGAACCTGGCGAAAACCGTGTTTATCATATTCATGATCTTCGTGCCGATCCTGTT
GTTGAACATGTTGATCGCTATGATGGGCAACACCTACGCGTACGTCATTGAGCAAGCTGAAAAGGAAGGCATGAAAC
AGTGGGCCAAGATCGTGGTCAACCTGGAGCGGGCGGTCAAGCAGGAGGACGCCAAAAAGTACCTGGAGGAGTACTCG
ATCGGGTTGGGACCGTCGGATGATCCGAGGTACGAGATCCGTGGAGTCATGGTCATCAAGAGCAAGAGTAAGACCCG
TGCCAGGCAGCGCAAGGGAGCGGTAAGTAACTGGAAGAGCGTTCTGCGTGTCACGTTGAACGAGCTGAAGAAGCGTA
ACATGACCGGCGAGGAGCTGCGGAGGATCATGTGGGGACGATCGTCGATCACTTCTCCGGCCAAGATCTCCAAGAAG
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CATGGTAAGTAGCGAACCGACCGGACCGCCCACAATCGACCCCTCCAAACCGGCGACGATCGCCGTCAAGCCCCAAA
CGGCACCCGCAGCGCAACCGATCCCGGAGATTCCTCCTCAACCGCCGCTGGTCAAACGGCAGTCCGTGGTTAGTGCT
CCGCCGGCCTACGACGATTTCCCCCCGATGAAGGACTACAAGGATCCCCTGCGGGAGCTGGTCATCATCTCGGAGTC
GCCCTCGGTGGACGACCATTACGTGCAGAGCTGCAAGACCCTCGCGAATGATGCGTCCACCCTGGATCACGACACCT
TGGGTCAGTTAAATCCCTTCCTGGAGGCGAAGGACGTGGTCGATCCGGTGAAGGAACGCGAGTTTCTCAAAACACTG
GAGGCCCTGGAGGACACCGACAGCGAAGCGGCCGAAAAGCCGGTCCTGGGCAAGATCTCCCTGATACGACGCGCCAA
GTCAGCCGTCTCGAGAACCACTTCCAGGAAGAAGAAAACCGACCAGCATCCGCTGTTTACGATCGCTTGGGATGACA
AGAACCTGACCCGGACGCATCCGGAGGACTTTGGAGCGCTGAACACGGCCTACGAGTACAGTGCCGAAGATTTCAAG
CAAGACGTGGACGAGGAAGCGAGGGAGGAGGAGGAAGACGAGGGTGTGACGGTGGAGGAAGTGCACCGCCGAATGGA
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AAGGACAAACGGATGAAGTCGGCGCCGACGGGTGGAGGGACCTCGCCACCGGATCCACTGGAACCATGGAGCACAAG
GGATATTTGCAACATTAATAAACTTTTGGACACCGATACGCAGGATGAGTAA

FIGURE 68 - SEQ ID NO: 32

<> 9
<> 3414
<> DNA
<> Culex quinquefasciatus
<> XM_001864290.1
<> ?
>gi|170057086|ref|XM_001864290.1| Culex quinquefasciatus OSMotic avoidance abnormal family member, mRNA

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TCGATGCGTTCAAGATGGGCGGCCAGAAGGCGGTGGAGCAGCTGATCCGGGAACAGTTTGGGGTGTTTATGTATAAT
GCTGGCCGGGGTCAGATTATCAATCGGGCGGAGTATCTGCGGTGGAAGTATATGGATAACCATGAGGTTGTGATTCC
GATTGAGGCGTCGCTGTCCCCGCATGATCCTTTGGGGAAGTGGGTCGATCATAAGGCCTGTTGGCAGATGCAGTATC
GTGGGTTGCTGGGGGAGAGTCTACTTCATGTGTTGATCATCTGCGACACTAAGATTCATACCAAACTGTCCCGCATT
CTGCTGCGCGTGTTTCCGGAGCTGTCGATCGACGTGATGGAAGGCGAGGAGTACCTGGGCGCTAGCGCACTCCACCT
GGCGATCGCGTACAGCAACAACGAACTCGTTGGCGATCTGATCGACGCCGGGGCGAATGTGTCCCAGCGGGCCATCG
GGCGCTTCTTCCTTCCACGGGACCAGCAGAAGATGCATCCGGCCAAGACCACCGACTACGAGGGGTTGGCCTACCTG
GGCGAGTACCCACTGGCTTGGGCCGCTTGCTGCTCGAACGAATCGGTCTACAACCTGCTGCTCGAGTGTGGCGCAGA
TCCGAACGCGCAAGACAGCTTCGGAAACATGATCCTGCACATGGTCGTCGTGTGCGACAAGCTGGACATGTTTGGGT
ACGCGCTGCGGCACCCGAAGCTACCATGCAAGAACGGGATCGTCAACGAGGCCGGACTGACCCCGTTGACGCTGGCC
TGCCGCATCGGTCGAGACGAGGTGTTCCGTGAGATGTTGGAGCTGTCGGCGAGGGAGTTTTGGCGGTACAGTAACAT
CACCTGTTCCGGGTATCCGTTGAACGCGCTGGACACGTTGATGCCGGATGGTTCGACGAACTGGAACTCTGCGCTGT
TCATCATACTTAACGGAACAAAGGAGGAACATTTGAACATGCTGGACGGTGGTATCGTGGAGCGTCTGCTGGACGAG
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CTCGATTTACCTGCGACCGGTACATGTCTTCAAGGATGATGACGATGCAGATGACACCGATGGGGTTACTGATTCCC
CTGATACAACCGACGACGAGGGGATTGACCTGACCACGTGGTTCCGGTACGGGTTTGAAGTTGCCACCGTGATGGGC
GTGCTGAGCTATGTCGTAGTTCAGCAGGGTGAAGAAATCAAGAATCAGGGGTTTATATCGTTCCTCAAATCGCTGGC
TGGAGCTCCCGCTAAAGCGATTTTCTTGATTTCCAACCTGATGATTTTGTGCTGCATACCTCTGCGGATTCTCGGCG
ATAGAGAAGCTGAGGAAGCGGTGTTGTTGTTTGCCGTCCCCGGCAGCTGGTTTCTGTTGATGTTCTTCGCCGGTGCA
ATCGGACTAACTGGACCCTTCGTAACCATGATCTTTTCTATGATAACCGGTGACATGTTCACCTTTGGTATCATTTA
CACGATCGTACTGTTCGGATTCTCGCAAGCGTTTTACTTCCTGTACAAGGGTCATCCCAACGCGGACGAATCACCTT
TTGGCACGTACTTTGGAACCTGGATGGGACTGTTCCAGACGACCCTGGGCGATTACGATTACGCCGATTTGAACCTG
ACCACGTACCCCAACCTCGCCAAAACGGTCTTTATCACGTTCATGATCTTCGTGCCGATTCTGCTGCTTAACATGTT
GATCGCCATGATGGGTAACACCTACGCGTACGTCATTGAGCAAGCCGAAAAGGAAGGTATGAAGCAGTGGGCCAAGA
TTGTGGTCAACCTGGAGCGTGCCGTCAAGCAGGAGGATGCCAAAAAGTATCTGGAAGAGTACTCGATCGGGCTGGGA
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CAAGGGAGCGGTCAGCAACTGGAAGAGTGTGCTGCGTGTGACGTTGAACGAGTTGAAGAAGCGCAGCATGACTGGCG
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CAAGCGGTATCGGCCACCGCCGGAACTGCTGCTCCGGAGGATGACTTTGGGGCACTGAACACGGCGTACGAGTGCTC
GGCGGAAGATTTGAAGCACGACGTGGACGAAGAAGCACGGGAGGACGATCCAGACGAGGGCGTGACGGTGGAGGAGG
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AGCAAGAAGCAGGCCAAGGGAGACAAACGCATGAAGTCGGCACCCAGCGGCCATGGGCCGCGCCATCGGCAGATGAT
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TCGATACGGATACCCAGGACGAGTAG

FIGURE 69 - SEQ ID NO: 33

<> 11
<> 3651
<> DNA
<> Anopheles gambiae
<> XM_310685.5
>gi|347963768|ref|XM_310685.5| Anopheles gambiae str. PEST AGAP000413-PA (AgaP_AGAP000413) mRNA, complete cds

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TCGACGCGTTCCAGATCGGCGGCCAGAAGGCGGTGGAGCAGCTGATCCGCGAGCAGTTCGGCGTGTTCATGTACAAC
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GATCGAGGCCTCCCTGTCGCCGCACGACCCGCTCAGCAAGTGGGACGACCATAAGGCCTGCTGGCAGATGCAGTACC
GGGGCCTGCTGGGCGAAAGTCTGCTGCACGTGCTCATCATCTGCGACACGAAGGTGCACACCAAGCTGGCCCGCATC
CTGCTGCGCGTCTTCCCGGAGCAGTCGATCGACGTGATGGAGGGCGAGGAGTATCTTGGCGCGTCCGCCCTCCATCT
AGCCATCGCGTACAGCAACAACGAGCTGGTCGGCGACCTGATCGATGCCGGCGCGGACGTGTCCCAGCGGGCGACCG
GGCGCTTCTTTCTGCCCCGCGACCAGCAGGGCCTGCGGCCGGCCAAGACGACCGACTACGAGGGGCTGGCGTACCTC
GGCGAGTACCCACTGGCCTGGGCGGCCTGCTGCGCGAACGAGTCGGTGTACAACCTGCTGCTCGAGTGTGGCGCCGA
CCCGAACGCCCAGGACAGCTTCGGCAACATGATCCTGCACATGGTGGTCGTGTGCGACAAGCTGGACATGTTCGGGT
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TGCCGGCTCGGCCGCGACGAGGTGTTCCGCGAGATGTTGGAGCTTTCTGCGCGCGAATTCTGGCGGTACAGTAACAT
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CTCGGTCTACCTGCGCCCGGTCCGCGTGTTTGCTGATGACGAGGGCGAGGAGGGCGGAGACGCAACCGATGACGATG
GTGCGGACGATGGTGGGCCGATGGCGGTGGACGCGGTCGACGACGACATCGACCTGACGACCTGGGTGCGGTACGGC
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GCATACCGCTGCGCATGATGGGCGACACCGAGACGGAGGAAGCCATCCTGCTGTTTGCCGTACCGGGCAGCTGGTTT
CTGCTAATGTTCTTTGCTGGTGCGATCGGACTGACCGGACCGTTCGTGACGATGATCTTCTCCATGATTACGGGCGA
CATGTTCACGTTCGGCATCATCTACATGATCGTGCTGTTTGGCTTTTCGCAAGCGTTCTACTTCCTCTACAAGGGCC
ACCCGAACGCGGAGGACAGCCCGTTCGGCAGCTATTTCGGCACGTGGATGGCGCTGTTCCAGACCACGCTCGGCGAC
TACGATTACGCCGATCTGAACCTCACCACCTACCCGAACCTGGCGAAGACGGTGTTTGTCATCTTTATGATCTTCGT
GCCGATCCTGCTGCTGAACATGCTGATCGCGATGATGGGCAACACGTACGCGTACGTGATCGAGCAGGCGGAGAAGG
AGGGCATGAAGCAGTGGGCGAAGATAGTGGTCAATCTCGAGCGGGCGGTGACGCAGGACGACGCGAAGCGCTACCTG
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TGAAGAAGCGCAGCATGACGGGCGAGGAGCTGCGACGCATCATGTGGGGCCGCTCGTCCATCACGTCGCCGGCGAAG
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GATGTCGTTCACGCAGGACATCGTGATGGTTAGCACGGACACGGTCTGCCCGATCACGATACCGCCAGCGGCTGCCC
CGGGCACGGCGGCCCCGAAGGCTGGTGGCACCAAACCGGTAGTAGTGGCACCGCCGCCGCCAGCAGCAGCAACAGCA
GTACAGCAACCACCGCCGCCAGCGACGACGCGGCGCCACTCGACGGCAAGCGCACCGGCCACGATGGGGCTGGGCGT
GGAGGCGGCCCTGCCCGGCTACAAGGATCCGCTGCGCGAGCTCGTCATCATCTCCGAGTCGGCCTCGGTCGACGAGA
ACTACGCGCAGAACGTGAAAACGCTCGCGATCGACGCGTCCACGCTCGACCACGTGCACGAGATCGACATCAGCCAG
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CCTCTTCCAGAACCCGAAGGACGTCGTGGATCCGGTGCGGGAGCGCGAGTTTCTCAAAACGCTCGAAGCGCTCGAGG
ACACGGACAGCGAGGCGGGCGAGAAGCCCGTCCTCGGCAAGATCTCGCTGATCCGGCGGGCCAAATCGGCCGTCTCG
CGCAGCACGTCGCGCAAGCGCAAAACCGACCAGCACCCGCTGTTCATGATCGCGTGGGAGGACAAGGGCGACCAGCA
GCGGCACAGCACAGCGCTGTACGATGGCGCGACGGGTGCGGCCCCGTCGGTCGGTGCGCCCGGCGAGCTGGGGCAGC
CGGAGCAGCCCGAGGACGCCGTCACGGTCGAGGAGCTGCACCGGCGGATGGAGCAGTTCCACCAGCGGGCGTCCGTG
CGCGAACGGGACGCGAACTCGAGCGAGAGCGGCAGCGGCAAGCAGCACGCCGGCCCGAAGGCACGGAAGCCGTCCCA
CCATCGGGACGGTGGCGGCTCCCATCATCACCATGGGCTCGGGCGGGGCAAGCACAACAAGATATCGCCCGACAACT
CGAACGAAAGTACGGGCGGTGGCGGCGGTGGCGGCGCCAGTGGCCACGGGCGCAAGCAGGACAAGCGCATGAAGTCG
GCCCCGATACTGGGCAGCGGCGGTGCGGGCAGTGCCGGTAGCAGTGCCGGCGGGCGGACGGTGGCGCCCGGTGGTGC
CCGACCGGACGATGGTACCGGGTCGCCGCCGGACCCGCTCGAACCATGGAGCACCAAGAACATCATGAACATCAACA
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FIGURE 70 - SEQ ID NO: 34

<> 13
<> 3261
<> DNA
<> Tribolium castaneum
<> TC012368
<> ?
>TC012368-PA TC012368
ATGGGTGCAAAAGTGTGCAAACCGTGTAAAAAGCGCAAAGCCAACACCTTCCAAGGGGGCTCCATCCTCGACCGGGT
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ACGCGTACAACCAAGGGGGCCAAGCCGAGGTGGAAAAATTAATACGCGAGCAATTCGGCCAGTTGATGTACCAGGAA
GGCAAAGGCCAGATAATCAACCGCTCGGAGTATCTCAGGTGGAAATTTCGCGACCACGAGCAGGTCATTCTCCCAAT
CGAGGCCTCCTTGAGCCGATACGACCCCCTGGCCAAGTGGAACGACCACGAGGCGTGCTGGCAGATGCAGTTCAGGG
GGTCTTTAGGCGAGTCTTTGCTGCACGTCCTCATAATTTGCGACACGAAAATTCACACAAGACTGGCGCGGACTCTG
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GAATACCCTCTGGCCTGGGCCGCGTGTTGCGCCAACGAAAGCGTCTACAATCTGTTGCTGGACAGTGGGGCGCACCC
CGACTATCAGGACAATTTTGGAAACATGATCTTGCACATGGTGGTGGTTTGCGACAAGTTGGACATGTTCGGCTACG
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TTATTTTAAACGGAACCAAGGAAGAGCATTTAGCCATGCTTGACGGTGGGATTATCCAACGACTGTTGGAGGAAAAA
TGGAAAACATTCGCACGGAACCAATTTTTGAAACGGCTTCTTATCCTCGTTGTGCATTTGTTGTTTCTGTCTTTGGC
GGTTTACTTGCGACCAGACGACCCAGACGAGTCTCTTCTCACCTGGTCTGATGATGTTACACTGATAGCTAGATATG
TGTGTGAAGTGGGCACGATTTTGGGCGTCCTCAGTTATCTGGTTTTGCAACAAGGGGACGAAATCCGTAATCAGGGA
CTTACTGCGTTCTTGAAACAACAACTGAATTCACCCCCGAAATTAATTTTCCTCATTTCGAATTTCCTAATTTTGGC
GTGCATTCCATGCAGGTTGTATGGCGATAAGGAAACCGAGGAGGCTATTCTGTGTTTTGCGGTACCTGGGTCTTGGT
TTCTTCTCATGTTTTTTGCAGGGGCCGTTCGTTTGACTGGTCCTTTTGTCACAATGATTTACAGCATGATTACCGGC
GATATGTTGACTTTTGGCATCATTTACACCGTTTTCTTATTTGGTTTTTCGCAGTCGTTCTATTTCCTGTATAAGGG
ATTCCCCGGGGTCAAAACTTCCTTATACAACACGTACATGTCGACTTGGATGGCCTTATTCCAAATTACTTTGGGCA
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AAACGATGCGAGTGCAGGGCTCCGGGGACGGGGCCGAAGTCCAGTCATCCAACGTCAAACCAAAGCGCAAAAAACGG
AGCAAAACAGCCAAAAACAACAAGTAA

FIGURE 71 - SEQ ID NO: 35

<> 15
<> 3306
<> DNA
<> Megachile rotundata
<> XM_003704618.1
<> ?
>gi|383858352|ref|XM_003704618.1| PREDICTED: Megachile rotundata uncharacterized LOC100877549 (LOC100877549), mRNA

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ATCAAGGTGGCCAGGCAGAGGTGGAAAAATTGATCAGGGAACAGTTTGGTGTACTGATGTACGCGGACGGCAAGGGT
CAGATGATCAATCGGGCAGAGTATCTGCGCTGGAAATTCCGGGACCTGGAACAGGTCGTGCTTCCTATAGAAGCTTC
CTTGTCACGATTCGATCCTCTGGCTCAATGGAACGATCACCAGGCATGCTGGCAGATGCAATACAGAGGTTCCCTCG
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TGTTTTTTGCTGGCGCTATCCGGCTGACCGGTCCATTCGTCACCATGGTCTACAGCATGATAACCGGCGACATGTTG
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AGTGAAATCATCCCTCTATAGTTCCTATCACTCGACATGGATGGCACTGTTTCAAGTAACCCTCGGCGATTATAACT
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CTACTCCTGAACATGCTAATTGCCATGATGGGCAACACTTACGCACACGTGATTGAGCAAAGCGAGAAGGAGTGGGT
GAAGCAATGGGCGAAAATCGTGGTCTCTCTGGAGCGAGCAGTATCTCAAAAAGACGCTCAGAATTATTTGCAAGAAT
ACAGTATTAAATTAGGACCTGGAGATGACCCGAACAACCCAGCGTCGGAGCAACGTGGTGTTCTGGTGATTAAAAGT
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GATTGCTTCGGAAAGTATGAACGATCCTGAAACGCTACTAAAAATGGCGGAACGTGTTGCTGCAGAATTTGATTCGT
CTGCGAATCCCAAAATAAATTTGCAAATTTTGGAACAGTTCACGATGACGAAAATACCGATGGAGGAACAAGCTGCA
GCTGTTAAGAAACAATATTTTATCGAATCCAGCGATAACGATTTTGGCGGCGACAACTTGCTAGGAACGGTGGCCCG
TTTACGTAGAATAAGATCAGCTAACAGCAGATTTATCACGGCACGGAGACATTCACGGCATGTCAATGACGACATGT
CATCGACGTCTTCCGCATCCGGCGACGGAAATCCTCGATACCAGCAGTTGCTAAACGACACTGAAGAGGTACCGTCG
AATCAACGGACCGAAAATCGAGATGAGTCAATCGTGGCGAACAAATCGGAAGTAAAACAAAACGATGCTAACTGCGG
ATCGAGGTGCAAAGCTCAGAAGCGTCGACCAAAAACTGCTAGAAACAGGGTATCGCCGAAGGAAACGGAGGATTCCG
GCCAAAGGAGAAGAGAATCGATGGAGCGGAATAAGGCGGTTTCACCGGCGACATCGCCCACCGATCCGCTCGAGCCA
TGGAGCACACGCGGAATTAAAGACATGAACACGATATTGGCTTGGGAGGAAAATGTGCCGGACAGTCCTTAA

FIGURE 72 - SEQ ID NO: 36

<> 17
<> 3306
<> DNA
<> Apis mellifera
<> XM_001121881.2
<> ?
>gi|328783035|ref|XM_001121881.2| PREDICTED: Apis mellifera inactive (Iav), mRNA

ATGGGTGGTGTCTGCTCGTTTCGAGGTCGCGGTAGCCAGGTGAACGCTGGCTCGATCCTCGATCGTGTGATCAGTCA
AGCGAGCGACGAGGATCAATGCCTGTTGTATCGTCTGGCCAATTACAAAAAGGGTGGCGAGCTGATCGAGTCGTACA
ATCAGGGTGGCCAGTTCGAGGTAGAAAAATTGATCAGGGAACAGTTCGGTGTGTTGATGTATGCGGACGGTAAGGGG
CAGGTGATCAATCGTGCCGAGTATCTACGCTGGAAATTCCGAGACCTCGAGCAAGTTGTGCTCCCTATCGAGGCTTC
TTTGTCGCAGTTCGATCCTCTGGCTCAATGGAACGATCACGAGGCGTGCTGGCAAATGCAGTACAGGGGCTCGCTGG
GAGAGACCCTCCTTCATGTCCTGATTATATGCGATACCAGGATACACACGCGAGTGGCCCGTATTCTGCTCAAGTGC
TTTCCACGATTGGCCATTGACGTAGTCGAGGGCGAGGAGTACCTTGGCGCTAGCGCGCTCCATCTAGCGATCGCGTA
CAACAATAATGAACTGGTGCAAGACCTGGTTGAGGCGGGGGCGATCATTTCTCAGCGGGCGATAGGCAGCTTTTTCC
TACCGAGGGACCAACAACGAACGAATCCGGCTAAGAATACGGATTACGAGGGATTAGCTTATCTGGGGGAATATCCC
CTCGCCTGGGCCGCTTGTTGTGCAAACGAGAGCGTTTACAACTTATTACTCGACTCTGGCGCTGATCCCGACGAGCA
AGACTCTTTTGGAAACATGATATTGCATATGGTCGTGGTTTGTGATAAATTGGACATGTTCGGATATGCTCTCCGTC
ATCCGAAGCTTCCTGCTCGCAATGGGATTGTGAATGCTGCCGGACTGACCCCATTGACGCTCGCCTGCCAGCTGGGC
CGTGCTGAGGTCTTTCGGGAGATGTTGGAACTGTCCGCACGAGAATTCTGGCGCTACAGTAACATCACCTGCTCGGC
GTATCCCCTGAATGCGCTCGACACGCTGTTGCCCGATGGCAGAACAAACTGGAACTCGGCGCTATTTATCATTCTGA
ACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTATTATTCAGCGATTACTCGAGGAAAAATGGAAGACC
TTTGCGCGGTTGCAGTTCTTAAAACGACTGATCATCTTGGCATTCCATCTGACGTCCTTGTCGCTGGCAGTATATCT
GAGGCCTTCCAACACAGATGCTCAGCTCTTGAAATGGCCGGAAGAAATCACGGAAGTCGCACGCACGATCGCCGAGT
GCATCACGGTGCTGGGCGTGCTCAGTTACATTCTGGTCCAACTAGGCGGTGAGATCATCAACATTGGTCTCTTGTCC
TTCATGAAACAGTTGAGTCACGAGCCCGCCAAGCTCATATTCTTGATCAGCAACCTGCTCATACTCGCGTGCATTCC
ATGTCGTCTTGCCGGTAATAGGCATGCGGAAGACGCGATTCTCATAGTCGCTGTGCCCGGCTCTTGGTTCCTTCTCA
TGTTCTTCGCTGGGGCTGTCCGGCTGACCGGTCCATTCGTCACCATGGTGTACAGCATGATAACGGGAGACATGTTG
ACCTTCGGTATAATATACATGGTGGTGCTGTTCGGCTTCTGCCAGTCGTTCTACTTTTTGTACAAAGGATTCCCGGG
AGTGAAATCATCCCTCTACAGTTCCTATCACTCGACCTGGATGGCACTGTTTCAGATAACCCTCGGCGATTACAACT
ACACGGATCTCAGCTACACGACCTATCCTAATTTATCGAAGATGGTGTTCGCCATATTTATGGTACTGGTGCCTATA
CTATTGTTGAACATGCTAATCGCCATGATGGGCAACACATACGCTCATGTGATCGAGCAGAGTGAAAAGGAGTGGGT
GAAACAATGGGCTAAAATCGTGGTTTCTCTGGAACGTGCAGTCTCACAGAAGGATGCACAGAATTATTTGCAAGAAT
ATAGCATTAAACTGGGACCTGGAGATGACCCAAACAATCCTGCCGCGGAGCAGCGAGGAGTTTTGATTATTAAAAGT
AAATCGAAAACCAAGGCGAAGCAACGCAAAGGCGCGGTAGCTAATTGGAAGCGTGTGGGCAAAGTGACGATAAACGA
ATTAAAAAAACGTGGTTTAACAGGAGAGGAATTGCGACGAATTATGTGGGGACGAGCTTCTTTTTCTACACCTGTCA
GAGTAAGTCCAAAAGGGGTCGAGCCTCAAGTTTCTGTGGTGACCGCCGGTTTCGGGGACGCATTGACCACAGCTTTG
GATGTCATGACGTTCGCCCACGATCTCGACTTGTCCACCGCAACGGAAGGAATTCCAACCAACATCGATGCCAAGCA
GTCGAAACCAAAGAGTGCTACCAAGGAGACGAAATCGACGGTGAATAATCAGCAGAACGTGACGACAAACATAGAAC
CATTGAAATCGACCACGGAAAATGTGGACGATCAGGCGAACAATCCTAGGGAAAAAAAAGTAACTAGCCAAGCTGCG
ACCGTACACGAGATGAATTTGAAGAATGCGAATCATTCGAGCGTGACCGAGGATTTTCAGGATCCGCTTTTGGAACT
TGTGATTGCTTCCGAAAATACGAACGATCCCGAAACCCTGCTCGAAATAGCGAAACGTGCCGCGGCAGGCTTCGAAA
CAGAAACCAGCTCTAAAATAAATCTTCAAATTTTAGAACAATTCACGATGACGAAGATACCCATGGATGAGAAGGTC
AACGTTACGAGGAAACAATATTTCGTCGAATCCAGTGACAATGACTTTGGAGGCGACAACTTGCTCGGGACTGAGGC
CCGTCTACGTAGAATAAGATCAGCGAACAACAGATTTATCACGACACGTAGACGGTCACGGAACGTCGACGACGACC
TGTCATCCACATCTTCCACGTCTATGGACAGAAATCCTCGATATCAGTCGTTGCTCAACGGCCATGAAAACTCGATC
GACCGTCCAATCGAGAGTCGAGAGTGTTCCATAGAAGCAATTAACTCGCAAATAAAGCAGAACGGACCGTGCGAAAC
GATGAAGGCCAAGGTCCAGAAGAAAAGACCAAAAACGGCCAGAAATAGGGTATCGCCGAAGGAAATAGAGAAGGCTG
GTCCGAGGAGAAGAGAATCGATCGAGCGGAATAAGGCGGTTTCACCGGCAACATCGCCCACGGATCCGCTCGAGCCA
TGGAGCACACGCGGCATTAAGGACATGAACACGATATTGGCTTGGGAAGAGACCGCGCCGGACAGTCCTTAA

FIGURE 73 - SEQ ID NO: 37

<> 19
<> 3318
<> DNA
<> Apis florea
<> XM_003690679.1
<> ?
>gi|380013352|ref|XM_003690679.1| PREDICTED: Apis florea uncharacterized LOC100868270 (LOC100868270), mRNA

ATGGGTGGTGTCTGCTCGTTTCGAGGTCGCGGTAGCCAGGTGAACTCTGGCTCGATCCTTGATCGTGTGATCAGTCA
AGCGAGCGACGAGGATCAATGTCTGTTGTATCGTCTGGCCAATTACAAAAAGGGTGGCGAGCTGATCGAGTCGTACA
ATCAAGGTGGCCAGTTCGAGGTAGAAAAATTGATCAGGGAACAATTCGGTGTATTGATGTATGCGAACGGTAAGGGC
CAGGTGATTAATCGTGCCGAGTATCTACGCTGGAAATTCCGAGACCTCGAGCAAGTTGTGCTCCCTATCGAAGCTTC
TTTGTCACAGTTCGACCCTTTGGCTCAATGGAACGATCACGAAGCGTGCTGGCAAATGCAGTACAGAGGTTCGCTAG
GAGAGACTCTCCTGCATGTTCTGATTATATGCGATACCAGGATACACACACGAGTGGCGCGTATTCTGCTCAAGTGC
TTTCCACGATTGGCCATTGACGTAGTCGAGGGTGAGGAGTACCTTGGCGCTAGCGCGCTCCATCTAGCGATCGCGTA
CAACAATAATGAACTGGTGCAAGACCTCGTTGAGGCGGGAGCGATCATTTCTCAGCGGGCGATAGGCAGCTTTTTCC
TACCCAGGGACCAACAACGAATGAATCCGGCTAAGAATACGGATTACGAGGGATTAGCTTATCTGGGGGAATATCCC
CTCGCCTGGGCCGCTTGTTGTGCAAACGAGAGCGTTTACAACTTATTACTCGACTCTGGCGCTGATCCCGACGAGCA
AGACTCTTTCGGAAACATGATACTGCATATGGTAGTGGTTTGTGATAAATTGGACATGTTCGGATATGCTCTCCGTC
ATCCGAAGCTTCCTGCTCGCAATGGGATTGTGAATGCTGCCGGACTGACCCCATTGACGCTCGCCTGCCAGTTGGGC
CGTGCTGAAGTCTTTCGGGAGATGTTGGAACTGTCCGCACGAGAATTCTGGCGCTACAGTAACATCACCTGCTCGGC
ATATCCCCTGAATGCGCTCGATACGCTGTTGCCCGATGGTAGAACAAACTGGAACTCGGCGCTATTTATCATTCTGA
ACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTATTATTCAGCGATTACTCGAGGAAAAATGGAAGACC
TTTGCGCGGTTGCAGTTTTTAAAACGACTAATCATCTTGGCATTCCATCTGACGTCCTTGTCGCTGGCAGTGTACCT
GAGACCTTCCAACACAGATGCTCAACTCTTGAAATGGCCGGAAGAAATCACGGAAGTCGCACGCACGATCGCCGAGT
GCATCACGGTGCTAGGCGTGCTCAGTTATATTCTGGTCCAACTAGGTGGCGAGATCATCAACATTGGTCTCCTGTCC
TTCATGAAACAGTTGAGTCACGAGCCCGCCAAGCTCATATTCTTGATCAGCAACCTGCTCATACTCGCGTGCATTCC
ATGTCGTCTTGCCGGTAATAGGCATGCGGAAGACGCGATACTCATAGTCGCTGTGCCCGGCTCTTGGTTCCTTCTCA
TGTTCTTCGCTGGGGCTGTCCGGCTGACCGGTCCATTCGTCACCATGGTGTATAGCATGATAACGGGAGACATGTTG
ACCTTCGGTATAATATACATGGTGGTACTGTTCGGCTTCTGTCAGTCGTTCTACTTTTTGTACAAAGGATTCCCGGG
AGTGAAATCATCCCTCTACAGTTCCTATCACTCGACCTGGATGGCACTGTTTCAGATAACCCTCGGCGATTACAACT
ACACGGATCTCAGCTACACGACCTATCCTAATTTATCGAAGATGGTGTTCGCTATATTTATGGTACTGGTGCCTATA
CTATTGTTGAACATGCTAATCGCCATGATGGGCAACACGTATGCCCACGTGATTGAGCAGAGTGAAAAGGAATGGGT
GAAACAATGGGCGAAAATCGTGGTTTCTCTGGAACGTGCAGTTTCACAGAAGGATGCACAGAATTATTTGCAAGAAT
ATAGCATTAAACTGGGACCTGGAGATGACCCAAACAATCCTGCCTCGGAGCAACGAGGAGTCTTGATTATTAAAAGT
AAATCGAAAACCAAGGCGAAGCAACGCAAAGGCGCGGTGGCTAATTGGAAGCGTGTGGGCAAGGTGACGATAAATGA
ATTAAAGAAACGTGGCTTAACAGGAGAGGAATTGCGACGAATTATGTGGGGTCGAGCTTCTTTTTCTACACCTGTAA
GAGTAAGTCCAAAAGGGGTCGAGCCTCAAGTTTCTGTGGTGACTGCCGGTTTCGGAGACGCGTTGACCACAGCTTTG
GATGTCATGGCGTTCGCCCATGATCTCGACTTGTCTACCGCAACGGAAGGAATTCCAACCAACATCGATGCCAAGCA
GTCGAAACCGAAGAGTGCTATCAAGGAGCAGATGAAATTGACGACGAATAATCAGGAGAACGTGTCGACTAACGTAG
AACCGCAGCTGAAATCGACCACGGAAAATGCGAACGATCAGGCGAACAATCCTAGGGAAATTAAAAAAGTAACTAAC
CAGGTTACAGGCATACACGAGATGAATTTGAAGAACGCGAATCATTCGAGCGTGACCGAGGATTTTCAGGATCCACT
TTTGGAACTTGTGATTGCTTCCGAAAATACGAACGATCCCGAAACCCTGCTCGAAATAGCGAAACGTGCCGCGGCAG
GCTTCGAAACAGAAGCCAGCTCTAAAATAAATCTTCAAATTTTAGAACAATTCACGATGACGAAGATACCTATGGAG
GAGAAGGTCAGCGTTACAAGGAAACAATATTTCGTCGAGTCTAGTGACAATGACTTTGGAGGCGACAACCTGCTCGG
GACTGAGGCCCGTCTACGTAGAATAAGATCAGCGAACAACAGATTTATCACGACACGTAGACGGTCACGGAACGTCG
ACGACGACCTGTCATCCACATCTTCCACGTCCATGGACAGAAATCCTCGATATCAGTCGTTGTTCAACGGCCATGAA
AACTCGATCGACCGTCCAATCGAGAGTCGAGAGTGTTCCATGGAAGCAATTAACTCGCAAATAAAGCAGAACGGGCC
ACCGTGCGAAACAGTGAAGGCCAAGGTCCAGAAGAAAAGACCAAAAACGGCCAAAAATAGGGTATCGCCGAAGGAAA
TAGAGAAGGCTGGTCCGAGGAGAAGAGAATCGATCGAGCGGAATAAGGCGGTTTCACCGGCAACATCGCCCACGGAT
CCGCTCGAGCCATGGAGCACACGCGGCATTAAGGACATGAACACGATATTGGCTTGGGAAGAGACCGCGCCGGACAG
TCCTTAA

FIGURE 74 - SEQ ID NO: 38

<> 21
<> 3168
<> DNA
<> Pediculus humanus corporis
<> XM_002432337.1
<> ?
>gi|242023926|ref|XM_002432337.1| Pediculus humanus corporis conserved hypothetical protein, mRNA

ATGGGAGCTGGATTATGTGGAACTTCTCAAGATCCTCAAAATCAAGGTTCGGTTTTGGATAGAGTCATTTCTCAAGC
TTCTAACAAAGATGATTGTCTTTTATATAAACTTGCCAACTACAAAAACAGTGGAGAATTGATCGAAGCATACAATA
TTGGAGGTCAAGCTGAGGTTGAAAAACTGATTAAAGAACAATTTGGAGTTTTAATGTATGCCGATGGCAAAGGTGAA
GTAATTAAACGTGCAGAATACCTTAGGTGGAAATTTCGAGATCAAGCTCAGGTCGTTTTACCTATCGAAGCTTCTTT
ATCTATTTACGATCCTTTGGCAAAATGGGAAGACCACGAAGCTTGTTGGCAAATGCAGTACAGGGGTAGTTTAGGAG
AAACGCTTCTTCATGTTTTGATAATTTGCGATTCTAAAATACACACAAAACTTGCTCGTACCCTTTTAAAATGCTTT
CCTAAACTTGCTTTGGATATAGTAGAAGGAGAAGAATATTTGGGAGCTAGTGCTCTTCATTTAGCCATTGCTTATAA
TAATAACGAATTAGTTGAAGATTTGGTAGATGCTGGAGCCAACATTAATCAAAGAGCAGTAGGTAGTTTTTTTCTTC
CTAAAGATCAACAACGAGCAAAACCTTTAAAAACCACAGATTACGAAGGTTTGGCATATTTAGGAGAATATCCTTTA
TCGTGGGCAGCTTGCTGCTCGAATGAAAGCGTCTACAATTTACTTCTTGATGTCGGTGCCGATCCTGACAGTCAGGA
TTCTTTTGGAAATATGATATTGCACATGGTGGTCGTTTGTGATAAACTGGACATGTTTGGTTATGCTCTTCGTCATC
CAAAAGTACCAGCTAGTAATGGAATAATTAACAACGAGGGACTTACTCCCCTAACATTGGCATGTAAATTGGGTAGA
GCAGATGTTTTTAAAGAAATGTTAGAACTGAGTGCTAAAGAATTTTGGCGTTACAGCAACATCACTTGTTCGGCATA
TCCACTAAATGCACTTGACACTCTATTACCAGATGGAAGAACCAATTGGAATTCTGCAATTTTTATTATTTTAAACG
GTACCAAAGAAGAACATTTAGACATGTTAGATGGTGGAATAATCCAAAGGCTTTTGGAAGAAAAATGGAAAACTTTT
GCAAGAAACCAATTTTTAAAACGTTTGGTTATTTTCTTCTTACATATATTTTGCCTAAGTGGTTCTGTATATTTAAG
ACCGGACGATAGAAATAAACCACTTTTGGGTGGTACTTCCGTTCAAGATGTTGTCAGGTATTGTTTCGAAATCGGTA
CCATACTCGGAGTTCTTTGTTATTTATGTTTTCAACAAGGAGATGAAATTAGAAATCAAGGATTGATTAGTTTTTTA
AAACAATTGCCGCATGATCCTGCAAAGTTTATATTTCTCATATCAAATCTTTTAATTTTGGCCTGTATACCTTACCG
TGTGGCTGGTGATACGGATACGGAAGAAGCCATACTTGTATTTGCGGTACCTAGTTCGTGGTTTCTGTTAATGTTTT
TTGCCGGAGCGATTCGATTAACTGGTCCATTTGTCACCATGATTTACAGTATGATCACTGGAGATATGTTAACCTTT
GGTATTATATATTCGGTATTTTTATTTGGTTTTTCTCAAAGTTTTTTTTTCCTATACAAAGGCTCTAAAAATGTGAG
CAGTTCTCTATTTACTTCATATCCATCAACTTGGATGGCTCTTTTTCAAGTCACAATGGGAGATTATAACTACAATG
ATTTATCTCTAACAGCATATCCAGCCATTAGCAAAATGGTATTCACAATATTTATGGTTTTGGTACCCATTCTTTTG
TTAAACATGTTGATTGCCATGATGGGCAATACTTATGCTCATGTTATTGAACAAAGCGAAAAAGAATGGATGAAACA
GTGGGCTAAAATTGTTGTGGCTTTGGAACGTGCGGTAAATCAGGAAGATTGTCATCGTTACTTACAAGAATATTCTA
TTAAATTAGGTCCTGGTGATGATCCTAGCACCGAGCAAAGAGGTGTTTTGGTAATTAAATCTAAAAGTAAAACAAGA
GCAAAACAAAGAAAAGGCGCACTTTGTAATTGGAAGAGGGTTGGAAAAGTAACCATTCGAGAATTGCATAAGAGAGG
AATGACCGGAGAACAATTGCGACGTCTTATGTGGGGAAGATCATCAATTTCAACCCCCGTCAAACCTGCACCAATAA
AATTAGGCCACGTTACGAGCATCTCGGGTGTGGCTGATATAACCGTTCCAGAAACGACAGGAAACACTGTTGGAACG
GGAGGAGGCGGTTTGTTAGCTGCTTTGGACGTTATGGCATTTACAAATGATTTGGAATTCAGTTCGGAAAATCAAAC
TTCGACCAGTTTCAAAACTCAACCTCAACCATCAGAAGTTTCTTGCGTTGAATCGGATTCGAATTCAGATCCTTTAT
ATAATGATCCTCTGAGGCAATTGAATGAAGAACTCAATAAAACTCGGGAAGAAATTTTAACTTTAGCTCGAGTTGCA
GCAAATAATGATGGAATTGAAGAGATACCACCGCAAATATGTCAATACGGTTGGATTAATAATTATAATTTTTTCGG
TAATACATTTGCACAAAATCAAAAAGTTGAGGATCCTGTTCAACAGCCTACATTTCAATCTACACCAAATCATAGCG
ACAGTGATGGTTTAGGAGATGGATTACTCCTTGGAAGTAATCGAAGATTAAAAAGAACTCGATCGGCAAATATAAAA
AGAAAGTTTTCTGGAAGTTCGACAAATGAAAAAAATTTATTAGAACCTGAGGATTCAAGTTCAACTAATTCCGAGGA
TTTTTCATGTTTAACCGAAAATTACATAAATAAAAATATTAAAGTTAATGCAAATTTTTCGGAGAATTCTTTACGAA
GTAATAGAAGTTCTGCCAATCTCGTGGTGAAAAAATTTGGAAGAAGGTCGGGTTTGAAATCCTCTACCAACAGAATT
GCTCCTGCTGATTTAAGTCCAGTTGGTAATGTTTCCAAATACTCTGAAACTTTGTGTAACTCATATTGTATTACTTC
TTCATCGGATGTTTTGTATCAATGGAGTATAAAAGGAATAACAAATATGAATACACTTTTAGGATTGGAAAATGAGG
ATTCAATGTAA

FIGURE 75 - SEQ ID NO: 39

<> 23
<> 3330
<> DNA
<> Acromyrmex echinatior
<> gi|332020355
<> ?
>(gi|332020355:c165202-164378, c163792-163567, c156295-156180, c153678-153442, c150494-150343, c142816-142600, c141823-141662, c140745-140548, c140090-139981, c138782-138433, c138023-137772, c137679-137370, c136361-136187) Acromyrmex echinatior unplaced genomic scaffold scaffold532, whole genome shotgun sequence

ATGGGTGGTGTTTGCTCGTGCCGCGTTGGTCGCAACAGCCAGGTCAACGCCGGTTCGATCCTCGACCGCGTGATCAG
CCAGGCAAGCAACGAGGACCAGTGTTTATTGTATCGATTGGCGAACTACAAGAAGGGCGGTGAGCTAATCGAGGCGT
ACAACCAGGGCGGTCAGCCTGAGGTGGAGAAGCTGATCCGCGAGCAATTTGGTATCCTGATGTATATGGATGGCAAA
GGCCAGATAATCAATCGTGCCGAGTATCTACGTTGGAAATTTCGTGACCTCGAGCAAGTCGTGTTGCCGATCGAGGC
CTCGCTGTCGCGTTTTGATCCACTAGCGCAGTGGAATGATCATGAAGCCTGCTGGCAGATGCAGTACAGAGGCTCGC
TGGGCGAGACCTTGTTGCATGTTCTTATCATATGTGACACGCGGATGCATACTAGAATAGCGCGCATACTGCTCAAG
TGTTTTCCGCGGCTAGCTATTGACGTCGTCGAGGGCGAAGAGTATCTGGGTGCGAGTGCTCTTCATCTGGCGATCGC
CTATGCGAACAACGAGCTCGTGCAGGATCTGGTCGAGGCGGGCGCGATTATCTCGCAGCGGGCCATCGGTAGCTTCT
TCCTGCCGCGGGATCAGCAAAGGATGAATCCCGCCAGAAATACCGATTACGAGGGTCTCGCGTATCTGGGAGAGTAT
CCTCTCGCCTGGGCCGCCTGCTGCGCTAATGAGAGCGTCTACAACCTGCTGCTTGATTCCGGCGCTGATCCTGACGA
GCAGGATACTTTTGGAAATATGATTTTGCACATGGTCGTAGTTTGCGACAAATTGGACATGTTCGGCTACGCATTGC
GACATCCGAAGCTTCCTGCTCGCAATGGAATTGTGAATGCCGCGGGCCTGACCCCGTTGACACTCGCCTGCCAGCTG
GGGCGTGCCGAGGTCTTCCGTGAGATGTTGGAGCTGTCCGCGCGGGAGTTTTGGCGTTACAGTAATATCACTTGCTC
GGCGTACCCTCTCAATGCTCTCGACACGCTGTTGCCCGATGGCAGAACAAACTGGAACTCTGCGCTATTTATCATTC
TGAACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTATTATTCAGCGATTACTTGAGGAAAAATGGAAG
ACCTTCGCGCGATTGCAGTTCCTGAAGCGATTGATTATCTTGGTGTTTCACCTGGCCTCGCTGTCCTTAGCCATGTA
CTTCAGGCCCGCGGACATGGAGGCTGTGCTGCTGCAGTGGCCCGAGGAGATAACGGACGTCGTCCGCACCGCGGCGG
AGTGCATCACCGTGCTGGGCGTGCTGAATTACATCCTGGTGCAGCTGGGATGCGAAATGATCAACGTCGGTCCGCTA
TCATTCCTGAAGCAACTGAGCCACGAACCGGCCAAGTTGATATTCGTGATCAGCAATCTGCTCATTCTCGCGTGCAT
TCCATGTCGTATCGCTGGCGATCGGCACGCGGAGGATGCGATACTGATGTTCGCTGTGCCGGGCTCATGGTTTCTTC
TTATGTTTTTCGCCGGAGCGATTCGATTGACTGGTCCATTTGTCACAATGGTATACAGCATGATAACGGGCGATATG
CTGACCTTTGGTATTATCTACACGGTTATGCTCTTTGGATTCTCGCAATCATTTTACTTTCTTTATAAGGGATTCCC
CGGAGTGAAATCATCTCTGTATCATTCCTATCCTTCGACCTGGATGGCACTGTTTCAGATAACCCTCGGCGATTATA
ACTACGCGGATTTGAGTAACACGACCTATCCTAACTTGAGCAAGACCGTCTTTGCGATTTTCATGGTACTTGTGCCC
ATACTGCTGCTCAACATGCTAATTGCCATGATGGGTAATACATATGCACATGTTATCGAGCAAAGCGAAAAGGAATT
CGTCAAGCAGTGGGCAAAAATCGTGGTGTCTTTGGAACGCGCCGTATCTCAGAAAGATGCTCATAATTACCTACAGG
AATACAGCATTAAACTGGGACCCGGCGATGATCCGAACAACCCCGCGTCGGAACAAAGGGGCGTGTTGGTTATTAAA
AGTAAATCGAAAACCAGAGCAAAGCAGCGTAAGGGCGCTGTGTCTAATTGGAAGCGAGTCGGAAAAGTCACGATACT
CGAATTGAGAAAACGAGGTATGACTGGCGAGGAACTCCGTCGTATAATGTGGGGTCGCGCGTCCTTTTCCACCCCTG
TGCGAGTCAGTCCCAATGCCGGTCAACCGCAAGTGTCGGCAGTTACTGCAGGTTTTGATGATGCGTTAACCGCAGCT
TTGGACGTAATGGCCTTTGCACATGACTTTGACTTATCCACTGCGACGGAAGGCATACCTACCAATATCGACGCAAA
ACAGATAAAGACAGCGCAGTCGAAAGCCGCTCTCAACGACCAGCAGACGAAAACAACCCAAAATAATCCAGAAGTGG
TGATAAATGTGCAACCGCATAATCAACCCATTAAAGAGGAAACTAAATTATCAGGTCTCACAGATTTAATCGATAAG
TCTATCGATCCCGTAAAGGATGTGGAGGCAATGAATTTGAGAAATATGAATCAAACGAAAGCGCTCGAAGAAACCGT
CGAAGATCCATTTTTGGAACTCGCTATCGCTTCTGAGACTACAACGGATTACAAAACTCTACTGCAAATAGCGAAGT
CCGCTTTAGCCACAAGCGAAGCTTCAATGAAAACCACAATCGACCCGCAAATTCTAGCACACTTCGCCATGGTCGCG
CCGCCGACCATTGAGAAATCTTCTATCGTTAAGAAACAGTATTTCATGGAGTCCAGCGACAATGACCTCGGCGGCGA
TAATTTACTTGGCACCGAAGCTCGCCTTCGAAGGATAAAATCCGCGAATAACAGATTCACTACATCGAAACGGTCAC
GCCGTGATGACGATGGCGACAGTTCCTCATCTACAACATCCGTCGAACAAAGTCTGCGATATCGACCACTACTGAAT
GATCCGGAACAGAGACCGATGAATCGTATCGAGACTGAAGGACGAAAGACCACCGTGGAAACAATTAAGCCGGAGGT
CAAACAGAATGGCAGCATTCCTACCAAACCACTCGATAAAATCCAAAAACGTCGACCAAAAACGGCCAAGAATAGGG
TATCGCCTAAAGAAACTGAGGAACCAGCGAGGAGAAGGGAATCGATTGAGCGGAATAAGGCGGCTTCACCACCTACG
TCGTCCTCGGATCCGCTCGAGCCATGGAGCACGCGTGGCATTACCGACATGAACACAATATTGGCTTGGCGGGAAAA
CGCACCGGACAGTCCTTAA

