

**Phylogenetic approach to identification of short linear motifs (SLiMs)  
in the Kekkoon protein family**

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Caitlin O'Reilly  
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Joseph B. Duffy, Ph. D.  
Biology and Biotechnology  
WPI Project Advisor

## **ABSTRACT**

The Kekkon (Kek) family of proteins are a group of six transmembrane proteins characterized by an extracellular domain with seven leucine rich repeats and one immunoglobulin domain. The intracellular domain has no known functional motifs and is poorly conserved across species. A short intracellular motif (SLiM) is a short (3-10 residues), linear group of amino acids that mediate protein interactions, and because of the short length and high specificity tend to be well conserved during evolution. Identification of highly conserved residues across a taxonomic range could lead to the discovery of SLiMs, broadening our understanding of Kek protein function and mechanisms. This project identified Kek1, 2, 3, 5, and 6 orthologs in a group of sixteen arthropods, and from this group of orthologs putative SLiMs with unknown functions were identified.

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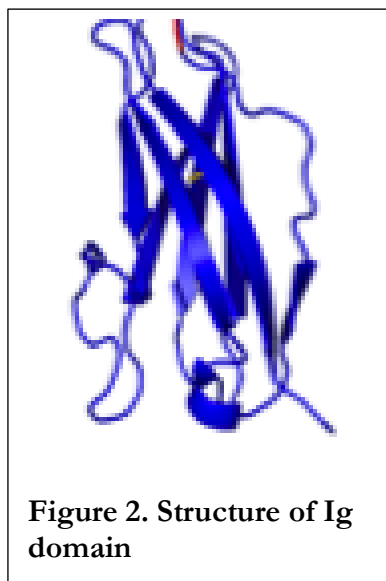
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# INTRODUCTION

## *Kekkon Protein Family*

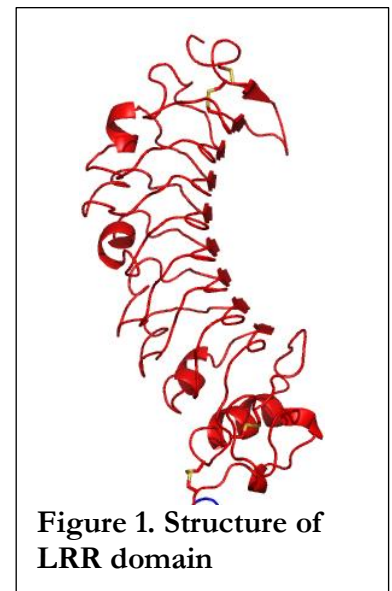
Leucine-rich repeats (LRR) and immunoglobulin (Ig) domains are some of the most ubiquitous motifs in the metazoan proteome (MacLaren et al, 2004). LRR domains are present in many proteins with diverse functions and form an underlying structure that facilitates protein-protein interactions (Figure 1) (Kobe and Kajava, 2001). Ig domains are characterized by an immunoglobulin fold, two antiparallel  $\beta$  sheets with a disulfide bond, and, like LRR domains, are found in a wide variety of proteins, especially those that participate in cell-cell interaction (Figure 2) (Barclay, 2003). The *Drosophila melanogaster* proteome contains 124