FIGURE 76 - SEQ ID NO: 40

<> 25
<> 3339
<> DNA
<> Harpegnathos saltator
<> gi|307206889
<> ?
>(gi|307206889:1112686-1113507, 1113778-1114003, 1120594-1120709, 1123877-1124113, 1127231-1127382, 1135454-1135670, 1136818-1136979, 1137310-1137507, 1138165-1138274, 1139575-1139909, 1140105-1140350, 1140588-1140924, 1141746-1141926) Harpegnathos saltator unplaced genomic scaffold scaffold219, whole genome shotgun sequence

ATGGGTGGTGTTTGCTCGTGTCGCGGCCGCGGCAGCCAGGTCAACGCCGGCTCGATCCTCGACCGCGTGATCAGCCA
GGCGAGCAACGAGGACCAGTGTTTGTTGTATCGGCTGGCCAACTACAAGAAGGGCGGCGAGCTGATAGAGGCTTACA
ACCAGGGCGGCCAGCCGGAGGTCGAGAGACTGATAAGAGAGCAATTCGGCATCCTGATGTACGCGGACGGCAAGGGT
CAGGTGATCAATCGCGCCGAGTATCTACGCTGGAAGTTTCGCGACCTGGAGCAGGTCGTGCTGCCGATCGAGGCGTC
GTTGTCGCGCTTCGACCCGTTGGCACAGTGGTACGACCACGAAGCCTGCTGGCAGATGCAGTACAGAGGCTCGCTGG
GAGAGAGCCTGCTGCACGTGCTCATCATATGCGACACGCGTATGCACACGAGGATAGCGCGCACGTTGCTCAAGTGC
TTCCCACGGCTGGCCATCGACGTGGTCGAGGGCGAGGAATACCTCGGCGCTAGTGCCCTTCATCTGGCGATCGCCTA
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TGCCCAGAGACCAGCAGAGGATGAATCCCGTAAGGAACACCGATTACGAGGGACTCGCGTATCTCGGGGAGTACCCG
CTCGCGTGGGCCGCGTGCTGCGCCAACGAAAGCGTTTACAACCTGCTGCTCGACTCCGGCGCCGATCCTGACGAGCA
GGATTCTTTCGGAAATATGATTTTGCACATGGTTGTAGTGTGCGACAAATTGGACATGTTCGGCTATGCCCTGCGAC
ATCCCAAGCTTCCCACTCGCAACGGAATCGTGAATGCCGCAGGCCTGACCCCATTGACACTCGCCTGCCAGCTGGGG
CGTGCCGAGGTCTTCCGTGAGATGCTGGAGCTGTCCGCACGGGAGTTCTGGCGTTACAGTAATATCACCTGCTCGGC
GTATCCACTCAATGCTCTCGACACGCTGCTCCCGGACGGTAGAACAAACTGGAACTCTGCGCTATTTATCATTCTGA
ACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTGTTATTCAGCGATTACTTGAGGAAAAATGGAAGACC
TTTGCGCGATTGCAGTTCCTGAAGCGATTGATTATCTTGGTGTTTCACCTGGCCTCGCTGTCCTTAGCCGTGTACTT
CAGGCCCGCGGACATGGACGCCGAGTTGCTGCAGTGGCCCGACGAGATTACGGACGCCGCCCGCATCGCGGCGGAAT
GCAGTACCGTGCTGGGTGTGCTAAGTTACATCCTGGTGCAACTGGGCGGCGAGATGATCAACATCGGTCCGCTGTCG
TTCCTGAAGCAACTGAGCCACGAACCGGCCAAGTTGATATTCGTGATCAGCAATCTGCTCATTCTCGCGTGCATTCC
ATGTCGTATCGCCGGCAATCGGCACGCGGAGGATGCGATACTGGTGTTCGCCGTGCCGGGCTCGTGGTTTCTTCTCA
TGTTTTTCGCCGGAGCTATCCGACTGACCGGTCCGTTCGTCACGATGGTGTACAGCATGATAACCGGCGACATGCTG
ACCTTCGGCATCATTTACACGGTCATGCTCTTTGGATTTTCTCAATCGTTTTATTTCCTCTACAAGGGATTCCCGGG
CGTGAAGTCGTCCCTCTACCATTCCTATCCTTCGACCTGGATGGCGTTATTTCAGATAACCTTGGGCGATTATAACT
ACGCAGACCTAAGTAACACGACCTATCCCAACTTGAGTAAGACGGTCTTTGCGATCTTCATGGTGCTCGTGCCGATA
TTGCTGCTCAATATGCTGATCGCCATGATGGGTAATACGTACGCGCACGTTATCGAGCAGAGCGAGAAGGAATTTGT
GAAGCAGTGGGCCAAAATTGTGGTATCTTTGGAACGCGCTGTGTCGCAGAAGGACGCCCATAATTATCTACAGGAAT
ACAGTATCAAGTTGGGGCCGGGCGACGATCCGAATAATCCCGCATCGGAGCAGAGAGGTGTGCTGATTATTAAAAGC
AAATCGAAAACTAGAGCGAAACAGCGCAAGGGCGCCGTGGCTAATTGGAAGCGAGTCGGAAAAGTCACGATAAACGA
GCTGAGAAAACGAGGTATGACTGGCGAGGAGCTACGCCGTATAATGTGGGATCGTGCGTCCATCTCCACTCCTGTGC
GAGTCAGTCCTAATGTCAACGAGCCACAAGTGTCGGCAGTTACTGCAGGTTTTGGTGACGCGCTAACCGCAGCTTTG
GACGTAATGGCCTTTGCGCACGACTTTGACTTATCCACTGCGACGGAAGGCGTACCGAGCAATATCGACACGAGGCA
GACGAAAGCCATCCCCGACGAGCAGACGAGAACGGCTCGGAATAATCCAAAGGCGGTGACGGATGTCCAACCGCACA
AACAAGCCATCGGGGGGGGAGGAGACCAAGTTGTCAGGTCTCACGGATCTAATTGATATGTCCGCCGCCGAACCGGCG
CGCGTGGAAGCGATGAACTTGAAGAACGCGAGTCAAGCAAAGGCGCACGAGGGAGCTGTCGAGGATCCATTCCTGGA
GCTCGCTATCGCCTCCGAGACTACGGAAGATTACGATACTTTATTGCAAATGGCCAAGTCCGCCCTAGCTACCAGTG
AGGCTTCAACCACGGTCGACCCACAAATTCTAGCACACTTCACTATGATCGCCCCGCCGCCCGTTGAAAAACCCATC
GTTGTTAAGAAACAATACTTGGTGGAGTCCAGTGACAACGATCTCGGTGGCGACAATTTGCTCGGTACCGAAGCTCG
CATCAGGAGGATAAAGTCGGCGAATGATAGATTCATCAGCACATCCAAACGATCACACCATGACGACGATAACGACA
GTTCCTCGTCCGTCACTTCCGTCGACCGGAGTCAGCCGCAGTATCGACCGCTGCTGAATGATTCGGAAGAGAGCCTG
GCGAACCGCGTCGAGAACGAAGGACGAAGAACTTCCGACGTCGAAACAATTAAGTCGGAAGTCAAGCAGAACGGCCG
CGGCGGCGGCGGCGGCGGTGTTTCCAAGCCGTCGGATAAACGCGTCCAGAAACGCCGGCCGAAAACGGCCAAGAACA
GGGTATCGCCTAAGGAAATAGAGGAACCGGCGAGGAGACGAGAAGAATCGATTGAGCGGAATAAGGCGGCTCTTTCA
CCTCCGGCGTCGCCCTCGGATCCGCTCGAGCCATGGAGCACGCGTGGCATTACCGACATGAACACGATATTGGCCTG
GCGGGAGAATGCACCGGACAGTCCTTAA

FIGURE 77 - SEQ ID NO: 41

<> 27
<> 3315
<> DNA
<> Bombus impatiens
<> XM_003485651.1
<> ?
>gi|350399982|ref|XM_003485651.1| PREDICTED: Bombus impatiens hypothetical protein LOC100747394, transcript variant 1 (LOC100747394), mRNA

ATGGGTGGTGTCTGCTCGTGTCGAGGTCGCGGTAGCCAGGTGAATGCTGGCTCGATCCTTGATCGAGTGATCAGTCA
TGCGAGCGACGAGGATCAATGTCTATTGTATCGTCTGGCCAATTATAAGAAGGGCGGCGAGCTGATCGAGTCGTACA
ATCAAGGTGGCCAAGCGGAAGTGGAAAAATTGATCAGGGAACAGTTCGGTGTACTGATGTACGCAGATGGGAAGGGT
CAGGCGATCAATCGGGCGGAATATCTACGTTGGAAATTCCGTGACCTCGAGCAGGTTGTGCTACCAATAGAGGCTTC
TTTGTCACAGTTTGATCCTCTGGCTCAATGGAACGATCATGAAGCATGTTGGCAGATGCAATATAGAGGATCACTCG
GAGAGACTCTCCTGCATGTCCTGATTATATGCGATACCAGGATACACACACGACTAGCGCGTATTCTGCTTAAGTGC
TTTCCACGATTGGCTATTGACGTAGTCGAGGGCGAGGAGTACCTCGGCGCTAGCGCTCTGCATCTCGCTATCGCGTA
CAACAATAATGAACTGGTTCAAGATCTCGTGGAGGCGGGAGCGATTATTTCTCAGAGGGCGATAGGCAGCTTTTTCC
TGCCTAGGGACCAACAACGAACGAATCCAGCTAAGAATACGGATTACGAGGGATTAGCATACCTGGGAGAGTATCCC
CTCGCCTGGGCTGCTTGCTGTGCAAACGAGAGTGTTTACAACTTATTACTCGACTCTGGCGCTGATCCCGACGAGCA
GGACTCTTTTGGGAACATGATACTACATATGGTAGTCGTTTGTGATAAATTGGACATGTTCGGGTATGCCCTCCGTC
ATCCGAAGCTTCCTGCTCGCAATGGGATCGTGAATGCCGCCGGACTGACCCCATTGACGCTCGCCTGCCAGCTGGGT
CGCGCAGAGGTCTTTCGGGAGATGTTGGAACTGTCTGCACGAGAATTCTGGCGTTACAGTAATATCACCTGCTCGGC
ATATCCGCTGAATGCACTCGACACGCTGTTACCTGACGGCAGAACAAACTGGAACTCCGCGCTATTTATCATTCTGA
ACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTATTATTCAGCGATTACTCGAGGAAAAATGGAAGACC
TTTGCGCGGTTGCAGTTCTTGAAACGGTTGATCATCCTGGTGTTCCATCTGACATCACTCTCGCTAGCCGTGTATAT
GAGACCGTCAAACATCGATGCCACCCTCCTGGAATGGCCGGAAGAAATCACGGAAGTTGGACGCATGATCGCGGAGT
GCACCACGGTAATAGGTGTGCTGAGCTACATTTTGGTGCAACTAGGCGGCGAGGTAGTCAACATTGGTCTTCTATCG
TTCATGAAACAATTGAGTCACGAGCCTGCCAAGCTCATATTCTTGATCAGCAATCTGCTCATACTCGCGTGCATACC
ATGTCGTCTTGCTGGTAATAGGCATGCTGAAGACGCGATACTCGTGGTTGCTGTTCCCGGCTCTTGGTTCCTCCTCA
TGTTCTTTGCTGGCGCTATCCGGTTGACCGGTCCATTCGTTACCATGGTCTACAGTATGATAACCGGTGACATGTTG
ACCTTCGGGATAATCTACATGGTGGTGCTGTTCGGATTTTGCCAGTCGTTCTACTTTTTGTACAAAGGCTTCCCGGG
AGTGAAATCATCCCTCTACAGTTCCTATCACTCGACCTGGATGGCACTGTTTCAGATAACCCTCGGCGATTATAACT
ATACGGACCTCGGCTACACAACCTACCCTAATTTATCGAAGATGGTGTTCGCCATATTTATGGTCCTGGTGCCCATA
CTGCTGTTGAATATGCTGATTGCGATGATGGGCAACACTTACGCGCATGTGATCGAGCAGAGCGAGAAGGAATGGGT
GAAGCAATGGGCGAAAATCGTGGTTTCTCTGGAGCGTGCAGTCGCGCAGAAAGATGCGCAGAATTATTTGCAAGAAT
ACAGTATTAAACTGGGACCTGGAGATGACCCGAACAACCCCGCCTCGGAACAGCGCGGAGTCCTGATTATTAAAAGT
AAATCGAAAACCAAGGCGAAGCAACGCAAAGGCGCGGTGGCTAATTGGAAGCGCGTAGGCAAAGTGACGATAAACGA
ATTGAAGAAACGTGGTATAACAGGAGAGGCGTTGCGACGAGTCATGTGGGGCCGAGCATCTTTCTCCACTCCTGTTA
GAACGAGTCCAAACACTGCCGAGCCTCAAGTTTCAGCGGTTACGGCCGGTTTTGGAGACGCATTGACTGCAGCGCTG
GATGTGATGGCGTTCGCCCACGATCTCGACTTGTCTACTGCTACGGAAGGAATTCCGACCAACATCGGCGCGAAGCA
GTCGAAATCGAAGACCGCCTGCAAGGATCAAGCGAAATCGGCGACGAATAATCAGGAGAAAGGGTCGACGGACGTTC
AGCAACAACGGAAACTAACCACGGAAAATCTGGATAATCTGGCGAGCAGTCATAATGATATTGACAAAACATCCAGC
GAATTTGTGGCCGTTCGCGAGATGAATTCGAAGAACGCGAGTCATTCGAGCATGGCCGAGGATTTTCAGGATCCGCT
TTTGGAGCTTGTGATTGCTTCCGAAAATACGGACGATCCTGAAACGCTGCTGAAAATAGCGGAGCGGGCCGCAGCGA
ATTTCGAAGTGGAGAGCAGTTCGAAAATAAATCTGCAAATTTTGGAGCAATTCACGATGACTAAGCTACCTATGGAG
GAGAAAGTTGCCGCTACAAAGAAGCAGTACTTTGTTGAATCGAGTGACAACGATTTTGGTGGCGACAACCTACTCGG
AACCGAGGCCCGTCTACGTAGAATAAGATCAGCGAACAACAGATTTATCACGACACGGAGACGGTCGCGGCACACCG
ATGACGACCTGTCATCTACGTCGTCCACATCCGCCGACAGAAATCCTCAATATCAGCCATTGCTCAACGGCCCTGAG
AACTTGGCGAGCCGTCAAATCGAAAGTCGAGAGAGCTCTATCGAAGCAATTAAGCCGCAAGTAAAGCAGAACGGGTC
ATGCGATTCAGTGAAGATCAAGGTTCAGAAGCGTCGACCGAAAACGGCGAAAAATAGGGTATCACCGAAGGAAATAG
AGGAGGCTGGTCCGAGGAGAAGAGAATCGATCGAGCGGAATAAGGCGGTTTCGCCGGCGACGTCGCCTACTGATCCG
CTCGAACCATGGAGCACACGCGGCATTAAGGACATGAACACGATATTGGCTTGGGAGGAGAATACGCCGGACAGTCC
TTAA

FIGURE 78 - SEQ ID NO: 42

<> 29
<> 3075
<> DNA
<> Bombus terrestris
<> XM_003396143.1
<> ?
>gi|340715376|ref|XM_003396143.1| PREDICTED: Bombus terrestris transient receptor potential cation channel subfamily V member 6-like (LOC100648205), mRNA

ATGGGTGGTGTCTGCTCGTGTCGAGGTCGCGGTAGCCAGGTGAATGCTGGCTCGATCCTTGATCGAGTGATCAGTCA
TGCAAGCGACGAGGATCAATGTCTATTGTATCGTCTGGCCAATTACAAGAAGGGTGGCGAGCTGATCGAGTCGTACA
ATCAAGGTGGCCAAGCGGAAGTGGAAAAATTGATCAGGGAACAGTTCGGTGTACTGATGTACGCAGATGGGAAGGGT
CAGGCGATCAATCGGGCGGAATATCTACGTTGGAAATTCCGTGACCTCGAGCAGGTTGTGCTGCCAATAGAGGCTTC
TTTGTCACAGTTCGATCCTCTAGCTCAATGGAACGATCATGAAGCATGTTGGCAGATGCAATATAGAGGATCACTCG
GAGAGACTCTCCTGCATGTCCTGATTATATGCGATACCAGGATACACACACGACTAGCGCGTATTCTGCTTAAGTGC
TTTCCACGATTGGCTATTGACGTAGTCGAGGGCGAGGAGTACCTCGGCGCTAGCGCTCTGCATCTCGCTATCGCGTA
CAACAATAATGAACTGGTTCAAGATCTCGTGGAGGCGGGCGCGATTATTTCTCAGAGGGCGATAGGCAGCTTTTTCC
TGCCTAGGGACCAACAACGAACGAATCCAGCTAAGAATACGGATTACGAGGGATTAGCATACCTGGGAGAGTATCCC
CTCGCCTGGGCTGCTTGCTGTGCAAACGAGAGTGTTTACAACTTATTACTCGACTCTGGCGCTGATCCCGACGAGCA
GGACTCTTTTGGGAACATGATACTACATATGGTAGTCGTTTGTGATAAATTGGACATGTTCGGGTATGCCCTCCGTC
ATCCGAAGCTTCCTGCTCGCAATGGGATCGTGAATGCCGCCGGACTGACCCCATTGACGCTCGCCTGCCAGCTGGGT
CGCGCAGAGGTCTTTCGGGAGATGTTGGAACTGTCTGCACGAGAATTCTGGCGTTACAGTAATATCACCTGCTCGGC
ATATCCGCTGAATGCACTCGACACGCTGTTACCTGACGGCAGAACAAACTGGAACTCCGCGCTATTTATCATTCTGA
ACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTATTATTCAGCGATTACTCGAGGAAAAATGGAAGACC
TTTGCGCGGTTGCAGTTCTTGAAACGGTTGATCATCCTGGTGTTCCATCTGACATCACTCTCGCTAGCCGTGTATAT
GAGACCGTCGAACATCGATGCCACTCTCCTGGAATGGCCAGAAGAAATCACGGAGGTTGGACGCATGATTGCGGAGT
GCACCACGGTGATAGGTGTGCTGAGCTACATTTTGGTGCAACTAGGCGGCGAGGTCGTCAACATTGGTCTTCTATCG
TTCATGAAACAATTGAGTCACGAGCCTGCCAAGCTCATATTCTTGATCAGCAATCTGCTCATACTCGCGTGCATACC
ATGTCGTCTTGCTGGTAATAGGCATGCTGAAGACGCGATACTCGTGGTTGCTGTTCCCGGCTCTTGGTTCCTCCTCA
TGTTCTTTGCTGGCGCTATCCGGTTGACCGGTCCATTCGTTACCATGGTCTACAGTATGATAACCGGTGACATGTTG
ACCTTTGGGATAATCTACATGGTGGTGCTGTTCGGATTTTGCCAGTCGTTCTACTTTTTGTACAAAGGCTTCCCGGG
AGTGAAATCATCCCTCTACAGTTCCTATCATTCGACCTGGATGGCACTGTTTCAGATAACCCTCGGCGATTATAACT
ATACGGACCTTGGTTACACGACCTACCCTAATTTATCGAAGATGGTGTTCGCCATATTTATGGTCCTGGTGCCCATA
CTGCTTTTGAATATGCTGATTGCGATGATGGGCAACACTTACGCGCATGTGATCGAGCAGAGCGAGAAGGAATGGGT
GAAGCAATGGGCGAAAATCGTGGTTTCTCTGGAGCGTGCAGTCGCGCAAAAAGATGCGCAGAATTATTTGCAAGAAT
ACAGTATTAAACTGGGGCCTGGAGATGACCCGAACAACCCCGCCTCGGAACAGCGCGGAGTCCTGGTTATTAAAAGT
AAATCGAAAACCAAGGCGAAGCAACGCAAAGGCGCGGTGGCTAATTGGAAGCGCGTAGGCAAAGTGACGATAAACGA
ATTGAAGAAACGTGGCATAACAGGAGAGGCGTTGCGACGAGTCATGTGGGGTCGAGCATCTTTCTCCACTCCTCGAG
ACACTTTGAGAGCTCTCGGATCTGTAGGTATTGTGAGAGCTGTAGGAACTCTCGGACCTGTAGGTACTGTGAGAGCT
GTAGGAGCTCTCGGACCTGTAGGCACTGTGAGAGATTCGAGCATGGCCGAGGATTTTCAGGATCCGCTTTTGGAGCT
TGTGATTGCTTCCGAAAATACGGACGATCCTGAAACGCTGTTGAAAATAGCGGAGCGGGCCGCGGCGAATTTCGAAG
TGGAGAGCAGTTCGAAAATAAATCTGCAAATTTTGGAGCAATTCACGATGACTAAGCTACCTATGGAGGAGAAAGTT
GCCGCTACAAAGAAGCAGTACTTTGTTGAATCGAGTGACAACGATTTTGGTGGCGACAACCTACTCGGAACCGAGGC
CCGTCTACGTAGAATAAGATCAGCGAACAACAGATTTATCACGACACGGAGACGGTCGCGGCACACCGACGACGACC
TGTCATCCACGTCGTCCACATCCGCCGATAGAAATCCTCAATATCAGCCATTGCTTAACGGCCCTGAGAACTTGGTG
AGCCGTCAAATCGAAAGTCGGGAGAGCTCTATCGAAGCAATTAAGCCGCAAGTAAAGCAGAACGGATCATGCGATTC
AGTGAAGATCAAGGTTCAGAAGCGTCGACCGAAAACGGCGAAAAATAGGGTATCACCGAAGGAAATAGAGGAGGCTG
GTCCGAGGAGAAGAGAATCGATCGAGCGGAATAAGGCGGTTTCACCGGCGACGTCGCCTACTGATCCGCTCGAACCA
TGGAGCACACGCGGCATTAAGGACATGAACACGATATTGGCTTGGGAGGAGAATACGCCGGACAGTCCTTAA

FIGURE 79 - SEQ ID NO: 43

<> 31
<> 2898
<> DNA
<> Dendroctonus ponderosae
<> gi|478256802
<> ?
>(gi|478256802:c>97259-97121, c97009-96855, c96447-96225, c96069-95928, c95914-95701, c95626-95527, c95477-95289, c95232-94892, c94761-94610, c94557-94341, c94257-94030, c93923-93801, c93748-93636, c93571-93415, c93133-92729) Dendroctonus ponderosae unplaced genomic scaffold Seq_1102706, whole genome shotgun sequence

ATGGGTGGGTGCCAATGTAAGCCATGCTGCAGACACAAGAAATCGCACTACACTGGAGGCTCAATTTTGGATCGAGT
AATTAGCCAAAGCTCCAATCAAGACCAGTGTTTGTTATACCGATTGGCCAACTACAAGAAGGGAGGGGAATTAATTG
ATGCCTACAATGCAGGCGGGCAGATTGAGTGCGAGAAGCTGATCCGCGACCAATTCGCGCAACTGATGTATCAGGAT
GGCAAAGGGAAGATTATCAACCGATCTGAGTATCTAAGATGGAAATTCAGGGATCATGAGCATGTGATTCTTCCAAT
CGAAGCGTCACTAAGTCGTTACGACCCATTAGGCAAATGGACCGACCATGAAGCCTGCTGGCAAATGCAGTACAGAG
GCTCTCTAGGCGAATCCCTGCTCCATCTGCTCATTATTTGCGACAGCAAAATCCACACCAGACTGGCAAGAACGTTA
ATTAAATGCTTCCCGAAACTGGCGCTTGATGTTGTCGAGGGAGAAGAGTACTTAGGGGCTAGTGCTCTTCACCTAGC
TATAGCCTACAGCAACAACGAACTAGTGCAGGACCTAGTTGAGGCTGGAGCTAACGTGAACCAACGAGCTATCGGTA
AGCAAATCGCTGATAAAACCGGCAAAATTAACGCAAAAAACCGTTTTTTTCTGCCGAGAGATCAGCAAAAACAGCGA
CCAGCTAAGCATACAGACTACGAAGGTTTGGCTTATTTGGGCGAGTATCCACTGGCTTGGGCGGCGTGTTGTGCCAA
CGAAAGCGTCTACAATCTGCTTCTGGACAGCGGCGCTCATCCAGATTTGCAGGACAATTTCGGCAACATGATCCTTC
ATATGGTGGTCGTTTGCGATAAATTGGATATGTTTGGCTACGCGCTTCGACATCCCAAACTGCCGGCTAGTAATGGG
ATTATTAACAAAGCTGGATTGACTCCACTCACTTTGGCCTGCAAACTAGGTCGTGCGGAAGTGTTCAGGGAGATGTT
GGAACTGTCCTGCAAAGAGTTTTGGAGATACAGCAACATTACATGTTCGGCGTATACTCTGAACGCTTTGGACACTT
TGCTGCCTGATGGTCGCACCAATTGGAACTCTGCCCTGTTCATTATCCTCAATGGCACCAAGGAGGCGCATCTCGAT
ATGTTGGATGGAGGCATCATTCAAAGACTGCTGGAGGAAAAATGGAAAGCCTTTGCTCGGAACCAGTTCCTCAAACG
CTTAATTATCCTGATAGTTCATCTAGCTTTTATGTCACTGGCTGTGTATATGAGGCCTGATGATCCGGACGAACCGT
TACTGGAATGGTCCGACGATCCTACAGTTATCATTCGGTATCGTCGGCTTTTCCAAGAGAATCCAGAGGTTTTACTG
GGGTTTTGTAGATTTACTGCTGAAATTGGGACGCTACTAAATGTGCTCAGTTACGTTGTTGTACAGCAGGGAGACGA
AATAAGGAACCAAGGATTTCTCTCTTTTTTGAAACAACAAACAAATTCCCCGCCAAAGTGCATTTTCTTAGTGTCCA
ACTTGATGATTCTGGCATGCATCCCTTGTAGACTGGCCGGAAACCGAGGGTTGGAAGAAACAATTTTGATCTTTGCT
GTGCCCGGATCCTGGTTTTTGCTCATGTTTTTTGCCGGTGCTGTTCGCTTAACCGGACCATTCGTCACAATGATCTA
CAGCATGATCACCGGGGACATGTTAACTTTTGGAATAATCTACACAATTTTCCTTTTCGGTTTTTCCCAGTCGCTTT
TCTTCTTGTACAAGGGAAATCCCAGCGTTAATGGCACGTTGTATCACAGCTACAGCTCCACTTGGATGGCACTGTTT
CAAGTCACAATGGGAAATTACGATTACTCTGAACTGGCGCTAACAACATATCCAGGTGTGGCCAAGTCCGTATTCGG
TCTTTTCATGGTATTCGTCCCAATATTGCTCTTCAACATGTTGATTGCCATGATGGGAAACACTTACGCTCATGTTA
CCGAACAGAGTGAAAAGGAATGGGTAAAACAATGGGCGAAAATCGTAATTTCCTTGGAAAGGGCCATCCCACAAAAG
GAGGCTCATAATTACCTACAGGAATATAGCATATCCTTGGGACCAGCTGAAGATCCAGCAACCGAACAACGAGGAGT
GATGGTGATAAAATCGAAAAACAAAACTAGAGCCAAACAACGAAAGGGAGCAGTCAGCAATTGGAAGAGAGTGGGAA
AAGTTACAATAAAAGCGCTAAAGAAAAAAGGGATGACTGGGGAAGAGATGCGCTGCCTAATGTGGGGGCGAGAGTCA
ATTAACACGCCGGTAAAAGTAAAAGGGCCTAAAAGAGACCCTTTGGCAAACCCCCAAGGCCCAGACTTGGCCAATGG
CTTCGGGGATGCTCTAACTTCTGCTCTGGATGTAATGGCGTTTACCCACGATTTGGACATTAATGCTCAAGGCCTAA
ATTTAGCAAAACAAACTCTAAATCCTAAGCCTTTTACGGACCCTCTAAGAACTCTGGTTTTGGAGTCTCTAGTGGAG
ACCAATTCAGCCAGATTGAGCGTTTTGGCTGCACAAGCAGCCAATTTGCCTGATACTGCCGAGATCGTCTCATGCCC
AAATACGGCCACCACTTCCGTGAAGAACCTCGCAGGAATTTTTGCAGGGACTGGCAATTTTGTGAAGAAAATTGAGG
AGAAAGTGAAGAAGAAAAAATATGCCGTTTTGGAATGCAGCGATAGCGAGAGCTTCGGAGGCAAGTGCCAGGGCATT
TCAACGCATTTCCAGTCAAAGACTTTGAAATATTGCAGAAGTGCTGCTGGGGACAATATCACGGGTGAAGAGGGCCA
GACTGATACATATGCGACATTCTGCAAACAGGAAAAGGAATTTAGATAA

FIGURE 80 - SEQ ID NO: 44

<> 33
<> 3444
<> DNA
<> Nasonia vitripennis
<> XM_001602538.2
<> ?
>gi|345485101|ref|XM_001602538.2| PREDICTED: Nasonia vitripennis inactive (Iav), mRNA

ATGGGTGGGGCATGCTCCTGTCAGGGTCGAGACAGCCAGGTCAATGCTGGCTCGATCCTCGATCGCGTGATCAGCCA
GGCGAGCGACGAGGACCAATGTCTGCTCTACCGGCTGGCCAACTACAAGAAGGGCGGCGAGCTGATCGAGGCCTACA
ACCAGGGCGGTCAAGCCGAGGTCGAGCGTCTGATCCGCGAGCAGTTCGGCATCCTCATGTACGCCGACGGCAAGGGT
CAGACGATCAACCGGGCAGAGTACCTCCGCTGGAAGTTCCGGGACCTGGACCAGGTCATCCTGCCGATCGAGGCGTC
CCTCTCGCGCTTCGATCCCTTGGCCCAGTGGTCGGATCACGAGGCCTGCTGGCAGATGCAGTACCGCGGCTCGCTGG
GAGAGACGCTGCTCCACGTGCTCATTATCTGCGACACCCGCACCCACACCCGGATCGCGAGGACGCTGCTCAAGTGC
TTCCCCAGACTGGCCATAGACGTGGTCGAGGGAGAGGAGTACCTCGGCGCGAGCGCGCTGCACCTGGCCATAGCCTA
CGCTAACAACGAGCTGGTCCAGGATCTCGTCGAGGCCGGGGCCATAGTGTCGCAGCGGGCCATAGGAAGCTTCTTCC
TGCCGAGGGACCAGCAGAGGCCCCGACCGGCTAAGAGCACCGACTACGAGGGACTGGCCTATCTCGGCGAGTACCCG
CTCGCCTGGGCGGCCTGCTGCGCCAACGAGAGCGTCTACAACCTGCTCCTCGACTCGGGAGCCCACCCCGACGAGCA
GGACACCTTCGGCAACAGCATCCTCCACATGGTCGTCGTCTGCGACAAGCTGGTCAGATTCGGCTACGCTCTGCGTC
ACCCGAAGCTACCAGCGAGCAACGGCATAGCTAACGCAGCCGGCCTGACCCCGCTGACACTCGCCTGCCAGCTGGGA
CGTGCCGAAGTCTTCCGCGAGATGCTCGAGCTCTCCGCCCGGGAGTTCTGGCGATACAGTAATATCACTTGCTCGGC
GTATCCGCTCAACGCACTCGACACGCTGCTGCCCGACGGAAGGACGAGTNNNAACTCGGCCCTGTTCATCATTCTCA
ACGGTACGAAGGAGGAGCACCTGGACATGCTGGACGGCGGCATCATACAGCGGCTGCTGGAAGAGAAGTGGAAGACC
TTCGCTCGGCTGCAGTTCTTGAAGCGGCTCGTAATCCTCGTCTTTCACCTGGTGTCGCTGTCGCTGGCCGTTTACTT
TCGGCCCGCGGACACTGACGCCGAGTTGGCCCAGTGGCCCGAGGAGATCACCGACGTCGTCAGAGTCATCGCCGAGT
GCGTCACCGTCCTCGGCGTCTTGGGTTACATTCTACTCCAGCTCGGAGGGGAGATCGTCAACATCGGCTTCTTCTCC
TTTTTCAAACAGCTGAGCCACGAACCTGCCAAGTTCATATTTCTCATCAGCAACCTCCTGATTCTGGCCTGCATCCC
GTGCAGACTGTCCGGCGACCGACACACCGAGGACGCCATTCTCGTGGTCGCCGTTCCGGGCTCCTGGTTTCTCCTGA
TGTTTTTCGCCGGGGCAGTACGTCTGACCGGACCCTTCGTCACGATGGTCTATAGCATGATACTCGGCGACATGCGG
ACTTTTGGCATCATCTACATGATCGTCATCTGCGGCTTCACCCAGGCGTTCTACTTCCTCTACAAGGGCTACCCGGG
AGTGAAGACGACCCTCTTCCATTCCTACCCCTCGACGTGGATGGCGCTATTTCAGATAACTCTCGGCGATTACAGCT
ACTCGGACCTCAGCATGACGACCTACCCCAATCTCAGCAAAGCGGTCTTCACCATCTTCATGGTCCTCGTGCCGATC
CTCCTGCTCAATATGCTGATAGCCATGATGGGAAACACGTACGCGCACGTGATCGAGCAGAGCGAGAAAGAATGGAT
GAAACAGTGGGCGAAAATCGTGGTTTCGCTGGAACGAGCTGTGTCGCAGGACGACGCGCACAATTACCTCCAGGAGT
ACAGCATAAAATTGGGCCCAGGAGACGACCCGAACGATCCAGCCTCGGAGCAACGGGGCGTCATGGTCATAAAGAGC
AAATCGAAGACTCGGGCTCGTCAGCGGAAAGGCGCCGTTGCTAATTGGAAGAGAGTCGGAAAGGTAACGATCGCCGA
GCTGAAAAAGCGTGGCATGACCGGGGAGGAGCTTCGTCGCATCATGTGGGGCCGAGCGTCCTTTTCCACGCCGGTCA
GGTCCAGCCCGATCCTGATGGAGCCGGTGTCATCAGTGCCAGGCGGTTTCGGCGACGCCCTGACGTCAGCCCTCGAC
GTTATGACTTTCGCCGCCGATGTGCCGGTGCCCATTGAGGGTAGTATACCCAAGCCAGTCGCCGTCGCCCCGGGCCA
ACAGCCGACTACAACACTTGCACTACCCAATGGAGCTGCGAAACCTCAACAGCCGATGATGACAACGTCGACGACAA
CGACGACGATCACGACGACAGTGCAGAAGACTCTCGTTACCGGCACTGCTACAACACCGGCGGTGGGCGTTACGAAG
ACCGTCGCGGTTCCAGCGGCGACCACCGTCAGCACCACAACGACTCGAGCATCAGCATCAGCAGTGCCCCCCACAGT
TCGGCCGTCAGAGCTCGGTCCAGCCTCGGCCCCTTGCAGCGCCGACCCACTGCTGGAGTTGATGCTCGCGACGGAGG
ATCCAGGCTCGTCGGAGGAGACTCTGCAGCGTCTGGCGCACTCGGCCCGGATCGTGGGCGAGAGCGCCACCACCAGC
GCCAAGTCCGATATCGATTCGAGCTTCCTCGAGAGGCTTGCGCTCGGAGGTCTCGGACTCGCCGCGATGCCCGAACA
GCCTGACAAGCCCGTCGAGCCCAAGAAGAAGCAGTATCTCGTCGAGTCCAGCGATAACGATATCTGTGCGAACGACG
GTCAGCTGGGAACGGAGGCTCGACTGCGGCGCATCAGGTCGGCCAGTAGCCGGCTAGCCCCGACGACGACGACGTCG
ACGTCGCGACGGAAGTCCGGCCAGCAGAAGCAGCAACGCGAAGCCAGGGACGACGAGAGCACCTCGTCCGCCGCTTC
GCTCGACAACATTTCCGGCTACCAGCCGCTCCTGAACGAGCCGGACACCACCGCGGACCAGCCTGCCACGGGAACAG
AGGACAATAAGCCGGCCAACGGCAGGAACCTACGCAAGAGACCCAAGACCACGAGTAACGAAGGCAAGGTCTTCTGT
AGTAGAAGGACAATTGTTGTACTTAATAAAAATAAGAAGAATAAAAAGCTCGAGACATCTGAAGCCAACATGAACGC
CAGGAAAAAGGAAACTCTTCTTGCACTGCACGACATGACAAGTTTGATCTCAGGCCGTGTACTCACCCTGGAACAGG
CCAATGAAAATGGCTATGAAATGCTGGAGCAGTTGAAGCATAAGTTGGACCCATAA

FIGURE 81 - SEQ ID NO: 45

<> 35
<> 3330
<> DNA
<> Camponotus floridanus
<> gi|307168683
<> ?
>(gi|307168683:95300-96124, 96482-96707, 102648-102763, 105291-105527, 107874-108025, 113417-113633, 114465-114626, 115036-115233, 115678-115787, 116993-117339, 117477-117731, 123276-123588, 124554-124725) Camponotus floridanus unplaced genomic scaffold scaffold2146, whole genome shotgun sequence

ATGGGTGGTGTTTGCTCGTGTCGCGTTGGTCGAGGTAACCAGCTTAACGCAGGCTCAATTCTCGATCGCGTCATCAG
CCAGGCAAGCAACGAGGATCAGTGCTTGTTGTATCGGCTGGCCAATTACAAAAAGGGCGGCGAGCTGATCGAGGCGT
ACAATCAAGGTGGCCAGCCAGAAGTGGAGAAATTGGTGCGCGAGCAATTCGGCATTCTGATGTACGCCGATGGTAAG
GGCCAGGTGATCAATCGCGCCGAGTATCTGCGTTGGAAGTTTCGTGACCTCGAGCAGGTCGTGCTGCCGATCGAGGC
ATCGCTGTCGCGCTTCGATCCACTCGCCCAATGGAACGATCACGAGGCCTGCTGGCAGATGCAATACAGAGGCTCGC
TGGGCGAGGCTCTGCTTCATGTCCTCATCATATGCGACACGCGGATACACACCAGAATAGCGCGTATATTACTCAAG
TGCTTCCCGCGACTCGCTATCGACGTCGTCGAGGGCGAAGAGTATCTCGGAGCGAGCGCCCTTCACCTGGCGATCGC
TTATAACAACAACGAACTCGTGCAGGATCTGGTCGATGCGGGCGCGATTATCTCGCAGCGGGCCATCGGTAGCTTTT
TTCTACCGCGTGATCAGCAGGGAATGAATCCCGTTAGAAACACCGATTACGAAGGACTCGCGTATTTAGGCGAGTAC
CCGCTCGCCTGGGCCGCTTGCTGCGCTAATGAAAGCGTCTACAATCTGCTGCTTGATTCCGGTGCGGATCCTGACGA
GCAGGATTCTTTCGGAAATATGATTTTGCATATGGTCGTAGTTGGCGATAAATTGGATATGTTCGGCTATGCTCTGC
GACATCCGAAGCTTCCCGCTCGCAACGGAATCGCGAATGCTGCGGGTCTGACCCCGTTGACACTCGCCTGCCAACTT
GGGCGTGCCGAGGTCTTCCGTGAGATGCTGGAACTGTCCGCGCGGGAGTTCTGGCGTTACAGTAATATCACCTGCTC
GGCGTATCCCCTCAATGCCCTCGACACGCTACTACCAGACGGCAGAACAAACTGGAACTCTGCGCTATTTATCATTC
TGAACGGTACGAAGGAGGAGCACTTGGACATGCTGGACGGTGGTATTATTCAGCGATTACTTGAGGAAAAATGGAAG
ACCTTCGCGCGATTGCAGTTCCTGAAGCGATTGATTATCTTGGTGTTTCACCTGGCCTCGCTGTCCTTAGCGGTATA
CTTCAGACCCGCGGATACGGATGCCGTGCTGCTGCAGTGGCCCGAGGAGATAACGGACGTCATCCGTACCGCGGCGG
AGTGCATCACCGTGCTGGGCGTGCTCAATTACATCCTGGTACAACTGGGTGGCGAGATGATCAACGTCGGACCGCTG
TCGTTTCTGAAGCAACTGAGCCACGAGCCAGCCAAGTTGATATTCGTGATCAGCAATCTACTCATTCTCGCGTGCAT
TCCATGTCGTATCGCCGGAAATCGGCACGCGGAGGATGCGATATTGGTGTTCGCCGTCCCGGGCTCCTGGTTTCTTC
TCATGTTTTTCGCCGGAGCAATTCGATTGACCGGTCCATTCGTCACGATGGTATACAGCATGATAACCGGTGATATG
CTGACTTTCGGTATAATCTATACAATCATGCTCTTCGGATTTTCGCAGTCGTTTTATTTTCTCTACAAGGGATTCCC
AGGCGTGAAATCATCTCTTTATCATTCTTATGTTTCGACCTGGATGGCATTGTTTCAGATAACCCTCGGCGATTATA
ACTATGCGGAATTGAATAACACGATCTATCCCAACTTGAGCAAAACCGTCTTCGCGATTTTTATGGTGCTTGTGCCC
ATTCTGCTACTTAACATGTTGATTGCCATGATGGGTAATACGTACGCACATGTTATCGAGCAAAGCGAGAAAGAATT
CGTTAAGCAGTGGGCAAAAATAGTGGTGTCTCTGGAACGTGCCGTATCGCAAAAAGACGCTCATAATTATCTGCAAG
AATACAGCATCAAGCTAGGACCCGGCGACGATCCAAACAATCCTGCTTCGGAGCAAAGAGGCGTGCTCGTTATTAAA
AGTAAATCGAAAACCAAAGCGAAGCAGCGTAAGGGCGCCGTAGCTAATTGGAAGCGAGTCGGAAAAGTTACGATAAA
CGAACTGAGAAAACGAGGGATGACTGGGGAGGAGCTTCGACATATAATGTGGGGTCGTGAGTCCTTCTCTACTCCTG
TACGAGTCAGTCCCAATGCTGGCCAACCGCAAGTGTCGGCAGTTACTGCAGGTTTTGGTGATGCACTAACCGCAGCT
TTGGACGTAATGGCCTTTGCACATGACTTTGACTTATCCGCGGCGACAGAAGGCATACCCACCAATATCGATGCGAA
ACAAACAAAAACGACACAATCGAAAGCCATTCCCAACGATCAGATGAAAACGACCCAGAATAATCCAGAAACAGTGA
CGAATGTCCAACCACATAAACAGCCTATTGGGGAGCCAACTAAATTGTTAGGTCTTACGGATTTAATCGATAATTCC
ATTGGTCCCGTGAAGGATGTGGAAGCGATGAATTTAAAAAATACGAACCAAACAAAAGCGCTCGAAGCATCTATGGA
GTTCGAAGATCCATTTTTGGAACTAGCCATCGCTTCTGAGACTACGACAAATTACGAAATCTTACTACAAATAGCGA
AGTCTGCTCTAGCTGCCAGTGAAGCTTCGGTGAAAACTGCAATTGATCCACAAATTCTCGCACATTTTGCTATGATT
CCTCCGCCGATCACTGAGAAATTCATCGTTAAGAAGCAATACTTTATGGAATCTAGTGATAACGATGTCGGTGGGGA
TAATTTATTAGGCACTGAAGCTCGTCTTCGAAGGATAAAATCTGCGAATAACAGGTTCATAACTACATCAAAACGGC
CACATCGTGATGATGATGGCGACAGTTCTTCGTCCACTATATCAATTGAACGAAATCAACGATATCGACCATTATTC
AACGATCCGGAAGAAAGATCGATAAATCATGTCGAAACTGAAGGTCAAAAAACTCCCATGGAAACAATTAAATCGGA
AATCCAGCAGAATGGTAGCATTCCACTCAAGCCACCCGATAAAATTCAAAAGCGTCGACCGAAAACAGCCAAGAACA
GAGTATCACCTAAGGAAATAGAGGAGCCGAGGAGAAGGGAATCGATTGAGCAGAATAAGGCGGCCTCACCACCGACG
TCGTCCTCGGATCCGCTCGAGCCATGGAGCACGCGTGGCATTACCGACATGAACACAATATTGGCTTGGAGGGATAA
CGCACCGGATAGTCCTTAA

FIGURE 82 - SEQ ID NO: 46

<> 37
<> 2974
<> DNA
<> Danaus plexippus
<> gi|357618515
<> ?
>gi|357618515|gb|AGBW01005481.1| Danaus plexippus, whole genome shotgun sequence