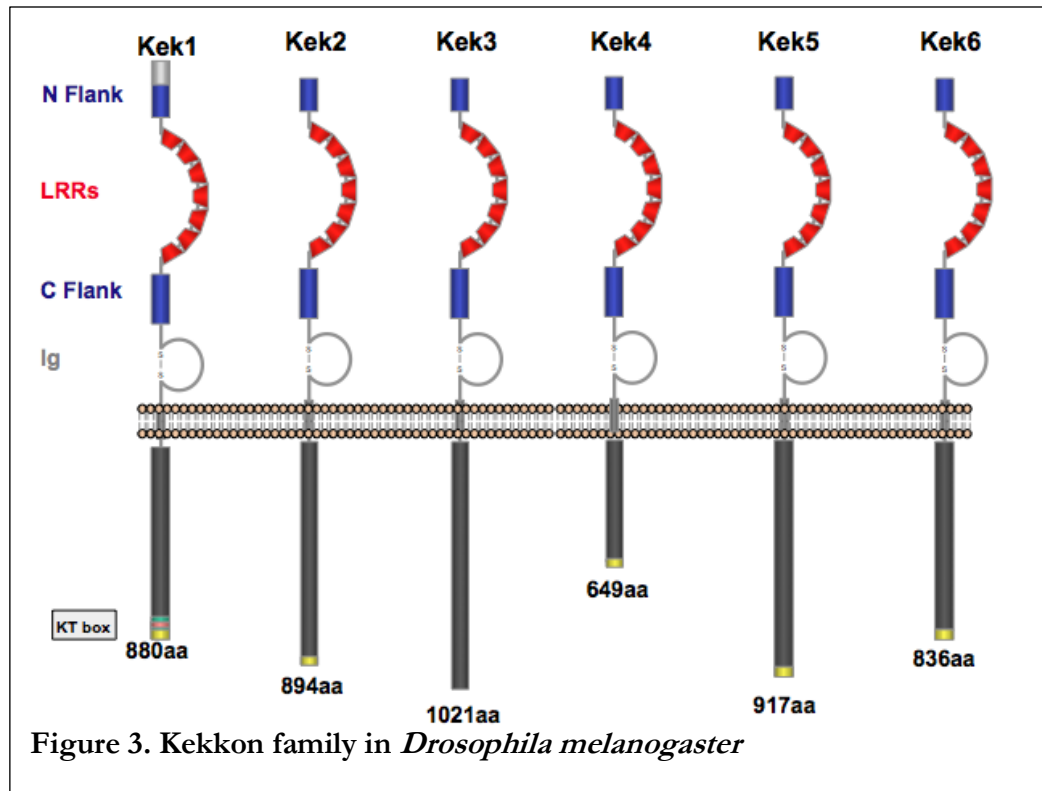


proteins with an LRR domain and 228 proteins with an Ig domain, while the

human proteome contains 375 proteins with an LRR domain and 750 proteins with an Ig domain. Despite the ubiquity of the LRR and Ig domains in metazoan proteomes, only nine proteins in the *Drosophila melanogaster* proteome contain both an LRR domain and an Ig domain. Of these nine members of the LIG protein family, six of them are Kekkon (Kek) proteins.

The Kekkon family of proteins is a group of six transmembrane LIG proteins characterized by an extracellular domain with seven leucine rich repeats capped by cytosine rich repeats and a single immunoglobulin domain (Figure 3). The intracellular region has no known functional motifs. (MacLaren et al, 2004).





Unlike the extracellular domain, the intracellular domain of Kek family members is poorly conserved across species (MacLaren et al, 2004). Poor conservation of intracellular domains and the presence of multiple Keks, suggest each member of the Kek family performs a unique function. The exact function of all Kek proteins remains unclear, but preliminary studies of their function suggest that they play a role in cell signaling and neural development. Kek1, Kek2 and Kek5 are abundant in the *Drosophila melanogaster* embryonic central nervous system (Musacchio and Perrimon, 1996 ; Evans et al, 2009).

In *Drosophila melanogaster*, Kek1 has been shown to inhibit the Epidermal Growth Factor Receptor (dEGFR) during oogenesis (Alvarado et al, 2004). Kek1 is expressed in tissues with dEGFR activity such as follicle cells, the eye, and wing imaginal disks, and conversely, Kek1 is not expressed without dEGFR activity (Ghiglione et al, 2003). Loss of Kek1 function during eye development is associated with altered eye phenotype (Alvarado et al, 2004). Furthermore, overexpression of human EGFR and mutated human EGFR are associated with many forms of cancer, especially lung and breast cancers and glioblastoma (Sigismund et al, 2017). Given that Kek1 inhibits dEGFR, and the role of aberrant EGFR signaling in cancer, Kek1 may have potential for therapeutic uses as an inhibitor.

Kek5 has been shown to regulate bone morphogenetic protein (BMP). In *Drosophila*, BMP regulates wing growth and vein formation during larval and pupal stages respectively. Gain- and loss-of-function studies show that Kek5 likely inhibits BMP, and loss-of-function results in abnormal wing morphology and reduced viability (Evans et al, 2009).

Kek6 interacts with *Drosophila* neurotrophins to regulate neuronal plasticity. Kek6 acts as a receptor for *Drosophila* neurotrophin 2 (DNT2) to regulate synaptic structure, plasticity, and vesicle release via CaMKIII and VAP33A. Furthermore, Kek6 interacts with Toll-6, another DNT2 receptor, to regulate neuromuscular junction growth (Ulian-Benitez et al, 2017).

To date, limited work has been done on Kek2, Kek3, and Kek4 function. Kek2 is abundant in developing *Drosophila* central nervous systems, and may play a role in regulating synaptic structure, but is otherwise poorly understood (Guan et al, 2005). Kek3 appears to play a role in BMP regulation, but Kek3 BMP regulation appears to be a different mechanism than Kek5 BMP regulation (Krishnan, 2015). Kek4 has not been studied and appears to only be present in *Drosophila*.

Unlike the extracellular domain, the intracellular domain is poorly conserved across species (MacLaren et al, 2004). This has led to an unresolved question – How do the Kek family members transduce an extracellular cue to produce an intracellular response? Identifying portions of the intracellular domain, that are well conserved across species and among the different Kek proteins, could provide better insights into the functions and signal transduction mechanism by which Kek family proteins act.

### *Short Linear Motifs*

A short linear motif (SLiM) is a small, linear group of residues that facilitate protein binding, and therefore, function (Krystkowiak and Davey, 2017). SLiMs are approximately 3-10 amino acids in length, and it is estimated that SLiMs mediate 15%-40% of protein interactions (Edwards et al, 2007). Identifying and understanding SLiMs are critical in understanding protein function and mechanism, but due to their relatively short length they are difficult to identify. Identification of SLiMs in proteins with poorly understood functions and interactions could lead to new understandings into protein function and cellular regulation (Davey et al, 2012).

Because SLiMs play an essential role in protein function, the SLiM residues tend to be well conserved compared to non-functional residues. While the specificity of a SLiM's interactions lends itself to evolutionary conservation, it can also lend itself to convergent evolution (Davey et al, 2012). A phylogenetic approach to SLiM identification takes advantage of these inherent characteristics. This is accomplished by first identifying protein orthologs in different species, then comparing the protein sequences to identify areas of the protein sequence with conservation across a taxonomic range.

The presence of Kek proteins in the *Drosophila* genus is well documented, and Kek orthologs have been found in *Anopheles gambiae* and *Apis mellifera* (MacLaren et al, 2004). This project aimed to identify Kek orthologs in more evolutionarily distant arthropods **and** to identify conserved short linear motifs, SLiMs, using a phylogenetic approach. Through this I hoped to address the unresolved question of how Kek family members transduce signals via their intracellular domains.