ATGGGTGTACCGTTAAGTAAGCTGTGTTCAGCAACGAGTGTCCCAGCCGTTGGCTCGGTTCTCGACCGTGTCATATC
CCAGCCCAGCAGCGAAGATCACACTGTCTTATATAAGCTCGCTGATTATAAAGAGGTTTACTATTAGAAACCTATAC
TAAGGGCGGCGTGGTAGCCGCCGAGCGCCTCATCAGAGAGGAGTTCTCGGCATATATGTACGCTGGTGGACGGGGCC
GGGTCATCAACAGAGCTGAATACCTCCGATGGAAGTTTCGAGACCAGGAAGTTGTTCTCCCAATAGAAGCGTCTCTC
TCACCTCACGATCCTCTAGCGAAATGGGAAGATCACACAGCTTGCTGGCAGATGAGTTACCGCGGAGCACTGGGGGA
GTCACTTCTTCATGTTCTCATTATATGCGACATCCACACAAGATTGGCGAGAACTTTGGTCAAATGTTTTCCGAAAT
TGTCCCTGGATGTCGTCGAAGGTGAAGAATGTGCTAGTTCGTTACATTTGGCCATCGCCTATAGTAATAATGAATTA
GTCCAAGACTTGGTCGAAGCTGGCGCGGATGTTAGTCAGAAAGCTGTAGTTTCTTTCTCCCGAGAGACCAACAAAAA
AATCCACCAGCTCGTCAGACAAATTACGAAGGTTTGGCGTATTTAGGGGAGTACCCACTAGCGTGGGCTGCTTGTTG
CGCTAACGAGGCCGTATATAACCTCCTTCTGGACTCTGGAGCTGATCCAGACGCCCAGGATTCATTTGGAAATATGA
TCCTGCATATGGTTGTAGTTTGTGATAAGTTGGATATGTTCGGCTATGCCCTTCGTCATCCAAAGGTACCAGCCAGT
AACGGCAGACTAAATAAGGCTGGGTTCACACCGCTCACCCTTGCCTGCCAATTGGGGCGAGCCTCGGTGTTCAGGGA
AATGTTGGAGCTTTCATCCAGGGAATTTTGGAGATATTCCAACATCACCTGTTCTGCATATCCATTGAATGCTCTAG
ACACTTTGCTACCTGATGGACGTACAAATTGGAATTCCGCATTATTCATCATACTTAATGGCACTAAACAAGAGCAT
CTTAATATGTTGGACGGGGGAATCATACAAAGGCTCTTAGAAGAGAAATGGAAAACATTTGCCAGAACAAAATTTTT
AAAGCGTCTATTAATCCTCATGCTACATCTGATCTTGCTATCCATATCTGTGTATCTACGTCACAGCAGTCTGGAAG
CGGATGTAGACCCCGACTGGGGTTTAGAGGTCAATGATGCAAGGTCCGGGATAAGATTGGCCTGCGAACTAGGAACT
ATCATAAGCACTCTTTGCTATATTATTCTGCAGCAAGGCGATGAGATCAAAAACCAAGGTGTTGTTGCGTACTTCAA
GCAACTAATCCATGAACCAGCCAAATTTATATTCCTAGCTTCAAACATATTGTTACTGGCGTGTATTCCAGCAAGAA
TAAGCCAAAGAACTACTTTGGAAGAAGCAATACTAATATTCGTACTACCCGGTTCTTGGTTCCTTATGATGTTTTTT
GCAGGAGCCGTGAAGTTGACTGGCCCGTTTGTTACAATGATATACAGCATGATCACTGGGGACATGTTCACATTCGG
CATTATCTACTGCATAGTATTGTTCGGATTCTCGCAATCTTTTTACTTCCTGTATAAAGGGTTTCCGAACGTACATT
CAACTCTGTACTCCAGCTATCCCAGCACCTGGATGGCTCTTTTTCAAATCACGTTAGGCGACTACAGTTACACAGAT
CTCGGTCTGACGATGTATCCTAATTTGTCGAAGACAGTGTTCACTGTTTTCATGGTGTTCGTCCCCATTCTGCTACT
CAACATGCTGATAGCCATGATGGGTAACACATACGCACACGTTATAGAGCAATCAGAGAAGGAATGGGTAAAACAGT
GGGCGAAGATTGTTGTGTCTCTGGAGCGTTCAGTATCCCAGGAAGATGCTCATCGTTACCTTCAGGAGTATTCAATA
GGTCTGGGACCCTCAGACGACCCTCGTTATGAGCAACGAGGTGTTATGGTAATTAAGAGCAAGGCCAAAACTCGCGC
CAAGCAAAGAAAGGGCGCGCTGTCTAATTGGAAGCGTGTGGGTAAAGTTACTATAGCAGAGCTGCGGCGCCGCGGCA
TTAGTGGAGAAGAATTGAGAAGACTCATGTGGGGGAGAGTCTCAATATCTACTCCAACCAAAGCACCCTTAAAATGT
GTGCCTCCCCCGGAGTTAGTGACTTCAGAAATTCCAGGAAGTGGAGTTGGACCAGCGTTGTCATCAGCTCTTAACGT
GATGGCGTACACACAAGATCTAGACCTCACCAACACCGGATCAGAACTGCATAAACAGATAACGCCCGATTTGCTCG
TCAATGGCAAGACGCCTGTGACAGCACAGAATACAGCAACCACTCCCAAAGTACCACTTGTAAATCTACCAAATAAA
GCGGGATTGGACGTTCAAAGTACGGGAAGTGATCAGAGCGTGCCAACTGCATTAACTAAGAATATGGACGTTTTGGG
CATAAATATGTCAACACAGGATTTGCTAAAGAATCAAACTATAAACAATCCCGCTACAGCCAACGAAATAGTGTTCA
AAGATTATCTCAGGGATATCATAAAGGCGGAGCAACTTGGTCTAGATAATATTGACATAAAGGCCCTCGCAGAGAAA
GCGGCCAACCTCACCGACGTACCAGAGATAGACATTAACATATCTACGGCTGCAAGGTCTGCCCGTCGTGTGGTAGC
CGGCGCTGTTTCTGGTCTGTTCGGTGTGACAGCAGAGACTCCGCGGGACGCAGGCTGGCGCAGAGAGAGACACGAAC
ATACAGACAGTGACCCTGTCCCAGAGTGCGTCATACTGGGTCGTGCGGCGCGCGCTCGCCGTGCACGATCTGCTTCC
CGGCGCGCGCCCCCTCCCCCACCTCACCTCTACGTTCCTGCGAGGTAA

FIGURE 83 - SEQ ID NO: 47

<> 39
<> 3540
<> DNA
<> Bombyx mori
<> XM_004925264.1
<> ?
>gi|512902215|ref|XM_004925264.1| PREDICTED: Bombyx mori uncharacterized LOC101737437 (LOC101737437), mRNA

ATGGGTAATGCCATTGGAAAATTTCTAACTGCGGGCAACGTTCAAGGTGCTGGCTCGGTTCTCGATAGAGTCATATC
CCAGCCGAGCAGCGAAGACCACACCGTACTTTACAAATTAGCTGATTATAAGAAAGGCGGTCTACTTTTAGAGACCT
ACGCGAAAGGTGGCATGACAGCCGCTGAAAAGTTAATGAGAGACGAATTCGCTGCATACATGTACGGCGGAGGGAGG
GGCCGGGTCATCAATCGTGCTGAATACTTGAGATGGAAGTTCAGAGACCAAGAACAGGTTGTACTTCCAATTGAAGC
ATCGCTCTCACCTTATGACCCGCTCGCCAAATGGGAAGATCACACCGCCTGTTGGCAGATGTGTTATAGAGGAGCTC
TCGGCGAATCATTGCTTCATGTACTCATTATTTGTGATACTAAGATTCATACAAGATTAGCTCGAACTCTAGTAAAA
TGTTTTCCGAAGCTGTCACTAGATGTCGTTGAAGGTGAAGAATATTTAGGGGCAAGCTCTTTACATCTGGCAATAGC
GTACAGCAATAACGAACTAGTACAAGATCTAGTTGAGGCCGGAGCTGATGTCAACCAGAGAGCCATTGGTAGCTTTT
TCCTACCCCGCGACCAACAAAGAGTTCCGCCAGCGCGACAAACAAATTACGAAGGTCTGGCATACTTGGGCGAATAC
CCCCTAGCCTGGACGGCTTGTTGCGCGAACGAAGCAGTCTACAACCTCTTACTAGATTCCGGGGCAGATCCCGATGC
TCAGGATTCGTTCGGGAACATGATACTACACATGGTGGTCGTTTGTGATAAACTGGACATGTTTGGATATGCCCTGC
GTCACCCTAAAGTTCCGGCCAGTAACGGTCGAATGAATAAAGCAGGTTTCACCCCACTAACCTTGGCTTGTCAGTTG
GGTCGGGCCTCTGTCTTCAGAGAGATGCTGGAGCTATCAGCCAGAGAGTTCTGGCGCTACTCCAACATTACGTGCTC
CGCTTACCCTTTGAACGCTTTAGATACCTTGCTGCCTGATGGGCGAACAAATTGGAATTCGGCTTTATTCATTATAC
TGAACGGAACAAAGCAAGAACACTTGAACATGTTAGACGGCGGTATCATACAAAGGTTGCTTGAAGAAAAATGGAAG
ACTTTCGCCAGGACGAAATTCCTCAAACGTCTCCTCATACTGATGCTGCATCTTCTCCTGCTCTCCGTTTCTGTGTA
CCTACGTCACAGCAGCGCAGAAGCTGATGCCCACCCCAACTGGGGCTTGGAGATCAACGACGCTAGAAGCGGACTGA
GACTTGCCAGTGAACTTGGGACTATATTGAGCACATTGTGTTATATTATACTGCAACAAGGCGACGAGCTAAAGAAT
CAAGGATTGGTCGCTTATTTTAAGCAGTTGATTCACGAGCCGGCCAAATTTATATTTTTGGCGTCAAACATCCTTGT
GTTAGCGTGCATACCGGCCAGACTCCTTAAGGAGACCAACGTGGAGGAAGCCATACTGCTTTTCCTGCTGCCGGGAT
CGTGGTTTTTGTTGATGTTTTTTGCTGGCGCGGTGAAATTGACCGGTCCATTCGTGACAATGATCTACAGTATGATA
ACAGGGGACATGTTCACGTTCGGTATCATCTACTGTATTGTCCTCTTCGGCTTCTCGCAGTCATTCTACTTCTTGTA
TAGAGGTTTTCCAAACGTACAGTCGACTTTGTACTCGAGCTACCCCAGCACGTGGATGGCACTATTCCAAATCACCT
TAGGAGATTACAGCTACTCGGATCTCAGTCAGACAACATACCCTAATCTCTCGAAGACTGTGTTCACGGTGTTCATG
ATATTCGTGCCAATTCTACTATTGAACATGTTGATCGCCATGATGGGGAACACGTACGCCCACGTCATTGAGCAATC
CGAGAAGGAATGGGTCAAACAGTGGGCGAAAATTGTGGTATCACTAGAGCGTTCAGTGGCCCAGGATGACGCACATA
AGTACTTGCAGGAGTATTCTATAGGACTTGGGCCTTCCGACGATCCGAGATACGAGCAACGAGCGGTCATGGTCATC
AAGAGCAAAGCTAAAACTAGAGCGAAACAGAAGAAAGACGCTTTAACTAATTGGAAGCACGTCGGTAAAGTGACAAT
AGCAGAGTTGAGAAGACGCGGTATCAGCGGTGAAGAGTTACGTAGATTGATGTGGGGCCGTATTTCAATTTCGACAC
CAACAAAAGCTCCCTTGCCGCGAAGAGTCCCAGCCCCGCCTCCAGACTGCGTGGTTTCGTCAGACGTGGGTTTAGCT
AGTGACGTAGGGAACGGTGTAGCACCAGCTCTCTCGTCAGCTCTCAACGTCATGGCCTTCACTCACGAATTAGACAT
TGGCACTACTGGTTCTGATCAAAAACAAACTACACCGGACTTGTTGGTCAACGGCAAAACTTCCAATGCCCCAATCT
TAACTACCGGTACCCAAATGCCAAAAGTTTCAAGCAAAACTCTCGGTACACCAGTGGCACGTATTGAAGCATCTTCA
CTTAAGACGCCTTTGGATGTTAAATTAAACCCAACAACATTGACACAGTCCACGGTTCAGGGTAATATAGGTAATGT
CAATATTCCTATAAGTGGAGTGAAAATAACAACAAATGTTGGACAAAACTCCGCGGTAGTACCTGAGATTCAACAGT
CGAATGAAAATCAGAAACCTGAGCAAGTACACCAAGATTATCTGCGTGAACTCATAGTTCTTGCTGAGAAACCTGCA
ACCACTAATCTTGAACTCAAACAACTTGCTGAGAAAGCGGCTGATCTGAGAGATGTACCGGAAATTGATATTAACAT
CAATATGGCTGCAAAATCTGCGCGTAAAATGGTAGCGGGTGCTGTGTCGGGTTTATTCGGTGTCGCCGCTGACACTC
CTGCCCCCGATGCTGGCTGGAGGCGGGATCGTCATGACAACAGCGACAGTGATCCGATATCGGAGTCAGTGCTGTTA
AGTCGAGCATCAAGAGCAAGACGCGCGAGGTCAGCATCGCGACGAGCCGCACCACCGCCCCCACATCTATATGTACC
GGCTAGGTCTATGTACTTAGTGGCATCTGAGAGCAGTGCTATAGAAAGTGATGCACCTTGGGATGATCAACCCAGTT
CAGAGAACAATTCAGCTGTAGGTGGTCGTAGAGAAGAGATCGCCCACATTAAAGCTGCAAGACCCTTGTGTATTCAA
CATGCTGCGTCAGGGAGAACGGCTCAAGTAGAACACTCATTATTTGTTGTAGGTCCTGGAACCGGAGCCGAAGTTGA
AAGTACTCCTACTGTACAAAAATCCGAAAAAAAGGCTAGACCTAAAACAACGCGATCTAGACGAAACAGAATATCTC
CAACACCGGTACAAGAAGCGGGCAGCCCTTTGGAGCCCTGGGCCACAGCACAACTATCGAAGCTATCACGTCTCATA
CGCTATTCCAGCTCATCAGCAGCTTCTATCACCTCGCAGACGTCCACGGAACAGGAGCAATCGCCAAGATACTGA

FIGURE 84 - SEQ ID NO: 48

<> 41
<> 2982
<> DNA
<> Acyrthosiphon pisum
<> XM_001950061.2
<> ?
>gi|328710193|ref|XM_001950061.2| PREDICTED: Acyrthosiphon pisum transient receptor potential cation channel subfamily V member 6-like (LOC100162897), mRNA

ATGGGAAATTCTTGTGCGAGTTGCACAGATTTCTCATTCTCGAAAACAGCTTCAGGATCTGTTCTGGATAGAGTGAT
TTCTCAAGCGTCAAATGAAGACGATTGTTTGTTGTATAAGTTAGCGGATTATAAAAAAGGAGGAGAATTGATCAATG
TGTATAATAATGGTGGTCAGGACGAAGCGGAACGATTTATTGTTGAAAAATTACCCGGCCTTATGTATAACAACGGT
AAAGGTCAAGTGATAAATCGAAATGATTATTTGAGATGGAAATTTCAAAATCGTAAACACGTGGCTGTTAATGTCGA
GGAAAGGCCGGGTCCTCACGATCCGTTAACAAGATGGGTGGACCATGTGGCGTGCTGGCAAATGCAGTATAGAGGAT
CATTAGGCGAAAGTTTGTTGCACGTATTAATCATATGCGATACCGTGATACACACTCGGCTGTCCCGACTACTTCTC
AAACACTACCCGATGTTAAGTCAAGATGTTGTGGAAGGCGAAGAATATCTCGGCGCTAGTGCATTACATTTGTCTAT
TGCTTATAACAACAACGATTTAATCCAAGACCTGGTTGATGCTGGTGCTAATATTTGTCAAAGAGCCATAGGGAGCT
TTTTCTTACCACGCGATCAACAGAATAAAGAAATCAATAACAAACACACGGATTACGAGGGTCTAGCGTATCTCGGG
GAGCTGCCATTAGCGTGGGCTGCTTGTTGCGGGAACCAAACGGTATACAACCTGTTGATTGATGCTGGAGCAAACCC
TGACGCCCAGGACTCATTTGGAAATATGATTCTCCATATGGTGGTCGTTTGTGATAAACTGAGTATGTTTGGTTATG
CTTTGAAACACCCTAAAGTGAAAGCAAGTAACGGTATCATGAACGTGGCAGGACTAACACCTTTAACACTATCGTGC
AAACTTGCAAGAACTAGTGTTTTCCGTGAAATGTTGGAACTAAGTGCACGGGAATTTTGGAGATATAGTAATATTAC
GTGTTCGGCATACCCTTTAAGCGCGTTAGACACGTTACTTCCAGACGGAAGAACAAATTGGAATTCAGTATTGTTTA
TAATTTTGGACGGTACCAAAGAAGAACATTTGGACATGCTCGATGGAGGCATTATTCAAAAATTATTAGAAGAAAAG
TGGAAAACTTTTGCTCGGAAACAATTTATGAAACGTTTAGTTATATTATCCATCCATCTAATCATGTTGAGTATTTC
TATATACCTAAGACCCGTGGACCAAGACAAACCACTGTTAGGAGAAGCAGAAGACTGGCAAGACGTGGCAAGGTATT
GTTTTGAAGGCGGAACAGTAGTCGGAGTGCTGTCATATTTAATTGTTCAGCAAGGTGGAGAAATACTCAATCAAGGT
CTGGTAGGATTTTTAAAACAAACGTTCAAAGAACCGGCCAAACTGATATTTCTGATTTCAAATTTATTGATATTGGC
TTGTATACCACCCAGGATGATGGGCGACAAACAGACGGAGGAAGCCATATTAGTATTTGCAGTTCCCGGATCATGGT
TTTTGTTAATGTTTTTTGCTGGCGCTATACGCCTGACTGGGCCTTTCGTAACTATGGTGTACTTGATGATCACAGGA
GACATGTTGACCTTTTTCGTCATCTACTCAGTAATTTTGTCTGGTTTTACGCAATCGTTTTTTTTCCTCTACAAAGG
ATCGCCAGACGTCAGTACGTCGTTATATAAATCTTACCCTTCTACGTGGATGGCCTTATTTCAAATTACTATGGGCG
ACTACAATTACGCGGATTTGAGTTACACCGTATATCCAGCGCTCAGCAAAACTGTGTTTACGGTTTTCATGGTGTTG
GTGCCAATTTTATTACTTAACATGTTAATAGCTATGATGGGCAACACTTATGCGCACGTCATCGAACAGAGCGAAAA
GGAATGGATGAAACAGTGGGCCAAGATTGTAGTTACCCTTGAAAGAGCTGTACCACAAAAAGCAGCCAGGAATTACC
TCGAAGAATATAGTATTCAGTTGGCTCCCGGCGACGATGTAAATCCAGAACAAAGAGGATTCATGGTTATCAAATGT
AAAAGCCAAACTAGAGCGAAACAGCGAAAAGGCGCCGTCATAAATTGGAAGAAAAGTGGAAAGTTGGTCATTCAAGA
GCTTCGTAGATTAGAAGGTACTGGCCAGAATCTAAGAGATATGATTTGGAAACGATCGTCTCTATCAGCGTCTTCTC
CGGTTGCTAAAAGTGTATCAATAACAAAAAATAAAAGCAAGTCCTATTCTGAAGCAAAAGATGACCAAATTCGGCTT
TCTGGTGCACTAGGAGCAGCACTAGACGCGATTGCAGTAGCTCATGACTTAGACATGACTCTGACAAAAGATCAATC
GATTGATGAATTACACGACCCTTTAAGACAATTAGTAATAATGTCAGAAAGTGATAAAAATATTGATAAAAGTCAAG
TCGAAATAGTGGCGAATGCAGCAGCAAAAATTGCAAATCAAGATTCTATAAAACCGATATCGATTAATTTAGAGCAA
CAAAATGACGTAAAAAATGAAAAAACCAAAATTCCAACTTCCAGTAACACAATAACAAATAGAAAACTCTTAAACAA
GCAATCTAAAAATTTAAGCATGTATGGTTTTGAGAGTCAGGACATGTCAGTAGATAAATACAGCAAAGCAATTGCAA
TCACAAGAAGTATATCAACTCAAACTGGAGGTATTGGTATCATCGAAAAAAACGAACGACAGATAATTCGACCGAAA
ACTGCAAAAATCAATCGCGTGACGCCCACGCAGAATTTCGCAGTGAAAAGAGGCCAATCGGCACAGCCGGACAAACG
GGAAGACCACAGGGATAACAAGGAGCAACAGTGTTATTGCATCAGTGGCAACAACATGTTGCGGCCGTGGAGCACGC
AAGACCTGGCGCCGTTGAACACGATCATGGCGTGGGGTCCCAACGACGATTTCTGA

FIGURE 85 - SEQ ID NO: 49

<> 43
<> 825, partial
<> DNA
<> Solenopsis invicta]
<> GL767538.1
<> ?
>gb|GL767538.1|:2073946-2074770 Solenopsis invicta unplaced genomic scaffold Si_gnG.scaffold06207, whole genome shotgun sequence
CAATTTATCGCCAACTACGACCATGTGTAAAATCATATTTCCGAAAGAATCCTGCTCGTCAGGATCCGCGCCGGAAT
CAAGCAGCAGATTGTAGACGCTCTCGTTAGCGCAGCAGGCTGCCCAGGCGAGCGGGTACTCTCCCAGATAGGCGAGA
CCCTCGTAATCGGTATTTCTGGCGGGATTCATCCTTTGCTGATCGCGCGGTAGGAAGAAGCTACCGATGGCGCGCTG
CGAGATAATCGCGCCCGCCTCAACCAGATCCTGCACGAGCTCGTTGTTGTTGTAGGCGATCGCCAGGTGAAGGGCGC
TCGCACCGAGATACTCCTCGCCCTCGACGACGTCGATAGACAGCCGCGGAAAGCACTTGAGCAGTATGCGCGCTATC
CTCGTGTGCATCCGCGTGTCGCATATGATCAGTACGTGCAACAAGGTCTCGCCCAGCGAGCCCCTGTACTGCATCTG
CCAGCAGGCCTCGTGGTCATTCCACTGCGCCAGAGGATCGAAGCGCGTCAGCGAGGCCTCGATCGGCAGCACGACTT
GCTCCAGGTCGCGGAACTTCCAACGTAAATACTCGGCGCGATTGATTGTCTGGCCCTTACCGTCCGCATACATCAGG
ATACCGAATTGCTCGCGAATTAGCTTCTCCACCTCCGGTTGACCGCCCTGATTGTACGCCTCGATCAGCTCGCCGCC
CTTCTTGTAGTTGGCCAGCCGATACAATAAACATTGATCCTCGTTGCTCGCCTGGCTGATCACGCGGTCGAGGATTG
AACCGGGATTGACCTGGCTGCCGCGACCAAAGCGGCACGAGCACGCACCACCCAT

FIGURE 86 - SEQ ID NO: 50

<> 45
<> 426
<> DNA
<> Schistocerca americana, DNA partial
<> In-house
<> ?
> Schistocerca americana, DNA partial
CACCACAATTTTGGCCCAYTGTTTCATCCACTCCTTCTCGCTCTGCTCGATRACGTGCGCGTACGTGTTTCCCATCA
TGGCGATCAGCATRTTGAGCAGCAGGATGGGCACCAGCACCATGAAAATGGCGAACACTGTCTTGGCCAGCGTTGGA
TATGTCGTGTGGCTCAGTTCTGGRTAGTTATAGTCGCCCATGGTGATCTGGAAGAGCGCCATCCAGGTGGTGGGGTA
GGAGTGGTAGAGCGACGTCTTCACGCCGGGGAAGCCCTTGTACAGAAAGTAGAAGGACTGAGAGAAGCCGAACAGCA
CAACCGTGTAGATGATGCCGAACGTCAACATGTCACCGGTGATCATCGAGTACACCATCGTCACGAACGGACCAGTC
AGCCGGRTGGCCCCCGCGAAAAACATCAGCAGGAACCAGGA

FIGURE 87 - SEQ ID NO: 51

<> 47
<> 2435, partial
<> DNA
<> Myzus persicae
<> In-house
<> ?

GAAAGGCCGGGCCCTCACGATCCGTTGACAAGATGGGTGGACCACGTGGCGTGCTGGCAAATGCAATACAGAGGATC
ATTAGGCGAAAGTCTGTTGCACGTATTAATCATATGCGATACTGTGATACACACTCGGCTCTCCCGACTACTTCTCA
AACACTACCCTATGTTAAGTCAAGATGTTGTGGAAGGTGAAGAATATCTCGGCGCCAGTGCATTACATTTGTCTATT
GCTTACAACAACAACGATTTAATCCAAGACTTGGTTGATGCTGGAGCAAATATTTGTCAAAGAGCCATAGGGAGCTT
TTTCTTACCACGCGATCAACAGAATAAAGAAATCAATAACAAACACACGGATTACGAGGGTCTAGCGTATCTCGGAG
AGCTACCGTTAGCGTGGGCTGCTTGTTGCGGAAACCAAACGGTATATAACCTGTTGATTGATGCTGGAGCAAACCCT
GACGCCCAGGACTCGTTTGGAAATATGATTCTCCATATGGTGGTCGTTTGTGACAAACTGAGTATGTTTGGTTATGC
TTTGAAGCACCCTAAAGTGCCGGCAAGTAATGGTATAATGAACGTGGCAGGACTAACACCTTTAACTCTATCGTGTA
AACTTGCAAGAACTAGTGTTTTCCGTGAAATGTTGGAACTAAGTGCAAGGGAATTTTGGAGATATAGTAATATTACA
TGTTCGGCGTATCCTTTAAGTGCTTTAGACACATTACTTCCAGACGGAAGAACAAATTGGAATTCAGTATTGTTTAT
AATTTTGGATGGTACAAAAGAAGAACATTTAGACATGCTCGATGGAGGCATAATTCAAAAATTATTAGAAGAAAAGT
GGAAAACTTTTGCTCGGNNNNNNNNNNNNNNNNNNNNNNTTATATTATCCATCCATTTAATCATGTTGAGTATTTCT
ATATACCTAAGACCCGTGGACCAGGACAAACCATTGTTAGGAGAAGCAGAAGACTGGCAAGACGTGGCAAGGTATTG
TTTTGAAGGCGGAACAGTAGTCGGAGTGCTGTCATATTTAATCGTTCAGCAAGGTGGAGAAATACTCAATCAAGGTC
TGGTAGGATTTTTAAAACAAACGTTCAAAGAACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGAG
ACATGTTAACCTTTTTCGTCATCTACTCAGTAATTTTGTCTGGTTTTACGCAATCGTTTTTTTTTCTCTACAAAGGA
TCGCCAGACGTCAGTACGTCGTTATATAAATCTTACCCTTCTACATGGATGGCCTTATTTCAAATTACTATGGGTGA
CTACAATTACGCGGATTTGAGTTACACCGTATACCCCGCTCTCAGCAAAACTGTGTTTACGGTTTTCATGGTGTTGG
TGCCCATTTTATTACTTAACATGTTAATAGCTATGATGGGAAACACTTATGCGCACGTCATCGAACAGAGCGAAAAA
GAATGGATGAAACAGTGGGCTAAGATTGTAGTTACTCTCGAGAGAGCTGTACCACAAAAAGCAGCCAGGAATTACCT
CGAAGAATATAGCATTCAGCTGGCACCCGGTGACGACGTAAATCCAGAACAAAGAGGATTCATGGTAATTAAATGTA
AAAGTCAAACACGAGCGAAACAGCGAAAAGGCGCAGTCATAAATTGGAAGAAAAGTGGAAAGTTGGTCATTCAAGAG
CTTCGTAGATTAGAAGGCACTGGCCAAAATTTAAGAGATATGATTTGGAAACGATCGTCTCTATCAGCGTCTTCTCC
GGTCGCTAAAAGTGTATCAATAACAAAAAATAAAAGCAAGTCTTATTCTGAAGCAAAAGATGACCAAATTCGGCTCT
CTGGTGCACTAGGAGCAGCACTAGACGCGATTGCTGTAGCTCATGATTTAGACATGACCCTGACAAAAGATCAATCG
ATTGATGAATTACATGATCCTTTAAGACAGTTAGTAATAATGTCGGAAAGTGATAAAAATATTGATAAAAGCCAAGT
CGAAATAGTGGCGAATGCAGCAGCAAAAATTGCAAACCAAGATTCTATAAAACCGATATCGGTTAATTTAGAGCAAC
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACAATTACAAATAGAAAACTGTTAAACAAGCAA
TCTAAAAATTTAAGCATGTATGGTTTTGAGAGTCAGGACATTTCAGTAGATAAATACAGCAAAGAAATTGTAATCAC
AAGAAGTATTTCAACTCAAACTGGAGGTATTGGTATCATCGAAAAAAACGAACGACCGATAATAAGACCAAAAACTG
CAAAAATCAATCGCGTGACGCCCACACAGAATTTCGCGGTGAAAAGAGGCCAATCAGCACAGCCGGACAAACGGGAA
GACCACAGGGATAACAAGGAGCAACAGTGTTATTGCATCAGTGGCAACAACATGTTGAGGCCGTGGAGCACTCAAGA
CCTGGCACCGTTAAACACGATCATGGCTTGGGGTCCCAACGACGATTTCTGA

FIGURE 88 - SEQ ID NO: 52

<> 49
<> 2904
<> DNA
<> Bemisia tabaci
<> In-house
<> ?

ATGTACAATGATGGCAAAGGACAGATCATCAAAAGAGCAGAGTATTTACGTTGGAAGTTCAGAGATCAGCAACAGGT
AACTCTACCTATTGAAGCATCTCTGAGTCCTCATGATCCCCTCGCCAAATGGGAGGACCATGAAGCTTGCTGGCAAA
TGCAGTACAGAGGCTCCTTGGGTGAAACCTTATTACACGTCTTGATAATCTGTGACACAAAAACCAACACTCGCCTG
GCCCGCACATTGCTTAAGTGCTTCCCTCGATTGGCTCAAGATATTGTAGAAGGAGAAGAGTATCTTGGTGCCAGTGC
TCTTCACCTTGCTATTGCATACAATAATAACGAATTAGTCCAGGATTTGGTAGAAGCAGGAGCAAATGTCAATCAAA
GAGCAATAGGTAGCTTTTTCCTGCCCAAAGATCAGCAAAGACCGAGACCTGCTAAACACACAGATTACGAAGGTTTG
GCTTACCTCGGAGAATTTCCTCTTTCGTGGGCAGCCTGTTGCGCCAATGAATCAGTTTACAATCTACTTCTAGATTC
AGGAGCCCATCCAGACATGCAGGACACTTTTGGGAATATGATTCTGCACATGGTTGTCGTTTGTGACAAGTTGGACA
TGTTTGGTTATGCTTTGAGACATCCAAAACTGCCAGCCAGTAATGGTATTACCAACACAGCTGGCCTCACGCCTCTC
ACATTAGCCTGCAAGTTGGGCCGTGCAGAAGTTTTTCGTGAAATGTTAGAACTGAGCGCAAGGGAATTTTGGAGGTA
CAGCAACATAACATGCTCAGCGTACCCTTTAAATGCTCTGGATACCCTGTTACCTGACGGACGAACTAACTGGAATT
CTGCTCTGTTCATCATTCTTAATGGTACCAAAGAAGAACATCTAGACATGTTAGATGGTGGAATCATTCAACGATTA
CTGGAGGAGAAGTGGAAAACGTTTGCAAGACGCCAGTTTTTAAAGCGGCTGGCAATTTTGTTTCTCCACCTTCTCAT
GCTAAGTATGGCCGTATACCTGAGACCAGTGGACAGGGAGCAGCCTCTTATAGGAGGAGATGACTGGTCGGATATTG
CGCGATACGGTTTTGAAGTTGGCACTATCATGGGCGTTTTATCGTATCTAGTTGTACAACAAGGTGGGGAGATTAAG
AATCAAGGTCTTGGAAGTTTCTTGAAGCAATTGATGGCAGAACCAGCCAAAGCAATATTCCTTGTTTCAAATCTTCT
AATTCTGGCTTGCATCCCTTTTCGGATGGCAGGGGACTCGCAAACAGAAGAGGCTATTTTAATTTTAGCCGTTCCTG
GGTCATGGTTTCTACTAATGTTTTTTGCTGGGGCTGTGCGGCTGACTGGTCCCTTTGTTACAATGATCTACAGTATG
ATTACTGGTGATATGTTTACGTTCGGAATTATCTACTCAATTCTTTTGTTTGGGTTCTCTCAGTCATTCTATTTCTT
GTACAAAGGCTCGCCAAATGTGAAGCAAACTTTATTTCACTCTTATCCAACAACTTGGATGGCTCTCTTCCAAATTA
CTTTGGGTGACTATAATTATCCAGAGTTGGCTTTCACCGTGTATCCAACTCTGAGCAAGATAGTTTTCACTAGTTTC
ATGGTTCTGGTGCCGATCTTGCTGCTGAACATGTTGATCGCTATGATGGGTAACACCTACGCTCATGTCATAGAACG
CAGTGAAAAGGAATGGATGAAGCAATGGGCGAAAATTGTTGTTGCTCTGGAGCGAGCTGTTCCCGCAGCAGATGCGC
ATAACTATTTGCAAGAGTACAGCATAAAACTAGGGCCTGGCGATGATCCATCAACGGAACAAAGAGGTGTCATGGTA
ATCAAAAGTAAGAGCAAAACACGTGCCAAGCAAAGAAAAGGAGCTGTATCCAACTGGAAGCGAGTTGGTAAAGTCAC
CATCAATGAATTACGGAAGCGAGGAATGACAGGTGAACAGCTGAATCGAATCATGTGGGGACGAGCTTCCATATCGA
CACCAGTTCGACAGCCTGCCATGGCTCTATTACTTGAAGATAGTGAAGAAGAAAATGCTGCAAACAATACTGGTCCA
TTTGGTGGAGCGCTGACAGCTGCCTTGGACGTAATGGCCTTCACCCACGACATAGACTTAAATATTGGTCAAACGCC
GGTCACAGTTTCTGGCCTTGGTGGTGTTTCCGTTCGCAGTGGAGCTGAAGGTCTTCCTCCAGAACAACCATTCCATG
ACCCATTCCGGCAGCTGGTGATTGAAGCAGAAAATCCTCATATTGATGAATCCGAATTAGCAGCTCTTGCAAATGCT
GCTGCAATGTCCGTTGTTGCGCCTGATGATATTCCGACTCCTGTGGTTACACCTGAGCCTGTATCTGCATTACCTCG
ATTGCCCTCTCTTCATCTAGAACCAAGTGACAGTGATGGACTTGGAGATGGACCTCTTCTTGGAAGAGGTAGTCGTG
TGCGCAGAGTTCGTTCTGCACATCTGAAGCAGCAAAAAGCATCTTCTACGAATGGGAATGGCTATTCAGACAGACAA
AGACTTTTTTCATCTAAGAATGAAGACTCAAGTTCAAATACTTCATTAGATTTCGACCTGACAAATCCTCCTTCTCA
ATTGAGGCTCACTCCACCTCCTAGACCGGTAACAGCTGAAATTGTGGCTGTAAATCCGAAGAAATACATAGGTGGAA
ACAGTCAAGAGAGGTTAAGGCCAAAAACAGCTAAAGTCAACAGGGTTGCGCCAACCCCCGATGTTCCTGTGCGTCGA
GGGATTTCTGCTAATGGTATCCCAGAATCACTGCCGTCTCCACCTGATCCACTAGAGCCATGGAGCACTCGTAATAT
CGTCAATATGAATGCAATTCTTGCATGGCAGCAAAGTGATCAGGATAGTTTGTAA

FIGURE 89 – SEQ ID NO: 53

<> 51
<> 2955
<> DNA
<> Euschistus heros
<> In-house
<> ?

ATGGGCATCATCTGGGGCAGTGGTGCTTCTTCAGTGAATGCTGGGACAGTACTTGACCGAGTGATCTCCCAAGCATC
AAATAAGGATGAATGCCTTCTTTACAAATTGGCCAACTACAAGAAGGGAGGAGAGCTGATAGATGCCTATAATGCAG
GAGGCCAAAGTGAGGTTGAGAAACTGATAAGGGAACAGTTCGGCCAATTGATGTATAATGAAGGAAAGGGTGCTCTC
ATCAACAGAGCTGAATATCTGCGATGGAAATTTAGGGACATGCAACAGGTACAGATCCCTATAGAGGCATCTTTATC
CAGCCAAGATCCATTGTCAAAATGGGAGGATCACCAAGCTTGCTGGCAGATGCAGTATCGAGGTTCACTGGGAGAAA
CATTGCTGCATGTACTTATAATTTGTGATACAAAGATACATACGAGACTAGCAAGGACACTATTAAAGTGTTTCCCT
AATCTTGCCATAGACGTTGTGGAAGGAGAAGAATAYTTAGGTGCTAGTGCCCTCCATTTGGCTATTGCATATTTCAA
CAATGAATTAGTTCAAGATCTTGTTGAAGCTGGAGCGAATGTAGAACAAAGGGCAATAGGCAGTTTCTTCCTTCCAA
GGGACCAGCAAGGGCAGAGACCATCAAAGCACACAGATTATGAGGGCTTAGCCTACCTCGGGGAGTAYCCATTGGCC
TGGGCAGCCTGCTGTGCTAATGAGAGTATATACAATTTACTTCTGGACAATGGAGCTAATCCTGATCACAGGGACAC
ATTCGGAAACATGATTCTTCATATGGTTGTGGTCTGTGACAAACTTGATATGTTTGGATATGCTCTCAGGCATCCCA
AGATGCCTGCTTCAAATGGGATAGCTAATGTCGCAGGCTTAACACCTCTTACTCTTGCCTGCAAACTAGGGCGTGCG
AAGGTCTTTCGAGAAATGTTGGAATTGAGTGCCAGAGAATTCTGGAGATACAGCAATATTACATGCTCTGCTTATCC
ATTGAATGCGCTTGATACACTGCTCCCTGATGGCAGAACAAACTGGAATTCAGCTCTCTTCATAATTCTAAATGGAA
CAAAAGAAGAGCACTTAGATATGTTAGACGGAGGTATAATTCAAAGGTTGCTAGAAGAAAAATGGAAARCATTTGCA
AGGAGGCAGTTTTTAAAACGGCTAGTAATCCTAATGCTTCATTTACTCTGCCTGAGCGGAGCAGTTTATCTTCGCCC
AACAGACAGAACTAAACCACTCTTAGGAGGAGATGATTGGAAATCAGTAGCGAGGCAAGGTTTTGAAGTAGCAACTG
TTTTAGGTGTTCTTTCGTATGTTATAGTACAGCAAGGAGGAGAAATAAGGAACCAGGGATTTATATCTTTCATCAAA
CAACTGGACYCAGCTAAAGCCATCTTCCTTGTATCAAATATCTTGATATTAATATGTATCCCATTTCGATTGATGGA
TGACAAAAGAACTGAGGAGGCAATATTAGTATTTGCAGTGCCTGGATCATGGTTCTTACTCATGTTTTTTGCAGGTG
CAGTGAGATTAACGGGACCATTTGTAACAATGGTATATAGTATGATAGTTGGAGACATGTTTACTTTTGGTATAATT
TATTCTATTGTGCTCTTTGGATTTTCCCAATCATTCTATTTTCTGTACAAAGGATTTCCAGGAGTTAAAAATACTCT
TTACAGCTCATACCACAGCACATGGATGGCTTTATTTCAGATCACTCTCGGTGATTATAATTATGCTGAATTGTCGC
ATACTTCATACCCGACATTAAGTAAGACAGTGTTTGCTATCTTCATGATTCTAGTCCCTATACTTCTGCTTAACATG
TTAATAGCTATGATGGGAAATACTTATGCCCATGTGATTGAACAAAGCGAGAAAGAATGGATGAAACAGTGGGCCAA
AATTGTGGTTTCACTGGAAARAGCGGTAAACCAGGAAGATTGCAAACAATATTTACAAGAATACAGCATAAAGCTAG
GACCTGGAGATGACCCATCGACAGAACAGCGTGGAGTAATGGTTATAAAAAGTAAAAGTAAAACCAGAGCTAAACAA
AGGAAAGGAGCTGTAGCTAATTGGAAGAGAGTGGGCAAGGTAACAATCAATGAGCTTAGAAAACGAGGGATGAACGG
AGAACAATTAAGAAGAATAATGTGGGATAGAGCTTCAATATCAACACCAGTTAAAGTACCTCAAAACCCTGTAGTAG
ATGTATTAATGGAAAACACGGCAGAACAACAAGCCCAACAAACTCCAGGAAGTTTTGGAGGAGCATTAACTGCAGCA
CTTGATGTAATGGCTTTCACACATGATTTAGATTTATCAGCATCTGGAATCACTTCTTCCGGCTTAAATGCAAAAGA
ACTTATTGTTAGCGATCCCTTCCGTGATCTGGTGTTGAGCTCCGAAATAGATGTGGGAGAGGAAGAATTGGCAACAC
TTGCGGAAGCTGCTGTTCTATCGGTGATGTCAGGCCAATCTGATGAATCAGAAAAACTAAAAATAGCTAAATTTAAT
AAGCAAATCAGTTTTGAACAGAATGCAGTTCTTGAAGTGAGTGACAGCGATGGATTCCTAGATGGCCAGCCATTGGG
TCAAGGATCACGAGCAAGAAAAGTTAAATCAGCTCAAGAGAGGCAAAGAGCAGAGAGGACGTGGGGTGGAACAAGCA
TATCGTCAATAGAGGAACCACCACCATACCTCCCTTTACCTCCCCCACCACCACTGCATTCCCATCAACGACCAAGG
CCCAAAACTGCGAAACCTAACAGAGTCGTCCCAGAAGCAGTGGTAGCAAAGCGTCCACAGAGCTCAGCTTTAGGGGA
CAGGGTTAAGTCCCCACCAGAACTCCTTGAACCATGGAGCACAAGAGGCATTGCAACCATAAATACAATACTTGCTT
GGCAACCTTCTGATCAAGATAGCATGTAG

FIGURE 90 – SEQ ID NO: 81

<> 2
<> 1123
<> PRT
<> Drosophila melanogaster
<> NP_572353.1
<> ?
>gi|24640231|ref|NP_572353.1| inactive [Drosophila melanogaster]
MKFLLKKCLRKKAPEMKPGAILDAVISQSSATACKCLLYKLADYKRGGDLIDAINSGGLIAVEQLIREQFGVFMYND
GKGQVINRAEFLRWKYRDHTEVTIPIEASLSIHDPLGKWEDHKACWQMQYRGALGESLLHVLIICDSKVHTKLARVL
LRVFPNLALDVMEGEEYLGASALHLSIAYSNNELVADLIEAGADIHQRAIGSFFLPRDQQRANPAKSTDYEGLAYMG
EYPLAWAACCANESVYNLLVDCGSDPDAQDSFGNMILHMVVVCDKLDMFGYALRHPKTPAKNGIVNQTGLTPLTLAC
KLGRAEVFREMLELSAREFWRYSNITCSGYPLNALDTLLPDGRTNWNSALFIILNGTKPEHLDMLDGGIIQRLLEEK
WKTFAQNQFLKRLLILSTHLLCLSVSVYLRPAHDGEAEDEDSEGSDASAAALLDIQSDEGDSGGGDYNAQTVARYCA
EFATLVGVLSYVIFQQGDEIKNQGLSAFLKQLSHAPAKAIFLFSNLLILACIPFRLIGDTDTEEAILIFAVPGSWFL
LMFFAGAIRLTGPFVTMIYSMITGDMFTFGIIYCIVLCGFSQAFYFLYKGHPQVQSTMFNTYTSTWMALFQTTLGDY
NYPDLNQTTYPNLSKTVFVIFMIFVPILLLNMLIAMMGNTYVTVIEQSEKEWMKQWAKIVVTLERAVPQADAKGYLE
AYSIPLGPSDDSGFEVRGVMVIKSKSKTRAKQRKGAVSNWKRVGRVTLTALKKRGMTGEEMRRLMWGRASISSPVKV
TKQKLKDPYNLHTDSDFTNAMDMLTFASNPASSNGVTLRSVTAPPPAPPAPDPFRELIMMSDQRPETHDPHYFAGLQ
QLANKAFDLVEQTMKTQPQAPVAKKVDPLPVASVAKASPAAPATQATATAAAASDLMAMPLPISNLSNLFQDPKDIV
DPKKLEEFMAMLAEVETEESDSGGPILGKLSLAKRTHNALSKAEIRRDQQGFEGHSHGQFQPMSSVWAPPGLDVDTG
FHFDEAVAEEVLTIEQEAEVETEDGNGGQDSEDIPTAEEVHATMKQFHLRKCQPAQDEAARRAKSARVRRRNKVSPE
QSDDPDERSQRGRSAYTRRTQSPPDPLEPWSTRELQDINKILARK

FIGURE 91 – SEQ ID NO: 82

<> 4
<> 1128
<> PRT
<> Musca domestica
<> XP_005181017.1
<> ?
>gi|557762606|ref|XP_005181017.1| PREDICTED: uncharacterized protein
LOC101887788 [Musca domestica]
MRLFMKKCLRKKPQELKPGAILDAVISQSSATASKCLLYKLADYKRGGDLIDAINTGGLVAVEQLIREQFGIFMYND
GKGQVINRAEFLRWKYRDHTEVTIPIEASLSIHDPLGKWKDHSACWQMQYRGALGESLLHVLIICDSKMHTKLARIL
LRVFPRLALDVIEGEEYLGASALHLAIAYSNNELVADLIEAGADINQRAIGSFFLPKDQQRANPAKSTDYEGLAYMG
EYPLSWAACCANESVYNLLLIDHDADPDAQDSFGNMILHMVVVCDKLDMFGYALRHPKTPAKNGIVNHSGLTPLTLAC
KLGRAEVFREMLELSAREFWRYSNITCSGYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEK
WKTFAQNQFLKRLLILVVHLLCLSTSVYLRPAHDGDDDEEDETAQANAGLQTNDPENEEYDIQTIVRYCAELCTIAG
VLSFLIFQQGDEIKNQGLSAFLKQLSHAPAKVIFLVSNLMILACIPFRLMGDTDTEEAILIFAVPGSWFLLMFFAGA
IRLTGPFVTMIYSMITGDMFTFGIIYSIVLCGFSQAFYFLYKGHPQLQSTMFDTFPSTWMALFQTTLGDYNYPDLNQ
TTYPNLSKTVFVIFMIFVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVTLERAVPQADAKNYLEAYSIPLG
PSDDSGFEVRGVMVIKSKSKTRAKQRKGAVSNWKRVGRVTLNALKKRGMTGEEMRRLMWGRASISSPIKVAKKKLKD
PYNLNQEPGGQSNLTSAMDMLNFANDPASSSGLAFRTSGTQDPKEKKDVPHIPAPDPLRDLVLLAEEKPEVHDPQFY
SALIQLANKAYDLVKKTLETQHQPQVEEPIPLTEATSLKDVTLTKQPDPVAADAGLLGDMAMGANLTNLFQDPKDIV
DPKKLEQFLKMVADVETEESDGGGPILGKLSLARRTRNALFKVPIPKSTLGDSSDKLINSVWDKVPADNDEDSIPAF
DFQEALAEHVLTVEQEADVETEDANDDSGETMDDIPTAEEVHATMKQFHLRKRQYQQDDAARRAKTARIRRKNKVAP
DYAGSEEQYGRGRSAPMKKKHDEDEMSPPDPLEPWSTRELQNINKILAKK

FIGURE 92 - SEQ ID NO: 83

<> 6
<> 1144
<> PRT
<> Ceratitis capitata
<> XP_004529475.1
<> ?
>gi|498980910|ref|XP_004529475.1| PREDICTED: uncharacterized protein LOC101456642 [Ceratitis capitata]
MKFFLKKCLRKKPEEMKPGAILDAVISQSSPMANKCLLYKLADYMRGGDLIDALNTGGLVAVEQLIREQFGIFMYND
GKGQVINRAEFLRWKYRDHTEVTIPIEASLSRHDPLGKWEDHKACWQMQFRGALGESLLHVLIICDSKIHTKLARVL
IRVFPNLAQDVMEGEEYLGASALHLAIAYSNNELVADLIEAGADINQRAIGSFFLPRDQQRRNPAKSTDYEGLAYLG
EYPLAWAACCANESVYNLLVDCGADPDAQDSFGNMILHMVVVCDKLDMFGYALRHPKTPAKNGIANHSGLTPLTLSC
KLGRAEVFREMLELSAREFWRYSNITCSGYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEK
WKTFAQNQFLKRLLILVIHLVFLSISVYMRPARVADDDDEDEIDASSKDTKALELATELDEDEYDVQTIVRYCAEFG
TIVGVLSYVIFQQGDEIKNQGLPAFLKQLTHAPAKAIFLVSNLLILACIPCRLMGDTDAEEAILIFAVPGSWFLLMF
FAGAIRLTGPFVTMIYSMITGDMFTFGIIYCIVLCGFSQAFYFLYKGHPQIQSTMFNTFPSTWMALFQTTLGDYNYP
DLNNTTYPNLSKTVFVIFMIFVPILLLNMLIAMMGNTYAQVIERSEKEWMKQWAKIVVTLERAVPQADAKNYLEAYS
IPLGPIDDSGYEVRGVMVIKSKAKTRAKQRKGAVSNWKRVGRVTLNALKKRGMTGEQMRRLMWGRASISSPIKITKK
KLKDPYNLNPQNDLTSAMDMLTFANDPAASAGLQLRSSLMDSGAEGKAAKVQEENQQPAPDPLRDLIFLADRRPEMH
DPQYFVGLQQLANQALDLVEQTMGIHPPPTPATDALLLSAAAATTTIGAVTMQTATTVAAPSADLITPLGANLTTLF
QDNKDVVDPQKLQEFLKMLAEIETEESDGGGRPILGKLSLSRRTKSALSKAQIKKDTVGGSPDKLIPSVWSHNLPQP
DEEPEFNFEAALAEEHTLTIEQEAEVETETGNEREDSEDCPTVEEVHATMKQFHLRKRQYQQDDAARRAKSARIKRK
NRISPEQSHECDDGSSGGGGGKSTHPRGASAPGRKHTVSERLSPPDPLEPWSTRELQNINKILARK