# METHODS AND MATERIALS

## Identification of Kek orthologs

To identify Kek orthologs in arthropod species of interest, the *Drosophila melanogaster* Kek protein sequence was used to search the National Center for Biotechnology Information (NCBI) protein database using the blastp search function ([blastp suite](#)). Using the ranked search results, potential Kek orthologs were identified based on a low e value and high percent identity. To confirm that the putative ortholog was indeed an ortholog for a specific Kek family member, its protein sequence was blasted against the *Drosophila melanogaster* proteome using FlyBase ([FlyBase](#)). If the top result obtained in this search was the same Kek protein used in the initial NCBI blastp search then the suspected Kek ortholog was confirmed as a true ortholog for that specific Kek family member. Once the ortholog's identity was confirmed in this manner, its NCBI accession number, open reading frame length and FASTA sequence were added to a master list of Kek orthologs. For Kek family members 1, 2, 3, 5, and 6, MS Word files containing all orthologs with their associated protein sequences, accession number, and species name were generated. The FASTA sequences of all identified orthologs can be found in appendix A.

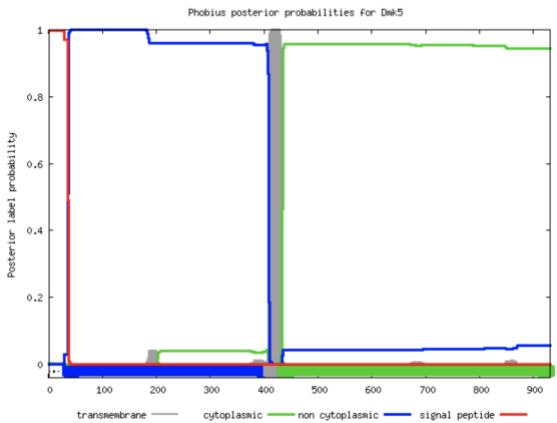
## Identification of the transmembrane and intracellular region

In order to identify the intracellular domain, the sequences were analyzed using Phobius ([Phobius](#)). Phobius uses hydrophobicity to predict the location of the signal sequence and transmembrane domain; allowing for identification of extracellular and intracellular domains based on the position of the signal sequence and transmembrane domain. The signal sequences were highlighted blue and intracellular domains red in the FASTA sequence list. See figure 4 for a sample output.

### Phobius prediction

#### Prediction of Dmk5

|    |          |     |     |                  |
|----|----------|-----|-----|------------------|
| ID | Dmk5     | 1   | 35  |                  |
| FT | SIGNAL   | 1   | 15  | N-REGION.        |
| FT | REGION   | 16  | 27  | H-REGION.        |
| FT | REGION   | 28  | 35  | C-REGION.        |
| FT | TOPO_DOM | 36  | 408 | NON CYTOPLASMIC. |
| FT | TRANSMEM | 409 | 434 |                  |
| FT | TOPO_DOM | 435 | 931 | CYTOPLASMIC.     |
| // |          |     |     |                  |



**Figure 4. Phobius prediction sample output.** Positions of the signal sequence, transmembrane, extracellular and intracellular domains are represented.

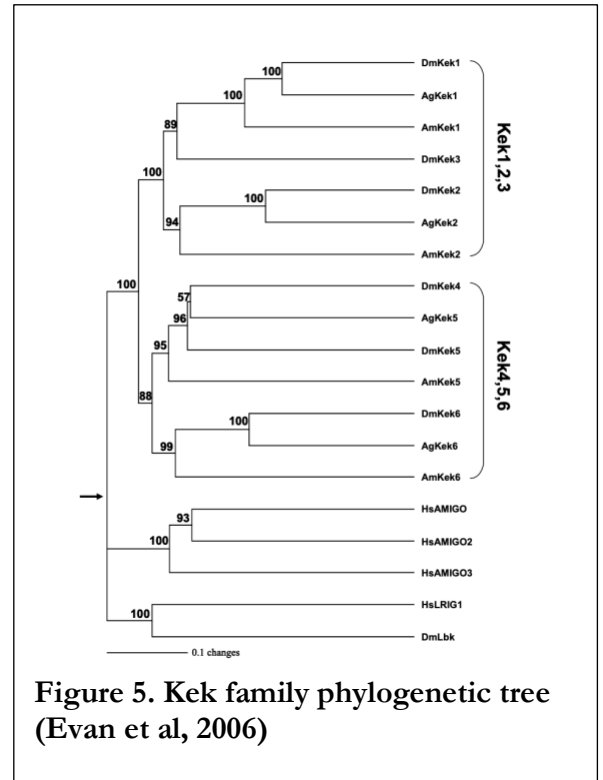
### *Sequence comparisons*

Once the transmembrane domains had been identified, intracellular regions were defined as the first amino acid following the transmembrane domain to the final amino acid. Based on this, the intracellular domains of a specific set of Kek family member orthologs were aligned using Clustal Omega ([Clustal Omega](#)) using standard parameters and an output format of Pearson/FASTA. The alignment output was then compared using BoxShade ([BoxShade](#)). The BoxShade fraction of sequences was set to 1.0, meaning only areas with 100% conservation were shaded. Conserved regions, here termed putative short linear motifs (SLiMs), were identified using BoxShade files. Using MS Excel, a master file was created with all SLiMs identified in this manner. For each Kek family member analyzed, a tab was generated that contains the putative SLiM for each species. Finally, using this Excel file, the residue frequency for each amino acid in an identified SLiM was depicted graphically using weblogo ([WebLogo](#)). WebLogos were created for each SLiM in each member of the Kek family, and additional composite WebLogos were created for SLiMs found in more than one Kek protein. In order to create the composite WebLogos the SLiMs with the same fingerprint motif were trimmed and aligned by hand so that the fingerprint motifs aligned.

## RESULTS

### Identification of *Kek* orthologs

Given the relatively low frequency of proteins with extracellular domain with both an Ig domain and LRR domain in the *Drosophila melanogaster* proteome, all members of the *Kek* protein family likely diverged from a single ancestral gene (MacLaren et al, 2004). Prior research into the evolution of *Kek* proteins suggest that *Kek*1, 2, and 3 form an intrafamilial clade and *Kek* 4, 5, and 6 form another intrafamilial clade (Figure 5) (Evans, 2006). Prior studies have found *Kek*1, 2, 3, 5, and 6 orthologs in species other than *Drosophila melanogaster*, *Kek*4 does not appear to be conserved, and therefore was not considered in this study.



In an attempt to identify conserved, and therefore likely functionally relevant, sequences within the intracellular domain in the *Kek* family, *Kek* orthologs among sixteen different arthropod species were identified. The sixteen species of interest represent approximately 530 million years of evolution. Among the five studied *Kek* proteins a total of seventy-four *Kek* family orthologs in sixteen species were identified in the NCBI database (Appendix A).

The presence of orthologs for each *Kek* in the species examined is summarized in Table 1. *Kek*1 was found in all sixteen species with a duplication in *Diaphorina citri* and *Acyrtosiphon pisum*. *Kek*2 was found in every species with a duplication in *Acromyrmex echinator* and *Acyrtosiphon pisum*. *Kek*3 was found in only half the species. *Kek*5 was found in every species except *Acyrtosiphon pisum*. One *Kek*6 protein was found in each species. *Daphnia magna* had a single protein that appeared to have characteristics of both *Kek*5 and *Kek*6.

**Table 1. Summary of *Kek* orthologs.**

| Species                           | Kek1 | Kek2 | Kek3 | Kek5 | Kek6 |
|-----------------------------------|------|------|------|------|------|
| <i>Drosophila melanogaster</i>    | +    | +    | +    | +    | +    |
| <i>Anopheles gambiae</i>          | +    | +    | -    | +    | +    |
| <i>Plutella xylostella</i>        | +    | +    | -    | +    | +    |
| <i>Tribolium castaneum</i>        | +    | +    | +    | +    | +    |
| <i>Leptinotarsa decemlineata</i>  | +    | +    | -    | +    | +    |
| <i>Apis mellifera</i>             | +    | +    | -    | +    | +    |
| <i>Habropoda laboriosa</i>        | +    | +    | -    | +    | +    |
| <i>Acromyrmex echinator</i>       | +    | +(2) | -    | +    | +    |
| <i>Nasonia vitripennis</i>        | +    | +    | -    | +    | +    |
| <i>Linipithema humile</i>         | +    | +    | -    | +    | +    |
| <i>Diaphorina citri</i>           | +(2) | +    | +    | +    | +    |
| <i>Cimex lectularius</i>          | +    | +    | +    | +    | +    |
| <i>Halymorphus balyi</i>          | +    | +    | +    | +    | +    |
| <i>Acyrtosiphon pisum</i>         | +(2) | +(2) | +    | -    | +    |
| <i>Pediculus humanus corporis</i> | +    | +    | +    | +    | +    |
| <i>Daphnia magna</i>              | +    | +    | +    | +    | +    |

### Identification of *Kek1* orthologs

At least one *Kek1* ortholog was identified in all species of interest (Table 2). Every species has one *Kek1* ortholog except *Diaphorina citri* (Asian citrus psyllid) and *Acyrtosiphon pisum* (Pea aphid) which both have two *Kek1* orthologs.