FIGURE 93 - SEQ ID NO: 84

<> 8
<> 1120
<> PRT
<> Aedes aegypti
<> XP_001659888.1
<> ?
>gi|157121231|ref|XP_001659888.1| hypothetical protein AaeL_AAEL009258 [Aedes aegypti]
MVQFDWRRMCRKKRKVPQGGAILDQVISQSANASNQCLLYKMANYKRGGDLIDAFQVGGQKAVEQLIREQFGVFMYN
NGRGQIINRAEYLRWKYMDNHEVVIPIEASLSPHDPLGKWVDHKACWQMQYRGLLGESLLHVLIICDTKIHTKLARI
LLRVFPELSIDVMEGEEYLGASALHLAIAYSNNELVGDLIDAGADVSQRAIGRFFLPRDQQGLKPAKNTDYEGLAYL
GEYPLAWAACCANESVYNLLLECGADPNAQDSFGNMILHMVVVCDKLDMFGYALRHPKLPCKNGIVNESGLTPLTLA
CRLGRDEVFREMLELSAREFWRYSNITCSGYPLNALDTLMPDGTTNWNSALFIILNGTKEEHLNMLDGGIVERLLDE
KWKTFARNQFIKRLLILALHLFCLSCSVYLRPVRVFKEESEEGSDGGDGAGTAAPDGVDDDEDIDLTTWFRYGFEIA
TVMGVLSYVVLQQGDEIKNQGLISFIKSLGNAPAKAIFLISNLMILACIPFRMMGDVEHEEAILLFAVPGSWFLLMF
FAGAIGLTGPFVTMIFSMITGDMFTFGIIYMIVLFGFSQAFYFLYKGHPEAEDSPFGSYFGTWMGLFQTTLGDYDYA
DLNLTTYPNLAKTVFIIFMIFVPILLLNMLIAMMGNTYAYVIEQAEKEGMKQWAKIVVNLERAVKQEDAKKYLEEYS
IGLGPSDDPRYEIRGVMVIKSKSKTRARQRKGAVSNWKSVLRVTLNELKKRNMTGEELRRIMWGRSSITSPAKISKK
KKIYEEEDPFAITNAIDVMSFTQDIVMVSSEPTGPPTIDPSKPATIAVKPQTAPAAQPIPEIPPQPPLVKRQSVVSA
PPAYDDFPPMKDYKDPLRELVIISESPSVDDHYVQSCKTLANDASTLDHDTLGQLNPFLEAKDVVDPVKEREFLKTL
EALEDTDSEAAEKPVLGKISLIRRAKSAVSRTTSRKKKTDQHPLFTIAWDDKNLTRTHPEDFGALNTAYEYSAEDFK
QDVDEEAREEEEDEGVTVEEVHRRMEELHHRGRASLERDSNSTESSKKHPHRKRQGMGRGRNNKVSPDTSNESVSGK
KDKRMKSAPTGGGTSPPDPLEPWSTRDICNINKLLDTDTQDE

FIGURE 94 - SEQ ID NO: 85

<> 10
<> 1137
<> PRT
<> Culex quinquefasciatus
<> XP_001864325.1
<> ?
>gi|170057087|ref|XP_001864325.1| OSMotic avoidance abnormal family member [Culex quinquefasciatus]
MVKFDWRRMCRKKKNVPQGGAILDQVISQSTNVQGQCLLYKMANYKGGGDLIDAFKMGGQKAVEQLIREQFGVFMYN
AGRGQIINRAEYLRWKYMDNHEVVIPIEASLSPHDPLGKWVDHKACWQMQYRGLLGESLLHVLIICDTKIHTKLSRI
LLRVFPELSIDVMEGEEYLGASALHLAIAYSNNELVGDLIDAGANVSQRAIGRFFLPRDQQKMHPAKTTDYEGLAYL
GEYPLAWAACCSNESVYNLLLECGADPNAQDSFGNMILHMVVVCDKLDMFGYALRHPKLPCKNGIVNEAGLTPLTLA
CRIGRDEVFREMLELSAREFWRYSNITCSGYPLNALDTLMPDGSTNWNSALFIILNGTKEEHLNMLDGGIVERLLDE
KWKTFARNQFLKRLLILALHLFCLSCSIYLRPVHVFKDDDDADDTDGVTDSPDTTDDEGIDLTTWFRYGFEVATVMG
VLSYVVVQQGEEIKNQGFISFLKSLAGAPAKAIFLISNLMILCCIPLRILGDREAEEAVLLFAVPGSWFLLMFFAGA
IGLTGPFVTMIFSMITGDMFTFGIIYTIVLFGFSQAFYFLYKGHPNADESPFGTYFGTWMGLFQTTLGDYDYADLNL
TTYPNLAKTVFITFMIFVPILLLNMLIAMMGNTYAYVIEQAEKEGMKQWAKIVVNLERAVKQEDAKKYLEEYSIGLG
PSDDPRFEIRGVMVIKSKSKTRARQRKGAVSNWKSVLRVTLNELKKRSMTGEELRRIMWGRSSITSPAKISKKKKIY
DEDEDPFAITAAIDVMSFTQDIVMVSTEPVGPLMIDPTKPPVTTVKPTAPTVPSAQPAPGVPMTTAQTAAPTAPQLV
KRQSVVSAPPAYDDFLPAKGFKDPLRELLILSESTSIDEHYAQTCRSLATDASTLDHEEHQQQQQQTVGQLNPFLDA
KDVVDPVKEREFLKTLEALEDTDSEAAEKPVLGKISLIRRARSAVSRTTSRKKKTDQHPLFMIAWDDKTTTIPGGGP
QAVSATAGTAAPEDDFGALNTAYECSAEDLKHDVDEEAREDDPDEGVTVEEVHRRMERFHQRPGRSSPERDSNSTES
SKKQAKGDKRMKSAPSGHGPRHRQMMDTGGGSPPDPLEPWSTKEIVPINKLLDTDTQDE

FIGURE 95 - SEQ ID NO: 86

<> 12
<> 1216
<> PRT
<> Anopheles gambiae
<> XP_310685.5
<> ?
>gi|347963769|ref|XP_310685.5| AGAP000413-PA [Anopheles gambiae str. PEST]
MVHLDPLRLCRKKRKLPQGGAILDQVISQSASASNQCLLYKMANYKRGGDLIDAFQIGGQKAVEQLIREQFGVFMYN
KGRGQIINRAEYLRWKYMDNHEVIIPIEASLSPHDPLSKWDDHKACWQMQYRGLLGESLLHVLIICDTKVHTKLARI
LLRVFPEQSIDVMEGEEYLGASALHLAIAYSNNELVGDLIDAGADVSQRATGRFFLPRDQQGLRPAKTTDYEGLAYL
GEYPLAWAACCANESVYNLLLECGADPNAQDSFGNMILHMVVVCDKLDMFGYALRHPKLPCKNGIVNAAGLTPLTLA
CRLGRDEVFREMLELSAREFWRYSNITCSGYPLNALDTLMPDGSTNWNSALFIILNGTKEEHLNMLDGGIVERLLDE
KWKTFARNQFIKRLLILAIHLFCLSCSVYLRPVRVFADDEGEEGGDATDDDGADDGGPMAVDAVDDDIDLTTWVRYG
FEVATVMGVLSYVVLQQGDEIKNQGFFSFLKSLSQAPAKAIFLISNILILACIPLRMMGDTETEEAILLFAVPGSWF
LLMFFAGAIGLTGPFVTMIFSMITGDMFTFGIIYMIVLFGFSQAFYFLYKGHPNAEDSPFGSYFGTWMALFQTTLGD
YDYADLNLTTYPNLAKTVFVIFMIFVPILLLNMLIAMMGNTYAYVIEQAEKEGMKQWAKIVVNLERAVTQDDAKRYL
EEYSIGLGPSDDPRYETRGVMVIKSKSKTRARQRKGAVSNWKSVLRVTLNELKKRSMTGEELRRIMWGRSSITSPAK
IAKKKRPGEVDDLLGDPFAITAAIDVMSFTQDIVMVSTDTVCPITIPPAAAPGTAAPKAGGTKPVVVAPPPPAAATA
VQQPPPPATTRRHSTASAPATMGLGVEAALPGYKDPLRELVIISESASVDENYAQNVKTLAIDASTLDHVHEIDISQ
QQQQQQQQQQQQPQQPQQQQNLGQLTLFQNPKDVVDPVRREREFLKTLEALEDTDSEAGEKPVLGKISLIRRAKSAVS
RSTSRKRKTDQHPLFMIAWEDKGDQQRHSTALYDGATGAAPSVGAPGELGQPEQPEDAVTVEELHRRMEQFHQRASV
RERDANSSESGSGKQHAGPKARKPSHHRDGGGSHHHHGLGRGKHNKISPDNSNESTGGGGGGGASGHGRKQDKRMKS
APILGSGGAGSAGSSAGGRTVAPGGARPDDGTGSPPDPLEPWSTKNIMNINKLLDQDTTEE

FIGURE 96 - SEQ ID NO: 87

<> 14
<> 1086
<> PRT
<> Tribolium castaneum
<> EFA10736.1
<> ?
>gi|270014288|gb|EFA10736.1| hypothetical protein TcasGA2_TC012368 [Tribolium castaneum]
MGAKVCKPCKKRKANTFQGGSILDRVISQASNQDQCLLYKLANYKKGGELIDAYNQGGQAEVEKLIREQFGQLMYQE
GKGQIINRSEYLRWKFRDHEQVILPIEASLSRYDPLAKWNDHEACWQMQFRGSLGESLLHVLIICDTKIHTRLARTL
IKCFPKLALDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGANVNQRAIGSFFLPRDQQRQKPAKHTDYEGLAYLG
EYPLAWAACCANESVYNLLLDSGAHPDYQDNFGNMILHMVVVCDKLDMFGYALRHPKLPASNGIVNKAGLTPLTLAC
KLGRAEVFREMLELSAKEFWRYSNITCSAYFLNALDTLLPDGRTNWNSALFIILNGTKEEHLAMLDGGIIQRLLEEK
WKTFARNQFLKRLLILVVHLLFLSLAVYLRPDDPDESLLTWSDDVTLIARYVCEVGTILGVLSYLVLQQGDEIRNQG
LTAFLKQQLNSPPKLIFLISNFLILACIPCRLYGDKETEEAILCFAVPGSWFLLMFFAGAVRLTGPFVTMIYSMITG
DMLTFGIIYTVFLFGFSQSFYFLYKGFPGVKTSLYNTYMSTWMALFQITLGNYEYSELSATTYPAVSKTVFAIFMVF
VPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVIALERAIPQSDAQHYLQEYSISLGPSEQDPSTEKRGVLVIK
SKSKTRAKQRKGAVANWKRVGKVTINALKKRGLTGEEMRCLMWGRESINTPVKTKKPVKDPLLDPQGPNLTGGFGDA
LTTALDVMTFTHDLDIVGASQGLNLATNPKPVPPTTTASAVTVNNQINSALNAQQKAVAGAGVGALAMIGTVTQLTD
SQGYIMQNSVKKEEKIVATLEDPFRELVINANDSNCDPEKLKMLALSAANLKDVEELSVAKPQTKSVKSLAGIFAGT
ETFVRKVEETIKKKYAALDPSDSEGFGEPPLLGKISRTRRAKSANLRNSSARSKASDKKKLVAGSQSSSTDTVNNEI
NEKNIENSDLDYAEERIKLVKESLKQVVDVAQIRPINIDVALEEQVSVTISETMRVQGSGDGAEVQSSNVKPKRKKR
SKTAKNNK

FIGURE 97 - SEQ ID NO: 88

<> 16
<> 1101
<> PRT
<> Megachile rotundata
<> XP_003704666.1
<> ?
>gi|383858353|ref|XP_003704666.1| PREDICTED: uncharacterized protein LOC100877549 [Megachile rotundata]
MGGVCSCRGLGSQVNAGSILDRVISQASDEDQCLLYRLANYKKSGELIDAYNQGGQAEVEKLIREQFGVLMYADGKG
QMINRAEYLRWKFRDLEQVVLPIEASLSRFDPLAQWNDHQACWQMQYRGSLGETLLHVLIICDTRLHTRLARILLKC
FPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEVGAIISQRAIGSFFLPRDQQRMNPAKNTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYALRHPKLPARNGIVNAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLNMLDGGIIQRLLEEKWKT
FARLQFLKRLIILVFHLTSLSLAVYLRPSNLDTVLLKWPEEVTEVGRTIAECITVLGVLSYILVQLGGEIINIGVLS
FLKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILVVAVPGSWFLLMFFAGAIRLTGPFVTMVYSMITGDML
TFGIIYMVVLFGFCQSFYFLYKGFPGVKSSLYSSYHSTWMALFQVTLGDYNYTDLSYTTYPNLSKMVFTIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAVSQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLVIKS
KSKTKAKQRKGAVANWKRVGKVTINELRKRGMTGEELRRIMWGRASFSTPVRVSPNVDEPQVSAVTAGFGDALTAAL
DVMAFAHDLDLSTATESIPTNIDVKQSKPKVVSSEQTKLTTNNQEKPSITEKAATEIANKQVNAKDETNKKPNEVVD
VEKMNVKNANNSSTVEEYHDLFLEFVIASESMNDPETLLKMAERVAAEFDSSANPKINLQILEQFTMTKIPMEEQAA
AVKKQYFIESSDNDFGGDNLLGTVARLRRIRSANSRFITARRHSRHVNDDMSSTSSASGDGNPRYQQLLNDTEEVPS
NQRTENRDESIVANKSEVKQNDANCGSRCKAQKRRPKTARNRVSPKETEDSGQRRRESMERNKAVSPATSPTDPLEP
WSTRGIKDMNTILAWEENVPDSP

FIGURE 98 - SEQ ID NO: 89

<> 18
<> 1101
<> PRT
<> Apis mellifera
<> XP_001121881.1
<> ?
>gi|110748981|ref|XP_001121881.1| PREDICTED: hypothetical protein LOC726119 [Apis mellifera]
MGGVCSFRGRGSQVNAGSILDRVISQASDEDQCLLYRLANYKKGGELIESYNQGGQFEVEKLIREQFGVLMYADGKG
QVINRAEYLRWKFRDLEQVVLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTRVARILLKC
FPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAIISQRAIGSFFLPRDQQRTNPAKNTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYALRHPKLPARNGIVNAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWKT
FARLQFLKRLIILAFHLTSLSLAVYLRPSNTDAQLLKWPEEITEVARTIAECITVLGVLSYILVQLGGEIINIGLLS
FMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILIVAVPGSWFLLMFFAGAVRLTGPFVTMVYSMITGDML
TFGIIYMVVLFGFCQSFYFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLSYTTYPNLSKMVFAIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAVSQKDAQNYLQEYSIKLGPGDDPNNPAAEQRGVLIIKS
KSKTKAKQRKGAVANWKRVGKVTINELKKRGLTGEELRRIMWGRASFSTPVRVSPKGVEPQVSVVTAGFGDALTTAL
DVMTFAHDLDLSTATEGIPTNIDAKQSKPKSATKETKSTVNNQQNVTTNIEPLKSTTENVDDQANNPREKKVTSQAA
TVHEMNLKNANHSSVTEDFQDPLLELVIASENTNDPETLLEIAKRAAAGFETETSSKINLQILEQFTMTKIPMDEKV
NVTRKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTRRRSRNVDDDLSSTSSTSMDRNPRYQSLLNGHENSI
DRPIESRECSIEAINSQIKQNGPCETMKAKVQKKRPKTARNRVSPKEIEKAGPRRRESIERNKAVSPATSPTDPLEP
WSTRGIKDMNTILAWEETAPDSP

FIGURE 99 - SEQ ID NO: 90

<> 20
<> 1105
<> PRT
<> Apis florea
<> XP_003690727.1
<> ?
>gi|380013353|ref|XP_003690727.1| PREDICTED: uncharacterized protein LOC100868270 [Apis florea]
MGGVCSFRGRGSQVNSGSILDRVISQASDEDQCLLYRLANYKKGGELIESYNQGGQFEVEKLIREQFGVLMYANGKG
QVINRAEYLRWKFRDLEQVVLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTRVARILLKC
FPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAIISQRAIGSFFLPRDQQRMNPAKNTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYALRHPKLPARNGIVNAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWKT
FARLQFLKRLIILAFHLTSLSLAVYLRPSNTDAQLLKWPEEITEVARTIAECITVLGVLSYILVQLGGEIINIGLLS
FMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILIVAVPGSWFLLMFFAGAVRLTGPFVTMVYSMITGDML
TFGIIYMVVLFGFCQSFYFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLSYTTYPNLSKMVFAIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAVSQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLIIKS
KSKTKAKQRKGAVANWKRVGKVTINELKKRGLTGEELRRIMWGRASFSTPVRVSPKGVEPQVSVVTAGFGDALTTAL
DVMAFAHDLDLSTATEGIPTNIDAKQSKPKSAIKEQMKLTTNNQENVSTNVEPQLKSTTENANDQANNPREIKKVTN
QVTGIHEMNLKNANHSSVTEDFQDPLLELVIASENTNDPETLLEIAKRAAAGFETEASSKINLQILEQFTMTKIPME
EKVSVTRKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTRRRSRNVDDDLSSTSSTSMDRNPRYQSLFNGHE
NSIDRPIESRECSMEAINSQIKQNGPPCETVKAKVQKKRPKTAKNRVSPKEIEKAGPRRRESIERNKAVSPATSPTD
PLEPWSTRGIKDMNTILAWEETAPDSP

FIGURE 100 - SEQ ID NO: 91

<> 22
<> 1055
<> PRT
<> Pediculus humanus corporis
<> XP_002432382.1
<> ?
>gi|242023927|ref|XP_002432382.1| conserved hypothetical protein [Pediculus humanus corporis]
MGAGLCGTSQDPQNQGSVLDRVISQASNKDDCLLYKLANYKNSGELIEAYNIGGQAEVEKLIKEQFGVLMYADGKGE
VIKRAEYLRWKFRDQAQVVLPIEASLSIYDPLAKWEDHEACWQMQYRGSLGETLLHVLIICDSKIHTKLARTLLKCF
PKLALDIVEGEEYLGASALHLAIAYNNNELVEDLVDAGANINQRAVGSFFLPKDQQRAKPLKTTDYEGLAYLGEYPL
SWAACCSNESVYNLLLDVGADPDSQDSFGNMILHMVVVCDKLDMFGYALRHPKVPASNGIINNEGLTPLTLACKLGR
ADVFKEMLELSAKEFWRYSNITCSAYPLNALDTLLPDGRTNWNSAIFIILNGTKEEHLDMLDGGIIQRLLEEKWKTF
ARNQFLKRLVIFFLHIFCLSGSVYLRPDDRNKPLLGGTSVQDVVRYCFEIGTILGVLCYLCFQQGDEIRNQGLISFL
KQLPHDPAKFIFLISNLLILACIPYRVAGDTDTEEAILVFAVPSSWFLLMFFAGAIRLTGPFVTMIYSMITGDMLTF
GIIYSVFLFGFSQSFFFLYKGSKNVSSSLFTSYPSTWMALFQVTMGDYNYNDLSLTAYPAISKMVFTIFMVLVPILL
LNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVALERAVNQEDCHRYLQEYSIKLGPGDDPSTEQRGVLVIKSKSKTR
AKQRKGALCNWKRVGKVTIRELHKRGMTGEQLRRLMWGRSSISTPVKPAPIKLGHVTSISGVADITVPETTGNTVGT
GGGGLLAALDVMAFTNDLEFSSENQTSTSFKTQPQPSEVSCVESDSNSDPLYNDPLRQLNEELNKTREEILTLARVA
ANNDGIEEIPPQICQYGWINNYNFFGNTFAQNQKVEDPVQQPTFQSTPNHSDSDGLGDGLLLGSNRRLKRTRSANIK
RKFSGSSTNEKNLLEPEDSSSTNSEDFSCLTENYINKNIKVNANFSENSLRSNRSSANLVVKKFGRRSGLKSSTNRI
APADLSPVGNVSKYSETLCNSYCITSSSDVLYQWSIKGITNMNTLLGLENEDSM

FIGURE 101 - SEQ ID NO: 92

<> 24
<> 1109
<> PRT
<> Acromyrmex echinatior
<> EGI60788.1
<> ?
>gi|332020367|gb|EGI60788.1| Transient receptor potential cation channel subfamily V member 6 [Acromyrmex echinatior]
MGGVCSCRVGRNSQVNAGSILDRVISQASNEDQCLLYRLANYKKGGELIEAYNQGGQPEVEKLIREQFGILMYMDGK
GQIINRAEYLRWKFRDLEQVVLPIEASLSRFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRMHTRIARILLK
CFPRLAIDVVEGEEYLGASALHLAIAYANNELVQDLVEAGAIISQRAIGSFFLPRDQQRMNPARNTDYEGLAYLGEY
PLAWAACCANESVYNLLLDSGADPDEQDTFGNMILHMVVVCDKLDMFGYALRHPKLPARNGIVNAAGLTPLTLACQL
GRAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWK
TFARLQFLKRLIILVFHLASLSLAMYFRPADMEAVLLQWPEEITDVVRTAAECITVLGVLNYILVQLGCEMINVGPL
SFLKQLSHEPAKLIFVISNLLILACIPCRIAGDRHAEDAILMFAVPGSWFLLMFFAGAIRLTGPFVTMVYSMITGDM
LTFGIIYTVMLFGFSQSFYFLYKGFPGVKSSLYHSYPSTWMALFQITLGDYNYADLSNTTYPNLSKTVFAIFMVLVP
ILLLNMLIAMMGNTYAHVIEQSEKEFVKQWAKIVVSLERAVSQKDAHNYLQEYSIKLGPGDDPNNPASEQRGVLVIK
SKSKTRAKQRKGAVSNWKRVGKVTILELRKRGMTGEELRRIMWGRASFSTPVRVSPNAGQPQVSAVTAGFDDALTAA
LDVMAFAHDFDLSTATEGIPTNIDAKQIKTAQSKAALNDQQTKTTQNNPEVVINVQPHNQPIKEETKLSGLTDLIDK
SIDPVKDVEAMNLRNMNQTKALEETVEDPFLELAIASETTTDYKTLLQIAKSALATSEASMKTTIDPQILAHFAMVA
PPTIEKSSIVKKQYFMESSDNDLGGDNLLGTEARLRRIKSANNRFTTSKRSRRDDDGDSSSSTTSVEQSLRYRPLLN
DPEQRPMNRIETEGRKTTVETIKPEVKQNGSIPTKPLDKIQKRRPKTAKNRVSPKETEEPARRRESIERNKAASPPT
SSSDPLEPWSTRGITDMNTILAWRENAPDSP

FIGURE 102 - SEQ ID NO: 93

<> 26
<> 1112
<> PRT
<> Harpegnathos saltator
<> EFN84766.1
<> ?
>gi|307206920|gb|EFN84766.1| Transient receptor potential cation channel subfamily V member 6 [Harpegnathos saltator]
MGGVCSCRGRGSQVNAGSILDRVISQASNEDQCLLYRLANYKKGGELIEAYNQGGQPEVERLIREQFGILMYADGKG
QVINRAEYLRWKFRDLEQVVLPIEASLSRFDPLAQWYDHEACWQMQYRGSLGESLLHVLIICDTRMHTRIARTLLKC
FPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAIISQRAIGSFFLPRDQQRMNPVRNTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYALRHPKLPTRNGIVNAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGVIQRLLEEKWKT
FARLQFLKRLIILVFHLASLSLAVYFRPADMDAELLQWPDEITDAARIAAECSTVLGVLSYILVQLGGEMINIGPLS
FLKQLSHEPAKLIFVISNLLILACIPCRIAGNRHAEDAILVFAVPGSWFLLMFFAGAIRLTGPFVTMVYSMITGDML
TFGIIYTVMLFGFSQSFYFLYKGFPGVKSSLYHSYPSTWMALFQITLGDYNYADLSNTTYPNLSKTVFAIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEFVKQWAKIVVSLERAVSQKDAHNYLQEYSIKLGPGDDPNNPASEQRGVLIIKS
KSKTRAKQRKGAVANWKRVGKVTINELRKRGMTGEELRRIMWDRASISTPVRVSPNVNEPQVSAVTAGFGDALTAAL
DVMAFAHDFDLSTATEGVPSNIDTRQTKAIPDEQTRTARNNPKAVTDVQPHKQAIGGEETKLSGLTDLIDMSAAEPA
RVEAMNLKNASQAKAHEGAVEDPFLELAIASETTEDYDTLLQMAKSALATSEASTTVDPQILAHFTMIAPPPVEKPI
VVKKQYLVESSDNDLGGDNLLGTEARIRRIKSANDRFISTSKRSHHDDDNDSSSSVTSVDRSQPQYRPLLNDSEESL
ANRVENEGRRTSDVETIKSEVKQNGRGGGGGGVSKPSDKRVQKRRPKTAKNRVSPKEIEEPARRREESIERNKAALS
PPASPSDPLEPWSTRGITDMNTILAWRENAPDSP

FIGURE 103 - SEQ ID NO: 94

<> 28
<> 1104
<> PRT
<> Bombus impatiens
<> XP_003485699.1
<> ?
>gi|350399983|ref|XP_003485699.1| PREDICTED: hypothetical protein LOC100747394 isoform 1 [Bombus impatiens]
MGGVCSCRGRGSQVNAGSILDRVISHASDEDQCLLYRLANYKKGGELIESYNQGGQAEVEKLIREQFGVLMYADGKG
QAINRAEYLRWKFRDLEQVVLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTRLARILLKC
FPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAIISQRAIGSFFLPRDQQRTNPAKNTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYALRHPKLPARNGIVNAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWKT
FARLQFLKRLIILVFHLTSLSLAVYMRPSNIDATLLEWPEEITEVGRMIAECTTVIGVLSYILVQLGGEVVNIGLLS
FMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILVVAVPGSWFLLMFFAGAIRLTGPFVTMVYSMITGDML
TFGIIYMVVLFGFCQSFYFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLGYTTYPNLSKMVFAIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAVAQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLIIKS
KSKTKAKQRKGAVANWKRVGKVTINELKKRGITGEALRRVMWGRASFSTPVRTSPNTAEPQVSAVTAGFGDALTAAL
DVMAFAHDLDLSTATEGIPTNIGAKQSKSKTACKDQAKSATNNQEKGSTDVQQQRKLTTENLDNLASSHNDIDKTSS
EFVAVREMNSKNASHSSMAEDFQDPLLELVIASENTDDPETLLKIAERAAANFEVESSSKINLQILEQFTMTKLPME
EKVAATKKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTRRRSRHTDDDLSSTSSTSADRNPQYQPLLNGPE
NLASRQIESRESSIEAIKPQVKQNGSCDSVKIKVQKRRPKTAKNRVSPKEIEEAGPRRRESIERNKAVSPATSPTDP
LEPWSTRGIKDMNTILAWEENTPDSP

FIGURE 104 - SEQ ID NO: 95

<> 30
<> 1024
<> PRT
<> Bombus terrestris
<> XP_003396191.1
<> ?
>gi|340715377|ref|XP_003396191.1| PREDICTED: transient receptor potential cation channel subfamily V member 6-like [Bombus terrestris]
MGGVCSCRGRGSQVNAGSILDRVISHASDEDQCLLYRLANYKKGGELIESYNQGGQAEVEKLIREQFGVLMYADGKG
QAINRAEYLRWKFRDLEQVVLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTRLARILLKC
FPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAIISQRAIGSFFLPRDQQRTNPAKNTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYALRHPKLPARNGIVNAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWKT
FARLQFLKRLIILVFHLTSLSLAVYMRPSNIDATLLEWPEEITEVGRMIAECTTVIGVLSYILVQLGGEVVNIGLLS
FMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILVVAVPGSWFLLMFFAGAIRLTGPFVTMVYSMITGDML
TFGIIYMVVLFGFCQSFYFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLGYTTYPNLSKMVFAIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAVAQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLVIKS
KSKTKAKQRKGAVANWKRVGKVTINELKKRGITGEALRRVMWGRASFSTPRDTLRALGSVGIVRAVGTLGPVGTVRA
VGALGPVGTVRDSSMAEDFQDPLLELVIASENTDDPETLLKIAERAAANFEVESSSKINLQILEQFTMTKLPMEEKV
AATKKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTRRRSRHTDDDLSSTSSTSADRNPQYQPLLNGPENLV
SRQIESRESSIEAIKPQVKQNGSCDSVKIKVQKRRPKTAKNRVSPKEIEEAGPRRRESIERNKAVSPATSPTDPLEP
WSTRGIKDMNTILAWEENTPDSP

FIGURE 105 - SEQ ID NO: 96

<> 32
<> 949
<> PRT
<> Dendroctonus ponderosae
<> ERL85467.1
<> ?
>gi|546673959|gb|ERL85467.1| hypothetical protein D910_02886 [Dendroctonus ponderosae]
MGGCQCKPCCKHKKSHYTGGSILDRVISQSSNQDQCLLYRLANYKKGGELIDAYNAGGQIECEKLIRDQFAQLMYQD
GKGKIINRSEYLRWKFRDHEHVILPIEASLSRYDPLGKWTDHEACWQMQYRGSLGESLLHLLIICDSKIHTRLARTL
IKCFPKLALDVVEGEEYLGASALHLAIAYSNNELVQDLVEAGANVNQRAIGKQIADKTGKINAKNRSFFLPRDQQKQ
RPAKHTDYEGLAYLGEYPLAWAACCANESVYNLLLDSGAHPDLQDNFGNMILHMVVVCDKLDMFGYALRHPKLPASN
GIINKAGLTPLTLACKLGRAEVFREMLELSCKEFWRYSNITCSAYTLNALDTLLPDGRTNWNSALFIILNGTKEAHL
DMLDGGIIQRLLEEKWKAFARNQFLKRLIILIVHLAFMSLAVYMRPDDPDEPLLEWSDDPTVIIRFTAEIGTLLNVL
SYVVVQQGDEIRNQGFLSFLKQQTNSPPKCIFLVSNLMILACIPCRLAGNRGLEETILIFAVPGSWFLLMFFAGAVR
LTGPFVTMIYSMITGDMLTFGIIYTIFLFGFSQSLFFLYKGNPSVNGTLYHSYSSTWMALFQVTMGNYDYSELALTT
YPGVAKSVFGLFMVFVPILLFNMLIAMMGNTYAHVTEQSEKEWVKQWAKIVISLERAIPQKEAHNYLQEYSISLGPA
EDPATEQRGVMVIKSKNKTRAKQRKGAVSNWKRVGKVTIKALKKKGMTGEEMRCLMWGRESINTPVKVKGPKRDPLA
NPQGPDLANGFGDALTSALDVMAFTHDLDINAQGLNLAKQTLNPKPFTDPLRTLVLESLVETNSARLSVLAAQAANL
PDTAEIVSCPNTATTSVKNLAGIFAGTGNFVKKIEEKVKKKKYAVLECSDSESFGGKCHGISTHFQSKTLKYCRSAA
GDNITGEEGQTDTYATFCKQEKEFR

FIGURE 106 - SEQ ID NO: 97

<> 34
<> 1147
<> PRT
<> Nasonia vitripennis
<> XP_001602588.2
<> ?
>gi|345485102|ref|XP_001602588.2| PREDICTED: hypothetical protein LOC100118680 [Nasonia vitripennis]
MGGACSCQGRDSQVNAGSILDRVISQASDEDQCLLYRLANYKKGGELIEAYNQGGQAEVERLIREQFGILMYADGKG
QTINRAEYLRWKFRDLDQVILPIEASLSRFDPLAQWSDHEACWQMQYRGSLGETLLHVLIICDTRTHTRIARTLLKC
FPRLAIDVVEGEEYLGASALHLAIAYANNELVQDLVEAGAIVSQRAIGSFFLPRDQQRPRPAKSTDYEGLAYLGEYP
LAWAACCANESVYNLLLDSGAHPDEQDTFGNSILHMVVVCDKLVRFGYALRHPKLPASNGIANAAGLTPLTLACQLG
RAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTSXNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWKT
FARLQFLKRLVILVFHLVSLSLAVYFRPADTDAELAQWPEEITDVVRVIAECVTVLGVLGYILLQLGGEIVNIGFFS
FFKQLSHEPAKFIFLISNLLILACIPCRLSGDRHTEDAILVVAVPGSWFLLMFFAGAVRLTGPFVTMVYSMILGDMR
TFGIIYMIVICGFTQAFYFLYKGYPGVKTTLFHSYPSTWMALFQITLGDYSYSDLSMTTYPNLSKAVFTIFMVLVPI
LLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVSLERAVSQDDAHNYLQEYSIKLGPGDDPNDPASEQRGVMVIKS
KSKTRARQRKGAVANWKRVGKVTIAELKKRGMTGEELRRIMWGRASFSTPVRSSPILMEPVSSVPGGFGDALTSALD
VMTFAADVPVPIEGSIPKPVAVAPGQQPTTTLALPNGAAKPQQPMMTTSTTTTTITTTVQKTLVTGTATTPAVGVTK
TVAVPAATTVSTTTTRASASAVPPTVRPSELGPASAPCSADPLLELMLATEDPGSSEETLQRLAHSARIVGESATTS
AKSDIDSSFLERLALGGLGLAAMPEQPDKPVEPKKKQYLVESSDNDICANDGQLGTEARLRRIRSASSRLAPTTTTS
TSRRKSGQQKQQREARDDESTSSAASLDNISGYQPLLNEPDTTADQPATGTEDNKPANGRNLRKRPKTTSNEGKVFC
SRRTIVVLNKNKKNKKLETSEANMNARKKETLLALHDMTSLISGRVLTLEQANENGYEMLEQLKHKLDP

FIGURE 107 - SEQ ID NO: 98

<> 36
<> 1109
<> PRT
<> Camponotus floridanus
<> EFN61724.1
<> ?
>gi|307168692|gb|EFN61724.1| Transient receptor potential cation channel subfamily V member 6 [Camponotus floridanus]
MGGVCSCRVGRGNQLNAGSILDRVISQASNEDQCLLYRLANYKKGGELIEAYNQGGQPEVEKLVREQFGILMYADGK
GQVINRAEYLRWKFRDLEQVVLPIEASLSRFDPLAQWNDHEACWQMQYRGSLGEALLHVLIICDTRIHTRIARILLK
CFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVDAGAIISQRAIGSFFLPRDQQGMNPVRNTDYEGLAYLGEY
PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVGDKLDMFGYALRHPKLPARNGIANAAGLTPLTLACQL
GRAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWK
TFARLQFLKRLIILVFHLASLSLAVYFRPADTDAVLLQWPEEITDVIRTAAECITVLGVLNYILVQLGGEMINVGPL
SFLKQLSHEPAKLIFVISNLLILACIPCRIAGNRHAEDAILVFAVPGSWFLLMFFAGAIRLTGPFVTMVYSMITGDM
LTFGIIYTIMLFGFSQSFYFLYKGFPGVKSSLYHSYVSTWMALFQITLGDYNYAELNNTIYPNLSKTVFAIFMVLVP
ILLLNMLIAMMGNTYAHVIEQSEKEFVKQWAKIVVSLERAVSQKDAHNYLQEYSIKLGPGDDPNNPASEQRGVLVIK
SKSKTKAKQRKGAVANWKRVGKVTINELRKRGMTGEELRHIMWGRESFSTPVRVSPNAGQPQVSAVTAGFGDALTAA
LDVMAFAHDFDLSAATEGIPTNIDAKQTKTTQSKAIPNDQMKTTQNNPETVTNVQPHKQPIGEPTKLLGLTDLIDNS
IGPVKDVEAMNLKNTNQTKALEASMEFEDPFLELAIASETTTNYEILLQIAKSALAASEASVKTAIDPQILAHFAMI
PPPITEKFIVKKQYFMESSDNDVGGDNLLGTEARLRRIKSANNRFITTSKRPHRDDDGDSSSSTISIERNQRYRPLF
NDPEERSINHVETEGQKTPMETIKSEIQQNGSIPLKPPDKIQKRRPKTAKNRVSPKEIEEPRRRESIEQNKAASPPT
SSSDPLEPWSTRGITDMNTILAWRDNAPDSP

FIGURE 108 - SEQ ID NO: 99

<> 38
<> 998
<> PRT
<> Danaus plexippus
<> EHJ71463.1
<> ?
>gi||gb| EHJ71463.1 hypothetical protein KGM_ [Danaus plexippus]
MGVPLSKLCSATSVPAVGSVLDRVISQPSSEDHTVLYKLADYKKGGLLLETYTKGGVVAAERLIREEFSAYMYAGGR
GRVINRAEYLRWKFRDQEQVVLPIEASLSPHDPLAKWEDHTACWQMSYRGALGESLLHVLIICDTKIHTRLARTLVK
CFPKLSLDVVEGEEYLGASSLHLAIAYSNNELVQDLVEAGADVSQKAIGSFFLPRDQQKNPPARQTNYEGLAYLGEY
PLAWAACCANEAVYNLLLDSGADPDAQDSFGNMILHMVVVCDKLDMFGYALRHPKVPASNGRLNKAGFTPLTLACQL
GRASVFREMLELSSREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKQEHLNMLDGGIIQRLLEEKWK
TFARTKFLKRLLILMLHLILLSISVYLRHSSLEADVDPDWGLEVNDARSGIRLACELGTIISTLCYIILQQGDEIKN
QGVVAYFKQLIHEPAKFIFLASNILLLACIPARISQRTTLEEAILIFVLPGSWFLMMFFAGAVKLTGPFVTMIYSMI
TGDMFTFGIIYCIVLFGFSQSFYFLYKGFPNVHSTLYSSYPSTWMALFQITLGDYSYTDLGLTMYPNLSKTVFTVFM
VFVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERSVSQEDAHRYLQEYSIGLGPSDDPRYEQRGVMVI
KSKAKTRAKQRKGALSNWKRVGKVTIAELRRRGISGEELRRLMWGRVSISTPTKAPLKCVPPPELVTSEIPGSGVGP
ALSSALNVMAYTQDLDLTNTGSELHKQITPDLLVNGKTPVTAQNTATTPKVPLVNLPNKAGLDVQSTGSDQSVPTAL
TKNMDVLGINMSTQDLLKNQTINNPATANEIVFKDYLRDIIKAEQLGLDNIDIKALAEKAANLTDVPEIDINISTAA
RSARRVVAGAVSGLFGVTAETPRDAGWRRERHEHTDSDPVPECVILGRAARARRARSASRRAPPPPPHLYVPAR

FIGURE 109 - SEQ ID NO: 100

<> 40
<> 1179
<> PRT
<> Bombyx mori
<> XP_004925321.1
<> ?
>gi|512902216|ref|XP_004925321.1| PREDICTED: uncharacterized protein
LOC101737437 [Bombyx mori]
MGNAIGKFLTAGNVQGAGSVLDRVISQPSSEDHTVLYKLADYKKGGLLLETYAKGGMTAAEKLMRDEFAAYMYGGGR
GRVINRAEYLRWKFRDQEQVVLPIEASLSPYDPLAKWEDHTACWQMCYRGALGESLLHVLIICDTKIHTRLARTLVK
CFPKLSLDVVEGEEYLGASSLHLAIAYSNNELVQDLVEAGADVNQRAIGSFFLPRDQQRVPPARQTNYEGLAYLGEY
PLAWTACCANEAVYNLLLDSGADPDAQDSFGNMILHMVVVCDKLDMFGYALRHPKVPASNGRMNKAGFTPLTLACQL
GRASVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKQEHLNMLDGGIIQRLLEEKWK
TFARTKFLKRLLILMLHLLLLSVSVYLRHSSAEADAHPNWGLEINDARSGLRLASELGTILSTLCYIILQQGDELKN
QGLVAYFKQLIHEPAKFIFLASNILVLACIPARLLKETNVEEAILLFLLPGSWFLLMFFAGAVKLTGPFVTMIYSMI
TGDMFTFGIIYCIVLFGFSQSFYFLYRGFPNVQSTLYSSYPSTWMALFQITLGDYSYSDLSQTTYPNLSKTVFTVFM
IFVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERSVAQDDAHKYLQEYSIGLGPSDDPRYEQRAVMVI
KSKAKTRAKQKKDALTNWKHVGKVTIAELRRRGISGEELRRLMWGRISISTPTKAPLPRRVPAPPPDCVVSSDVGLA
SDVGNGVAPALSSALNVMAFTHELDIGTTGSDQKQTTPDLLVNGKTSNAPILTTGTQMPKVSSKTLGTPVARIEASS
LKTPLDVKLNPTTLTQSTVQGNIGNVNIPISGVKITTNVGQNSAVVPEIQQSNENQKPEQVHQDYLRELIVLAEKPA
TTNLELKQLAEKAADLRDVPEIDININMAAKSARKMVAGAVSGLFGVAADTPAPDAGWRRDRHDNSDSDPISESVLL
SRASRARRARSASRRAAPPPPHLYVPARSMYLVASESSAIESDAPWDDQPSSENNSAVGGRREEIAHIKAARPLCIQ
HAASGRTAQVEHSLFVVGPGTGAEVESTPTVQKSEKKARPKTTRSRRNRISPTPVQEAGSPLEPWATAQLSKLSRLI
RYSSSSAASITSQTSTEQEQSPRY

FIGURE 110 - SEQ ID NO: 101

<> 42
<> 993
<> PRT
<> Acyrthosiphon pisum
<> XP_001950096.1
<> ?
>gi|193656992|ref|XP_001950096.1| PREDICTED: transient receptor potential cation channel subfamily V member 6-like [Acyrthosiphon pisum]
MGNSCASCTDFSFSKTASGSVLDRVISQASNEDDCLLYKLADYKKGGELINVYNNGGQDEAERFIVEKLPGLMYNNG
KGQVINRNDYLRWKFQNRKHVAVNVEERPGPHDPLTRWVDHVACWQMQYRGSLGESLLHVLIICDTVIHTRLSRLLL
KHYPMLSQDVVEGEEYLGASALHLSIAYNNNDLIQDLVDAGANICQRAIGSFFLPRDQQNKEINNKHTDYEGLAYLG
ELPLAWAACCGNQTVYNLLIDAGANPDAQDSFGNMILHMVVVCDKLSMFGYALKHPKVKASNGIMNVAGLTPLTLSC
KLARTSVFREMLELSAREFWRYSNITCSAYPLSALDTLLPDGRTNWNSVLFIILDGTKEEHLDMLDGGIIQKLLEEK
WKTFARKQFMKRLVILSIHLIMLSISIYLRPVDQDKPLLGEAEDWQDVARYCFEGGTVVGVLSYLIVQQGGEILNQG
LVGFLKQTFKEPAKLIFLISNLLILACIPPRMMGDKQTEEAILVFAVPGSWFLLMFFAGAIRLTGPFVTMVYLMITG
DMLTFFVIYSVILSGFTQSFFFLYKGSPDVSTSLYKSYPSTWMALFQITMGDYNYADLSYTVYPALSKTVFTVFMVL
VPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVTLERAVPQKAARNYLEEYSIQLAPGDDVNPEQRGFMVIKC
KSQTRAKQRKGAVINWKKSGKLVIQELRRLEGTGQNLRDMIWKRSSLSASSPVAKSVSITKNKSKSYSEAKDDQIRL
SGALGAALDAIAVAHDLDMTLTKDQSIDELHDPLRQLVIMSESDKNIDKSQVEIVANAAAKIANQDSIKPISINLEQ
QNDVKNEKTKIPTSSNTITNRKLLNKQSKNLSMYGFESQDMSVDKYSKAIAITRSISTQTGGIGIIEKNERQIIRPK
TAKINRVTPTQNFAVKRGQSAQPDKREDHRDNKEQQCYCISGNNMLRPWSTQDLAPLNTIMAWGPNDDF

FIGURE 111 - SEQ ID NO: 102

<> 44
<> 275, partial
<> PRT
<> Solenopsis invicta]
<> EFZ13594.1
<> ?
>gi|322787506|gb|EFZ13594.1| hypothetical protein SINV_13786 [Solenopsis invicta]
MGGACSCRFGRGSQVNPGSILDRVISQASNEDQCLLYRLANYKKGGELIEAYNQGGQPEVEKLIREQFGILMYADGK
GQTINRAEYLRWKFRDLEQVVLPIEASLTRFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRMHTRIARILLK
CFPRLSIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAIISQRAIGSFFLPRDQQRMNPARNTDYEGLAYLGEY
PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVGDKL

FIGURE 112 - SEQ ID NO: 103

<> 46
<> 142
<> PRT
<> Schistocerca americana, DNA partial
<> In-house
<> ?
> Schistocerca americana, DNA partial
SWFLLMFFAGAXRLTGPFVTMVYSMITGDMLTFGIIYTVVLFGFSQSFYFLYKGFPGVKTSLYHSYPTTWMALFQIT
MGDYNYPELSHTTYPTLAKTVFAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVV

FIGURE 113 - SEQ ID NO: 104

<> 48
<>
<> PRT
<> Myzus persicae
<> In-house
<> ?
ERPGPHDPLTRWVDHVACWQMQYRGSLGESLLHVLIICDTVIHTRLSRLLLKHYPMLSQDVVEGEEYLGASALHLSI
AYNNNDLIQDLVDAGANICQRAIGSFFLPRDQQNKEINNKHTDYEGLAYLGELPLAWAACCGNQTVYNLLIDAGANP
DAQDSFGNMILHMVVVCDKLSMFGYALKHPKVPASNGIMNVAGLTPLTLSCKLARTSVFREMLELSAREFWRYSNIT
CSAYPLSALDTLLPDGRTNWNSVLFIILDGTKEEHLDMLDGGIIQKLLEEKWKTFARXXXXXXXXILSIHLIMLSIS
IYLRPVDQDKPLLGEAEDWQDVARYCFEGGTVVGVLSYLIVQQGGEILNQGLVGFLKQTFKEXXXXXXXXXXXXXXX
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDMLTFFVIYSVILSGFTQSFFFLYKG
SPDVSTSLYKSYPSTWMALFQITMGDYNYADLSYTVYPALSKTVFTVFMVLVPILLLNMLIAMMGNTYAHVIEQSEK
EWMKQWAKIVVTLERAVPQKAARNYLEEYSIQLAPGDDVNPEQRGFMVIKCKSQTRAKQRKGAVINWKKSGKLVIQE
LRRLEGTGQNLRDMIWKRSSLSASSPVAKSVSITKNKSKSYSEAKDDQIRLSGALGAALDAIAVAHDLDMTLTKDQS
IDELHDPLRQLVIMSESDKNIDKSQVEIVANAAAKIANQDSIKPISVNLEQXXXXXXXXXXXXXXXTITNRKLLNKQ
SKNLSMYGFESQDISVDKYSKEIVITRSISTQTGGIGIIEKNERPIIRPKTAKINRVTPTQNFAVKRGQSAQPDKRE
DHRDNKEQQCYCISGNNMLRPWSTQDLAPLNTIMAWGPNDDF