**Table 2.** Identified *Kek1* orthologs

| Gene            | Species name                      | Order        | Subphylum | Common name                 | ORF length (aa) | Accession #                   | Taxid  |
|-----------------|-----------------------------------|--------------|-----------|-----------------------------|-----------------|-------------------------------|--------|
| DmK1<br>CG12283 | <i>Drosophila melanogaster</i>    | Diptera      | Hexapoda  | Fruit fly                   | 880             | AAC47404.1                    | 7227   |
| AgK1            | <i>Anopheles gambiae</i>          | Diptera      | Hexapoda  | Mosquito                    | 769             | None – genome assembly blastX | 7165   |
| PxK1            | <i>Plutella xylostella</i>        | Lepidoptera  | Hexapoda  | Diamondback moth            | 650             | XP_011548756.1                | 51655  |
| TcKek1          | <i>Tribolium castaneum</i>        | Coleoptera   | Hexapoda  | Flour beetle                | 605             | XP_973226.1                   | 7070   |
| LdecK1          | <i>Leptinotarsa decemlineata</i>  | Coleoptera   | Hexapoda  | Colorado potato beetle      | 670             | XP_023018029.1                | 7539   |
| AmK1            | <i>Apis mellifera</i>             | Hymenoptera  | Hexapoda  | Honeybee                    | 630             | XP_006563309.1                | 7460   |
| HIK1            | <i>Habropoda laboriosa</i>        | Hymenoptera  | Hexapoda  | Southeastern blueberry bee  | 511             | KOC62356.1                    | 597456 |
| AechinK1        | <i>Acromyrmex echinator</i>       | Hymenoptera  | Hexapoda  | New world ants              | 614             | XP_011062139.1                | 103372 |
| NvitriK1        | <i>Nasonia vitripennis</i>        | Hymenoptera  | Hexapoda  | Pteromalid parasitoid wasps | 669             | XP_031780070.1                | 7425   |
| LhumK1          | <i>Linepithema humile</i>         | Hymenoptera  | Hexapoda  | Argentine ant               | 634             | XP_012218825.1                | 83485  |
| DcK1(a)         | <i>Diaphorina citri</i>           | Hemiptera    | Uniramia  | Asian citrus psyllid        | 600             | XP_008471648.2                | 121845 |
| DcK1(b)         | <i>Diaphorina citri</i>           | Hemiptera    | Uniramia  | Asian citrus psyllid        | 591             | XP_008485548.1                | 121845 |
| CIK1            | <i>Cimex lectularius</i>          | Hemiptera    | Hexapoda  | Bed Bug                     | 592             | XP_014259547.1                | 79782  |
| HhK1            | <i>Halymorpha halys</i>           | Hemiptera    | Hexapoda  | Brown marmorated stink bug  | 561             | XP_014291404.1                | 286706 |
| ApK1(a)         | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                   | 669             | XP_029344215.1                | 7029   |
| ApK1(b)         | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                   | 748             | XP_003245526.1                | 7029   |
| PhumpK1         | <i>Pediculus humanus corporis</i> | Phthiraptera | Hexapoda  | Body louse                  | 752             | XP_002427512.1                | 121224 |
| DmagK1          | <i>Daphnia magna</i>              | Cladocera    | Crustacea | Water flea                  | 879             | KZS15226.1                    | 35525  |

### Identification of *Kek2* orthologs

*Kek2* was found in all species of interest (Table 3). Each species has one *Kek2* ortholog except *Acromyrmex echinator* (New world ants) and *Acyrtosiphon pisum* (Pea aphid), both of which have two *Kek2* orthologs. *Plutella xylostella* (Diamondback moth) has two accession numbers because the NCBI database entries that appeared to be the most likely orthologs were two partial protein sequences; the two sequences represent partial sequences that overlap to form a full sequence for a single protein.

**Table 3.** Identified *Kek2* orthologs

| Gene      | Species name                      | Order        | Subphylum | Common name                 | ORF length (aa) | Accession #                      | Taxid  |
|-----------|-----------------------------------|--------------|-----------|-----------------------------|-----------------|----------------------------------|--------|
| DmK2      | <i>Drosophila melanogaster</i>    | Diptera      | Hexapoda  | Fruit fly                   | 894             | NP_523551.1                      | 7227   |
| AgK2      | <i>Anopheles gambiae</i>          | Diptera      | Hexapoda  | Mosquito                    | 880             | CM000359.1                       | 7165   |
| PxK2      | <i>Plutella xylostella</i>        | Lepidoptera  | Hexapoda  | Diamondback moth            | 708<br>492      | XP_011553857.1<br>XP_011564835.1 | 51655  |
| TcKeK2a   | <i>Tribolium castaneum</i>        | Coleoptera   | Hexapoda  | Flour beetle                | 592             | XP_015835039.1                   | 7070   |
| TcKeK2b   | <i>Tribolium castaneum</i>        | Coleoptera   | Hexapoda  | Flour beetle                | 667             | EFA02723.2                       | 7070   |
| AmK2      | <i>Apis mellifera</i>             | Hymenoptera  | Hexapoda  | Honeybee                    | 725             | XP_026299571.1                   | 7460   |
| HlK2      | <i>Habropoda laboriosa</i>        | Hymenoptera  | Hexapoda  | Southeastern blueberry bee  | 725             | XP_017794268.1                   | 597456 |
| AechinK2a | <i>Acromyrmex echinator</i>       | Hymenoptera  | Hexapodas | New world ants              | 693             | EGI60801.1                       | 103372 |
| AechinK2b | <i>Acromyrmex echinator</i>       | Hymenoptera  | Hexapodas | New world ants              | 765             | XP_011061966.1                   | 103372 |
| NvitriK2  | <i>Nasonia vitripennis</i>        | Hymenoptera  | Hexapoda  | Pteromalid parasitoid wasps | 739             | XP_031777401                     | 7425   |
| LhumK2    | <i>Linepithema humile</i>         | Hymenoptera  | Hexapoda  | Argentine ant               | 762             | XP_012226521                     | 83485  |
| DcK2      | <i>Diaphorina citri</i>           | Hemiptera    | Uniramia  | Asian citrus psyllid        | 767             | XP_008477578.1                   | 121845 |
| ClK2      | <i>Cimex lectularius</i>          | Hemiptera    | Hexapoda  | Bed Bug                     | 695             | XP_014259906.1                   | 79782  |
| HhK2      | <i>Halyomorpha halys</i>          | Hemiptera    | Hexapoda  | Brown marmorated stink bug  | 672             | XP_024214678                     | 286706 |
| ApK2(a)   | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                   | 802             | XP_029343355.1                   | 7029   |
| ApK2(b)   | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                   | 671             | XP_008181523.1                   | 7029   |
| PhumpK2   | <i>Pediculus humanus corporis</i> | Phthiraptera | Hexapoda  | Body louse                  | 752             | XP_002427512.1                   | 121224 |
| DmagK2    | <i>Daphnia magna</i>              | Cladocera    | Crustacea | Water flea                  | 832             | KZS15230.1                       | 35525  |