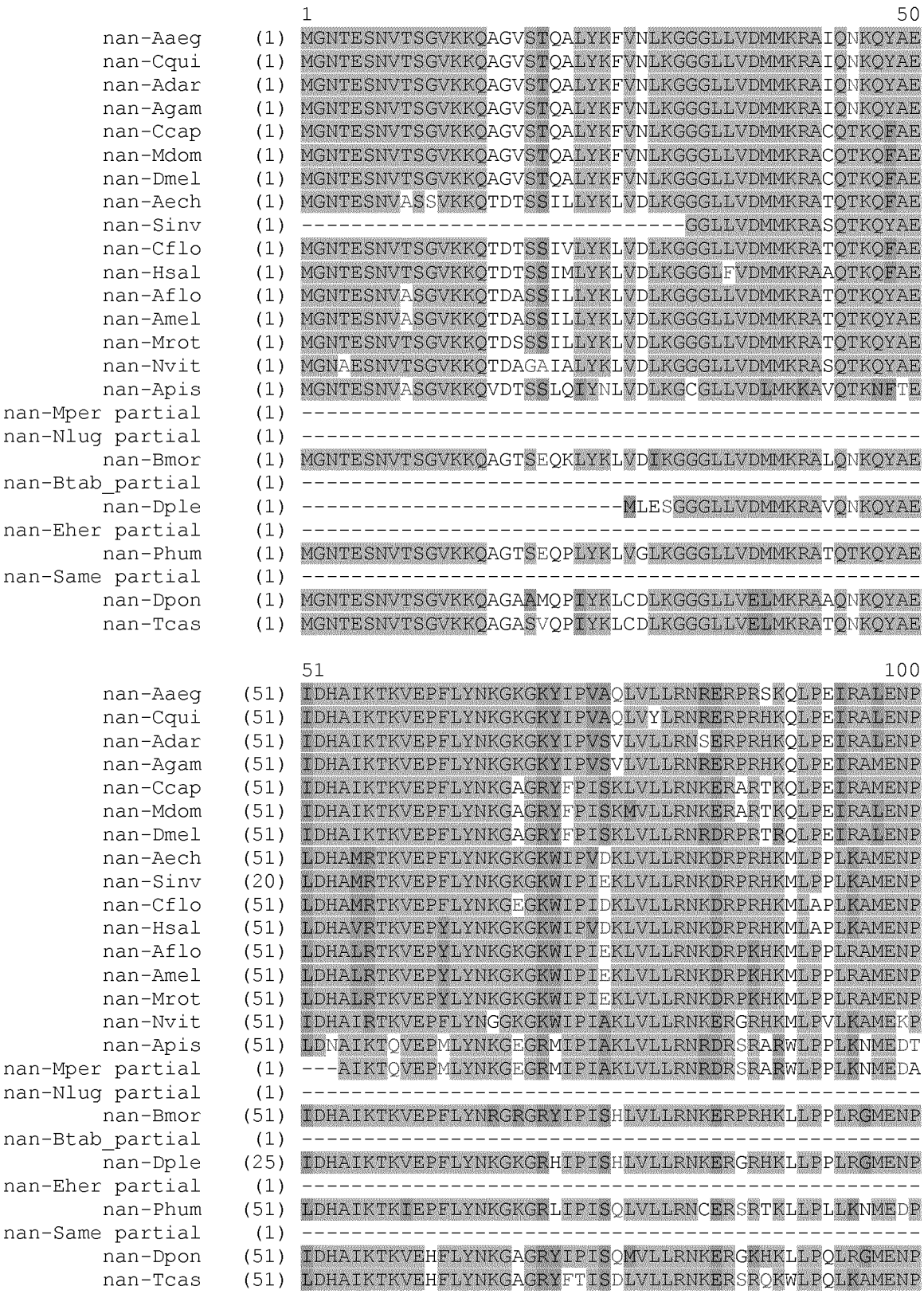
FIGURE 114 - SEQ ID NO: 105

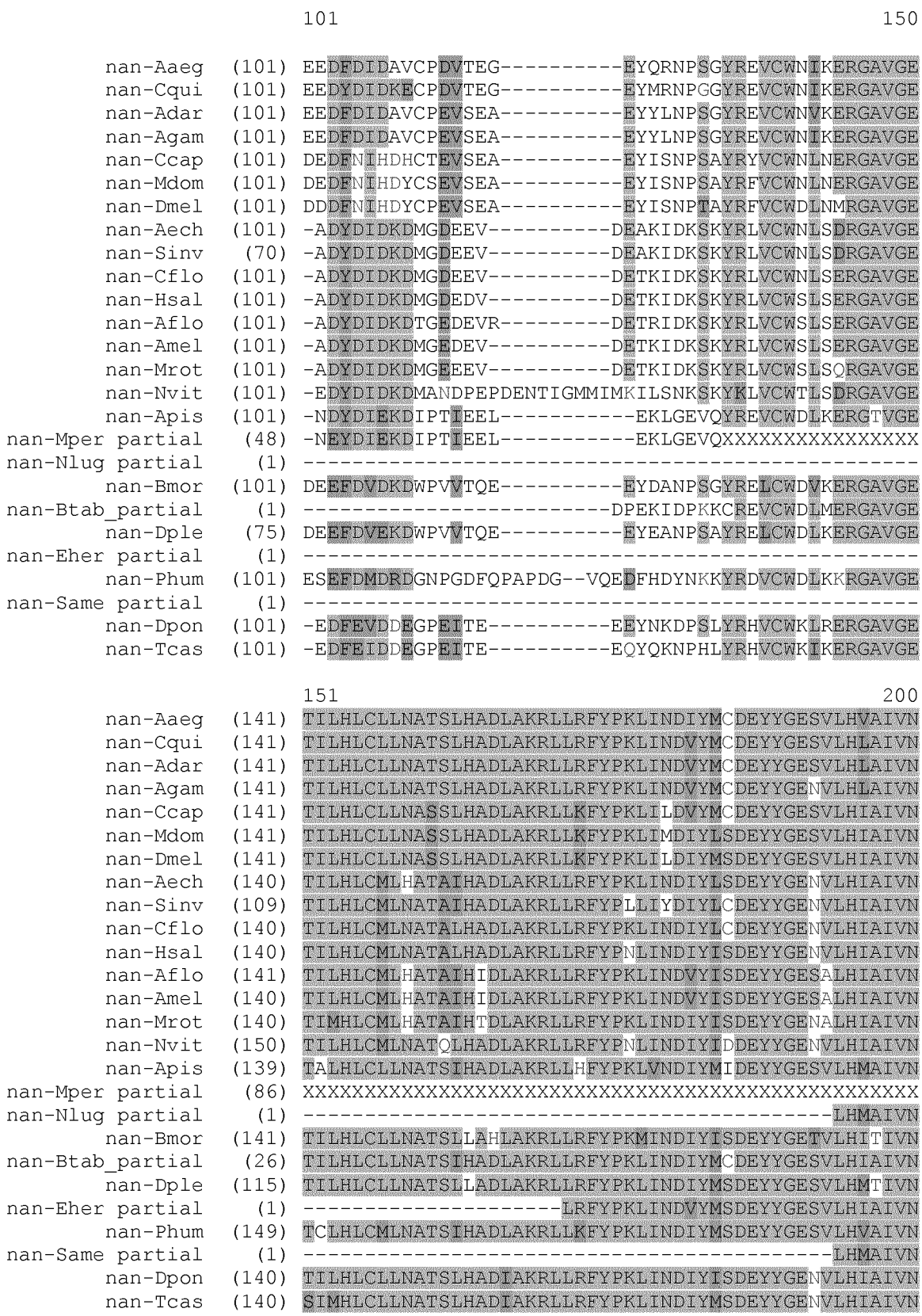
<> 50
<> 552
<> PRT
<> Bemisia tabaci
<> In-house
<> ?
MYNDGKGQIIKRAEYLRWKFRDQQQVTLPIEASLSPHDPLAKWEDHEACWQMQYRGSLGETLLHVLIICDTKTNTRL
ARTLLKCFPRLAQDIVEGEEYLGASALHLAIAYNNNELVQDLVEAGANVNQRAIGSFFLPKDQQRPRPAKHTDYEGL
AYLGEFPLSWAACCANESVYNLLLDSGAHPDMQDTFGNMILHMVVVCDKLDMFGYALRHPKLPASNGITNTAGLTPL
TLACKLGRAEVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRL
LEEKWKTFARRQFLKRLAILFLHLLMLSMAVYLRPVDREQPLIGGDDWSDIARYGFEVGTIMGVLSYLVVQQGGEIK
NQGLGSFLKQLMAEPAKAIFLVSNLLILACIPFRMAGDSQTEEAILILAVPGSWFLLMFFAGAVRLTGPFVTMIYSM
ITGDMFTFGIIYSILLFGFSQSFYFLYKGSPNVKQTLFHSYPTTWMALFQITLGDYNYPELAFTVYPTLSKIVFTSF
MVLVPILLLNMLIAMMGNTYAHVIERSEKEWMKQWAKIVVALERAVPAADAHNYLQEYSIKLGPGDDPSTEQRGVMV
IKSKSKTRAKQRKGAVSNWKRVGKVTINELRKRGMTGEQLNRIMWGRASISTPVRQPAMALLLEDSEEENAANNTGP
FGGALTAALDVMAFTHDIDLNIGQTPVTVSGLGGVSVRSGAEGLPPEQPFHDPFRQLVIEAENPHIDESELAALANA
AAMSVVAPDDIPTPVVTPEPVSALPRLPSLHLEPSDSDGLGDGPLLGRGSRVRRVRSAHLKQQKASSTNGNGYSDRQ
RLFSSKNEDSSSNTSLDFDLTNPPSQLRLTPPPRPVTAEIVAVNPKKYIGGNSQERLRPKTAKVNRVAPTPDVPVRR
GISANGIPESLPSPPDPLEPWSTRNIVNMNAILAWQQSDQDSL

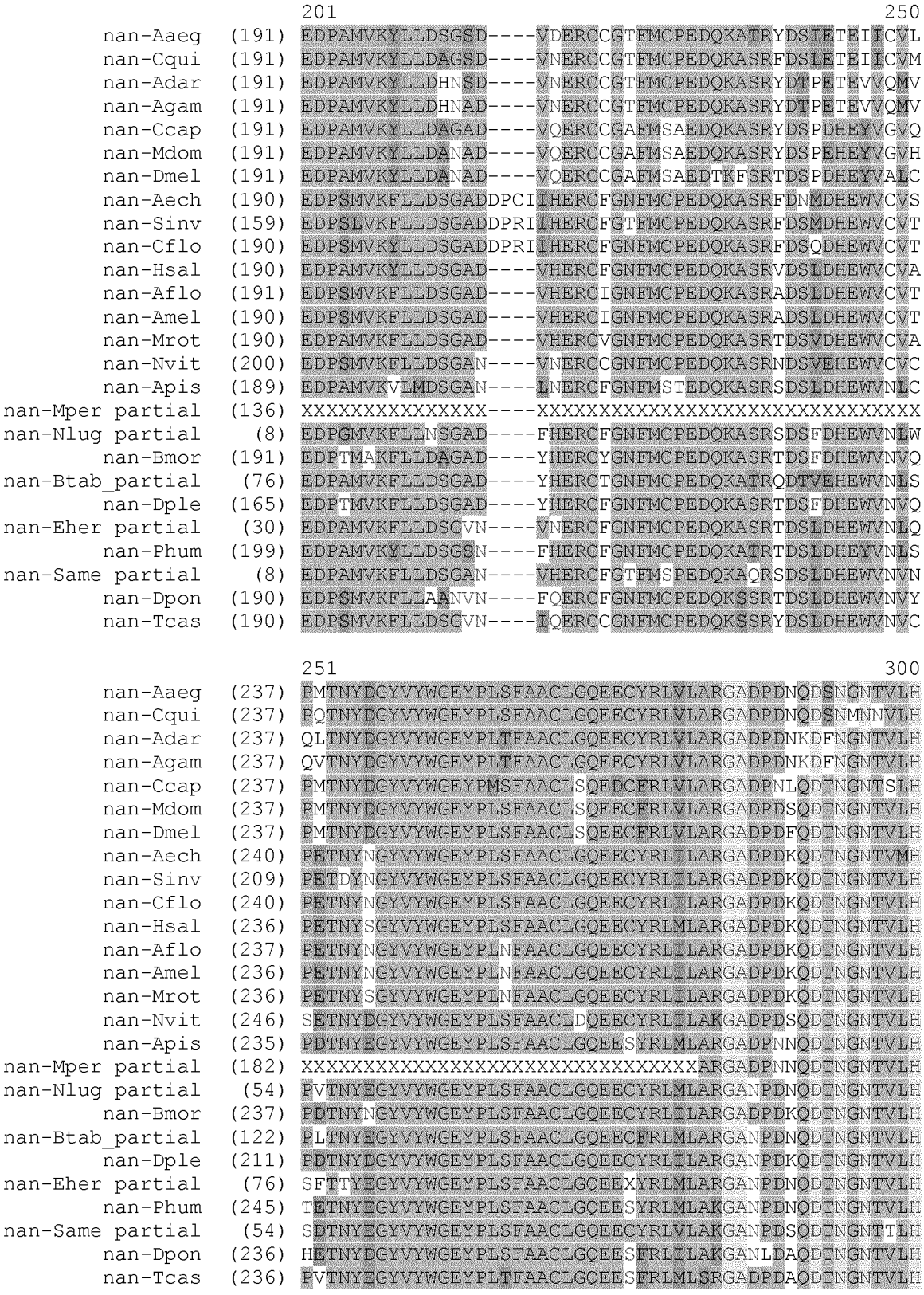
FIGURE 115 - SEQ ID NO: 106

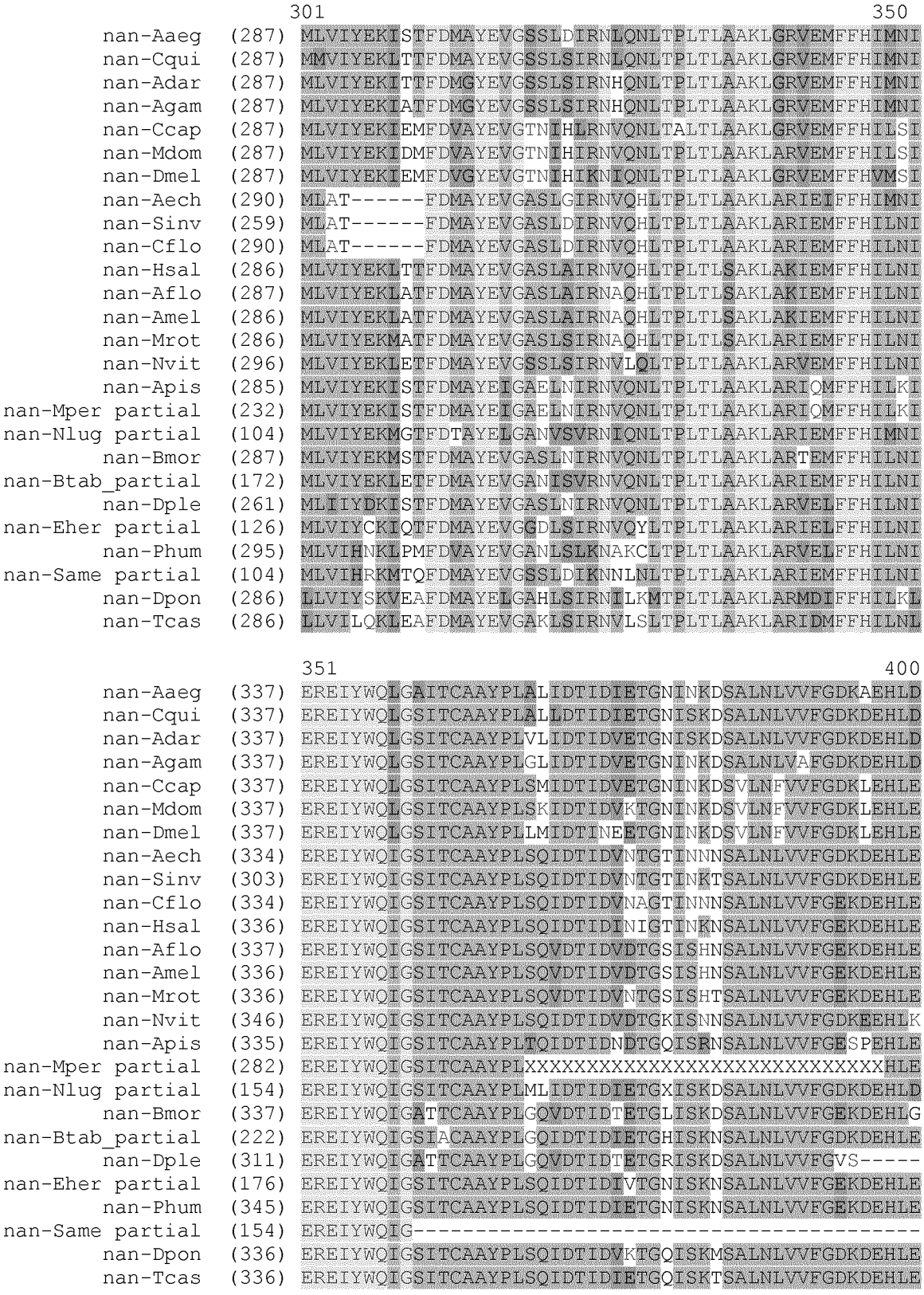
<> 52
<> 984
<> PRT
<> Euschistus heros
<> In-House
<> ?
MGIIWGSGASSVNAGTVLDRVISQASNKDECLLYKLANYKKGGELIDAYNAGGQSEVEKLIREQFGQLMYNEGKGAL
INRAEYLRWKFRDMQQVQIPIEASLSSQDPLSKWEDHQACWQMQYRGSLGETLLHVLIICDTKIHTRLARTLLKCFP
NLAIDVVEGEEYLGASALHLAIAYFNNELVQDLVEAGANVEQRAIGSFFLPRDQQGQRPSKHTDYEGLAYLGEYPLA
WAACCANESIYNLLLDNGANPDHRDTFGNMILHMVVVCDKLDMFGYALRHPKMPASNGIANVAGLTPLTLACKLGRA
KVFREMLELSAREFWRYSNITCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLEEKWKXFA
RRQFLKRLVILMLHLLCLSGAVYLRPTDRTKPLLGGDDWKSVARQGFEVATVLGVLSYVIVQQGGEIRNQGFISFIK
QLDXAKAIFLVSNILILICIPFRLMDDKRTEEAILVFAVPGSWFLLMFFAGAVRLTGPFVTMVYSMIVGDMFTFGII
YSIVLFGFSQSFYFLYKGFPGVKNTLYSSYHSTWMALFQITLGDYNYAELSHTSYPTLSKTVFAIFMILVPILLLNM
LIAMMGNTYAHVIEQSEKEWMKQWAKIVVSLEXAVNQEDCKQYLQEYSIKLGPGDDPSTEQRGVMVIKSKSKTRAKQ
RKGAVANWKRVGKVTINELRKRGMNGEQLRRIMWDRASISTPVKVPQNPVVDVLMENTAEQQAQQTPGSFGGALTAA
LDVMAFTHDLDLSASGITSSGLNAKELIVSDPFRDLVLSSEIDVGEEELATLAEAAVLSVMSGQSDESEKLKIAKFN
KQISFEQNAVLEVSDSDGFLDGQPLGQGSRARKVKSAQERQRAERTWGGTSISSIEEPPPYLPLPPPPPLHSHQRPR
PKTAKPNRVVPEAVVAKRPQSSALGDRVKSPPELLEPWSTRGIATINTILAWQPSDQDSM

FIGURE 116


1 50
nan-Aaeg (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAE
nan-Cqui (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAE
nan-Adar (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAE
nan-Agam (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRAIQNKQYAE
nan-Ccap (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAE
nan-Mdom (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAE
nan-Dmel (1) MGNTESNVTSGVKKQAGVSTQALYKFVNLKGGGLLVDMMKRACQTKQFAE
nan-Aech (1) MGNTESNVASSVKKQTDTSSILLYKLVDLKGGGLLVDMMKRATQTKQFAE
nan-Sinv (1) ----------GGLLVDMMKRASQTKQYAE
nan-Cflo (1) MGNTESNVTSGVKKQTDTSSIVLYKLVDLKGGGLLVDMMKRATQTKQFAE
nan-Hsal (1) MGNTESNVTSGVKKQTDTSSIMLYKLVDLKGGGLFVDMMKRAAQTKQFAE
nan-Aflo (1) MGNTESNVASGVKKQTDASSILLYKLVDLKGGGLLVDMMKRATQTKQYAE
nan-Amel (1) MGNTESNVASGVKKQTDASSILLYKLVDLKGGGLLVDMMKRATQTKQYAE
nan-Mrot (1) MGNTESNVTSGVKKQTDSSSILLYKLVDLKGGGLLVDMMKRATQTKQYAE
nan-Nvit (1) MGNAESNVTSGVKKQTDAGAIALYKLVDLKGGGLLVDMMKRASQTKQYAE
nan-Apis (1) MGNTESNVASGVKKQVDTSSLQIYNLVDLKGCGLLVDLMKKAVQTKNFTE
nan-Mper partial (1) ----------
nan-Nlug partial (1) ----------
nan-Bmor (1) MGNTESNVTSGVKKQAGTSEQKLYKLVDIKGGGLLVDMMKRALQNKQYAE
nan-Btab_partial (1) ----------
nan-Dple (1) ----------MLESGGGLLVDMMKRAVQNKQYAE
nan-Eher partial (1) ----------
nan-Phum (1) MGNTESNVTSGVKKQAGTSEQPLYKLVGLKGGGLLVDMMKRATQTKQYAE
nan-Same partial (1) ----------
nan-Dpon (1) MGNTESNVTSGVKKQAGAAMQPIYKLCDLKGGGLLVELMKRAAQNKQYAE
nan-Tcas (1) MGNTESNVTSGVKKQAGASVQPIYKLCDLKGGGLLVELMKRATQNKQYAE
51 100
nan-Aaeg (51) IDHAIKTKVEPFLYNKGKGKYIPVAQLVLLRNRERPRSKQLPEIRALENP
nan-Cqui (51) IDHAIKTKVEPFLYNKGKGKYIPVAQLVYLRNRERPRHKQLPEIRALENP
nan-Adar (51) IDHAIKTKVEPFLYNKGKGKYIPVSVLVLLRNSERPRHKQLPEIRALENP
nan-Agam (51) IDHAIKTKVEPFLYNKGKGKYIPVSVLVLLRNRERPRHKQLPEIRAMENP
nan-Ccap (51) IDHAIKTKVEPFLYNKGAGRYFPISKLVLLRNKERARTKQLPEIRAMENP
nan-Mdom (51) IDHAIKTKVEPFLYNKGAGRYFPISKMVLLRNKERARTKQLPEIRALENP
nan-Dmel (51) IDHAIKTKVEPFLYNKGAGRYFPISKLVLLRNRDRPRTRQLPEIRALENP
nan-Aech (51) LDHAMRTKVEPFLYNKGKGKWIPVDKLVLLRNKDRPRHKMLPPLKAMENP
nan-Sinv (20) LDHAMRTKVEPFLYNKGKGKWIPIEKLVLLRNKDRPRHKMLPPLKAMENP
nan-Cflo (51) LDHAMRTKVEPFLYNKGEGKWIPIDKLVLLRNKDRPRHKMLAPLKAMENP
nan-Hsal (51) LDHAVRTKVEPYLYNKGKGKWIPVDKLVLLRNKDRPRHKMLAPLKAMENP
nan-Aflo (51) LDHALRTKVEPYLYNKGKGKWIPIEKLVLLRNKDRPKHKMLPPLRAMENP
nan-Amel (51) LDHALRTKVEPYLYNKGKGKWIPIEKLVLLRNKDRPKHKMLPPLRAMENP
nan-Mrot (51) LDHALRTKVEPYLYNKGKGKWIPIEKLVLLRNKDRPKHKMLPPLRAMENP
nan-Nvit (51) IDHAIRTKVEPFLYNGGKGKWIPIAKLVLLRNKERGRHKMLPVLKAMEKP
nan-Apis (51) LDNAIKTQVEPMLYNKGEGRMIPIAKLVLLRNRDRSRARWLPPLKNMEDT
nan-Mper partial (1) ---AIKTQVEPMLYNKGEGRMIPIAKLVLLRNRDRSRARWLPPLKNMEDA
nan-Nlug partial (1) ----------
nan-Bmor (51) IDHAIKTKVEPFLYNRGRGRYIPISHLVLLRNKERPRHKLLPPLRGMENP
nan-Btab_partial (1) ----------
nan-Dple (25) IDHAIKTKVEPFLYNKGKGRHIPISHLVLLRNKERGRHKLLPPLRGMENP
nan-Eher partial (1) ----------
nan-Phum (51) LDHAIKTKIEPFLYNKGKGRLIPISQLVLLRNCERSRTKLLPLLKNMEDP
nan-Same partial (1) ----------
nan-Dpon (51) IDHAIKTKVEHFLYNKGAGRYIPISQMVLLRNKERGKHKLLPQLRGMENP
nan-Tcas (51) LDHAIKTKVEHFLYNKGAGRYFTISDLVLLRNKERSRQKWLPQLKAMENP


101 150
nan-Aaeg (101) EEDFDIDAVCPDVTEG----------EYQRNPSGYREVCWNIKERGAVGE
nan-Cqui (101) EEDYDIDKECPDVTEG----------EYMRNPGGYREVCWNIKERGAVGE
nan-Adar (101) EEDFDIDAVCPEVSEA----------EYYLNPSGYREVCWNVKERGAVGE
nan-Agam (101) EEDFDIDAVCPEVSEA----------EYYLNPSGYREVCWNIKERGAVGE
nan-Ccap (101) DEDFNIHDHCTEVSEA----------EYISNPSAYRYVCWNLNERGAVGE
nan-Mdom (101) DEDFNIHDYCSEVSEA----------EYISNPSAYRFVCWNLNERGAVGE
nan-Dmel (101) DDDFNIHDYCPEVSEA----------EYISNPTAYRFVCWDLNMRGAVGE
nan-Aech (101) -ADYDIDKDMGDEEV----------DEAKIDKSKYRLVCWNLSDRGAVGE
nan-Sinv (70) -ADYDIDKDMGDEEV----------DEAKIDKSKYRLVCWNLSDRGAVGE
nan-Cflo (101) -ADYDIDKDMGDEEV----------DETKIDKSKYRLVCWNLSERGAVGE
nan-Hsal (101) -ADYDIDKDMGDEDV----------DETKIDKSKYRLVCWSLSERGAVGE
nan-Aflo (101) -ADYDIDKDTGEDEVR---------DETRIDKSKYRLVCWSLSERGAVGE
nan-Amel (101) -ADYDIDKDMGEDEV----------DETKIDKSKYRLVCWSLSERGAVGE
nan-Mrot (101) -ADYDIDKDMGEEEV----------DETKIDKSKYRLVCWSLSQRGAVGE
nan-Nvit (101) -EDYDIDKDMANDPEPDENTIGMMIMKILSNKSKYKLVCWTLSDRGAVGE
nan-Apis (101) -NDYDIEKDIPTIEEL-----------EKLGEVQYREVCWDLKERGTVGE
nan-Mper partial (48) -NEYDIEKDIPTIEEL-----------EKLGEVQXXXXXXXXXXXXXXXX
nan-Nlug partial (1) ----------
nan-Bmor (101) DEEFDVDKDWPVVTQE----------EYDANPSGYRELCWDVKERGAVGE
nan-Btab_partial (1) ----------DPEKIDPKKCREVCWDLMERGAVGE
nan-Dple (75) DEEFDVEKDWPVVTQE----------EYEANPSAYRELCWDLKERGAVGE
nan-Eher partial (1) ----------
nan-Phum (101) ESEFDMDRDGNPGDFQPAPDG--VQEDFHDYNKKYRDVCWDLKKRGAVGE
nan-Same partial (1) ----------
nan-Dpon (101) -EDFEVDDEGPEITE----------EEYNKDPSLYRHVCWKLRERGAVGE
nan-Tcas (101) -EDFEIDDEGPEITE----------EQYQKNPHLYRHVCWKIKERGAVGE
151 200
nan-Aaeg (141) TILHLCLLNATSLHADLAKRLLRFYPKLINDIYMCDEYYGESVLHVAIVN
nan-Cqui (141) TILHLCLLNATSLHADLAKRLLRFYPKLINDVYMCDEYYGESVLHLAIVN
nan-Adar (141) TILHLCLLNATSLHADLAKRLLRFYPKLINDVYMCDEYYGESVLHLAIVN
nan-Agam (141) TILHLCLLNATSLHADLAKRLLRFYPKLINDVYMCDEYYGENVLHLAIVN
nan-Ccap (141) TILHLCLLNASSLHADLAKRLLKFYPKLILDVYMCDEYYGESVLHIAIVN
nan-Mdom (141) TILHLCLLNASSLHADLAKRLLKFYPKLIMDIYLSDEYYGESVLHIAIVN
nan-Dmel (141) TILHLCLLNASSLHADLAKRLLKFYPKLILDIYMSDEYYGESVLHIAIVN
nan-Aech (140) TILHLCMLHATAIHADLAKRLLRFYPKLINDIYLSDEYYGENVLHIAIVN
nan-Sinv (109) TILHLCMLNATAIHADLAKRLLRFYPLLIYDIYLCDEYYGENVLHIAIVN
nan-Cflo (140) TILHLCMLNATALHADLAKRLLRFYPKLINDIYLCDEYYGENVLHIAIVN
nan-Hsal (140) TILHLCMLNATALHADLAKRLLRFYPNLINDIYISDEYYGENVLHIAIVN
nan-Aflo (141) TILHLCMLHATAIHIDLAKRLLRFYPKLINDVYISDEYYGESALHIAIVN
nan-Amel (140) TILHLCMLHATAIHIDLAKRLLRFYPKLINDVYISDEYYGESALHIAIVN
nan-Mrot (140) TIMHLCMLHATAIHTDLAKRLLRFYPKLINDIYISDEYYGENALHIAIVN
nan-Nvit (150) TILHLCMLNATQLHADLAKRLLRFYPNLINDIYIDDEYYGENVLHIAIVN
nan-Apis (139) TALHLCLLNATSIHADLAKRLLHFYPKLVNDIYMIDEYYGESVLHMAIVN
nan-Mper partial (86) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
nan-Nlug partial (1) ----------LHMAIVN
nan-Bmor (141) TILHLCLLNATSLLAHLAKRLLRFYPKMINDIYISDEYYGETVLHITIVN
nan-Btab_partial (26) TILHLCLLNATSIHADLAKRLLRFYPKLINDIYMCDEYYGESVLHIAIVN
nan-Dple (115) TILHLCLLNATSLLADLAKRLLRFYPKLINDIYMSDEYYGESVLHMTIVN
nan-Eher partial (1) ----------LRFYPKLINDVYMSDEYYGESVLHIAIVN
nan-Phum (149) TCLHLCMLNATSIHADLAKRLLKFYPKLINDIYMSDEYYGESVLHVAIVN
nan-Same partial (1) ----------LHMAIVN
nan-Dpon (140) TILHLCLLNATSLHADIAKRLLRFYPKLINDIYISDEYYGENVLHIAIVN
nan-Tcas (140) SIMHLCLLNATSLHADIAKRLLRFYPKLINDIYMSDEYYGENVLHIAIVN


201 250
nan-Aaeg (191) EDPAMVKYLLDSGSD----VDERCCGTFMCPEDQKATRYDSIETEIICVL
nan-Cqui (191) EDPAMVKYLLDAGSD----VNERCCGTFMCPEDQKASRFDSLETEIICVM
nan-Adar (191) EDPAMVKYLLDHNSD----VNERCCGTFMCPEDQKASRYDTPETEVVQMV
nan-Agam (191) EDPAMVKYLLDHNAD----VNERCCGTFMCPEDQKASRYDTPETEVVQMV
nan-Ccap (191) EDPAMVKYLLDAGAD----VQERCCGAFMSAEDQKASRYDSPDHEYVGVQ
nan-Mdom (191) EDPAMVKYLLDANAD----VQERCCGAFMSAEDQKASRYDSPEHEYVGVH
nan-Dmel (191) EDPAMVKYLLDANAD----VQERCCGAFMSAEDTKFSRTDSPDHEYVALC
nan-Aech (190) EDPSMVKFLLDSGADDPCIIHERCFGNFMCPEDQKASRFDNMDHEWVCVS
nan-Sinv (159) EDPSLVKFLLDSGADDPRIIHERCFGTFMCPEDQKASRFDSMDHEWVCVT
nan-Cflo (190) EDPSMVKYLLDSGADDPRIIHERCFGNFMCPEDQKASRFDSQDHEWVCVT
nan-Hsal (190) EDPAMVKYLLDSGAD----VHERCFGNFMCPEDQKASRVDSLDHEWVCVA
nan-Aflo (191) EDPSMVKFLLDSGAD----VHERCIGNFMCPEDQKASRADSLDHEWVCVT
nan-Amel (190) EDPSMVKFLLDSGAD----VHERCIGNFMCPEDQKASRADSLDHEWVCVT
nan-Mrot (190) EDPAMVKFLLDSGAD----VHERCVGNFMCPEDQKASRTDSVDHEWVCVA
nan-Nvit (200) EDPSMVKFLLDSGAN----VNERCCGNFMCPEDQKASRNDSVEHEWVCVC
nan-Apis (189) EDPAMVKVLMDSGAN----LNERCFGNFMSTEDQKASRSDSLDHEWVNLC
nan-Mper partial (136) XXXXXXXXXXXXXXX----XXXXXXXXXXXXXXXXXXXXXXXXXXXX
nan-Nlug partial (8) EDPGMVKFLLNSGAD----FHERCFGNFMCPEDQKASRSDSFDHEWVNLW
nan-Bmor (191) EDPTMAKFLLDAGAD----YHERCYGNFMCPEDQKASRTDSFDHEWVNVQ
nan-Btab_partial (76) EDPAMVKFLLDSGAD----YHERCTGNFMCPEDQKATRQDTVEHEWVNLS
nan-Dple (165) EDPTMVKFLLDSGAD----YHERCFGNFMCPEDQKASRTDSFDHEWVNVQ
nan-Eher partial (30) EDPAMVKFLLDSGVN----VNERCFGNFMCPEDQKASRTDSLDHEWVNLQ
nan-Phum (199) EDPAMVKYLLDSGSN----FHERCFGNFMCPEDQKATRTDSLDHEYVNLS
nan-Same partial (8) EDPAMVKFLLDSGAN----VHERCFGTFMSPEDQKAQRSDSLDHEWVNVN
nan-Dpon (190) EDPSMVKFLLAANVN----FQERCFGNFMCPEDQKSSRTDSLDHEWVNVY
nan-Tcas (190) EDPSMVKFLLDSGVN----IQERCCGNFMCPEDQKSSRYDSLDHEWVNVC
251 300
nan-Aaeg (237) PMTNYDGYVYWGEYPLSFAACLGQEECYRLVLARGADPDNQDSNGNTVLH
nan-Cqui (237) PQTNYDGYVYWGEYPLSFAACLGQEECYRLVLARGADPDNQDSNMNNVLH
nan-Adar (237) QLTNYDGYVYWGEYPLTFAACLGQEECYRLVLARGADPDNKDFNGNTVLH
nan-Agam (237) QVTNYDGYVYWGEYPLTFAACLGQEECYRLVLARGADPDNKDFNGNTVLH
nan-Ccap (237) PMTNYDGYVYWGEYPMSFAACLSQEDCFRLVLARGADPNLQDTNGNTSLH
nan-Mdom (237) PMTNYDGYVYWGEYPLSFAACLSQEECFRLVLARGADPDSQDTNGNTVLH
nan-Dmel (237) PMTNYDGYVYWGEYPLSFAACLSQEECFRLVLARGADPDFQDTNGNTVLH
nan-Aech (240) PETNYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVMH
nan-Sinv (209) PETDYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVLH
nan-Cflo (240) PETNYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVLH
nan-Hsal (236) PETNYSGYVYWGEYPLSFAACLGQEECYRLMLARGADPDKQDTNGNTVLH
nan-Aflo (237) PETNYNGYVYWGEYPLNFAACLGQEECYRLILARGADPDKQDTNGNTVLH
nan-Amel (236) PETNYNGYVYWGEYPLNFAACLGQEECYRLILARGADPDKQDTNGNTVLH
nan-Mrot (236) PETNYSGYVYWGEYPLNFAACLGQEECYRLILARGADPDKQDTNGNTVLH
nan-Nvit (246) SETNYDGYVYWGEYPLSFAACLDQEECYRLILAKGADPDSQDTNGNTVLH
nan-Apis (235) PDTNYEGYVYWGEYPLSFAACLGQEESYRLMLARGADPNNQDTNGNTVLH
nan-Mper partial (182) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXARGADPNNQDTNGNTVLH
nan-Nlug partial (54) PVTNYEGYVYWGEYPLSFAACLGQEECYRLMLARGANPDNQDTNGNTVLH
nan-Bmor (237) PDTNYNGYVYWGEYPLSFAACLGQEECYRLILARGADPDKQDTNGNTVLH
nan-Btab_partial (122) PLTNYEGYVYWGEYPLSFAACLGQEECFRLMLARGANPDNQDTNGNTVLH
nan-Dple (211) PDTNYDGYVYWGEYPLSFAACLGQEECYRLILARGANPDKQDTNGNTVLH
nan-Eher partial (76) SFTTYEGYVYWGEYPLSFAACLGQEEXYRLMLARGANPDNQDTNGNTVLH
nan-Phum (245) TETNYEGYVYWGEYPLSFAACLGQEESYRLMLAKGANPDNQDTNGNTVLH
nan-Same partial (54) SDTNYEGYVYWGEYPLSFAACLGQEECYRLVLAKGANPDSQDTNGNTTLH
nan-Dpon (236) HETNYDGYVYWGEYPLSFAACLGQEESFRLILAKGANLDAQDTNGNTVLH
nan-Tcas (236) PVTNYEGYVYWGEYPLTFAACLGQEESFRLMLSRGADPDAQDTNGNTVLH

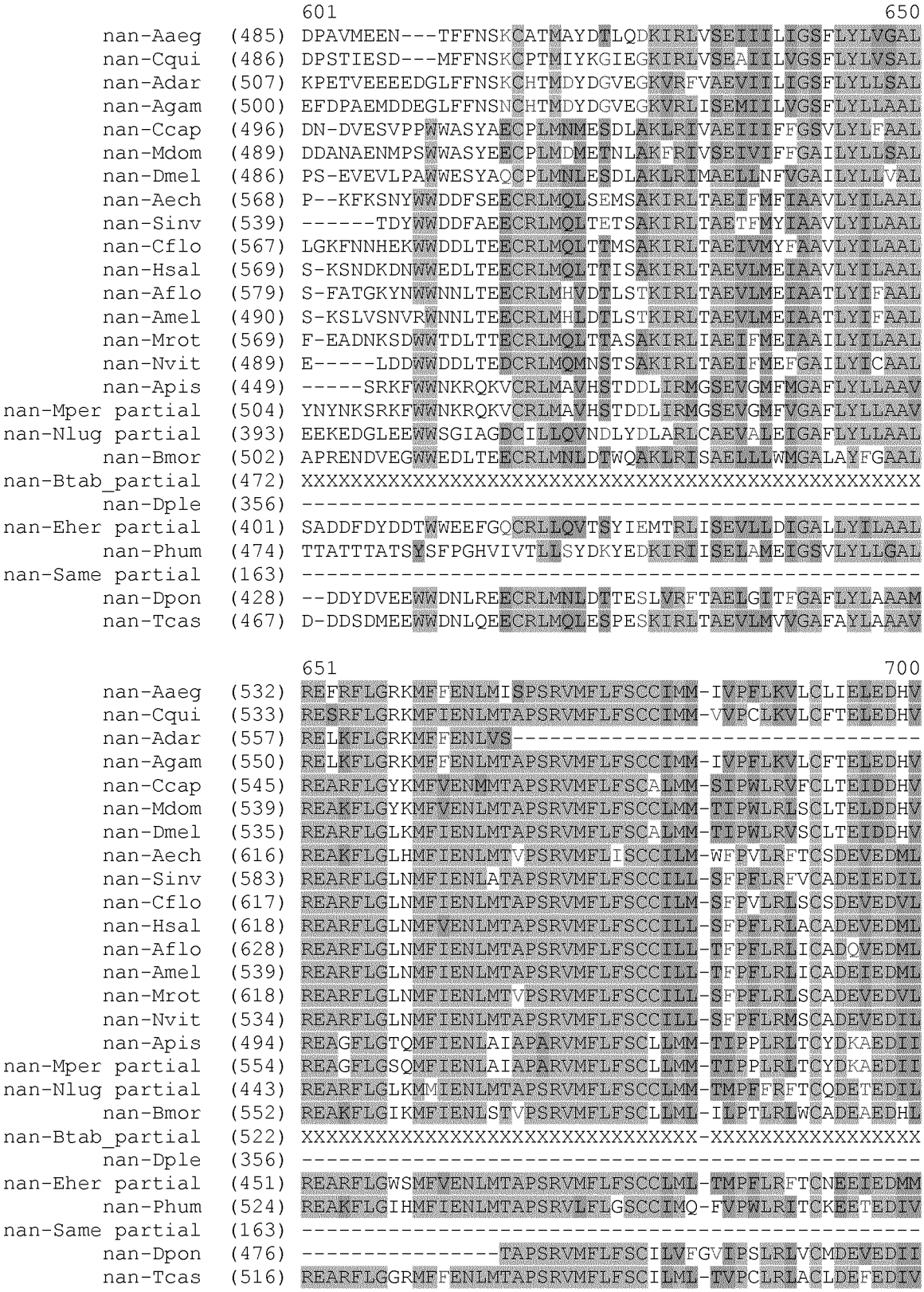

301 350
nan-Aaeg (287) MLVIYEKISTFDMAYEVGSSLDIRNLQNLTPLTLAAKLGRVEMFFHIMNI
nan-Cqui (287) MMVIYEKLTTFDMAYEVGSSLSIRNLQNLTPLTLAAKLGRVEMFFHIMNI
nan-Adar (287) MLVIYEKITTFDMGYEVGSSLSIRNHQNLTPLTLAAKLGRVEMFFHIMNI
nan-Agam (287) MLVIYEKIATFDMGYEVGSSLSIRNHQNLTPLTLAAKLGRVEMFFHIMNI
nan-Ccap (287) MLVIYEKIEMFDVAYEVGTNIHLRNVQNLTALTLAAKLGRVEMFFHILSI
nan-Mdom (287) MLVIYEKIDMFDVAYEVGTNIHIRNVQNLTPLTLAAKLARVEMFFHILSI
nan-Dmel (287) MLVIYEKIEMFDVGYEVGTNIHIKNIQNLTPLTLAAKLGRVEMFFHVMSI
nan-Aech (290) MLAT------FDMAYEVGASLGIRNVQHLTPLTLAAKLARIEIFFHIMNI
nan-Sinv (259) MLAT------FDMAYEVGASLDIRNVQHLTPLTLAAKLARIEMFFHILNI
nan-Cflo (290) MLAT------FDMAYEVGASLDIRNVQHLTPLTLAAKLARIEMFFHILNI
nan-Hsal (286) MLVIYEKLTTFDMAYEVGASLAIRNVQHLTPLTLSAKLAKIEMFFHILNI
nan-Aflo (287) MLVIYEKLATFDMAYEVGASLAIRNAQHLTPLTLSAKLAKIEMFFHILNI
nan-Amel (286) MLVIYEKLATFDMAYEVGASLAIRNAQHLTPLTLSAKLAKIEMFFHILNI
nan-Mrot (286) MLVIYEKMATFDMAYEVGASLSIRNAQHLTPLTLSAKLARIEMFFHILNI
nan-Nvit (296) MLVIYEKLETFDMAYEVGSSLSIRNVLQLTPLTLAAKLARVEMFFHILNI
nan-Apis (285) MLVIYEKISTFDMAYEIGAELNIRNVQNLTPLTLAAKLARIQMFFHILKI
nan-Mper partial (232) MLVIYEKISTFDMAYEIGAELNIRNVQNLTPLTLAAKLARIQMFFHILKI
nan-Nlug partial (104) MLVIYEKMGTFDTAYELGANVSVRNIQNLTPLTLAAKLARIEMFFHIMNI
nan-Bmor (287) MLVIYEKMSTFDMAYEVGASLNIRNVQNLTPLTLAAKLARTEMFFHILNI
nan-Btab_partial (172) MLVIYEKLETFDMAYEVGANISVRNVQNLTPLTLAAKLARIEMFFHILNI
nan-Dple (261) MLIIYDKISTFDMAYEVGASLNIRNVQNLTPLTLAAKLARVELFFHILNI
nan-Eher partial (126) MLVIYCKIQTFDMAYEVGGDLSIRNVQYLTPLTLAAKLARIELFFHILNI
nan-Phum (295) MLVIHNKLPMFDVAYEVGANLSLKNAKCLTPLTLAAKLARVELFFHILNI
nan-Same partial (104) MLVIHRKMTQFDMAYEVGSSLDIKNNLNLTPLTLAAKLARIEMFFHILNI
nan-Dpon (286) LLVIYSKVEAFDMAYELGAHLSIRNILKMTPLTLAAKLARMDIFFHILKL
nan-Tcas (286) LLVILQKLEAFDMAYEVGAKLSIRNVLSLTPLTLAAKLARIDMFFHILNL
351 400
nan-Aaeg (337) EREIYWQLGAITCAAYPLALIDTIDIETGNINKDSALNLVVFGDKAEHLD
nan-Cqui (337) EREIYWQLGSITCAAYPLALLDTIDIETGNISKDSALNLVVFGDKDEHLD
nan-Adar (337) EREIYWQLGSITCAAYPLVLIDTIDVETGNISKDSALNLVVFGDKDEHLD
nan-Agam (337) EREIYWQLGSITCAAYPLGLIDTIDVETGNINKDSALNLVAFGDKDEHLD
nan-Ccap (337) EREIYWQLGSITCAAYPLSMIDTIDVETGNINKDSVLNFVVFGDKLEHLE
nan-Mdom (337) EREIYWQLGSITCAAYPLSKIDTIDVKTGNINKDSVLNFVVFGDKLEHLE
nan-Dmel (337) EREIYWQLGSITCAAYPLLMIDTINEETGNINKDSVLNFVVFGDKLEHLE
nan-Aech (334) EREIYWQIGSITCAAYPLSQIDTIDVNTGTINNNSALNLVVFGDKDEHLE
nan-Sinv (303) EREIYWQIGSITCAAYPLSQIDTIDVNTGTINKTSALNLVVFGDKDEHLE
nan-Cflo (334) EREIYWQIGSITCAAYPLSQIDTIDVNAGTINNNSALNLVVFGEKDEHLE
nan-Hsal (336) EREIYWQIGSITCAAYPLSQIDTIDINIGTINKNSALNLVVFGEKDEHLE
nan-Aflo (337) EREIYWQIGSITCAAYPLSQVDTIDVDTGSISHNSALNLVVFGEKDEHLE
nan-Amel (336) EREIYWQIGSITCAAYPLSQVDTIDVDTGSISHNSALNLVVFGEKDEHLE
nan-Mrot (336) EREIYWQIGSITCAAYPLSQVDTIDVNTGSISHTSALNLVVFGEKDEHLE
nan-Nvit (346) EREIYWQIGSITCAAYPLSQIDTIDVDTGKISNNSALNLVVFGDKEEHLK
nan-Apis (335) EREIYWQIGSITCAAYPLTQIDTIDNDTGQISRNSALNLVVFGESPEHLE
nan-Mper partial (282) EREIYWQIGSITCAAYPLXXXXXXXXXXXXXXXXXXXXXXXXXXXHLE
nan-Nlug partial (154) EREIYWQIGSITCAAYPLMLIDTIDIETGXISKDSALNLVVFGDKDEHLD
nan-Bmor (337) EREIYWQIGATTCAAYPLGQVDTIDTETGLISKDSALNLVVFGEKDEHLG
nan-Btab_partial (222) EREIYWQIGSIACAAYPLGQIDTIDIETGHISKNSALNLVVFGDKDEHLE
nan-Dple (311) EREIYWQIGATTCAAYPLGQVDTIDTETGRISKDSALNLVVFGVS-----
nan-Eher partial (176) EREIYWQIGSITCAAYPLSQIDTIDIVTGNISKNSALNLVVFGEKDEHLE
nan-Phum (345) EREIYWQIGSITCAAYPLSQIDTIDIETGNISKNSALNLVVFGEKDEHLE
nan-Same partial (154) EREIYWQIG----------
nan-Dpon (336) EREIYWQIGSITCAAYPLSQIDTIDVKTGQISKMSALNLVVFGDKDEHLE
nan-Tcas (336) EREIYWQIGSITCAAYPLSQIDTIDIETGQISKTSALNLVVFGDKDEHLE