### Identification of Kek3 orthologs

With the exception of Kek4, Kek3 appears to be the least well conserved member of the Kek family. In contrast to Keks1, 2, 5 and 6, only eight of the sixteen species appear to have a Kek3 protein ortholog (Table 4). For organisms without an accession number, I was unable to identify a Kek3 ortholog based on NCBI blast searches. Interestingly, while Kek3 is found in *Drosophila melanogaster*, orthologs appear absent in numerous hexapoda, but an ortholog can be identified in the extremely divergent crustacean, *Daphnia magna*, representing conservation over an evolutionary distance of ~ 524 million years (Kumar et al, 2017).

**Table 4.** Identified Kek3 orthologs

| Gene    | Species name                      | Order        | Subphylum | Common name                | ORF length (aa) | Accession #    | Taxid  |
|---------|-----------------------------------|--------------|-----------|----------------------------|-----------------|----------------|--------|
| DmK3    | <i>Drosophila melanogaster</i>    | Diptera      | Hexapoda  | Fruit fly                  | 1021            | NP_001162986.1 | 7227   |
|         | <i>Anopheles gambiae</i>          | Diptera      | Hexapoda  | Mosquito                   |                 |                | 7165   |
|         | <i>Plutella xylostella</i>        | Lepidoptera  | Hexapoda  | Diamondback moth           |                 |                | 51655  |
| TcKek3  | <i>Tribolium castaneum</i>        | Coleoptera   | Hexapoda  | Flour beetle               | 814             | XP_008192538.1 | 7070   |
|         | <i>Apis mellifera</i>             | Hymenoptera  | Hexapoda  | Honeybee                   |                 |                | 7460   |
|         | <i>Habropoda laboriosa</i>        | Hymenoptera  | Hexapoda  | Southeastern blueberry bee |                 |                | 597456 |
|         | <i>Acromyrmex echinatior</i>      | Hymenoptera  | Hexapoda  | New world ants             |                 |                | 103372 |
|         | <i>Nasonia vitripennis</i>        | Hymenoptera  | Hexapoda  | Pteromalid parasitoid wasp |                 |                | 7425   |
|         | <i>Linepithema humile</i>         | Hymenoptera  | Hexapoda  | Argentine ant              |                 |                | 83485  |
| DcK3    | <i>Diaphorina citri</i>           | Hemiptera    | Uniramia  | Asian citrus psyllid       | 610             | XP_026683561.1 | 121845 |
| ClK3    | <i>Cimex lectularius</i>          | Hemiptera    | Hexapoda  | Bed Bug                    | 703             | XP_014250349.1 | 79782  |
| HhK3    | <i>Halymorpha halys</i>           | Hemiptera    | Hexapoda  | Brown marmorated stink bug | 670             | XP_024218178.1 | 286706 |
| ApK3    | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                  | 904             | XP_008183139.1 | 7029   |
| PhumpK3 | <i>Pediculus humanus corporis</i> | Phthiraptera | Hexapoda  | Body louse                 | 456             | XP_002431502.1 | 121224 |
| DmagK3  | <i>Daphnia magna</i>              | Cladocera    | Crustacea | Water flea                 | 833             | KZS21093.1     | 35525  |

### Identification of Kek5 orthologs

Each species of interest has one Kek5 ortholog, except *Diaphorina citri* (Asian citrus psyllid) which does not appear to have a Kek5 ortholog at all (Table 5). *Daphnia magna* (Water flea) is unique amongst the Kek5 orthologs because a clear ortholog could not be identified. When the reciprocal blast in Flybase was performed using the putative Kek5 sequence both Kek5 and Kek6 matched equally well. Upon further examination, it appears that *Daphnia magna* has a single Kek ortholog that has characteristics of both Kek5 and Kek6 and represents both Kek5 and Kek6.

**Table 5.** Identified Kek5 orthologs

| Gene      | Species name                      | Order        | Subphylum | Common name                 | ORF length (aa) | Accession #    | Taxid  |
|-----------|-----------------------------------|--------------|-----------|-----------------------------|-----------------|----------------|--------|
| DmK5      | <i>Drosophila melanogaster</i>    | Diptera      | Hexapoda  | Fruit fly                   | 931             | NP_001245746.1 | 7227   |
| AgK5      | <i>Anopheles gambiae</i>          | Diptera      | Hexapoda  | Mosquito                    | 901             | XP_312632.5    | 7165   |
| PxK5      | <i>Plutella xylostella</i>        | Lepidoptera  | Hexapoda  | Diamondback moth            | 783             | XP_011554456.1 | 51655  |
| TcK5      | <i>Tribolium castaneum</i>        | Coleoptera   | Hexapoda  | Flour beetle                | 738             | XP_015834875.1 | 7070   |
| AmK5      | <i>Apis mellifera</i>             | Hymenoptera  | Hexapoda  | Honeybee                    | 766             | XP_026297157.1 | 7460   |
| HlK5      | <i>Habropoda laboriosa</i>        | Hymenoptera  | Hexapoda  | Southeastern blueberry bee  | 760             | XP_017789119.1 | 597456 |
| AechinK5a | <i>Acromyrmex echinator</i>       | Hymenoptera  | Hexapoda  | New world ants              | 739             | EGI59898.1     | 103372 |
| AechinK5b | <i>Acromyrmex echinator</i>       | Hymenoptera  | Hexapoda  | New world ants              | 776             | XP_011063371.1 | 103372 |
| NvtriK5   | <i>Nasonia vitripennis</i>        | Hymenoptera  | Hexapoda  | Pteromalid parasitoid wasps | 802             | XP_031781470.1 | 7425   |
| LhumK5    | <i>Linepithema humile</i>         | Hymenoptera  | Hexapoda  | Argentine ant               | 783             | XP_012216137.1 | 83485  |
|           | <i>Diaphorina citri</i>           | Hemiptera    | Uniramia  | Asian citrus psyllid        |                 |                |        |
| ClK5      | <i>Cimex lectularius</i>          | Hemiptera    | Hexapoda  | Bed Bug                     | 736             | XP_014260449.1 | 79782  |
| HhK5      | <i>Halyomorpha halys</i>          | Hemiptera    | Hexapoda  | Brown marmorated stink bug  | 730             | XP_024214681.1 | 286706 |
| ApK5      | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                   | 799             | XP_001946145.1 | 7029   |
| PhumpK5   | <i>Pediculus humanus corporis</i> | Phthiraptera | Hexapoda  | Body louse                  | 475             | XP_002426780.1 | 121224 |
| DmagK5/6  | <i>Daphnia magna</i>              | Cladocera    | Crustacea | Water flea                  | 955             | KZS18598.1     | 35525  |

### Identification of *Kek6* orthologs

Each of the sixteen species of interest had one *Kek6* ortholog, (Table 6) with the exception of the crustacean *Daphnia magna* as described above.

**Table 6.** Identified *Kek6* orthologs

| Gene     | Species name                      | Order        | Subphylum | Common name                 | ORF length (aa) | Accession #    | Taxid  |
|----------|-----------------------------------|--------------|-----------|-----------------------------|-----------------|----------------|--------|
| DmK6     | <i>Drosophila melanogaster</i>    | Diptera      | Hexapoda  | Fruit fly                   | 836             | NP_651880.1    | 7227   |
| AgK6     | <i>Anopheles gambiae</i>          | Diptera      | Hexapoda  | Mosquito                    | 805             | XP_310646.5    | 7165   |
| PxK6     | <i>Plutella xylostella</i>        | Lepidoptera  | Hexapoda  | Diamondback moth            | 585             | XP_011558577   | 51655  |
| TcKeK6   | <i>Tribolium castaneum</i>        | Coleoptera   | Hexapoda  | Flour beetle                | 561             | XP_974068.1    | 7070   |
| AmK6     | <i>Apis mellifera</i>             | Hymenoptera  | Hexapoda  | Honeybee                    | 660             | XP_006559862   | 7460   |
| HlK6     | <i>Habropoda laboriosa</i>        | Hymenoptera  | Hexapoda  | Southeastern blueberry bee  | 662             | XP_017790179.1 | 597456 |
| AechinK6 | <i>Acromyrmex echinator</i>       | Hymenoptera  | Hexapodas | New world ants              | 680             | XP_011064989   | 103372 |
| NvitriK6 | <i>Nasonia vitripennis</i>        | Hymenoptera  | Hexapoda  | Pteromalid parasitoid wasps | 669             | XP_001606266   | 7425   |
| LhumK6   | <i>Linepithema humile</i>         | Hymenoptera  | Hexapoda  | Argentine ant               | 676             | XP_012216988   | 83485  |
| DcK6     | <i>Diaphorina citri</i>           | Hemiptera    | Uniramia  | Asian citrus psyllid        | 610             | XP_008472857.1 | 121845 |
| ClK6     | <i>Cimex lectularius</i>          | Hemiptera    | Hexapoda  | Bed Bug                     | 616             | XP_024085325   | 79782  |
| HhK6     | <i>Halyomorpha halys</i>          | Hemiptera    | Hexapoda  | Brown marmorated stink bug  | 611             | XP_014272847   | 286706 |
| ApK6     | <i>Acyrtosiphon pisum</i>         | Homoptera    | Hexapoda  | Pea aphid                   | 624             | XP_003246846   | 7029   |
| PhumpK6  | <i>Pediculus humanus corporis</i> | Phthiraptera | Hexapoda  | Body louse                  | 648             | XP_002425241   | 121224 |
| DmagK5/6 | <i>Daphnia magna</i>              | Cladocera    | Crustacea | Water flea                  | 955             | KZS18598       | 35525  |