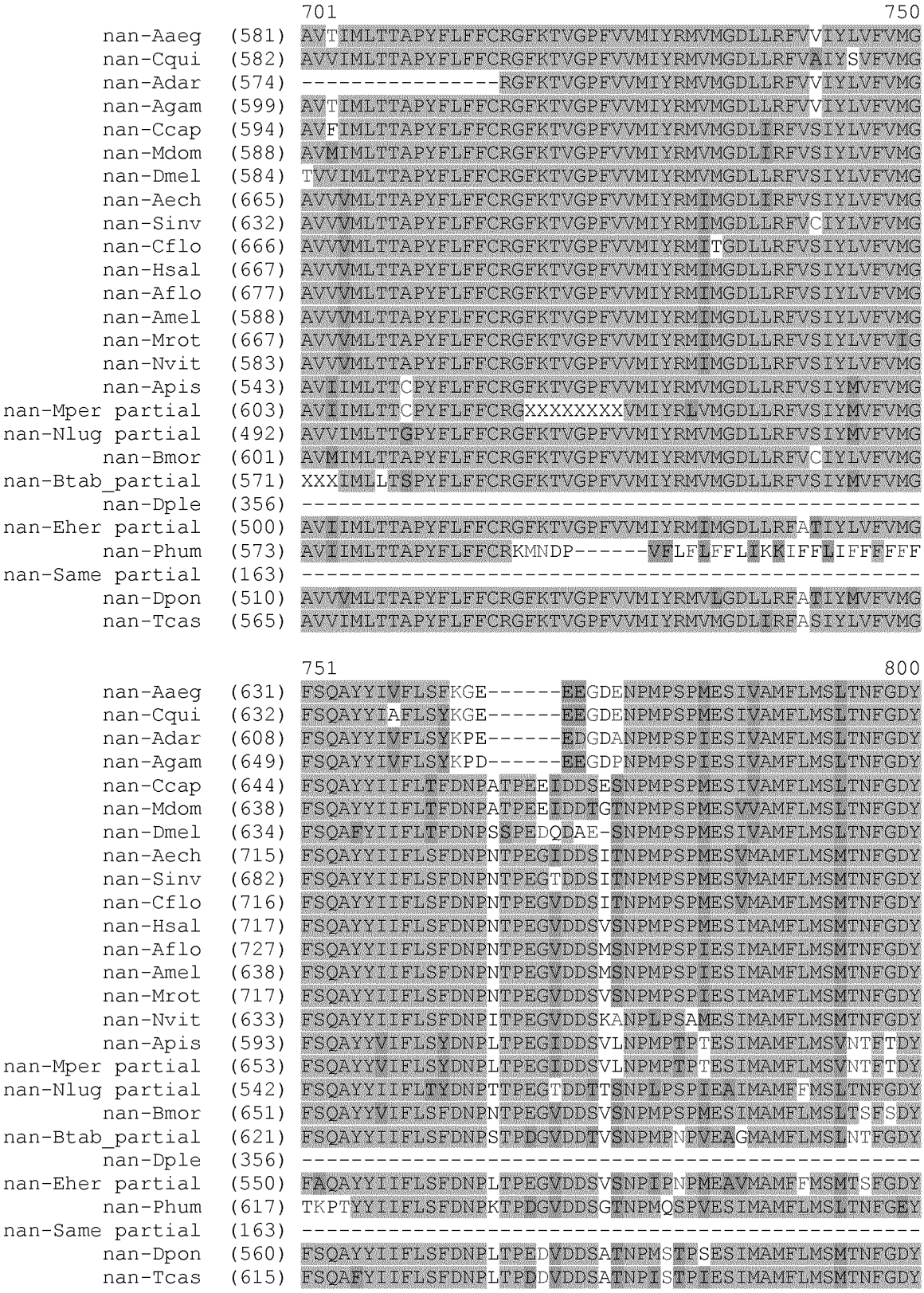
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                          401                                                450
        nan-Aaeg  (387) LLEGVLIDLLKTKWNSFVKDKFYRQFFVFFWYFCVSLVSFTLRRGPM---
        nan-Cqui  (387) LLEGVLIDLLKTKWNTFVKDKFYSQFFVFFCYFCVSLISFTLREGPM---
        nan-Adar  (387) LLDGVLIDLLKTKWNTFVKDKFYRQFFMFFCYFCVSLIGFTLRNGPP---
        nan-Agam  (387) LLDGVLIDLLKTKWNTFVKDKFYRQFFMFFCYFCVSLVSFTLRNGPP---
        nan-Ccap  (387) LLDGVVIDLLKTKWESFVKSRFYKQFYMFSFYFLFSLISFISRPGP----
        nan-Mdom  (387) LLDGVVIDLLKTKWETFVKSRFYKQFYMFSFYFLFSLVSFISRPGPKI--
        nan-Dmel  (387) LLDGVVIDLLKTKWDTFCKSRFYKQFYMFALYFLISLFSFILRPGP----
        nan-Aech  (384) LMDGVLVDLLNAKWNTFVKSRFYNQFFLFCFYFVLSLISFTLRPGPSTIE
        nan-Sinv  (353) LMDGMLVDLLNAKWNTFVKSRFYRQFFLFCFHFVLSLISFTLRPGPSTME
        nan-Cflo  (384) LMDGVLIDLLNAKWNTFVKFRFYRQFILFYFYFVLSLISFTLRPGP---Q
        nan-Hsal  (386) LMDGMLVDLLNAKWNTFVKSRFYRQFFLFCFYFVLSLISFTLRPGP-LPQ
        nan-Aflo  (387) LMDGILVDLLNAKWNTFVKFRFYRQFFXFCFYFVLSLISFTLRPGPATTS
        nan-Amel  (386) LMDGILVDLLNAKWNTFVKFRFYRQFFLFCFYFVLSLISFTLRPGPATTS
        nan-Mrot  (386) LMDGTMVDLLNAKWNTFVKSRFYRQFFLFCFYFILYLISFTLRPGPSVTS
        nan-Nvit  (396) LLEGVLIDLLNAKWNTFVKSRFYQQFYLFFCYFILSLISCTLRPGP----
        nan-Apis  (385) MMDGVLVDLLNAKWNAFVKFRFYRQFILFAFYFSISMVCFVLRPGPPPTG
nan-Mper partial  (332) MMDGVLVDLLNAKWNAFVKFRFYRQFILFAFYFSISMVCFVLRPGPPPTG
nan-Nlug partial  (204) LMEGVLVDLLHAKWNAFVKFRFYRQFIMFFQYFLISCVCFILRPGPPEAH
        nan-Bmor  (387) LLEGMLIDLLKTKWNTFVKFRFYRQFILFSCYFLVSLICFTLRPGPPD--
nan-Btab_partial  (272) LMDGVLVDLLNAKWNAFVKLRXXXXXXXXXXXXXXXXXXXXXXXXXXXX
        nan-Dple  (356) ------------------------------------------------------
nan-Eher partial  (226) LMDGVLIDLLNAKWNAFVKFRFYRQFFLFLFYFLISLICFTLRPGPPPVK
        nan-Phum  (395) LMDGVLVDLLVAKWNTYVKFRFYRQFISFFFYFLISVICFTLRPGPP---
nan-Same partial  (163) ------------------------------------------------------
        nan-Dpon  (386) LLDGVLVDLLNAKWNTFVKSKFYRQFFTFAFYFTVSLVDTSN--------
        nan-Tcas  (386) LMDGVLIDLLNAKWNTFVKFKFYKQFFTFAFYFLISLVAFTLRPGP----

                          451                                                500
        nan-Aaeg  (434) ------------------------------------------------------
        nan-Cqui  (434) ------------------------------------------------------
        nan-Adar  (434) ------------------------------------------------------
        nan-Agam  (434) ------------------------------------------------------
        nan-Ccap  (433) ------------------------------------------------------
        nan-Mdom  (435) ------------------------------------------------------
        nan-Dmel  (433) ------------------------------------------------------
        nan-Aech  (434) TDEN------ANDTSTRTNSSNITEPIIHKTLQSSDLSELVTNSLVAAFT
        nan-Sinv  (403) TDEN------ANDTSTKTNSSNITEPIILKPLQSSDLSELVTNSFVAAFA
        nan-Cflo  (431) TDEN------ANDTLTNSFN-TTRESMILKSLHSSDLSELVTNSFTAAFT
        nan-Hsal  (435) ETEN------ANDTRTNSSN--ATAMEILRLFQSSDLSNLVTNSLAAAFA
        nan-Aflo  (437) SVPNPVAQTPLTSTELSTISPKVDPPVSNVTVNRSSNAFQHDSNLSLLLD
        nan-Amel  (436) ------------------------------------------------------
        nan-Mrot  (436) --------TATTAPTTESTTPKLPDPPPN-FIPVTNQKTFLEASLSSSLD
        nan-Nvit  (442) ------------------------------------------------------
        nan-Apis  (435) LKPPLINYTSTSTT------------------------------------------
nan-Mper partial  (382) LKPPLINYTSTSTTVATTPFDFMDNESMLPDNV------MYDEMMIGGGG
nan-Nlug partial  (254) DGMNITANATLNLSFGVLEVRPEALQALLYRLEKLSLPQSGDLERFILES
        nan-Bmor  (435) ------------------------------------------------------
nan-Btab_partial  (322) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
        nan-Dple  (356) ------------------------------------------------------
nan-Eher partial  (276) PISSFNSTKPS-GNNITAELSPESNATTVPKWIYKTEIKKYDPEDNSSQN
        nan-Phum  (442) ------------------------------------------------------
nan-Same partial  (163) ------------------------------------------------------
        nan-Dpon  (428) ------------------------------------------------------
        nan-Tcas  (432) ------------------------------------------------------
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                        501                                                 550
        nan-Aaeg  (434) ----------------------NLEETAANRTTTSITLKNLTFSDSTNA
        nan-Cqui  (434) ----------------------KLEDGEANKTTTSIQLKNMTLADLTNA
        nan-Adar  (434) ----------------------PPEEDDENRAGGGSGNKTSSASKQDLR
        nan-Agam  (434) ----------------------PAEDDDGKESEAG-GNKTAAVTKEELR
        nan-Ccap  (433) ----------------------TEKNEDDDDDDDADASVEATVTRAANS
        nan-Mdom  (435) ----------------------EDEDEEGDANDSAGKGNDSTTNARLLY
        nan-Dmel  (433) ----------------------DAKDEDEDGANSTTAKSDLYRQNGSDS
        nan-Aech  (478) SNFKSSLN-----MTQESLEK--IQLQVTSNITSALKSILLLTLNENEGI
        nan-Sinv  (447) SNLKSSLN-----MTQESLEK--IQLQVTSNITSALKSILLLTLNENEGI
        nan-Cflo  (474) SNFKSSLN-----VTQESLEK--IQLQVTSNVTSALRSILLLTLSNNEDL
        nan-Hsal  (477) SNLKSSLN-----VTQESLEK--IQLQVTSNITSALKNILPS-LSDNEGI
        nan-Aflo  (487) KILSTASVKYPWNVTRTRLDK--LKLDIIENLTTALNNLLST----HRDE
        nan-Amel  (436) ----------------------S-LDIVENLTSALSDMLGT----YRNE
        nan-Mrot  (477) EIVTNALNLNFPSNATARFDD--LKLDLVTHIMSNLKNILNG----NETK
        nan-Nvit  (442) --------------------------------ITKTDAPT-------T
        nan-Apis  (449) --------------------------------------------------
nan-Mper partial  (426) P----------------------TEFETPVVTTEMATVNDNATTNNGTGI
nan-Nlug partial  (304) LADEKSISEAALENDENRX-----------PGWNNSVFSTYETLARDTGY
        nan-Bmor  (435) ----------------------RALNTTVLNSTIGPNVTDAELVSDVEN
nan-Btab_partial  (372) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
        nan-Dple  (356) --------------------------------------------------
nan-Eher partial  (325) SRLNVILREVILTSLKVED--------------ID----KVVSFSNAEPQ
        nan-Phum  (442) -------------------------------TGTTTTTNGIVVLNNNNNNI
nan-Same partial  (163) --------------------------------------------------
        nan-Dpon  (428) --------------------------------------------------
        nan-Tcas  (432) ----------------------------------PHKEA--------

                        551                                                 600
        nan-Aaeg  (461) -TLPTLLAADVNEKIVQFIAN-------------------------ETLF
        nan-Cqui  (461) STLSSLLVTDVSGKIVGLNGS-------------------------ETFF
        nan-Adar  (461) QRLWNRTVTLEDADNVSSLLSDIMGIDALGKLA----EQLLNGSEGSGAF
        nan-Agam  (460) RQLWNETTLEDALAALAGNGS------FAGRLS----NLEQSNGSSDAMG
        nan-Ccap  (460) TAPLQRGDQWFKRLIKRAIDKMEYKTFWLN--------------FTDYFD
        nan-Mdom  (462) ATPASR---------VTGIEKLPYKTFWLN--------------FSEYID
        nan-Dmel  (460) YHLHSK----------RATMTTEYKTFWLN--------------FTEYYD
        nan-Aech  (521) LSPPDEATIHTLWYTDSPPNASDYFMNTYNKT---DANSTVKTIIDGVAR
        nan-Sinv  (490) LSPPDEATIHTPWYTDSSPNTSDYFTDLYNKTV-VAENSTVKAVVDDVAQ
        nan-Cflo  (517) LSSPDEAAIHTLWYTDNPQNASDYFINMYNKTVTIDTNSTAKTTIDDVTL
        nan-Hsal  (519) LSAPDEAAIRTLWYTSSPYNESDYLTDAYNENVTSDANSTAGTIIGSIEV
        nan-Aflo  (531) IEFFNHSYKTTEYFHSTRNDTTPIDNLKITINE--TVLSVNSTILFNDGI
        nan-Amel  (458) IKLFNRSDKTSIYSS--RNDAKPID----------------ETIFFPSYF
        nan-Mrot  (521) NEPFNSSQLARFDKHLFRENDTDYSTSILNETA--DVDSTTKFSFDNSVL
        nan-Nvit  (451) --TPHPMNDTSLYADVNETSASDPF----------DLNASDIVILKKGKK
        nan-Apis  (449) --------------------------------------------------
nan-Mper partial  (454) IRTPLIYEDGAGGGGGSGTVSLHGKSSGSDRGKHRSTWNPANHTFKTNYT
nan-Nlug partial  (343) QTDESPHDGLSSSMDYAEVAERLTKLMIDVNLTERSGAVNEIILKALPSL
        nan-Bmor  (462) CTMTPNADFDTNAVEVLNGTKFGGSHCARFKSH----P------KEKSTE
nan-Btab_partial  (422) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
        nan-Dple  (356) --------------------------------------------------
nan-Eher partial  (357) DNSREDADGLVCNGDSVHSCLGNGSDVVAVFGKGKSPKVPK------PGA
        nan-Phum  (462) TSVVDN--------S-----------------------------NNVTT
nan-Same partial  (163) --------------------------------------------------
        nan-Dpon  (428) --------------------------------------------------
        nan-Tcas  (437) -------KLVNVTINATVSNTSKWE-------------NLTSIPFGKTPD
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601 650
nan-Aaeg (485) DPAVMEEN---TFFNSKCATMAYDTLQDKIRLVSEIIILIGSFLYLVGAL
nan-Cqui (486) DPSTIESD---MFFNSKCPTMIYKGIEGKIRLVSEAIILVGSFLYLVSAL
nan-Adar (507) KPETVEEEEDGLFFNSKCHTMDYDGVEGKVRFVAEVIILIGSFLYLLSAL
nan-Agam (500) EFDPAEMDDEGLFFNSNCHTMDYDGVEGKVRLISEMIILVGSFLYLLAAL
nan-Ccap (496) DN-DVESVPPWWASYAECPLMNMESDLAKLRIVAEIIIFFGSVLYLFAAL
nan-Mdom (489) DDANAENMPSWWASYEECPLMDMETNLAKFRIVSEIVIFFGAILYLLSAL
nan-Dmel (486) PS-EVEVLPAWWESYAQCPLMNLESDLAKLRIMAELLNFVGAILYLLVAL
nan-Aech (568) P--KFKSNYWWDDFSEECRLMQLSEMSAKIRLTAEIFMFIAAVLYILAAL
nan-Sinv (539) ------TDYWWDDFAEECRLMQLTETSAKIRLTAETFMYIAAVLYILAAL
nan-Cflo (567) LGKFNNHEKWWDDLTEECRLMQLTTMSAKIRLTAEIVMYFAAVLYILAAL
nan-Hsal (569) S-KSNDKDNWWEDLTEECRLMQLTTISAKIRLTAEVLMEIAAVLYILAAL
nan-Aflo (579) S-FATGKYNWWNNLTEECRLMHVDTLSTKIRLTAEVLMEIAATLYIFAAL
nan-Amel (490) S-KSLVSNVRWNNLTEECRLMHLDTLSTKIRLTAEVLMEIAATLYIFAAL
nan-Mrot (569) F-EADNKSDWWTDLTTECRLMQLTTASAKIRLIAEIFMEIAAILYILAAL
nan-Nvit (489) E-----LDDWWDDLTEDCRLMQMNSTSAKIRLTAEIFMEFGAILYICAAL
nan-Apis (449) -----SRKFWWNKRQKVCRLMAVHSTDDLIRMGSEVGMFMGAFLYLLAAV
nan-Mper partial (504) YNYNKSRKFWWNKRQKVCRLMAVHSTDDLIRMGSEVGMFVGAFLYLLAAV
nan-Nlug partial (393) EEKEDGLEEWWSGIAGDCILLQVNDLYDLARLCAEVALEIGAFLYLLAAL
nan-Bmor (502) APRENDVEGWWEDLTEECRLMNLDTWQAKLRISAELLLWMGALAYFGAAL
nan-Btab_partial (472) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
nan-Dple (356) ----------
nan-Eher partial (401) SADDFDYDDTWWEEFGQCRLLQVTSYIEMTRLISEVLLDIGALLYILAAL
nan-Phum (474) TTATTTATSYSFPGHVIVTLLSYDKYEDKIRIISELAMEIGSVLYLLGAL
nan-Same partial (163) ----------
nan-Dpon (428) --DDYDVEEWWDNLREECRLMNLDTTESLVRFTAELGITFGAFLYLAAAM
nan-Tcas (467) D-DDSDMEEWWDNLQEECRLMQLESPESKIRLTAEVLMVVGAFAYLAAAV
651 700
nan-Aaeg (532) REFRFLGRKMFFENLMISPSRVMFLFSCCIMM-IVPFLKVLCLIELEDHV
nan-Cqui (533) RESRFLGRKMFIENLMTAPSRVMFLFSCCIMM-VVPCLKVLCFTELEDHV
nan-Adar (557) RELKFLGRKMFFENLVS----------
nan-Agam (550) RELKFLGRKMFFENLMTAPSRVMFLFSCCIMM-IVPFLKVLCFTELEDHV
nan-Ccap (545) REARFLGYKMFVENMMTAPSRVMFLFSCALMM-SIPWLRVFCLTEIDDHV
nan-Mdom (539) REAKFLGYKMFVENLMTAPSRVMFLFSCCLMM-TIPWLRLSCLTELDDHV
nan-Dmel (535) REARFLGLKMFIENLMTAPSRVMFLFSCALMM-TIPWLRVSCLTEIDDHV
nan-Aech (616) REAKFLGLHMFIENLMTVPSRVMFLISCCILM-WFPVLRFTCSDEVEDML
nan-Sinv (583) REARFLGLNMFIENLATAPSRVMFLFSCCILL-SFPFLRFVCADEIEDIL
nan-Cflo (617) REARFLGLNMFIENLMTAPSRVMFLFSCCILM-SFPVLRLSCSDEVEDVL
nan-Hsal (618) REARFLGLNMFVENLMTAPSRVMFLFSCCILL-SFPFLRLACADEVEDML
nan-Aflo (628) REARFLGLNMFIENLMTAPSRVMFLFSCCILL-TFPFLRLICADQVEDML
nan-Amel (539) REARFLGLNMFIENLMTAPSRVMFLFSCCILL-TFPFLRLICADEIEDML
nan-Mrot (618) REARFLGLNMFIENLMTVPSRVMFLFSCCILL-SFPFLRLSCADEVEDVL
nan-Nvit (534) REARFLGLNMFIENLMTAPSRVMFLFSCCILL-SFPFLRMSCADEVEDIL
nan-Apis (494) REAGFLGTQMFIENLAIAPARVMFLFSCLLMM-TIPPLRLTCYDKAEDII
nan-Mper partial (554) REAGFLGSQMFIENLAIAPARVMFLFSCLLMM-TIPPLRLTCYDKAEDII
nan-Nlug partial (443) REARFLGLKMMIENLMTAPSRVMFLFSCCLMM-TMPFFRFTCQDETEDIL
nan-Bmor (552) REAKFLGIKMFIENLSTVPSRVMFLFSCLLML-ILPTLRLWCADEAEDHL
nan-Btab_partial (522) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX-XXXXXXXXXXXXXXXXX
nan-Dple (356) ----------
nan-Eher partial (451) REARFLGWSMFVENLMTAPSRVMFLFSCCLML-TMPFLRFTCNEEIEDMM
nan-Phum (524) REAKFLGIHMFIENLMTAPSRVLFLGSCCIMQ-FVPWLRITCKEETEDIV
nan-Same partial (163) ----------
nan-Dpon (476) ----------TAPSRVMFLFSCILVFGVIPSLRLVCMDEVEDII
nan-Tcas (516) REARFLGGRMFFENLMTAPSRVMFLFSCILML-TVPCLRLACLDEFEDIV


701 750
nan-Aaeg (581) AVTIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVVIYLVFVMG
nan-Cqui (582) AVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVAIYSVFVMG
nan-Adar (574) ----------RGFKTVGPFVVMIYRMVMGDLLRFVVIYLVFVMG
nan-Agam (599) AVTIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVVIYLVFVMG
nan-Ccap (594) AVFIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLIRFVSIYLVFVMG
nan-Mdom (588) AVMIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLIRFVSIYLVFVMG
nan-Dmel (584) TVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVSIYLVFVMG
nan-Aech (665) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLIRFVSIYLVFVMG
nan-Sinv (632) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVCIYLVFVMG
nan-Cflo (666) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMITGDLLRFVSIYLVFVMG
nan-Hsal (667) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVSIYLVFVMG
nan-Aflo (677) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVSIYLVFVMG
nan-Amel (588) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVSIYLVFVMG
nan-Mrot (667) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVSIYLVFVIG
nan-Nvit (583) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFVSIYLVFVMG
nan-Apis (543) AVIIMLTTCPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVSIYMVFVMG
nan-Mper partial (603) AVIIMLTTCPYFLFFCRGXXXXXXXXVMIYRLVMGDLLRFVSIYMVFVMG
nan-Nlug partial (492) AVVIMLTTGPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVSIYMVFVMG
nan-Bmor (601) AVMIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVCIYLVFVMG
nan-Btab_partial (571) XXXIMLLTSPYFLFFCRGFKTVGPFVVMIYRMVMGDLLRFVSIYMVFVMG
nan-Dple (356) ----------
nan-Eher partial (500) AVIIMLTTAPYFLFFCRGFKTVGPFVVMIYRMIMGDLLRFATIYLVFVMG
nan-Phum (573) AVIIMLTTAPYFLFFCRKMNDP------VFLFLFFLIKKIFFLIFFFFFF
nan-Same partial (163) ----------
nan-Dpon (510) AVVVMLTTAPYFLFFCRGFKTVGPFVVMIYRMVLGDLLRFATIYMVFVMG
nan-Tcas (565) AVVIMLTTAPYFLFFCRGFKTVGPFVVMIYRMVMGDLIRFASIYLVFVMG
751 800
nan-Aaeg (631) FSQAYYIVFLSFKGE------EEGDENPMPSPMESIVAMFLMSLTNFGDY
nan-Cqui (632) FSQAYYIAFLSYKGE------EEGDENPMPSPMESIVAMFLMSLTNFGDY
nan-Adar (608) FSQAYYIVFLSYKPE------EDGDANPMPSPIESIVAMFLMSLTNFGDY
nan-Agam (649) FSQAYYIVFLSYKPD------EEGDPNPMPSPIESIVAMFLMSLTNFGDY
nan-Ccap (644) FSQAYYIIFLTFDNPATPEEIDDSESNPMPSPMESIVAMFLMSLTNFGDY
nan-Mdom (638) FSQAYYIIFLTFDNPATPEEIDDTGTNPMPSPMESVVAMFLMSLTNFGDY
nan-Dmel (634) FSQAFYIIFLTFDNPSSPEDQDAE-SNPMPSPMESIVAMFLMSLTNFGDY
nan-Aech (715) FSQAYYIIFLSFDNPNTPEGIDDSITNPMPSPMESVMAMFLMSMTNFGDY
nan-Sinv (682) FSQAYYIIFLSFDNPNTPEGTDDSITNPMPSPMESVMAMFLMSMTNFGDY
nan-Cflo (716) FSQAYYIIFLSFDNPNTPEGVDDSITNPMPSPMESVMAMFLMSMTNFGDY
nan-Hsal (717) FSQAYYIIFLSFDNPNTPEGVDDSVSNPMPSPMESIMAMFLMSMTNFGDY
nan-Aflo (727) FSQAYYIIFLSFDNPNTPEGVDDSMSNPMPSPIESIMAMFLMSMTNFGDY
nan-Amel (638) FSQAYYIIFLSFDNPNTPEGVDDSMSNPMPSPIESIMAMFLMSMTNFGDY
nan-Mrot (717) FSQAYYIIFLSFDNPNTPEGVDDSVSNPMPSPIESIMAMFLMSMTNFGDY
nan-Nvit (633) FSQAYYIIFLSFDNPITPEGVDDSKANPLPSAMESIMAMFLMSMTNFGDY
nan-Apis (593) FSQAYYVIFLSYDNPLTPEGIDDSVLNPMPTPTESIMAMFLMSVNTFTDY
nan-Mper partial (653) FSQAYYVIFLSYDNPLTPEGIDDSVLNPMPTPTESIMAMFLMSVNTFTDY
nan-Nlug partial (542) FSQAYYIIFLTYDNPTTPEGTDDTTSNPLPSPIEAIMAMFFMSLTNFGDY
nan-Bmor (651) FSQAYYVIFLSFDNPNTPEGVDDSVSNPMPSPMESIMAMFLMSLTSFSDY
nan-Btab_partial (621) FSQAYYIIFLSFDNPSTPDGVDDTVSNPMPNPVEAGMAMFLMSLNTFGDY
nan-Dple (356) ----------
nan-Eher partial (550) FAQAYYIIFLSFDNPLTPEGVDDSVSNPIPNPMEAVMAMFFMSMTSFGDY
nan-Phum (617) TKPTYYIIFLSFDNPKTPDGVDDSGTNPMQSPVESIMAMFLMSLTNFGEY
nan-Same partial (163) ----------
nan-Dpon (560) FSQAYYIIFLSFDNPLTPEDVDDSATNPMSTPSESIMAMFLMSMTNFGDY
nan-Tcas (615) FSQAFYIIFLSFDNPLTPDDVDDSATNPISTPIESIMAMFLMSMTNFGDY

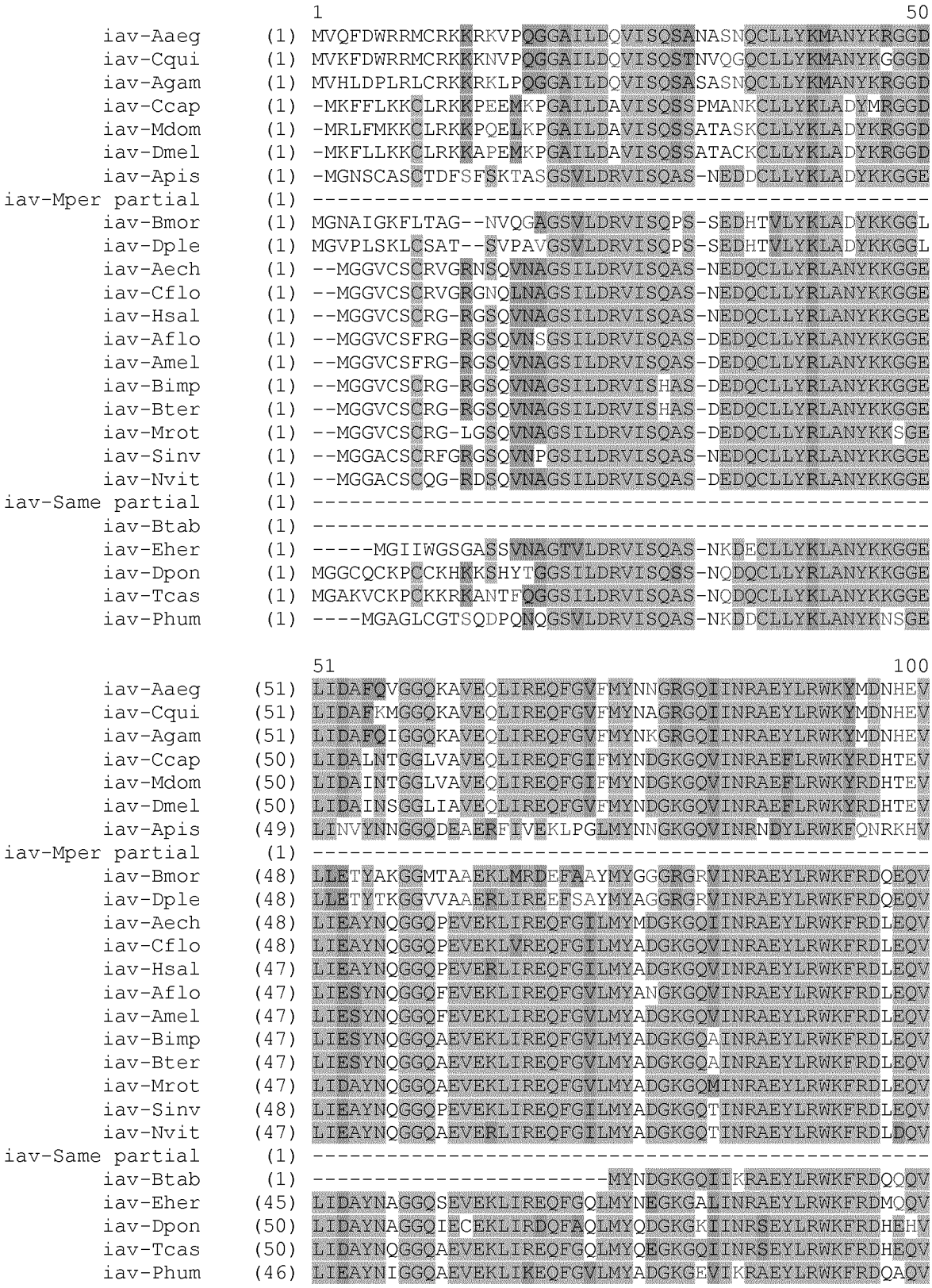
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                          801                                                 850
        nan-Aaeg  (675) YGALEKTEHEGCAKVLFVIFMVIVAVLLVNLLIAMMGNTYTMIAETKNEW
        nan-Cqui  (676) YAALEDTAHEGCAKVLFVTYMVIVAVLLVNLLIAMMGNTYTKIAETKNEW
        nan-Adar  (652) YGALENTDHEMCAKILFVLFMVIVAVLLVNMLIAMMGNTYQKIAETKNEW
        nan-Agam  (693) YGALENTDHEMCAKILFVLFMVIVAVLLVNMLIAMMGNTYQKIAETKNEW
        nan-Ccap  (694) FGGMASTQHEYEAKTLFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEW
        nan-Mdom  (688) YGAMGSTQHEYEAKILFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEW
        nan-Dmel  (683) YGAMVSTQHEYEAKILFFLFMVIVSVLLVNMLIAMMGNTYQKIAEIRNEW
        nan-Aech  (765) FGAFDRTEHEFEAKLLFVLYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Sinv  (732) FGAFERTEHEFEAKLLFVLYMVIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Cflo  (766) YATFDRTEHEFEAKLLFVLYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Hsal  (767) YGAFERTEHESEAKLLFVLYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Aflo  (777) YGAFERTQHEIEAKFLFVVYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Amel  (688) YGAFERTQHEMEAKFLFVVYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Mrot  (767) YGAFERTRHEMEAKFLFVVYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Nvit  (683) YDAFENTEHEMLAKCLFVVYMAIVSVLLVNMLIAMMGNTYQKIAETRNEW
        nan-Apis  (643) YTAFDKTSHTLVAKFCFIVFMVIVAILLVNMLIAMMGNTYQKIAETRNEW
nan-Mper partial  (703) YTAFDKTSHTLVAKFCFIVFMVIVAILPVNMLIAMMGDTYQKIAETRNEW
nan-Nlug partial  (592) YSAFENTEHEIEAKAFFVIYMVIVAILLINMLIAMMGNTYQKIAETKNEW
        nan-Bmor  (701) YTAFDRTDHEIEAKLLFVIYMIIVAILLVNMLIAMMGNTYQKIAETRNEW
nan-Btab_partial  (671) FSAFEKTEHELEAKVCFVIFMGIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Dple  (356) ----------------------------------------------------
nan-Eher partial  (600) YPALERTAHEFCAKLCFVIYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
        nan-Phum  (667) YGAFEKTEHEFVAKLMFVVYMAIVAILLVNMLIAMMGNTYQKIAETRNEW
nan-Same partial  (163) ----------------------------------------------------
        nan-Dpon  (610) YTAFARTEHEYEAKILFVIFMAIVAILLINMLIAMMGNTYQKIAETRNEW
        nan-Tcas  (665) YAAFEKTDHEYEAKMLFVVFMVIVSILLINMLIAMMGNTYQKIAETRNEW

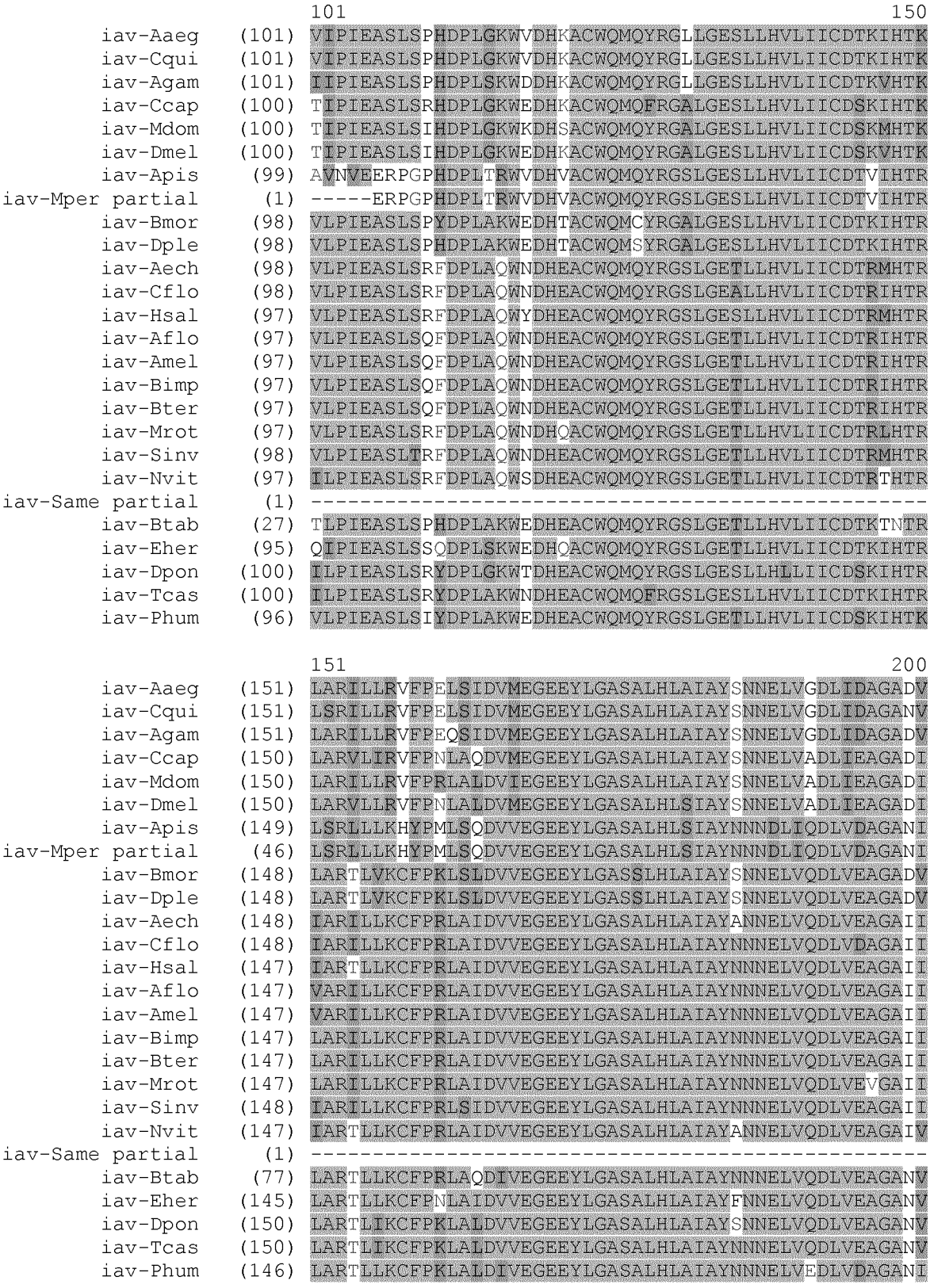
                          851                                                 900
        nan-Aaeg  (725) QRQWARIVLVVERGVPPSERLKNFMSYSQPMSDGRRALVLRLHMTDEDKE
        nan-Cqui  (726) QRQWARIVLVVERGVPPAERLKNLMNYSQPMSDGRRALVLRLNMTEEDKE
        nan-Adar  (702) QRQWARIVLVVERGVPPKERLKNLMSYSQPMSDGRRALVLRLNMTDEDKE
        nan-Agam  (743) QRQWARIVLVVERGVPPKERLKNLMSYSQPMSDGRRALVLRLNMT-EDKE
        nan-Ccap  (744) QRQWARIVLVVERSVPPAERLKNFMHYSQPMSDGRRALVLRLNMSDEVKE
        nan-Mdom  (738) QRQWARIVLVVERSVPPAERLKNFMQYSQPMSDGRRALVLRLNMSDEDKE
        nan-Dmel  (733) QRQWARIVLVVERSVPPAERLKNFMQYSQSMSDGRRALVLRLNMTEE-KE
        nan-Aech  (815) QRQ-----------------------------------------EEDKE
        nan-Sinv  (782) QRQWARIVLVVERGVSPAERLKKLTDYSQPMSDGRPALVLRLHQTEEDKE
        nan-Cflo  (816) QRQWARIVLVVERGVSPAERLKKLMDYSQPMSDGRKALVLRLNQTEEDKE
        nan-Hsal  (817) QRQWARIVLVVERGVSPAERLKKLMDYSQPMSGGRRALVLRLNQSEEDKE
        nan-Aflo  (827) QRQWARIVLVVERGVSPEERLKKLMDYSQPMSDGRRALVLRLNQSEEDKE
        nan-Amel  (738) QRQWARIVLVVERGVSPDERLKKLMDYSQPMSDGRRALVLRLNQSEEDKE
        nan-Mrot  (817) QRQWARIVLVVERGVSPQERLKKLMDYSQPMSDGRRALVLRLNQSEEDKE
        nan-Nvit  (733) QRQWARIVLVVERGVAPAERLKKLNVYSQPMSDGRKALVLRLNQTDKDKE
        nan-Apis  (693) QRQWARIVLVVERGVSPSQRLIKLMYYSQPMSDGRRALVLRLNQTDEDKE
nan-Mper partial  (753) QRQWARIVLVVERGVSPSQRLKKLMYYSQPMSDGRRALVLRLNQTDEDKE
nan-Nlug partial  (642) QRQWARIVLVVERGVSPKERLKKLMSYSQPMSDGGRALVLRLNMTEEDKE
        nan-Bmor  (751) QRQWARIVLVVERGVPPAQRLKQLMTYSQPMANGKRALVLRINQKDEDKE
nan-Btab_partial  (721) QRQWARIVLVVERGVPPKERLTKLMWYSQPMSDGRRALVLRLNQTEQDKE
        nan-Dple  (356) ----------------------------------------------------
nan-Eher partial  (650) QRQWARIVLVVERGVSPSERLTKLMWYSQPMSDGRRALVLRLNQSEEDKE
        nan-Phum  (717) QRQWARIVLVVERGVSPQERLKKLMLYSQPMSDGRRALVLRLHQTPEDKE
nan-Same partial  (163) ----------------------------------------------------
        nan-Dpon  (660) QRQWARIVLVVERGVSPPERLKQLNVYSQPMSDGKRALVLRLNQSVRY--
        nan-Tcas  (715) QRQWARIVLVVERGVSPSERLKQLMVYSQPMSDGRRALVLRLNQSDEDKE
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```
                          901                                                 950
        nan-Aaeg  (775) EMKEILEMKRVHERLKKKRQVERELRAEQRRLIME------KYANVP---
        nan-Cqui  (776) EMKEILDMKRVHERLSKKRAVEREARAEQRRLIAE------KYANVP---
        nan-Adar  (752) EMKEILEMKRVHERLSKKRQVERDARAEQRRLLRE------KYLNMT---
        nan-Agam  (792) EMKEILEMKRVHERLSIKRQIERDARAEQRRLLRE------KYLNMSS--
        nan-Ccap  (794) EMKEVQETKRIHQRFSKKRQIEREARAQKRQEEYE------KFFGKKP-S
        nan-Mdom  (788) EMKEVQEMKRIHQRFSKKRQMEREARAKKRQEEYE------KFFGATP-T
        nan-Dmel  (782) EMKEVQEMKRIHQRFAKKRQMEREARALRRQQEYE------KFFGTAPKS
        nan-Aech  (823) EMKEILEMKRTHDRLLKKRQNRMSKEKIIFETEPI------ITKN-----
        nan-Sinv  (832) EMKEILEMKRTHEKLLKKRQCRMSKEKILS----------------------
        nan-Cflo  (866) EMKEILEMKRTHDKLIKKRQDKILKEKALAETEAV------ITRK-----
        nan-Hsal  (867) EMKEILEMKRTHDRLLKKRQGRMSKEKVLAESEII------ITRN-----
        nan-Aflo  (877) EMKEILEMKRTHDKLYKKRQSK-IMKKILTSEDNV------IL-------
        nan-Amel  (788) EMKEILEMKRTHDKLYKRRQSK-TMKKILTSEDNV------IL-------
        nan-Mrot  (867) EMKEILEMKRTHERLYKKRQLKTTKEKTTITEENV------TL-------
        nan-Nvit  (783) EMKDILEMKRIHIKSIKRRKDKLQKAKEDAEKLQQ------QMADKDNKD
        nan-Apis  (743) QMKEILEMKRIHNRYVERMRARDLSSKLSSSCGKNANNGTFNLKANE---
nan-Mper partial  (803) QMKEILEMKRIHNRYVERMRARDLSSKLSSSCGKNANDGTINLKANK---
nan-Nlug partial  (692) EMKEILEMKRVRDKIVMKR-KKGLKLLGTTTPSPK------RMKGRETPI
        nan-Bmor  (801) EMKEILEMKRTHERIVAKRKQREALKPGEIPPPAR------DYPIRK---
nan-Btab_partial  (771) EMKEILEMKRVHNRIVEKRQKRLAKLSNNASPSNKPLVDLPNLSNHDSPT
        nan-Dple  (356) --------------------------------------------------
nan-Eher partial  (700) EMKEILEMKRIHNRMVQKR-KEREKSMNKS----------PNLINLNSPA
        nan-Phum  (767) EMKEILDMKRIHNRTVQRRKAKENKNVTFAGTPKN------GIKNRLLGP
nan-Same partial  (163) --------------------------------------------------
        nan-Dpon  (708) --------------------------------------------------
        nan-Tcas  (765) EMKEILEMRRRHERHIKKRSEKLKENAKKN------------------

                          951        964
        nan-Aaeg  (816) --------------
        nan-Cqui  (817) --------------
        nan-Adar  (793) --------------
        nan-Agam  (834) --------------
        nan-Ccap  (837) GNSDNNNA------
        nan-Mdom  (831) SDNENNNF------
        nan-Dmel  (826) ECSDNNNF------
        nan-Aech  (862) --------------
        nan-Sinv  (862) --------------
        nan-Cflo  (905) --------------
        nan-Hsal  (906) --------------
        nan-Aflo  (913) --------------
        nan-Amel  (824) --------------
        nan-Mrot  (904) --------------
        nan-Nvit  (827) KAVIIQ--------
        nan-Apis  (790) --------------
nan-Mper partial  (850) --------------
nan-Nlug partial  (735) --------------
        nan-Bmor  (842) --------------
nan-Btab_partial  (821) KPLLDLASNLSKF-
        nan-Dple  (356) --------------
nan-Eher partial  (739) ENVKNTNPFS----
        nan-Phum  (811) VPPLKSIPSKPKI-
nan-Same partial  (163) --------------
        nan-Dpon  (708) --------------
        nan-Tcas  (795) --------------
```

FIGURE 117


1 50
iav-Aaeg (1) MVQFDWRRMCRKKRKVPQGGAILDQVISQSANASNQCLLYKMANYKRGGD
iav-Cqui (1) MVKFDWRRMCRKKKNVPQGGAILDQVISQSTNVQGQCLLYKMANYKGGGD
iav-Agam (1) MVHLDPLRLCRKKRKLPQGGAILDQVISQSASASNQCLLYKMANYKRGGD
iav-Ccap (1) -MKFFLKKCLRKKPEEMKPGAILDAVISQSSPMANKCLLYKLADYMRGGD
iav-Mdom (1) -MRLFMKKCLRKKPQELKPGAILDAVISQSSATASKCLLYKLADYKRGGD
iav-Dmel (1) -MKFLLKKCLRKKAPEMKPGAILDAVISQSSATACKCLLYKLADYKRGGD
iav-Apis (1) -MGNSCASCTDFSFSKTASGSVLDRVISQAS-NEDDCLLYKLADYKKGGE
iav-Mper partial (1) ----------
iav-Bmor (1) MGNAIGKFLTAG--NVQGAGSVLDRVISQPS-SEDHTVLYKLADYKKGGL
iav-Dple (1) MGVPLSKLCSAT--SVPAVGSVLDRVISQPS-SEDHTVLYKLADYKKGGL
iav-Aech (1) --MGGVCSCRVGRNSQVNAGSILDRVISQAS-NEDQCLLYRLANYKKGGE
iav-Cflo (1) --MGGVCSCRVGRGNQLNAGSILDRVISQAS-NEDQCLLYRLANYKKGGE
iav-Hsal (1) --MGGVCSCRG-RGSQVNAGSILDRVISQAS-NEDQCLLYRLANYKKGGE
iav-Aflo (1) --MGGVCSFRG-RGSQVNSGSILDRVISQAS-DEDQCLLYRLANYKKGGE
iav-Amel (1) --MGGVCSFRG-RGSQVNAGSILDRVISQAS-DEDQCLLYRLANYKKGGE
iav-Bimp (1) --MGGVCSCRG-RGSQVNAGSILDRVISHAS-DEDQCLLYRLANYKKGGE
iav-Bter (1) --MGGVCSCRG-RGSQVNAGSILDRVISHAS-DEDQCLLYRLANYKKGGE
iav-Mrot (1) --MGGVCSCRG-LGSQVNAGSILDRVISQAS-DEDQCLLYRLANYKKSGE
iav-Sinv (1) --MGGACSCRFGRGSQVNPGSILDRVISQAS-NEDQCLLYRLANYKKGGE
iav-Nvit (1) --MGGACSCQG-RDSQVNAGSILDRVISQAS-DEDQCLLYRLANYKKGGE
iav-Same partial (1) ----------
iav-Btab (1) ----------
iav-Eher (1) -----MGIIWGSGASSVNAGTVLDRVISQAS-NKDECLLYKLANYKKGGE
iav-Dpon (1) MGGCQCKPCCKHKKSHYTGGSILDRVISQSS-NQDQCLLYRLANYKKGGE
iav-Tcas (1) MGAKVCKPCKKRKANTFQGGSILDRVISQAS-NQDQCLLYKLANYKKGGE
iav-Phum (1) ----MGAGLCGTSQDPQNQGSVLDRVISQAS-NKDDCLLYKLANYKNSGE
51 100
iav-Aaeg (51) LIDAFQVGGQKAVEQLIREQFGVFMYNNGRGQIINRAEYLRWKYMDNHEV
iav-Cqui (51) LIDAFKMGGQKAVEQLIREQFGVFMYNAGRGQIINRAEYLRWKYMDNHEV
iav-Agam (51) LIDAFQIGGQKAVEQLIREQFGVFMYNKGRGQIINRAEYLRWKYMDNHEV
iav-Ccap (50) LIDALNTGGLVAVEQLIREQFGIFMYNDGKGQVINRAEFLRWKYRDHTEV
iav-Mdom (50) LIDAINTGGLVAVEQLIREQFGIFMYNDGKGQVINRAEFLRWKYRDHTEV
iav-Dmel (50) LIDAINSGGLIAVEQLIREQFGVFMYNDGKGQVINRAEFLRWKYRDHTEV
iav-Apis (49) LINVYNNGGQDEAERFIVEKLPGLMYNNGKGQVINRNDYLRWKFQNRKHV
iav-Mper partial (1) ----------
iav-Bmor (48) LLETYAKGGMTAAEKLMRDEFAAYMYGGGRGRVINRAEYLRWKFRDQEQV
iav-Dple (48) LLETYTKGGVVAAERLIREEFSAYMYAGGRGRVINRAEYLRWKFRDQEQV
iav-Aech (48) LIEAYNQGGQPEVEKLIREQFGILMYMDGKGQIINRAEYLRWKFRDLEQV
iav-Cflo (48) LIEAYNQGGQPEVEKLVREQFGILMYADGKGQVINRAEYLRWKFRDLEQV
iav-Hsal (47) LIEAYNQGGQPEVERLIREQFGILMYADGKGQVINRAEYLRWKFRDLEQV
iav-Aflo (47) LIESYNQGGQFEVEKLIREQFGVLMYANGKGQVINRAEYLRWKFRDLEQV
iav-Amel (47) LIESYNQGGQFEVEKLIREQFGVLMYADGKGQVINRAEYLRWKFRDLEQV
iav-Bimp (47) LIESYNQGGQAEVEKLIREQFGVLMYADGKGQAINRAEYLRWKFRDLEQV
iav-Bter (47) LIESYNQGGQAEVEKLIREQFGVLMYADGKGQAINRAEYLRWKFRDLEQV
iav-Mrot (47) LIDAYNQGGQAEVEKLIREQFGVLMYADGKGQMINRAEYLRWKFRDLEQV
iav-Sinv (48) LIEAYNQGGQPEVEKLIREQFGILMYADGKGQTINRAEYLRWKFRDLEQV
iav-Nvit (47) LIEAYNQGGQAEVERLIREQFGILMYADGKGQTINRAEYLRWKFRDLDQV
iav-Same partial (1) ----------
iav-Btab (1) ----------MYNDGKGQIIKRAEYLRWKFRDQQQV
iav-Eher (45) LIDAYNAGGQSEVEKLIREQFGQLMYNEGKGALINRAEYLRWKFRDMQQV
iav-Dpon (50) LIDAYNAGGQIECEKLIRDQFAQLMYQDGKGKIINRSEYLRWKFRDHEHV
iav-Tcas (50) LIDAYNQGGQAEVEKLIREQFGQLMYQEGKGQIINRSEYLRWKFRDHEQV
iav-Phum (46) LIEAYNIGGQAEVEKLIKEQFGVLMYADGKGEVIKRAEYLRWKFRDQAQV


101 150
iav-Aaeg (101) VIPIEASLSPHDPLGKWVDHKACWQMQYRGLLGESLLHVLIICDTKIHTK
iav-Cqui (101) VIPIEASLSPHDPLGKWVDHKACWQMQYRGLLGESLLHVLIICDTKIHTK
iav-Agam (101) IIPIEASLSPHDPLSKWDDHKACWQMQYRGLLGESLLHVLIICDTKVHTK
iav-Ccap (100) TIPIEASLSRHDPLGKWEDHKACWQMQFRGALGESLLHVLIICDSKIHTK
iav-Mdom (100) TIPIEASLSIHDPLGKWKDHSACWQMQYRGALGESLLHVLIICDSKMHTK
iav-Dmel (100) TIPIEASLSIHDPLGKWEDHKACWQMQYRGALGESLLHVLIICDSKVHTK
iav-Apis (99) AVNVEERPGPHDPLTRWVDHVACWQMQYRGSLGESLLHVLIICDTVIHTR
iav-Mper partial (1) -----ERPGPHDPLTRWVDHVACWQMQYRGSLGESLLHVLIICDTVIHTR
iav-Bmor (98) VLPIEASLSPYDPLAKWEDHTACWQMCYRGALGESLLHVLIICDTKIHTR
iav-Dple (98) VLPIEASLSPHDPLAKWEDHTACWQMSYRGALGESLLHVLIICDTKIHTR
iav-Aech (98) VLPIEASLSRFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRMHTR
iav-Cflo (98) VLPIEASLSRFDPLAQWNDHEACWQMQYRGSLGEALLHVLIICDTRIHTR
iav-Hsal (97) VLPIEASLSRFDPLAQWYDHEACWQMQYRGSLGESLLHVLIICDTRMHTR
iav-Aflo (97) VLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTR
iav-Amel (97) VLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTR
iav-Bimp (97) VLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTR
iav-Bter (97) VLPIEASLSQFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRIHTR
iav-Mrot (97) VLPIEASLSRFDPLAQWNDHQACWQMQYRGSLGETLLHVLIICDTRLHTR
iav-Sinv (98) VLPIEASLTRFDPLAQWNDHEACWQMQYRGSLGETLLHVLIICDTRMHTR
iav-Nvit (97) ILPIEASLSRFDPLAQWSDHEACWQMQYRGSLGETLLHVLIICDTRTHTR
iav-Same partial (1) ----------
iav-Btab (27) TLPIEASLSPHDPLAKWEDHEACWQMQYRGSLGETLLHVLIICDTKTNTR
iav-Eher (95) QIPIEASLSSQDPLSKWEDHQACWQMQYRGSLGETLLHVLIICDTKIHTR
iav-Dpon (100) ILPIEASLSRYDPLGKWTDHEACWQMQYRGSLGESLLHLLIICDSKIHTR
iav-Tcas (100) ILPIEASLSRYDPLAKWNDHEACWQMQFRGSLGESLLHVLIICDTKIHTR
iav-Phum (96) VLPIEASLSIYDPLAKWEDHEACWQMQYRGSLGETLLHVLIICDSKIHTK
151 200
iav-Aaeg (151) LARILLRVFPELSIDVMEGEEYLGASALHLAIAYSNNELVGDLIDAGADV
iav-Cqui (151) LSRILLRVFPELSIDVMEGEEYLGASALHLAIAYSNNELVGDLIDAGANV
iav-Agam (151) LARILLRVFPEQSIDVMEGEEYLGASALHLAIAYSNNELVGDLIDAGADV
iav-Ccap (150) LARVLIRVFPNLAQDVMEGEEYLGASALHLAIAYSNNELVADLIEAGADI
iav-Mdom (150) LARILLRVFPRLALDVIEGEEYLGASALHLAIAYSNNELVADLIEAGADI
iav-Dmel (150) LARVLLRVFPNLALDVMEGEEYLGASALHLSIAYSNNELVADLIEAGADI
iav-Apis (149) LSRLLLKHYPMLSQDVVEGEEYLGASALHLSIAYNNNDLIQDLVDAGANI
iav-Mper partial (46) LSRLLLKHYPMLSQDVVEGEEYLGASALHLSIAYNNNDLIQDLVDAGANI
iav-Bmor (148) LARTLVKCFPKLSLDVVEGEEYLGASSLHLAIAYSNNELVQDLVEAGADV
iav-Dple (148) LARTLVKCFPKLSLDVVEGEEYLGASSLHLAIAYSNNELVQDLVEAGADV
iav-Aech (148) IARILLKCFPRLAIDVVEGEEYLGASALHLAIAYANNELVQDLVEAGAII
iav-Cflo (148) IARILLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVDAGAII
iav-Hsal (147) IARTLLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAII
iav-Aflo (147) VARILLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAII
iav-Amel (147) VARILLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAII
iav-Bimp (147) LARILLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAII
iav-Bter (147) LARILLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAII
iav-Mrot (147) LARILLKCFPRLAIDVVEGEEYLGASALHLAIAYNNNELVQDLVEVGAII
iav-Sinv (148) IARILLKCFPRLSIDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGAII
iav-Nvit (147) IARTLLKCFPRLAIDVVEGEEYLGASALHLAIAYANNELVQDLVEAGAIV
iav-Same partial (1) ----------
iav-Btab (77) LARTLLKCFPRLAQDIVEGEEYLGASALHLAIAYNNNELVQDLVEAGANV
iav-Eher (145) LARTLLKCFPNLAIDVVEGEEYLGASALHLAIAYFNNELVQDLVEAGANV
iav-Dpon (150) LARTLIKCFPKLALDVVEGEEYLGASALHLAIAYSNNELVQDLVEAGANV
iav-Tcas (150) LARTLIKCFPKLALDVVEGEEYLGASALHLAIAYNNNELVQDLVEAGANV
iav-Phum (146) LARTLLKCFPKLALDIVEGEEYLGASALHLAIAYNNNELVEDLVDAGANI

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                          201                                                 250
        iav-Aaeg   (201) SQRAIG---------------RFFLPRDQQ-GLKPAKNTDYEGLAYLGEY
        iav-Cqui   (201) SQRAIG---------------RFFLPRDQQ-KMHPAKTTDYEGLAYLGEY
        iav-Agam   (201) SQRATG---------------RFFLPRDQQ-GLRPAKTTDYEGLAYLGEY
        iav-Ccap   (200) NQRAIG---------------SFFLPRDQQ-RRNPAKSTDYEGLAYLGEY
        iav-Mdom   (200) NQRAIG---------------SFFLPKDQQ-RANPAKSTDYEGLAYMGEY
        iav-Dmel   (200) HQRAIG---------------SFFLPRDQQ-RANPAKSTDYEGLAYMGEY
        iav-Apis   (199) CQRAIG---------------SFFLPRDQQNKEINNKHTDYEGLAYLGEL
iav-Mper partial    (96) CQRAIG---------------SFFLPRDQQNKEINNKHTDYEGLAYLGEL
        iav-Bmor   (198) NQRAIG---------------SFFLPRDQQ-RVPPARQTNYEGLAYLGEY
        iav-Dple   (198) SQKAIG---------------SFFLPRDQQ-KNPPARQTNYEGLAYLGEY
        iav-Aech   (198) SQRAIG---------------SFFLPRDQQ-RMNPARNTDYEGLAYLGEY
        iav-Cflo   (198) SQRAIG---------------SFFLPRDQQ-GMNPVRNTDYEGLAYLGEY
        iav-Hsal   (197) SQRAIG---------------SFFLPRDQQ-RMNPVRNTDYEGLAYLGEY
        iav-Aflo   (197) SQRAIG---------------SFFLPRDQQ-RMNPAKNTDYEGLAYLGEY
        iav-Amel   (197) SQRAIG---------------SFFLPRDQQ-RTNPAKNTDYEGLAYLGEY
        iav-Bimp   (197) SQRAIG---------------SFFLPRDQQ-RTNPAKNTDYEGLAYLGEY
        iav-Bter   (197) SQRAIG---------------SFFLPRDQQ-RTNPAKNTDYEGLAYLGEY
        iav-Mrot   (197) SQRAIG---------------SFFLPRDQQ-RMNPAKNTDYEGLAYLGEY
        iav-Sinv   (198) SQRAIG---------------SFFLPRDQQ-RMNPARNTDYEGLAYLGEY
        iav-Nvit   (197) SQRAIG---------------SFFLPRDQQ-RPRPAKSTDYEGLAYLGEY
iav-Same partial     (1) ----------------------------------------------------
        iav-Btab   (127) NQRAIG---------------SFFLPKDQQ-RPRPAKHTDYEGLAYLGEF
        iav-Eher   (195) EQRAIG---------------SFFLPRDQQ-GQRPSKHTDYEGLAYLGEY
        iav-Dpon   (200) NQRAIGKQIADKTGKINAKNRSFFLPRDQQ-KQRPAKHTDYEGLAYLGEY
        iav-Tcas   (200) NQRAIG---------------SFFLPRDQQ-RQKPAKHTDYEGLAYLGEY
        iav-Phum   (196) NQRAVG---------------SFFLPKDQQ-RAKPLKTTDYEGLAYLGEY

                          251                                                 300
        iav-Aaeg   (235) PLAWAACCANESVYNLLLECGADPNAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Cqui   (235) PLAWAACCSNESVYNLLLECGADPNAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Agam   (235) PLAWAACCANESVYNLLLECGADPNAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Ccap   (234) PLAWAACCANESVYNLLVDCGADPDAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Mdom   (234) PLSWAACCANESVYNLLIDHDADPDAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Dmel   (234) PLAWAACCANESVYNLLVDCGSDPDAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Apis   (234) PLAWAACCGNQTVYNLLIDAGANPDAQDSFGNMILHMVVVCDKLSMFGYA
iav-Mper partial   (131) PLAWAACCGNQTVYNLLIDAGANPDAQDSFGNMILHMVVVCDKLSMFGYA
        iav-Bmor   (232) PLAWTACCANEAVYNLLLDSGADPDAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Dple   (232) PLAWAACCANEAVYNLLLDSGADPDAQDSFGNMILHMVVVCDKLDMFGYA
        iav-Aech   (232) PLAWAACCANESVYNLLLDSGADPDEQDTFGNMILHMVVVCDKLDMFGYA
        iav-Cflo   (232) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVGDKLDMFGYA
        iav-Hsal   (231) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYA
        iav-Aflo   (231) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYA
        iav-Amel   (231) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYA
        iav-Bimp   (231) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYA
        iav-Bter   (231) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYA
        iav-Mrot   (231) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVCDKLDMFGYA
        iav-Sinv   (232) PLAWAACCANESVYNLLLDSGADPDEQDSFGNMILHMVVVGDKL------
        iav-Nvit   (231) PLAWAACCANESVYNLLLDSGAHPDEQDTFGNSILHMVVVCDKLVRFGYA
iav-Same partial     (1) ----------------------------------------------------
        iav-Btab   (161) PLSWAACCANESVYNLLLDSGAHPDMQDTFGNMILHMVVVCDKLDMFGYA
        iav-Eher   (229) PLAWAACCANESIYNLLLDNGANPDHRDTFGNMILHMVVVCDKLDMFGYA
        iav-Dpon   (249) PLAWAACCANESVYNLLLDSGAHPDLQDNFGNMILHMVVVCDKLDMFGYA
        iav-Tcas   (234) PLAWAACCANESVYNLLLDSGAHPDYQDNFGNMILHMVVVCDKLDMFGYA
        iav-Phum   (230) PLSWAACCSNESVYNLLLDVGADPDSQDSFGNMILHMVVVCDKLDMFGYA
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                          301                                                 350
        iav-Aaeg   (285)  LRHPKLPCKNGIVNESGLTPLTLACRLGRDEVFREMLELSAREFWRYSNI
        iav-Cqui   (285)  LRHPKLPCKNGIVNEAGLTPLTLACRIGRDEVFREMLELSAREFWRYSNI
        iav-Agam   (285)  LRHPKLPCKNGIVNAAGLTPLTLACRLGRDEVFREMLELSAREFWRYSNI
        iav-Ccap   (284)  LRHPKTPAKNGIANHSGLTPLTLSCKLGRAEVFREMLELSAREFWRYSNI
        iav-Mdom   (284)  LRHPKTPAKNGIVNHSGLTPLTLACKLGRAEVFREMLELSAREFWRYSNI
        iav-Dmel   (284)  LRHPKTPAKNGIVNQTGLTPLTLACKLGRAEVFREMLELSAREFWRYSNI
        iav-Apis   (284)  LKHPKVKASNGIMNVAGLTPLTLSCKLARTSVFREMLELSAREFWRYSNI
iav-Mper partial   (181)  LKHPKVPASNGIMNVAGLTPLTLSCKLARTSVFREMLELSAREFWRYSNI
        iav-Bmor   (282)  LRHPKVPASNGRMNKAGFTPLTLACQLGRASVFREMLELSAREFWRYSNI
        iav-Dple   (282)  LRHPKVPASNGRLNKAGFTPLTLACQLGRASVFREMLELSSREFWRYSNI
        iav-Aech   (282)  LRHPKLPARNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Cflo   (282)  LRHPKLPARNGIANAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Hsal   (281)  LRHPKLPTRNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Aflo   (281)  LRHPKLPARNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Amel   (281)  LRHPKLPARNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Bimp   (281)  LRHPKLPARNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Bter   (281)  LRHPKLPARNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Mrot   (281)  LRHPKLPARNGIVNAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
        iav-Sinv   (276)  --------------------------------------------------
        iav-Nvit   (281)  LRHPKLPASNGIANAAGLTPLTLACQLGRAEVFREMLELSAREFWRYSNI
iav-Same partial     (1)  --------------------------------------------------
        iav-Btab   (211)  LRHPKLPASNGITNTAGLTPLTLACKLGRAEVFREMLELSAREFWRYSNI
        iav-Eher   (279)  LRHPKMPASNGIANVAGLTPLTLACKLGRAKVFREMLELSAREFWRYSNI
        iav-Dpon   (299)  LRHPKLPASNGITNKAGLTPLTLACKLGRAEVFREMLELSCKEFWRYSNI
        iav-Tcas   (284)  LRHPKLPASNGIVNKAGLTPLTLACKLGRAEVFREMLELSAKEFWRYSNI
        iav-Phum   (280)  LRHPKVPASNGITNNEGLTPLTLACKLGRADVFKEMLELSAKEFWRYSNI

                          351                                                 400
        iav-Aaeg   (335)  TCSGYPLNALDTLMPDGTTNWNSALFIILNGTKEEHLNMLDGGIVERLLD
        iav-Cqui   (335)  TCSGYPLNALDTLMPDGSTNWNSALFIILNGTKEEHLNMLDGGIVERLLD
        iav-Agam   (335)  TCSGYPLNALDTLMPDGSTNWNSALFIILNGTKEEHLNMLDGGIVERLLD
        iav-Ccap   (334)  TCSGYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Mdom   (334)  TCSGYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Dmel   (334)  TCSGYPLNALDTLLPDGRTNWNSALFIILNGTKPEHLDMLDGGIIQRLLE
        iav-Apis   (334)  TCSAYPLSALDTLLPDGRTNWNSVLFIILDGTKEEHLDMLDGGIIQKLLE
iav-Mper partial   (231)  TCSAYPLSALDTLLPDGRTNWNSVLFIILDGTKEEHLDMLDGGIIQKLLE
        iav-Bmor   (332)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKQEHLNMLDGGIIQRLLE
        iav-Dple   (332)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKQEHLNMLDGGIIQRLLE
        iav-Aech   (332)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Cflo   (332)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Hsal   (331)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGVIQRLLE
        iav-Aflo   (331)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Amel   (331)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Bimp   (331)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Bter   (331)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Mrot   (331)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLNMLDGGIIQRLLE
        iav-Sinv   (276)  --------------------------------------------------
        iav-Nvit   (331)  TCSAYPLNALDTLLPDGRTSXNSALFIILNGTKEEHLDMLDGGIIQRLLE
iav-Same partial     (1)  --------------------------------------------------
        iav-Btab   (261)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Eher   (329)  TCSAYPLNALDTLLPDGRTNWNSALFIILNGTKEEHLDMLDGGIIQRLLE
        iav-Dpon   (349)  TCSAYTLNALDTLLPDGRTNWNSALFIILNGTKEAHLDMLDGGIIQRLLE
        iav-Tcas   (334)  TCSAYFLNALDTLLPDGRTNWNSALFIILNGTKEEHLAMLDGGIIQRLLE
        iav-Phum   (330)  TCSAYPLNALDTLLPDGRTNWNSAIFIILNGTKEEHLDMLDGGIIQRLLE
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                          401                                                450
        iav-Aaeg   (385) EKWKTFARNQFIKRLLILALHLFCLSCSVYLRPVRVFKEESEE----GSD
        iav-Cqui   (385) EKWKTFARNQFLKRLLILALHLFCLSCSIYLRPVHVFKDD--------DD
        iav-Agam   (385) EKWKTFARNQFIKRLLILAIHLFCLSCSVYLRPVRVFADDEGEEGGDATD
        iav-Ccap   (384) EKWKTFAQNQFLKRLLILVIHLVFLSISVYMRPARVADDDDEDEIDASSK
        iav-Mdom   (384) EKWKTFAQNQFLKRLLILVVHLLCLSTSVYLRPAHDGDDDEEDET---AQ
        iav-Dmel   (384) EKWKTFAQNQFLKRLLILSTHLLCLSVSVYLRPAHDGEAEDEDSEGSDAS
        iav-Apis   (384) EKWKTFARKQFMKRLVILSIHLIMLSISIYLRPVDQDKPLLGEA------
iav-Mper partial   (281) EKWKTFARXXXXXXXXILSIHLIMLSISIYLRPVDQDKPLLGEA------
        iav-Bmor   (382) EKWKTFARTKFLKRLLILMLHLLLLSVSVYLRHSSAEADAHPNWGL----
        iav-Dple   (382) EKWKTFARTKFLKRLLILMLHLILLSISVYLRHSSLEADVDPDWGL----
        iav-Aech   (382) EKWKTFARLQFLKRLIILVFHLASLSLAMYFRPADMEAVLLQWP------
        iav-Cflo   (382) EKWKTFARLQFLKRLIILVFHLASLSLAVYFRPADTDAVLLQWP------
        iav-Hsal   (381) EKWKTFARLQFLKRLIILVFHLASLSLAVYFRPADMDAELLQWP------
        iav-Aflo   (381) EKWKTFARLQFLKRLIILAFHLTSLSLAVYLRPSNTDAQLLKWP------
        iav-Amel   (381) EKWKTFARLQFLKRLIILAFHLTSLSLAVYLRPSNTDAQLLKWP------
        iav-Bimp   (381) EKWKTFARLQFLKRLIILVFHLTSLSLAVYMRPSNIDATLLEWP------
        iav-Bter   (381) EKWKTFARLQFLKRLIILVFHLTSLSLAVYMRPSNIDATLLEWP------
        iav-Mrot   (381) EKWKTFARLQFLKRLIILVFHLTSLSLAVYLRPSNLDTVLLKWP------
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit   (381) EKWKTFARLQFLKRLVILVFHLVSLSLAVYFRPADTDAELAQWP------
iav-Same partial     (1) ------------------------------------------------------
        iav-Btab   (311) EKWKTFARRQFLKRLAILFLHLLMLSMAVYLRPVDREQPLIGGD------
        iav-Eher   (379) EKWKXFARRQFLKRLVILMLHLLCLSGAVYLRPTDRTKPLLGGD------
        iav-Dpon   (399) EKWKAFARNQFLKRLIILIVHLAFMSLAVYMRPDDPDEPLLEWS------
        iav-Tcas   (384) EKWKTFARNQFLKRLLILVVHLLFLSLAVYLRPDDPDESLLTWS------
        iav-Phum   (380) EKWKTFARNQFLKRLVIFFLHIFCLSGSVYLRPDDRNKPLLGGT------

                          451                                                500
        iav-Aaeg   (431) GGDGAGTAAPDGVDDDEDIDLTTWFRYGFEIATVMGVLSYVVLQQGDEIK
        iav-Cqui   (427) ADDTDGVTDSPDTTDDEGIDLTTWFRYGFEVATVMGVLSYVVVQQGEEIK
        iav-Agam   (435) DDGADDGGPMAVDAVDDDIDLTTWVRYGFEVATVMGVLSYVVLQQGDEIK
        iav-Ccap   (434) DTKALELATELDED---EYDVQTIVRYCAEFGTIVGVLSYVIFQQGDEIK
        iav-Mdom   (431) ANAGLQTNDPENEE----YDIQTIVRYCAELCTIAGVLSFLIFQQGDEIK
        iav-Dmel   (434) AAALLDIQSDEGDSGGGDYNAQTVARYCAEFATLVGVLSYVIFQQGDEIK
        iav-Apis   (428) ------------------EDWQDVARYCFEGGTVVGVLSYLIVQQGGEIL
iav-Mper partial   (325) ------------------EDWQDVARYCFEGGTVVGVLSYLIVQQGGEIL
        iav-Bmor   (428) ----------------EINDARSGLRLASELGTILSTLCYIILQQGDELK
        iav-Dple   (428) ----------------EVNDARSGIRLACELGTIISTLCYIILQQGDEIK
        iav-Aech   (426) ------------------EEITDVVRTAAECITVLGVLNYILVQLGCEMI
        iav-Cflo   (426) ------------------EEITDVIRTAAECITVLGVLNYILVQLGGEMI
        iav-Hsal   (425) ------------------DEITDAARIAAECSTVLGVLSYILVQLGGEMI
        iav-Aflo   (425) ------------------EEITEVARTIAECITVLGVLSYILVQLGGEII
        iav-Amel   (425) ------------------EEITEVARTIAECITVLGVLSYILVQLGGEII
        iav-Bimp   (425) ------------------EEITEVGRMIAECTTVIGVLSYILVQLGGEVV
        iav-Bter   (425) ------------------EEITEVGRMIAECTTVIGVLSYILVQLGGEVV
        iav-Mrot   (425) ------------------EEVTEVGRTIAECITVLGVLSYILVQLGGEII
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit   (425) ------------------EEITDVVRVIAECVTVLGVLGYILLQLGGEIV
iav-Same partial     (1) ------------------------------------------------------
        iav-Btab   (355) ------------------DWSDIARYGFEVGTIMGVLSYLVVQQGGEIK
        iav-Eher   (423) ------------------DWKSVARQGFEVATVLGVLSYVIVQQGGEIR
        iav-Dpon   (443) ------------------DDPTVIIRFTAEIGTLLNVLSYVVVQQGDEIR
        iav-Tcas   (428) ------------------DDVTLIARYVCEVGTILGVLSYLVLQQGDEIR
        iav-Phum   (424) ------------------SVQDVVRYCFEIGTILGVLCYLCFQQGDEIR
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                          501                                                 550
        iav-Aaeg   (481) NQGLISFIKSLGNAPAKAIFLISNLMILACIPFRMMGDVEHEEAILLFAV
        iav-Cqui   (477) NQGFISFLKSLAGAPAKAIFLISNLMILCCIPLRILGDREAEEAVLLFAV
        iav-Agam   (485) NQGFFSFLKSLSQAPAKAIFLISNILILACIPLRMMGDTETEEAILLFAV
        iav-Ccap   (481) NQGLPAFLKQLTHAPAKAIFLVSNLLILACIPCRLMGDTDAEEAILIFAV
        iav-Mdom   (477) NQGLSAFLKQLSHAPAKVIFLVSNLMILACIPFRLMGDTDTEEAILIFAV
        iav-Dmel   (484) NQGLSAFLKQLSHAPAKAIFLFSNLLILACIPFRLIGDTDTEEAILIFAV
        iav-Apis   (460) NQGLVGFLKQTFKEPAKLIFLISNLLILACIPPRMMGDKQTEEAILVFAV
iav-Mper partial   (357) NQGLVGFLKQTFKEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
        iav-Bmor   (462) NQGLVAYFKQLIHEPAKFIFLASNILVLACIPARLLKETNVEEAILLFLL
        iav-Dple   (462) NQGVVAYFKQLIHEPAKFIFLASNILLLACIPARISQRTTLEEAILIFVL
        iav-Aech   (458) NVGPLSFLKQLSHEPAKLIFVISNLLILACIPCRIAGDRHAEDAILMFAV
        iav-Cflo   (458) NVGPLSFLKQLSHEPAKLIFVISNLLILACIPCRIAGNRHAEDAILVFAV
        iav-Hsal   (457) NIGPLSFLKQLSHEPAKLIFVISNLLILACIPCRIAGNRHAEDAILVFAV
        iav-Aflo   (457) NIGLLSFMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILIVAV
        iav-Amel   (457) NIGLLSFMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILIVAV
        iav-Bimp   (457) NIGLLSFMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILVVAV
        iav-Bter   (457) NIGLLSFMKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILVVAV
        iav-Mrot   (457) NIGVLSFLKQLSHEPAKLIFLISNLLILACIPCRLAGNRHAEDAILVVAV
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit   (457) NIGFFSFFKQLSHEPAKFIFLISNLLILACIPCRLSGDRHTEDAILVVAV
iav-Same partial     (1) ------------------------------------------------------
        iav-Btab   (386) NQGLGSFLKQLMAEPAKAIFLVSNLLILACIPFRMAGDSQTEEAILILAV
        iav-Eher   (454) NQGFTSFIKQLDX--AKAIFLVSNILILICIPFRLMDDKRTEEAILVFAV
        iav-Dpon   (475) NQGFLSFLKQQTNSPPKCIFLVSNLMILACIPCRLAGNRGLEETILIFAV
        iav-Tcas   (460) NQGLTAFLKQQLNSPPKLIFLISNFLILACIPCRLYGDKETEEAILCFAV
        iav-Phum   (455) NQGLISFLKQLPHDPAKFIFLISNLLILACIPYRVAGDTDTEEAILVFAV

                          551                                                 600
        iav-Aaeg   (531) PGSWFLLMFFAGAIGLTGPFVTMIFSMITGDMFTFGIIYMIVLFGFSQAF
        iav-Cqui   (527) PGSWFLLMFFAGAIGLTGPFVTMIFSMITGDMFTFGIIYTIVLFGFSQAF
        iav-Agam   (535) PGSWFLLMFFAGAIGLTGPFVTMIFSMITGDMFTFGIIYMIVLFGFSQAF
        iav-Ccap   (531) PGSWFLLMFFAGAIRLTGPFVTMIYSMITGDMFTFGIIYCIVLCGFSQAF
        iav-Mdom   (527) PGSWFLLMFFAGAIRLTGPFVTMIYSMITGDMFTFGIIYSIVLCGFSQAF
        iav-Dmel   (534) PGSWFLLMFFAGAIRLTGPFVTMIYSMITGDMFTFGIIYCIVLCGFSQAF
        iav-Apis   (510) PGSWFLLMFFAGAIRLTGPFVTMVYLMITGDMLTFFVIYSVILSGFTQSF
iav-Mper partial   (407) XXXXXXXXXXXXXXXXXXXXXXXXXXXXXDMLTFFVIYSVILSGFTQSF
        iav-Bmor   (512) PGSWFLLMFFAGAVKLTGPFVTMIYSMITGDMFTFGIIYCIVLFGFSQSF
        iav-Dple   (512) PGSWFLMMFFAGAVKLTGPFVTMIYSMITGDMFTFGIIYCIVLFGFSQSF
        iav-Aech   (508) PGSWFLLMFFAGAIRLTGPFVTMVYSMITGDMLTFGIIYTVMLFGFSQSF
        iav-Cflo   (508) PGSWFLLMFFAGAIRLTGPFVTMVYSMITGDMLTFGIIYTIMLFGFSQSF
        iav-Hsal   (507) PGSWFLLMFFAGAIRLTGPFVTMVYSMITGDMLTFGIIYTVMLFGFSQSF
        iav-Aflo   (507) PGSWFLLMFFAGAVRLTGPFVTMVYSMITGDMLTFGIIYMVVLFGFCQSF
        iav-Amel   (507) PGSWFLLMFFAGAVRLTGPFVTMVYSMITGDMLTFGIIYMVVLFGFCQSF
        iav-Bimp   (507) PGSWFLLMFFAGAIRLTGPFVTMVYSMITGDMLTFGIIYMVVLFGFCQSF
        iav-Bter   (507) PGSWFLLMFFAGAIRLTGPFVTMVYSMITGDMLTFGIIYMVVLFGFCQSF
        iav-Mrot   (507) PGSWFLLMFFAGAIRLTGPFVTMVYSMITGDMLTFGIIYMVVLFGFCQSF
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit   (507) PGSWFLLMFFAGAVRLTGPFVTMVYSMILGDMRTFGIIYMIVICGFTQAF
iav-Same partial     (1) --SWFLLMFFAGAXRLTGPFVTMVYSMITGDMLTFGIIYTVVLFGFSQSF
        iav-Btab   (436) PGSWFLLMFFAGAVRLTGPFVTMIYSMITGDMFTFGIIYSILLFGFSQSF
        iav-Eher   (502) PGSWFLLMFFAGAVRLTGPFVTMVYSMIVGDMFTFGIIYSIVLFGFSQSF
        iav-Dpon   (525) PGSWFLLMFFAGAVRLTGPFVTMIYSMITGDMLTFGIIYTIFLFGFSQSL
        iav-Tcas   (510) PGSWFLLMFFAGAVRLTGPFVTMIYSMITGDMLTFGIIYTVFLFGFSQSF
        iav-Phum   (505) PSSWFLLMFFAGAIRLTGPFVTMIYSMITGDMLTFGIIYSVFLFGFSQSF
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                          601                                                650
        iav-Aaeg   (581) YFLYKGHPEAEDSPFGSYFGTWMGLFQTTLGDYDYADLNLTTYPNLAKTV
        iav-Cqui   (577) YFLYKGHPNADESPFGTYFGTWMGLFQTTLGDYDYADLNLTTYPNLAKTV
        iav-Agam   (585) YFLYKGHPNAEDSPFGSYFGTWMALFQTTLGDYDYADLNLTTYPNLAKTV
        iav-Ccap   (581) YFLYKGHPQIQSTMFNTFPSTWMALFQTTLGDYNYPDLNNTTYPNLSKTV
        iav-Mdom   (577) YFLYKGHPQLQSTMFDTFPSTWMALFQTTLGDYNYPDLNQTTYPNLSKTV
        iav-Dmel   (584) YFLYKGHPQVQSTMFNTYTSTWMALFQTTLGDYNYPDLNQTTYPNLSKTV
        iav-Apis   (560) FFLYKGSPDVSTSLYKSYPSTWMALFQITMGDYNYADLSYTVYPALSKTV
iav-Mper partial   (457) FFLYKGSPDVSTSLYKSYPSTWMALFQITMGDYNYADLSYTVYPALSKTV
        iav-Bmor   (562) YFLYRGFPNVQSTLYSSYPSTWMALFQITLGDYSYSDLSQTTYPNLSKTV
        iav-Dple   (562) YFLYKGFPNVHSTLYSSYPSTWMALFQITLGDYSYTDLGLTMYPNLSKTV
        iav-Aech   (558) YFLYKGFPGVKSSLYHSYPSTWMALFQITLGDYNYADLSNTTYPNLSKTV
        iav-Cflo   (558) YFLYKGFPGVKSSLYHSYVSTWMALFQITLGDYNYAELNNTIYPNLSKTV
        iav-Hsal   (557) YFLYKGFPGVKSSLYHSYPSTWMALFQITLGDYNYADLSNTTYPNLSKTV
        iav-Aflo   (557) YFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLSYTTYPNLSKMV
        iav-Amel   (557) YFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLSYTTYPNLSKMV
        iav-Bimp   (557) YFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLGYTTYPNLSKMV
        iav-Bter   (557) YFLYKGFPGVKSSLYSSYHSTWMALFQITLGDYNYTDLGYTTYPNLSKMV
        iav-Mrot   (557) YFLYKGFPGVKSSLYSSYHSTWMALFQVTLGDYNYTDLSYTTYPNLSKMV
        iav-Sinv   (276) ----------------------------------------------------
        iav-Nvit   (557) YFLYKGYPGVKTTLFHSYPSTWMALFQITLGDYSYSDLSMTTYPNLSKAV
iav-Same partial    (49) YFLYKGFPGVKTSLYHSYPTTWMALFQITMGDYNYPELSHTTYPTLAKTV
        iav-Btab   (486) YFLYKGSPNVKQTLFHSYPTTWMALFQITLGDYNYPELAFTVYPTLSKIV
        iav-Eher   (552) YFLYKGFPGVKNTLYSSYHSTWMALFQITLGDYNYAELSHTSYPTLSKTV
        iav-Dpon   (575) FFLYKGNPSVNGTLYHSYSSTWMALFQVTMGNYDYSELALTTYPGVAKSV
        iav-Tcas   (560) YFLYKGFPGVKTSLYNTYMSTWMALFQITLGNYEYSELSATTYPAVSKTV
        iav-Phum   (555) FFLYKGSKNVSSSLFTSYPSTWMALFQVTMGDYNYNDLSLTAYPAISKMV

                          651                                                700
        iav-Aaeg   (631) FIIFMIFVPILLLNMLIAMMGNTYAYVIEQAEKEGMKQWAKIVVNLERAV
        iav-Cqui   (627) FITFMIFVPILLLNMLIAMMGNTYAYVIEQAEKEGMKQWAKIVVNLERAV
        iav-Agam   (635) FVIFMIFVPILLLNMLIAMMGNTYAYVIEQAEKEGMKQWAKIVVNLERAV
        iav-Ccap   (631) FVIFMIFVPILLLNMLIAMMGNTYAQVIERSEKEWMKQWAKIVVTLERAV
        iav-Mdom   (627) FVIFMIFVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVTLERAV
        iav-Dmel   (634) FVIFMIFVPILLLNMLIAMMGNTYVTVIEQSEKEWMKQWAKIVVTLERAV
        iav-Apis   (610) FTVFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVTLERAV
iav-Mper partial   (507) FTVFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVTLERAV
        iav-Bmor   (612) FTVFMIFVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERSV
        iav-Dple   (612) FTVFMVFVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERSV
        iav-Aech   (608) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEFVKQWAKIVVSLERAV
        iav-Cflo   (608) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEFVKQWAKIVVSLERAV
        iav-Hsal   (607) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEFVKQWAKIVVSLERAV
        iav-Aflo   (607) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAV
        iav-Amel   (607) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAV
        iav-Bimp   (607) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAV
        iav-Bter   (607) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAV
        iav-Mrot   (607) FTIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVVSLERAV
        iav-Sinv   (276) ----------------------------------------------------
        iav-Nvit   (607) FTIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVSLERAV
iav-Same partial    (99) FAIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVV------
        iav-Btab   (536) FTSFMVLVPILLLNMLIAMMGNTYAHVIERSEKEWMKQWAKIVVALERAV
        iav-Eher   (602) FAIFMILVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVSLEXAV
        iav-Dpon   (625) FGLFMVFVPILLFNMLIAMMGNTYAHVTEQSEKEWVKQWAKIVISLERAI
        iav-Tcas   (610) FAIFMVFVPILLLNMLIAMMGNTYAHVIEQSEKEWVKQWAKIVIALERAI
        iav-Phum   (605) FTIFMVLVPILLLNMLIAMMGNTYAHVIEQSEKEWMKQWAKIVVALERAV
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                          701                                                750
        iav-Aaeg   (681) KQEDAKKYLEEYSIGLGP---SDDPRYEIRGVMVIKSKSKTRARQRKGAV
        iav-Cqui   (677) KQEDAKKYLEEYSIGLGP---SDDPRFEIRGVMVIKSKSKTRARQRKGAV
        iav-Agam   (685) TQDDAKRYLEEYSIGLGP---SDDPRYETRGVMVIKSKSKTRARQRKGAV
        iav-Ccap   (681) PQADAKNYLEAYSIPLGP---IDDSGYEVRGVMVIKSKAKTRAKQRKGAV
        iav-Mdom   (677) PQADAKNYLEAYSIPLGP---SDDSGFEVRGVMVIKSKSKTRAKQRKGAV
        iav-Dmel   (684) PQADAKGYLEAYSIPLGP---SDDSGFEVRGVMVIKSKSKTRAKQRKGAV
        iav-Apis   (660) PQKAARNYLEEYSIQLAPG---DDVNPEQRGFMVIKCKSQTRAKQRKGAV
iav-Mper partial   (557) PQKAARNYLEEYSIQLAPG---DDVNPEQRGFMVIKCKSQTRAKQRKGAV
        iav-Bmor   (662) AQDDAHKYLQEYSIGLGP---SDDPRYEQRAVMVIKSKAKTRAKQKKDAL
        iav-Dple   (662) SQEDAHRYLQEYSIGLGP---SDDPRYEQRGVMVIKSKAKTRAKQRKGAL
        iav-Aech   (658) SQKDAHNYLQEYSIKLGPGDDPNNPASEQRGVLVIKSKSKTRAKQRKGAV
        iav-Cflo   (658) SQKDAHNYLQEYSIKLGPGDDPNNPASEQRGVLVIKSKSKTKAKQRKGAV
        iav-Hsal   (657) SQKDAHNYLQEYSIKLGPGDDPNNPASEQRGVLIIKSKSKTRAKQRKGAV
        iav-Aflo   (657) SQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLIIKSKSKTKAKQRKGAV
        iav-Amel   (657) SQKDAQNYLQEYSIKLGPGDDPNNPAAEQRGVLIIKSKSKTKAKQRKGAV
        iav-Bimp   (657) AQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLIIKSKSKTKAKQRKGAV
        iav-Bter   (657) AQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLVIKSKSKTKAKQRKGAV
        iav-Mrot   (657) SQKDAQNYLQEYSIKLGPGDDPNNPASEQRGVLVIKSKSKTKAKQRKGAV
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit   (657) SQDDAHNYLQEYSIKLGPGDDPNDPASEQRGVMVIKSKSKTRARQRKGAV
iav-Same partial   (143) ------------------------------------------------------
        iav-Btab   (586) PAADAHNYLQEYSIKLGPG---DDPSTEQRGVMVIKSKSKTRAKQRKGAV
        iav-Eher   (652) NQEDCKQYLQEYSIKLGPG---DDPSTEQRGVMVIKSKSKTRAKQRKGAV
        iav-Dpon   (675) PQKEAHNYLQEYSISLGP---AEDPATEQRGVMVIKSKNKTRAKQRKGAV
        iav-Tcas   (660) PQSDAQHYLQEYSISLGPS--EQDPSTEKRGVLVIKSKSKTRAKQRKGAV
        iav-Phum   (655) NQEDCHRYLQEYSIKLGPG---DDPSTEQRGVLVIKSKSKTRAKQRKGAL

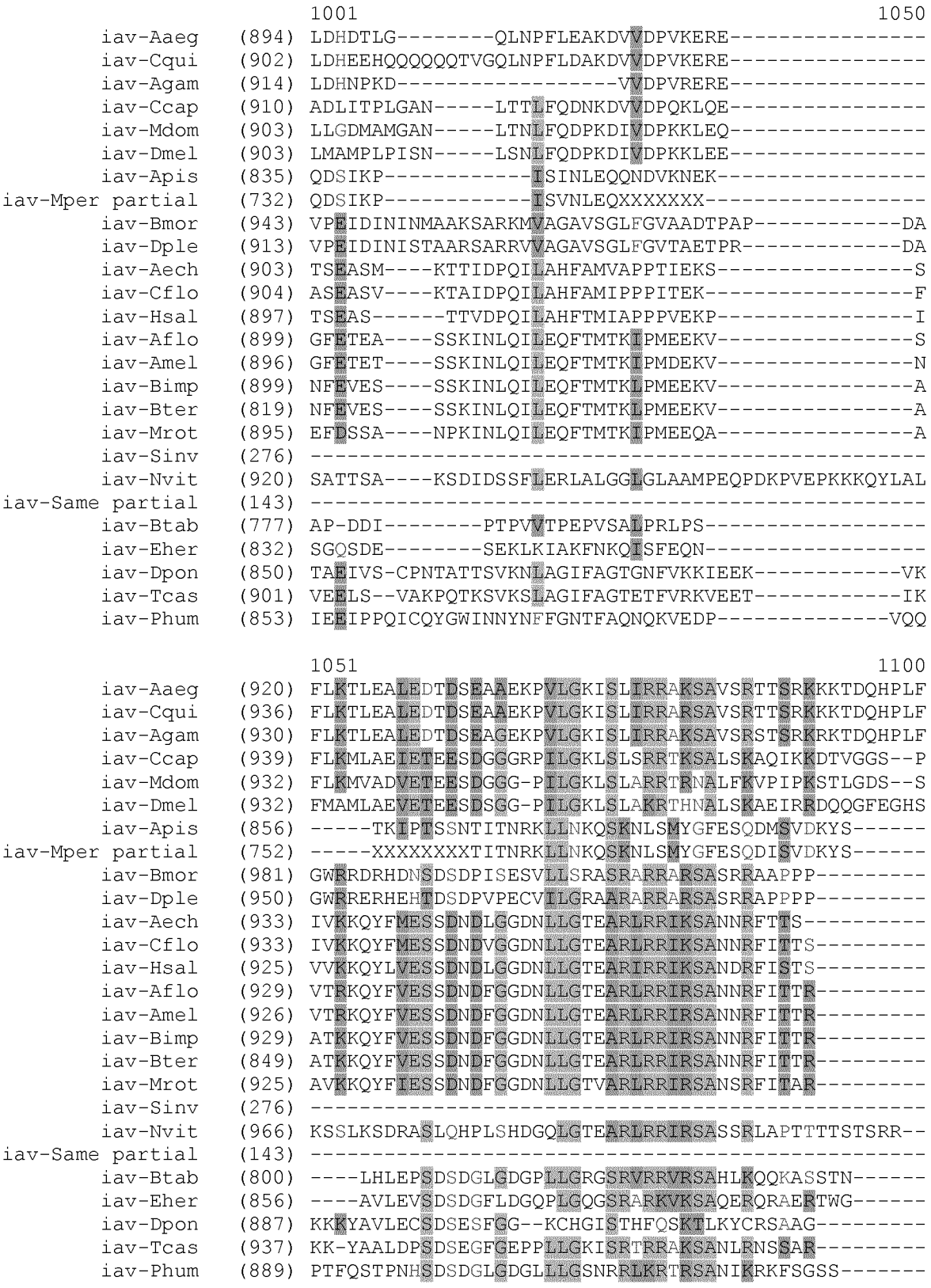
                          751                                                800
        iav-Aaeg   (728) SNWKSVLRVTLNELKKRNMTGEELRRIMWGRSSITSPAKISKKK------
        iav-Cqui   (724) SNWKSVLRVTLNELKKRSMTGEELRRIMWGRSSITSPAKISKKKK-----
        iav-Agam   (732) SNWKSVLRVTLNELKKRSMTGEELRRIMWGRSSITSPAKIAKKKR--P--
        iav-Ccap   (728) SNWKRVGRVTLNALKKRGMTGEQMRRLMWGRASISSPIKITKKKLKDP--
        iav-Mdom   (724) SNWKRVGRVTLNALKKRGMTGEEMRRLMWGRASISSPIKVAKKKLKDP--
        iav-Dmel   (731) SNWKRVGRVTLTALKKRGMTGEEMRRLMWGRASISSPVKVTKQKLKDP--
        iav-Apis   (707) INWKKSGKLVIQELRRLEGTGQNLRDMIWKRSSLSASSPVAKSVSITK--
iav-Mper partial   (604) INWKKSGKLVIQELRRLEGTGQNLRDMIWKRSSLSASSPVAKSVSITK--
        iav-Bmor   (709) TNWKHVGKVTIAELRRRGISGEELRRLMWGRISISTPTKAPLPRRVPAPP
        iav-Dple   (709) SNWKRVGKVTIAELRRRGISGEELRRLMWGRVSISTPTKAPLK---CVPP
        iav-Aech   (708) SNWKRVGKVTILELRKRGMTGEELRRIMWGRASFSTPVRVSPNAGQPQ--
        iav-Cflo   (708) ANWKRVGKVTINELRKRGMTGEELRHIMWGRESFSTPVRVSPNAGQPQ--
        iav-Hsal   (707) ANWKRVGKVTINELRKRGMTGEELRRIMWDRASISTPVRVSPNVNEPQ--
        iav-Aflo   (707) ANWKRVGKVTINELKKRGLTGEELRRIMWGRASFSTPVRVSPKGVEPQ--
        iav-Amel   (707) ANWKRVGKVTINELKKRGLTGEELRRIMWGRASFSTPVRVSPKGVEPQ--
        iav-Bimp   (707) ANWKRVGKVTINELKKRGITGEALRRVMWGRASFSTPVRTSPNTAEPQ--
        iav-Bter   (707) ANWKRVGKVTINELKKRGITGEALRRVMWGRASFSTPRDTLRALGSVG--
        iav-Mrot   (707) ANWKRVGKVTINELRKRGMTGEELRRIMWGRASFSTPVRVSPNVDEPQ--
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit   (707) ANWKRVGKVTIAELKKRGMTGEELRRIMWGRASFSTPVRSSPILMEP---
iav-Same partial   (143) ------------------------------------------------------
        iav-Btab   (633) SNWKRVGKVTINELRKRGMTGEQLNRIMWGRASISTPVRQP---AMALLL
        iav-Eher   (699) ANWKRVGKVTINELRKRGMNGEQLRRIMWDRASISTPVKVPQNPVVDVLM
        iav-Dpon   (722) SNWKRVGKVTIKALKKKGMTGEEMRCLMWGRESINTPVKVKGPKR-----
        iav-Tcas   (708) ANWKRVGKVTINALKKRGLTGEEMRCLMWGRESINTPVKTKKPVK-----
        iav-Phum   (702) CNWKRVGKVTIRELHKRGMTGEQLRRLMWGRSSISTPVKPAPIKLGHVTS
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                          801                                                 850
        iav-Aaeg   (772) -------------KIYEEEDPFAITNAIDVMSFTQDIVM-----------
        iav-Cqui   (769) -------------IYDEDEDPFAITAAIDVMSFTQDIVM-----------
        iav-Agam   (778) -----------GEVDDLLGDPFAITAAIDVMSFTQDIVM-----------
        iav-Ccap   (776) -----------YNLNP----QNDLTSAMDMLTFANDPAA-----------
        iav-Mdom   (772) -----------YNLNQEPGGQSNLTSAMDMLNFANDPAS-----------
        iav-Dmel   (779) -----------YNLHT----DSDFTNAMDMLTFASNPAS-----------
        iav-Apis   (755) ----NKSKSYSEAKDDQIRLSGALGAALDAIAVAHDLDMT----------
iav-Mper partial   (652) ----NKSKSYSEAKDDQIRLSGALGAALDAIAVAHDLDMT----------
        iav-Bmor   (759) PDCVVSSDVGLASDVGNGVAPA-LSSALNVMAFTHELDIGTT--------
        iav-Dple   (756) PELVTSEIP------GSGVGPA-LSSALNVMAYTQDLDLTNT--------
        iav-Aech   (756) -----------VSAVTAGFDDA-LTAALDVMAFAHDFDL-----------
        iav-Cflo   (756) -----------VSAVTAGFGDA-LTAALDVMAFAHDFDL-----------
        iav-Hsal   (755) -----------VSAVTAGFGDA-LTAALDVMAFAHDFDL-----------
        iav-Aflo   (755) -----------VSVVTAGFGDA-LTTALDVMAFAHDLDL-----------
        iav-Amel   (755) -----------VSVVTAGFGDA-LTTALDVMTFAHDLDL-----------
        iav-Bimp   (755) -----------VSAVTAGFGDA-LTAALDVMAFAHDLDL-----------
        iav-Bter   (755) -----------IVRAVG-------------------------------------
        iav-Mrot   (755) -----------VSAVTAGFGDA-LTAALDVMAFAHDLDL-----------
        iav-Sinv   (276) -------------------------------------------------------
        iav-Nvit   (754) -----------VSSVPGGFGDA-LTSALDVMTFAADVPVPIEGSIPKPVA
iav-Same partial   (143) -------------------------------------------------------
        iav-Btab   (680) EDSEEEN-----AANNTGPFGGALTAALDVMAFTHDIDLNIGQT------
        iav-Eher   (749) ENTAEQQ-----AQQTPGSFGGALTAALDVMAFTHDLDLSASG-------
        iav-Dpon   (767) DPLANPQGP----DLANGFGDA-LTSALDVMAFTHDLDIN----------
        iav-Tcas   (753) DPLLDPQGP----NLTGGFGDA-LTTALDVMTFTHDLDIVGA--------
        iav-Phum   (752) ISGVADITVPETTGNTVGTGGGGLLAALDVMAFTNDLEFS----------

                          851                                                 900
        iav-Aaeg   (798) -------VSSEPTGPPTIDPSKP--A------------------------
        iav-Cqui   (795) -------VSTEPVGPLMIDPTKPPVT------------------------
        iav-Agam   (806) -------VSTDTVCPITIPPAAAPGT------------------------
        iav-Ccap   (800) -------SAGLQLRSSLMDSGAEGKA------------------------
        iav-Mdom   (800) -------SSGLAFRTSGTQDPKEKK------------------------
        iav-Dmel   (803) -------SNGVTLRSVTAPPPAP--------------------------
        iav-Apis   (791) -------------------------------------------------
iav-Mper partial   (688) -------------------------------------------------
        iav-Bmor   (800) -----G-SDQKQTTPDLLVNGKTSNAPILTTGTQMPKVSSKTLGTPVARI
        iav-Dple   (791) -----GSELHKQITPDLLVNGKT------------PVTAQNTATTPKVPL
        iav-Aech   (783) -----STATEGIPTNIDAKQIKTAQS----------------------KAA
        iav-Cflo   (783) -----SAATEGIPTNIDAKQTKTTQS----------------------KAI
        iav-Hsal   (782) -----STATEGVPSNIDTRQTKAIP------------------------
        iav-Aflo   (782) -----STATEGIPTNIDAKQSKPKS------------------------A
        iav-Amel   (782) -----STATEGIPTNIDAKQSKPK-------------------------S
        iav-Bimp   (782) -----STATEGIPTNIGAKQSKSKT------------------------A
        iav-Bter   (761) -----TLGPVGTVRAVGALG---P--------------------------
        iav-Mrot   (782) -----STATESIPTNIDVKQSKPKV----------------------V
        iav-Sinv   (276) -------------------------------------------------
        iav-Nvit   (792) VAPGQQPTTTLALPNGAAKPQQPMMT--------------------TST
iav-Same partial   (143) -------------------------------------------------
        iav-Btab   (719) ------PVTVSGLGGVSVRSGAEGL------------------------
        iav-Eher   (787) -------ITSSGLN-------------------------------------
        iav-Dpon   (802) -----AQGLNLAKQTLNPKP------------------------------
        iav-Tcas   (790) -----SQGLNLATNPKPVPPTTT--------------------------
        iav-Phum   (792) -------SENQTSTSFKTQPQPS--------------------------
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                          901                                                 950
        iav-Aaeg   (815) ------TIAVKPQTAPAAQPIPEIPPQ------------PPLVKRQSVVS
        iav-Cqui   (814) ------TVKPTAPTVPSAQPAPGVPMTT---AQTAAPTAPQLVKRQSVVS
        iav-Agam   (825) ------AAPKAGGTKPVVVAPPPPAAAT---AVQQPPP-PATTRRHSTAS
        iav-Ccap   (819) ------AKVQEENQQPAPDPLRDLIFLADRRPEMHDPQYFVGLQQLANQA
        iav-Mdom   (818) ----------DVPHIPAPDPLRDLVLLAEEKPEVHDPQFYSALIQLANKA
        iav-Dmel   (819) ---------------PAPDPFRELIMMSDQRPETHDPHYFAGLQQLANKA
        iav-Apis   (791) --------------------------------------------------
iav-Mper partial   (688) --------------------------------------------------
        iav-Bmor   (844) EASSLKTPLDVKLNPTTLTQSTVQGNIGNVNIPISGVKITTNVGQNSAVV
        iav-Dple   (824) VNLPNKAGLDVQSTGSDQSVPTALT----KNMDVLGINMSTQDLLKNQTI
        iav-Aech   (807) LNDQQTKTTQNNPEVVINVQPHNQPIK-EETKLSGLTDLIDKSIDPVKDV
        iav-Cflo   (807) PNDQMKTTQ-NNPETVTNVQPHKQPIG-EPTKLLGLTDLIDNSIGPVKDV
        iav-Hsal   (802) --DEQTRTARNNPKAVTDVQPHKQAIGGEETKLSGLTDLIDMSAAEPARV
        iav-Aflo   (803) IKEQMKLTTNNQENVSTNVEPQLKSTTENANDQANNPREIKKVTNQVTGI
        iav-Amel   (802) ATKETKSTVNNQQNVTTNIEP-LKSTTENVDDQANNPR-EKKVTSQAATV
        iav-Bimp   (803) CKDQAKSATNNQEKGSTDVQQQRKLTTENLDNLASSHNDIDKTSSEFVAV
        iav-Bter   (777) ----VG--------------------T------------VRD-------
        iav-Mrot   (803) SSEQTKLTTNNQEKPS----ITEKAATEIANKQVNAKDETNKKPNEVVDV
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit   (821) TTTTITTTVQKTLVTGTATTPAVGVTKTVAVPAATTVSTTTTRASASAVP
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (738) --------------------------------------------------
        iav-Eher   (794) --------------------------------------------------
        iav-Dpon   (817) --------------------------------------------------
        iav-Tcas   (808) ------ASAVTVNNQINSALNAQQKAVAGAGVGALAMIGTVTQLTDSQGY
        iav-Phum   (808) ---------E----------------------------------------

                          951                                                1000
        iav-Aaeg   (847) APPAY--DDFPPMKDYKDPLRELVIISE-SPSVDDHYVQSCKTLANDAST
        iav-Cqui   (855) APPAY--DDFLPAKGFKDPLRELLILSE-STSIDEHYAQTCRSLATDAST
        iav-Agam   (865) APATMGLGVEAALPGYKDPLRELVIISE-SASVDENYAQNVKTLAIDAST
        iav-Ccap   (863) LDLVEQTMGIHPPP--TPATDALLLSAA-AATTTIGAVTMQTATTVAAPS
        iav-Mdom   (858) YDLVKKTLETQHQP----QVEEPIPLTE-ATSLKDVTLTKQPDPVAADAG
        iav-Dmel   (854) FDLVEQTMKTQPQAPVAKKVDPLPVASV-AKASPAAPATQATATAAAASD
        iav-Apis   (791) ------LTKDQSIDELHDPLRQLVIMSESDKNIDKSQVEIVANAAAKIAN
iav-Mper partial   (688) ------LTKDQSIDELHDPLRQLVIMSESDKNIDKSQVEIVANAAAKIAN
        iav-Bmor   (894) PEIQQSNENQKPEQVHQDYLRELIVLAE-KPATTNLELKQLAEKAADLRD
        iav-Dple   (870) NNPATAN-----EIVFKDYLRD-IIKAE-QLGLDNIDIKALAEKAANLTD
        iav-Aech   (856) EAMNLRNMNQTKALEE--TVEDPFLELA-IASETTTDYKTLLQIAKSALA
        iav-Cflo   (855) EAMNLKNTNQTKALEASMEFEDPFLELA-IASETTTNYEILLQIAKSALA
        iav-Hsal   (850) EAMNLKNASQAKAHEG--AVEDPFLELA-IASETTEDYDTLLQMAKSALA
        iav-Aflo   (853) HEMNLKNA---NHSSVTEDFQDPLLELV-IASENTNDPETLLEIAKRAAA
        iav-Amel   (850) HEMNLKNA---NHSSVTEDFQDPLLELV-IASENTNDPETLLEIAKRAAA
        iav-Bimp   (853) REMNSKNA---SHSSMAEDFQDPLLELV-IASENTDDPETLLKIAERAAA
        iav-Bter   (783) -------------SSMAEDFQDPLLELV-IASENTDDPETLLKIAERAAA
        iav-Mrot   (849) EKMNVKNA---NNSSTVEEYHDLFLEFV-IASESMNDPETLLKMAERVAA
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit   (871) PTVRPSELGPASAPCSADPLLELMLATE-DPGSSEETLQRLAHSARIVGE
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (738) ----------PPEQPFHDPFRQLVIEAE-NPHIDESELAALANAAAMSVV
        iav-Eher   (794) ----------AKELIVSDPFRDLVLSSE-IDVGEE-ELATLAEAAVLSVM
        iav-Dpon   (817) ---------------FTDPLRTLVLES--LVETNSARLSVLAAQAANLPD
        iav-Tcas   (852) IMQNSVKKEEKIVATLEDPFRELVINAN-DSNCDPEKLKMLALSAANLKD
        iav-Phum   (809) -----VSCVESDSNSDPLYNDPLRQLNE-ELNKTREELTLLARVAANNDG
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1001 1050
iav-Aaeg (894) LDHDTLG--------QLNPFLEAKDVVDPVKERE----------
iav-Cqui (902) LDHEEHQQQQQQTVGQLNPFLDAKDVVDPVKERE----------
iav-Agam (914) LDHNPKD----------VVDPVRERE----------
iav-Ccap (910) ADLITPLGAN-----LTTLFQDNKDVVDPQKLQE----------
iav-Mdom (903) LLGDMAMGAN-----LTNLFQDPKDIVDPKKLEQ----------
iav-Dmel (903) LMAMPLPISN-----LSNLFQDPKDIVDPKKLEE----------
iav-Apis (835) QDSIKP----------ISINLEQQNDVKNEK----------
iav-Mper partial (732) QDSIKP----------ISVNLEQXXXXXXX----------
iav-Bmor (943) VPEIDININMAAKSARKMVAGAVSGLFGVAADTPAP----------DA
iav-Dple (913) VPEIDINISTAARSARRVVAGAVSGLFGVTAETPR----------DA
iav-Aech (903) TSEASM----KTTIDPQILAHFAMVAPPTIEKS----------S
iav-Cflo (904) ASEASV----KTAIDPQILAHFAMIPPPITEK----------F
iav-Hsal (897) TSEAS------TTVDPQILAHFTMIAPPPVEKP----------I
iav-Aflo (899) GFETEA----SSKINLQILEQFTMTKIPMEEKV----------S
iav-Amel (896) GFETET----SSKINLQILEQFTMTKIPMDEKV----------N
iav-Bimp (899) NFEVES----SSKINLQILEQFTMTKLPMEEKV----------A
iav-Bter (819) NFEVES----SSKINLQILEQFTMTKLPMEEKV----------A
iav-Mrot (895) EFDSSA----NPKINLQILEQFTMTKIPMEEQA----------A
iav-Sinv (276) ----------
iav-Nvit (920) SATTSA----KSDIDSSFLERLALGGLGLAAMPEQPDKPVEPKKKQYLAL
iav-Same partial (143) ----------
iav-Btab (777) AP-DDI--------PTPVVTPEPVSALPRLPS----------
iav-Eher (832) SGQSDE--------SEKLKIAKFNKQISFEQN----------
iav-Dpon (850) TAEIVS-CPNTATTSVKNLAGIFAGTGNFVKKIEEK----------VK
iav-Tcas (901) VEELS--VAKPQTKSVKSLAGIFAGTETFVRKVEET----------IK
iav-Phum (853) IEEIPPQICQYGWINNYNFFGNTFAQNQKVEDP----------VQQ
1051 1100
iav-Aaeg (920) FLKTLEALEDTDSEAAEKPVLGKISLIRRAKSAVSRTTSRKKKTDQHPLF
iav-Cqui (936) FLKTLEALEDTDSEAAEKPVLGKISLIRRARSAVSRTTSRKKKTDQHPLF
iav-Agam (930) FLKTLEALEDTDSEAGEKPVLGKISLIRRAKSAVSRSTSRKRKTDQHPLF
iav-Ccap (939) FLKMLAEIETEESDGGGRPILGKLSLSRRTKSALSKAQIKKDTVGGS--P
iav-Mdom (932) FLKMVADVETEESDGGG-PILGKLSLARRTRNALFKVPIPKSTLGDS--S
iav-Dmel (932) FMAMLAEVETEESDSGG-PILGKLSLAKRTHNALSKAEIRRDQQGFEGHS
iav-Apis (856) -----TKIPTSSNTITNRKLLNKQSKNLSMYGFESQDMSVDKYS------
iav-Mper partial (752) -----XXXXXXXXTITNRKLLNKQSKNLSMYGFESQDISVDKYS------
iav-Bmor (981) GWRRDRHDNSDSDPISESVLLSRASRARRARSASRRAAPPP---------
iav-Dple (950) GWRRERHEHTDSDPVPECVILGRAARARRARSASRRAPPPP---------
iav-Aech (933) IVKKQYFMESSDNDLGGDNLLGTEARLRRIKSANNRFTTS----------
iav-Cflo (933) IVKKQYFMESSDNDVGGDNLLGTEARLRRIKSANNRFITTS---------
iav-Hsal (925) VVKKQYLVESSDNDLGGDNLLGTEARIRRIKSANDRFISTS---------
iav-Aflo (929) VTRKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTR---------
iav-Amel (926) VTRKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTR---------
iav-Bimp (929) ATKKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTR---------
iav-Bter (849) ATKKQYFVESSDNDFGGDNLLGTEARLRRIRSANNRFITTR---------
iav-Mrot (925) AVKKQYFIESSDNDFGGDNLLGTVARLRRIRSANSRFITAR---------
iav-Sinv (276) ----------
iav-Nvit (966) KSSLKSDRASLQHPLSHDGQLGTEARLRRIRSASSRLAPTTTTSTSRR--
iav-Same partial (143) ----------
iav-Btab (800) ----LHLEPSDSDGLGDGPLLGRGSRVRRVRSAHLKQQKASSTN------
iav-Eher (856) ----AVLEVSDSDGFLDGQPLGQGSRARKVKSAQERQRAERTWG------
iav-Dpon (887) KKKYAVLECSDSESFGG--KCHGISTHFQSKTLKYCRSAAG---------
iav-Tcas (937) KK-YAALDPSDSEGFGEPPLLGKISRTRRAKSANLRNSSAR---------
iav-Phum (889) PTFQSTPNHSDSDGLGDGLLLGSNRRLKRTRSANIKRKFSGSS-------

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                        1101                                                1150
        iav-Aaeg   (970) TIAWDDKNLTR---------------THPEDFGALNTAYEYSAEDFKQDV
        iav-Cqui   (986) MIAWDDKTTTIPGGGPQAVSATAGTAAPEDDFGALNTAYECSAEDLKHDV
        iav-Agam   (980) MIAWEDKGDQQR-------------------HSTALYDGATGAAPSVGAP
        iav-Ccap   (987) DKLIPSVWSHNLPQPDEEPE--------FNFEAALAEEHTLTIEQEAEVE
        iav-Mdom   (979) DKLINSVWDKVPADNDEDSIP-------AFDFQEALAEHVLTVEQEADVE
        iav-Dmel   (981) HGQFQPMSSVWAPPGLDVDT--------GFHFDEAVAEEVLTIEQEAEVE
        iav-Apis   (895) ------------------------------------KAIAITRSISTQTG
iav-Mper partial   (791) ------------------------------------KEIVITRSISTQTG
        iav-Bmor  (1022) ------------------------------------PHLYVPARSMYLVA
        iav-Dple   (991) ------------------------------------PHLYVPAR------
        iav-Aech   (973) ---------------------------------KRSRRDDDGDSSSSTTS
        iav-Cflo   (974) ---------------------------------KRPHRDDDGDSSSSTIS
        iav-Hsal   (966) ---------------------------------KRSHHDDDNDSSSSVTS
        iav-Aflo   (970) ---------------------------------RRSRNVDDDLSSTSSTS
        iav-Amel   (967) ---------------------------------RRSRNVDDDLSSTSSTS
        iav-Bimp   (970) ---------------------------------RRSRHTDDDLSSTSSTS
        iav-Bter   (890) ---------------------------------RRSRHTDDDLSSTSSTS
        iav-Mrot   (966) ---------------------------------RHSRHVNDDMSSTSSAS
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit  (1014) ----------------------------KSGQQKQQREARDDESTSSAAS
iav-Same partial   (143) ------------------------------------------------------
        iav-Btab   (840) ------------------------------------GNGYSDRQRLFSSKN
        iav-Eher   (896) ------------------------------------GTSISSIE-------
        iav-Dpon   (926) -------------------------------------DNITGEE-----GQ
        iav-Tcas   (977) ------------------------------------SKASDKKKLVAGSQ
        iav-Phum   (932) ---------------------------------TNEKNLLEPEDSSSTNS

                        1151                                                1200
        iav-Aaeg  (1005) DEEA---REEEEDEGVTVEEVHRRMEELHHR-GRASLERDSNSTESSKKH
        iav-Cqui  (1036) DEEA---REDDPDEGVTVEEVHRRMERFHQRPGRSSPERDSNSTESSK--
        iav-Agam  (1011) GELG---QPEQPEDAVTVEELHRRMEQFHQR--ASVRERDANSSESGS--
        iav-Ccap  (1029) TETG--NEREDSEDCPTVEEVHATMKQFHLRKRQYQQDDAARRAKSARIK
        iav-Mdom  (1022) TEDANDDSGETMDDIPTAEEVHATMKQFHLRKRQYQQDDAARRAKTARIR
        iav-Dmel  (1023) TEDG--NGGQDSEDIPTAEEVHATMKQFHLRKCQPAQDEAARRAKSARVR
        iav-Apis   (909) GIGIIEKNERQIIRPKTAKINRVTPTQNFAVKRGQSAQPDKREDHRDN--
iav-Mper partial   (805) GIGIIEKNERPIIRPKTAKINRVTPTQNFAVKRGQSAQPDKREDHRDN--
        iav-Bmor  (1036) SESSAIESDAPWDDQPSSENNSAVGGRREEIAHIKAARPLCIQHAASG--
        iav-Dple   (999) ------------------------------------------------------
        iav-Aech   (990) VEQSL-RYRPLLNDPEQRPMNRI-ETEGR-KTTVETIKPEVKQNG-----
        iav-Cflo   (991) IERNQ-RYRPLFNDPEERSINHV-ETEGQ-KTPMETIKSEIQQNG-----
        iav-Hsal   (983) VDRSQPQYRPLLNDSEESLANRV-ENEGRRTSDVETIKSEVKQNGRGG--
        iav-Aflo   (987) MDRNP-RYQSLFNG-HENSIDR--PIESR-ECSMEAINSQIKQNGPP---
        iav-Amel   (984) MDRNP-RYQSLLNG-HENSIDR--PIESR-ECSIEAINSQIKQNGP----
        iav-Bimp   (987) ADRNP-QYQPLLNG-PENLASR--QIESR-ESSIEAIKPQVKQNGS----
        iav-Bter   (907) ADRNP-QYQPLLNG-PENLVSR--QIESR-ESSIEAIKPQVKQNGS----
        iav-Mrot   (983) GDGNP-RYQQLLND-TEEVPSNQ-RTENR-DESIVANKSEVKQNDAN---
        iav-Sinv   (276) ------------------------------------------------------
        iav-Nvit  (1036) LDNIS-GYQPLLNEPDTTADQPATGTEDNKPANGRNLRKRPKTTSNEGKV
iav-Same partial   (143) ------------------------------------------------------
        iav-Btab   (855) EDSSS---NTSLDFDLTNPPSQLRLTPPPRPVTAEIVAVNPKKYIG----
        iav-Eher   (904) -----------------EPPPYLPLPPPP-----------P---------
        iav-Dpon   (935) TDTYATFCKQEKEFR----------------------------------
        iav-Tcas   (991) SSSTDTVNNEINEKNIENSDLDYAEERIKLVKESLKQVVDVAQIRPIN--
        iav-Phum   (949) EDFSCLTENYINKNIKVNANFSENSLRSNRSSANLVVKKFGRRSG-----
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                          1201                                                1250
        iav-Aaeg  (1051) PHRKRQGMGRGRNNKVSPDTSNESVSG------------KKDKRMKSAP
        iav-Cqui  (1081) -K-----Q-------AKGDKRMKSAPS------------GHGPRHRQMM
        iav-Agam  (1054) --------GKQHAGPKARKPAGSSAGG------------RTVAPGGARP
        iav-Ccap  (1077) -----------RKNRISPEQSHECDDGSSGGGGGKSTHPRGASAPGRKHT
        iav-Mdom  (1072) -----------RKNKVAPDYAGSEEQ-----------YGRGRSAPMKKKH
        iav-Dmel  (1071) -----------RRNKVSPEQSDDPDE--------------RSQRGRSAY
        iav-Apis   (957) ------------------------------------K----------EQ
iav-Mper partial   (853) ------------------------------------K----------EQ
        iav-Bmor  (1084) ----RTAQVEHSLFVVGPGTGAEVESTPTVQKSEKKARPKTTRSRRNRIS
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1032) ------SIPTKPLDKIQKRRPKTAKNRVSPKETEEPARRR-ESIERN-KA
        iav-Cflo  (1033) ------SIPLKPPDKIQKRRPKTAKNRVSPKEIEEPRRR--ESIEQN-KA
        iav-Hsal  (1030) ---GGGGVSKPSDKRVQKRRPKTAKNRVSPKEIEEPARRREESIERNKAA
        iav-Aflo  (1029) --------CETVKAKVQKKRPKTAKNRVSPKEIEKAGPRRRESIERN-KA
        iav-Amel  (1025) --------CETMKAKVQKKRPKTARNRVSPKEIEKAGPRRRESIERN-KA
        iav-Bimp  (1028) --------CDSVKIKVQKRRPKTAKNRVSPKEIEEAGPRRRESIERN-KA
        iav-Bter   (948) --------CDSVKIKVQKRRPKTAKNRVSPKEIEEAGPRRRESIERN-KA
        iav-Mrot  (1026) --------CGSRCKAQ-KRRPKTARNRVSPKETEDSGQRRRESMERN-KA
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1085) FCSRRTIVVLNKNKKNKKLETSEANMNARKKETLLALHDMTSLISDNWIQ
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (898) ------------GNSQERLRPKTAKVNRVAPTPDVPVRRG----ISANGI
        iav-Eher   (917) ------------LHSHQRPRPKTAKPNRVVPEAVVAKRP------QSSAL
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1039) ----IDVALEEQVSVTISETMRVQGSGDGAEVQSSNVKPKRKKRSKTAKN
        iav-Phum   (994) ---------------------LKSSTNRIAPADLSPVGNVSKYSETLCN

                          1251                                                1300
        iav-Aaeg  (1088) TGGGTSPPDPLEPWSTRDICNINKLLDTDTQDE-----------------
        iav-Cqui  (1105) DTGGGSPPDPLEPWSTKEIVPINKLLDTDTQDE-----------------
        iav-Agam  (1083) DDGTGSPPDPLEPWSTKNIMNINKLLDQDTTEE-----------------
        iav-Ccap  (1116) VSERLSPPDPLEPWSTRELQNINKILARK----------------------
        iav-Mdom  (1100) DEDEMSPPDPLEPWSTRELQNINKILAKK----------------------
        iav-Dmel  (1095) TRRTQSPPDPLEPWSTRELQDINKILARK----------------------
        iav-Apis   (960) QCYCISGNNMLRPWSTQDLAPLNTIMAWGPNDDF----------------
iav-Mper partial   (856) QCYCISGNNMLRPWSTQDLAPLNTIMAWGPNDDF----------------
        iav-Bmor  (1130) PTPVQEAGSPLEPWATAQLSKLSRLIRYSSSSAASITSQTSTEQEQSPRY
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1074) ASPPTSSSDPLEPWSTRGITDMNTILAWRENAPDSP--------------
        iav-Cflo  (1074) ASPPTSSSDPLEPWSTRGITDMNTILAWRDNAPDSP--------------
        iav-Hsal  (1077) LSPPASPSDPLEPWSTRGITDMNTILAWRENAPDSP--------------
        iav-Aflo  (1070) VSPATSPTDPLEPWSTRGIKDMNTILAWEETAPDSP--------------
        iav-Amel  (1066) VSPATSPTDPLEPWSTRGIKDMNTILAWEETAPDSP--------------
        iav-Bimp  (1069) VSPATSPTDPLEPWSTRGIKDMNTILAWEENTPDSP--------------
        iav-Bter   (989) VSPATSPTDPLEPWSTRGIKDMNTILAWEENTPDSP--------------
        iav-Mrot  (1066) VSPATSPTDPLEPWSTRGIKDMNTILAWEENVPDSP--------------
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1135) INIARFQNNYSHSKVTKNLKKCHLHIESDVLLTSQQCCINISNSKAKMNQ
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (932) PESLPSPPDPLEPWSTRNIVNMNAILAWQQSDQDSL--------------
        iav-Eher   (949) GDRVKSPPELLEPWSTRGIATINTILAWQPSDQDSM--------------
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1085) NK------------------------------------------------
        iav-Phum  (1022) SYCITSSSDVLYQWSIKGITNMNTLLGLENEDSM----------------
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                          1301                                          1350
        iav-Aaeg  (1121) --------------------------------------------------
        iav-Cqui  (1138) --------------------------------------------------
        iav-Agam  (1116) --------------------------------------------------
        iav-Ccap  (1145) --------------------------------------------------
        iav-Mdom  (1129) --------------------------------------------------
        iav-Dmel  (1124) --------------------------------------------------
        iav-Apis   (994) --------------------------------------------------
iav-Mper partial   (890) --------------------------------------------------
        iav-Bmor  (1180) --------------------------------------------------
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1110) --------------------------------------------------
        iav-Cflo  (1110) --------------------------------------------------
        iav-Hsal  (1113) --------------------------------------------------
        iav-Aflo  (1106) --------------------------------------------------
        iav-Amel  (1102) --------------------------------------------------
        iav-Bimp  (1105) --------------------------------------------------
        iav-Bter  (1025) --------------------------------------------------
        iav-Mrot  (1102) --------------------------------------------------
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1185) ALLVVLSFFVVNEDQPVAGWTWGKSATSSSNNSINDDRARYCRICASHTM
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (968) --------------------------------------------------
        iav-Eher   (985) --------------------------------------------------
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1087) --------------------------------------------------
        iav-Phum  (1056) --------------------------------------------------

                          1351                                          1400
        iav-Aaeg  (1121) --------------------------------------------------
        iav-Cqui  (1138) --------------------------------------------------
        iav-Agam  (1116) --------------------------------------------------
        iav-Ccap  (1145) --------------------------------------------------
        iav-Mdom  (1129) --------------------------------------------------
        iav-Dmel  (1124) --------------------------------------------------
        iav-Apis   (994) --------------------------------------------------
iav-Mper partial   (890) --------------------------------------------------
        iav-Bmor  (1180) --------------------------------------------------
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1110) --------------------------------------------------
        iav-Cflo  (1110) --------------------------------------------------
        iav-Hsal  (1113) --------------------------------------------------
        iav-Aflo  (1106) --------------------------------------------------
        iav-Amel  (1102) --------------------------------------------------
        iav-Bimp  (1105) --------------------------------------------------
        iav-Bter  (1025) --------------------------------------------------
        iav-Mrot  (1102) --------------------------------------------------
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1235) CLFPYDDPGPKCAAVENGDLEPEEIEWILQRHNSLRDGIARAWKSQYRPL
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (968) --------------------------------------------------
        iav-Eher   (985) --------------------------------------------------
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1087) --------------------------------------------------
        iav-Phum  (1056) --------------------------------------------------
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                          1401                                                1450
        iav-Aaeg  (1121) --------------------------------------------------
        iav-Cqui  (1138) --------------------------------------------------
        iav-Agam  (1116) --------------------------------------------------
        iav-Ccap  (1145) --------------------------------------------------
        iav-Mdom  (1129) --------------------------------------------------
        iav-Dmel  (1124) --------------------------------------------------
        iav-Apis   (994) --------------------------------------------------
iav-Mper partial   (890) --------------------------------------------------
        iav-Bmor  (1180) --------------------------------------------------
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1110) --------------------------------------------------
        iav-Cflo  (1110) --------------------------------------------------
        iav-Hsal  (1113) --------------------------------------------------
        iav-Aflo  (1106) --------------------------------------------------
        iav-Amel  (1102) --------------------------------------------------
        iav-Bimp  (1105) --------------------------------------------------
        iav-Bter  (1025) --------------------------------------------------
        iav-Mrot  (1102) --------------------------------------------------
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1285) PARDMMQVFWDEELAKIARRWALQCNIHEKDQCRDVEEFSVAQSVSALDL
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (968) --------------------------------------------------
        iav-Eher   (985) --------------------------------------------------
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1087) --------------------------------------------------
        iav-Phum  (1056) --------------------------------------------------

                          1451                                                1500
        iav-Aaeg  (1121) --------------------------------------------------
        iav-Cqui  (1138) --------------------------------------------------
        iav-Agam  (1116) --------------------------------------------------
        iav-Ccap  (1145) --------------------------------------------------
        iav-Mdom  (1129) --------------------------------------------------
        iav-Dmel  (1124) --------------------------------------------------
        iav-Apis   (994) --------------------------------------------------
iav-Mper partial   (890) --------------------------------------------------
        iav-Bmor  (1180) --------------------------------------------------
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1110) --------------------------------------------------
        iav-Cflo  (1110) --------------------------------------------------
        iav-Hsal  (1113) --------------------------------------------------
        iav-Aflo  (1106) --------------------------------------------------
        iav-Amel  (1102) --------------------------------------------------
        iav-Bimp  (1105) --------------------------------------------------
        iav-Bter  (1025) --------------------------------------------------
        iav-Mrot  (1102) --------------------------------------------------
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1335) QDAGNRSEMERLKFHLRSWYSQLEPDFSNSAGVGLATPSVTNVGCGRATY
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (968) --------------------------------------------------
        iav-Eher   (985) --------------------------------------------------
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1087) --------------------------------------------------
        iav-Phum  (1056) --------------------------------------------------
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                          1501                                          1550
        iav-Aaeg  (1121) --------------------------------------------------
        iav-Cqui  (1138) --------------------------------------------------
        iav-Agam  (1116) --------------------------------------------------
        iav-Ccap  (1145) --------------------------------------------------
        iav-Mdom  (1129) --------------------------------------------------
        iav-Dmel  (1124) --------------------------------------------------
        iav-Apis   (994) --------------------------------------------------
iav-Mper partial   (890) --------------------------------------------------
        iav-Bmor  (1180) --------------------------------------------------
        iav-Dple   (999) --------------------------------------------------
        iav-Aech  (1110) --------------------------------------------------
        iav-Cflo  (1110) --------------------------------------------------
        iav-Hsal  (1113) --------------------------------------------------
        iav-Aflo  (1106) --------------------------------------------------
        iav-Amel  (1102) --------------------------------------------------
        iav-Bimp  (1105) --------------------------------------------------
        iav-Bter  (1025) --------------------------------------------------
        iav-Mrot  (1102) --------------------------------------------------
        iav-Sinv   (276) --------------------------------------------------
        iav-Nvit  (1385) SVAIDDSDVAAAVEVLVCNYGPIDDPETEDDSGCETRSRRYSELCQLTRR
iav-Same partial   (143) --------------------------------------------------
        iav-Btab   (968) --------------------------------------------------
        iav-Eher   (985) --------------------------------------------------
        iav-Dpon   (950) --------------------------------------------------
        iav-Tcas  (1087) --------------------------------------------------
        iav-Phum  (1056) --------------------------------------------------

                          1551
        iav-Aaeg  (1121) -
        iav-Cqui  (1138) -
        iav-Agam  (1116) -
        iav-Ccap  (1145) -
        iav-Mdom  (1129) -
        iav-Dmel  (1124) -
        iav-Apis   (994) -
iav-Mper partial   (890) -
        iav-Bmor  (1180) -
        iav-Dple   (999) -
        iav-Aech  (1110) -
        iav-Cflo  (1110) -
        iav-Hsal  (1113) -
        iav-Aflo  (1106) -
        iav-Amel  (1102) -
        iav-Bimp  (1105) -
        iav-Bter  (1025) -
        iav-Mrot  (1102) -
        iav-Sinv   (276) -
        iav-Nvit  (1435) E
iav-Same partial   (143) -
        iav-Btab   (968) -
        iav-Eher   (985) -
        iav-Dpon   (950) -
        iav-Tcas  (1087) -
        iav-Phum  (1056) -
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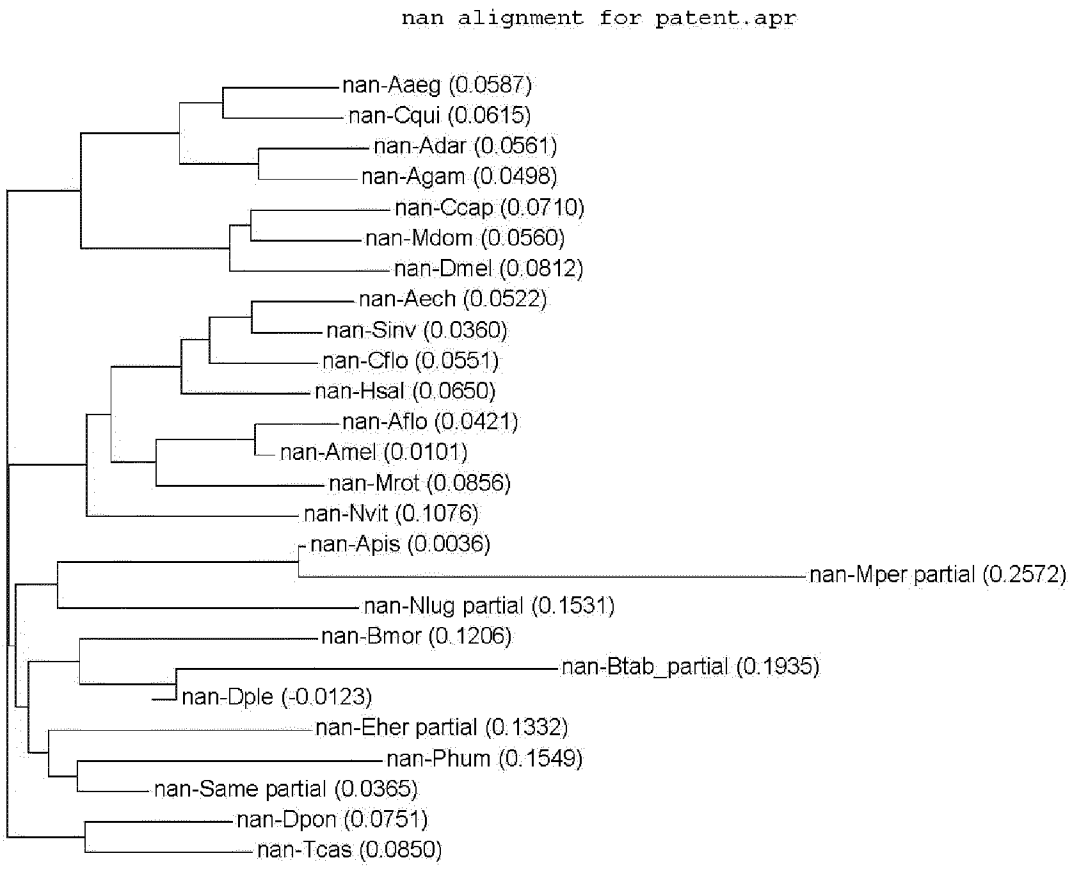

nan alignment for patent.apr
nan-Aaeg (0.0587)
nan-Cqui (0.0615)
nan-Adar (0.0561)
nan-Agam (0.0498)
nan-Ccap (0.0710)
nan-Mdom (0.0560)
nan-Dmel (0.0812)
nan-Aech (0.0522)
nan-Sinv (0.0360)
nan-Cflo (0.0551)
nan-Hsal (0.0650)
nan-Aflo (0.0421)
nan-Amel (0.0101)
nan-Mrot (0.0856)
nan-Nvit (0.1076)
nan-Apis (0.0036)
nan-Mper partial (0.2572)
nan-Nlug partial (0.1531)
nan-Bmor (0.1206)
nan-Btab_partial (0.1935)
nan-Dple (-0.0123)
nan-Eher partial (0.1332)
nan-Phum (0.1549)
nan-Same partial (0.0365)
nan-Dpon (0.0751)
nan-Tcas (0.0850)

FIGURE 118

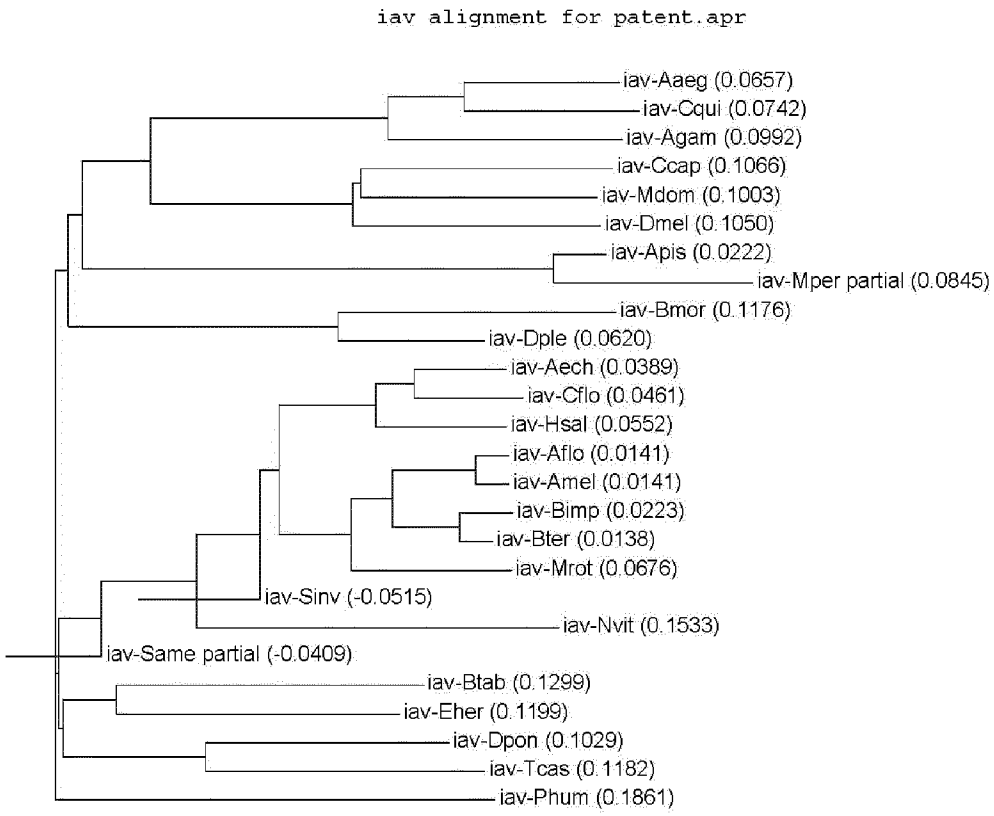

iav alignment for patent.apr
iav-Aaeg (0.0657)
iav-Cqui (0.0742)
iav-Agam (0.0992)
iav-Ccap (0.1066)
iav-Mdom (0.1003)
iav-Dmel (0.1050)
iav-Apis (0.0222)
iav-Mper partial (0.0845)
iav-Bmor (0.1176)
iav-Dple (0.0620)
iav-Aech (0.0389)
iav-Cflo (0.0461)
iav-Hsal (0.0552)
iav-Aflo (0.0141)
iav-Amel (0.0141)
iav-Bimp (0.0223)
iav-Bter (0.0138)
iav-Mrot (0.0676)
iav-Sinv (-0.0515)
iav-Nvit (0.1533)
iav-Same partial (-0.0409)
iav-Btab (0.1299)
iav-Eher (0.1199)
iav-Dpon (0.1029)
iav-Tcas (0.1182)
iav-Phum (0.1861)

FIGURE 119

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/064078

A. CLASSIFICATION OF SUBJECT MATTER
INV. G01N33/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, EMBASE, FSTA, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CHERYL A. LEICHTER ET AL: "The high potency of ME-5343 to aphids is due to a unique mechanism of action", PESTICIDE BIOCHEMISTRY AND PHYSIOLOGY, vol. 107, no. 2, 1 October 2013 (2013-10-01), pages 169-176, XP055218037, ISSN: 0048-3575, DOI: 10.1016/j.pestbp.2013.06.009 abstract; p. 169, left-hand col., 1st para. - right-hand col., 1st para.; p. 170, para 2.2.1	28-33, 35-37

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[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
23 September 2016	04/10/2016

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Ripaud, Leslie

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INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/064078

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ALEXANDRE NESTEROV ET AL: "TRP Channels in Insect Stretch Receptors as Insecticide Targets", NEURON, vol. 86, no. 3, 1 May 2015 (2015-05-01), pages 665-671, XP055201614, ISSN: 0896-6273, DOI: 10.1016/j.neuron.2015.04.001 abstract; p. 665, right-hand col., 1st-2nd para; p. 667, right-hand col., 2nd para.; p. 668, right-hand col., last para.; p. 670, left-hand col., 1st para.; fig. 3	1-31, 33-38
X,P	WO 2015/097560 A2 (BASF SE [DE]) 2 July 2015 (2015-07-02) the whole document	1-38
A	KEIICHI NAGATA: "TRP channels as target sites for insecticides: physiology, pharmacology and toxicology", INVERTEBRATE NEUROSCIENCE, SPRINGER, BERLIN, DE, vol. 7, no. 1, 7 February 2007 (2007-02-07), pages 31-37, XP019476061, ISSN: 1439-1104, DOI: 10.1007/S10158-007-0044-4 the whole document	1-38
A	US 2009/209633 A1 (PREMKUMAR LOUIS S [US]) 20 August 2009 (2009-08-20) para. 6, 7, 38, 39	1-38
A	G. R. SEABROOK: "Functional Properties of the High-Affinity TRPV1 (VR1) Vanilloid Receptor Antagonist (4-Hydroxy-5-iodo-3-methoxyphenylacetate ester) Iodo-Resiniferatoxin", JOURNAL OF PHARMACOLOGY AND EXPERIMENTAL THERAPEUTICS, vol. 303, no. 3, 1 December 2002 (2002-12-01), pages 1052-1060, XP055305053, US ISSN: 0022-3565, DOI: 10.1124/jpet.102.040394 abstract; p. 1053, right-hand col., last para. - p. 1054, left-hand col., 1st para.	1-38

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INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/064078

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	E. PHILLIPS ET AL: "Identification of Species-specific Determinants of the Action of the Antagonist Capsazepine and the Agonist PPAHV on TRPV1", JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 279, no. 17, 23 April 2004 (2004-04-23), pages 17165-17172, XP055305059, US ISSN: 0021-9258, DOI: 10.1074/jbc.M313328200 abstract; p. 17166, left-hand col., 3rd para.	1-38
A	CN 103 898 122 A (INST PLANT PROTECTION IPP CAAS) 2 July 2014 (2014-07-02) the whole document	1-38

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2016/064078

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2015097560 A2	02-07-2015	NONE	
US 2009209633 A1	20-08-2009	US 2009209633 A1	20-08-2009
		WO 2008011532 A2	24-01-2008
CN 103898122 A	02-07-2014	NONE	