### *Identification of SLiMs conserved in individual Kek family members*

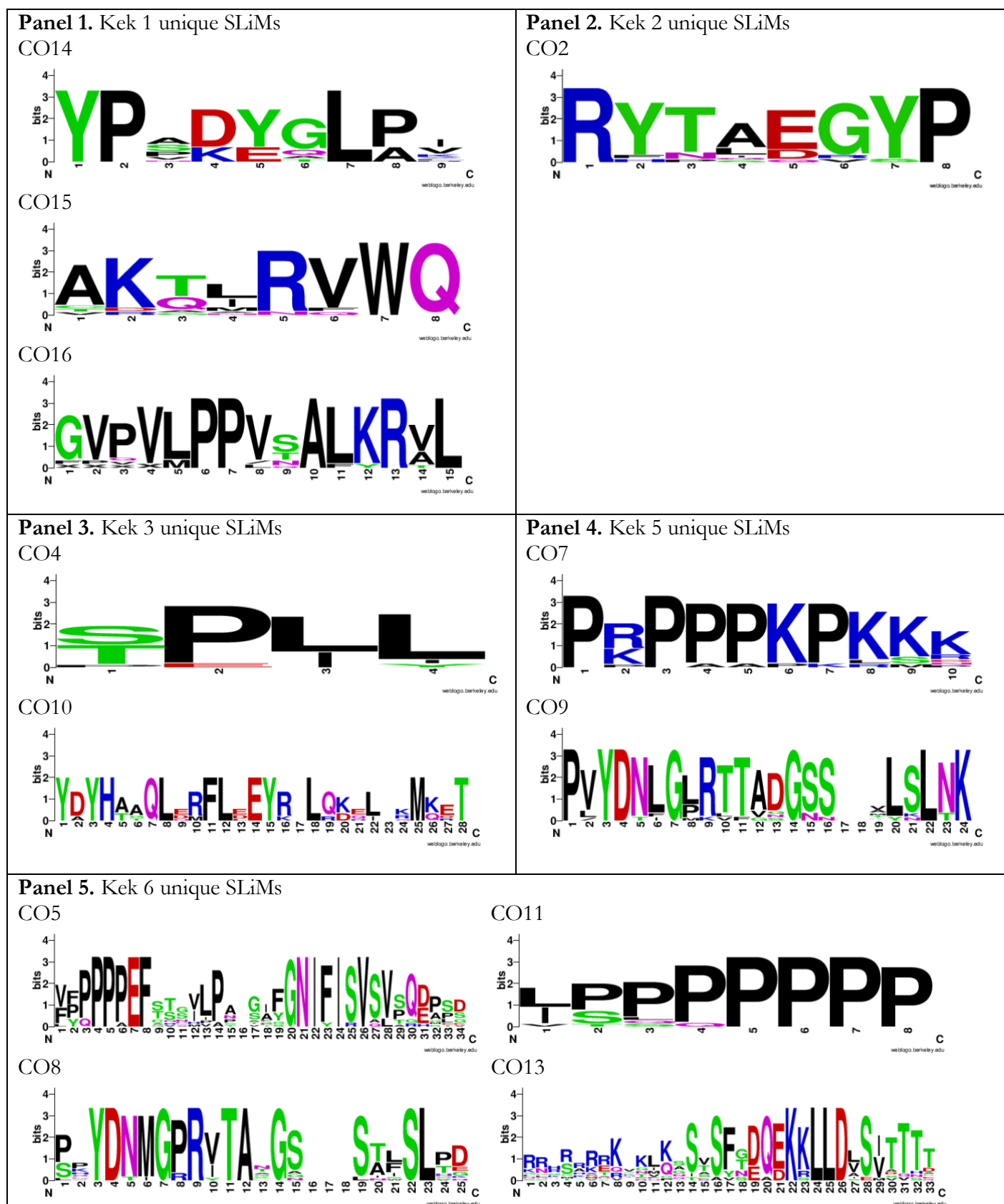
Having identified a broad set of Kek family member orthologs in an evolutionary diverse set of organisms, I embarked on a set of analyses to uncover conserved, and likely functional, intracellular sequence elements. A short intracellular motif (SLiM) is a linear group of 3-10 residues that facilitate protein interactions. In order to identify putative SLiMs, the intracellular regions of individual Kek orthologs were aligned using Clustal Omega and areas of 100% conservation in the alignments were identified using BoxShade. BoxShade outputs for each Kek can be found in Appendix B.

Among the five Kek proteins studied twenty-four SLiMs were identified. Of the twenty-four identified SLiMs, twelve were found in only a single Kek family member. Any SLiMs identified in each member of the Kek family were then compared to other family members. A fingerprint motif is a submotif within a particular SLiM that is conserved across multiple members of the Kek family. SLiMs with the same fingerprint motif share a common label in Table 7. SLiMs that appear in more than one Kek do not have identical sequences, but rather share a fingerprint motif and have some conserved residues that are unique to a single member of the Kek family.

**Table 7.** Presence of identified SLiMs in Kek proteins

| Protein | CO1 | CO2 | CO3 | CO4 | CO5 | CO6 | CO7 | CO8 | CO9 | CO10 | CO11 | CO12 | CO13 | CO14 | CO15 | CO16 |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|
| Kek1    | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| Kek2    | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| Kek3    | +   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| Kek5    | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| Kek6    | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| Dmag5/6 | +   | -   | +   | -   | -   | +   | +   | +   | +   | -    | -    | -    | +    | -    | -    | -    |

The majority of SLiMs were unique to a specific member of the Kek family, with only four CO1, CO3, CO6, and CO12 being conserved in more than one family member. Dmag5/6 was differentiated from Kek5 and Kek6 because it appears to have characteristics of both Kek5 and Kek6; this was supported by the presence of SLiMs that appeared in both Kek5 and Kek6. Figure 6 provides a graphical representation of SLiMs identified in only one member of the Kek family. WebLogos for all identified SLiMs can be found in Appendix C.



**Figure 6. Unique SLiMs.** The above WebLogos represent SLiMs found in only one Kek family member. Letter height represents residue frequency at that position, while the letter color represents residue chemical properties.

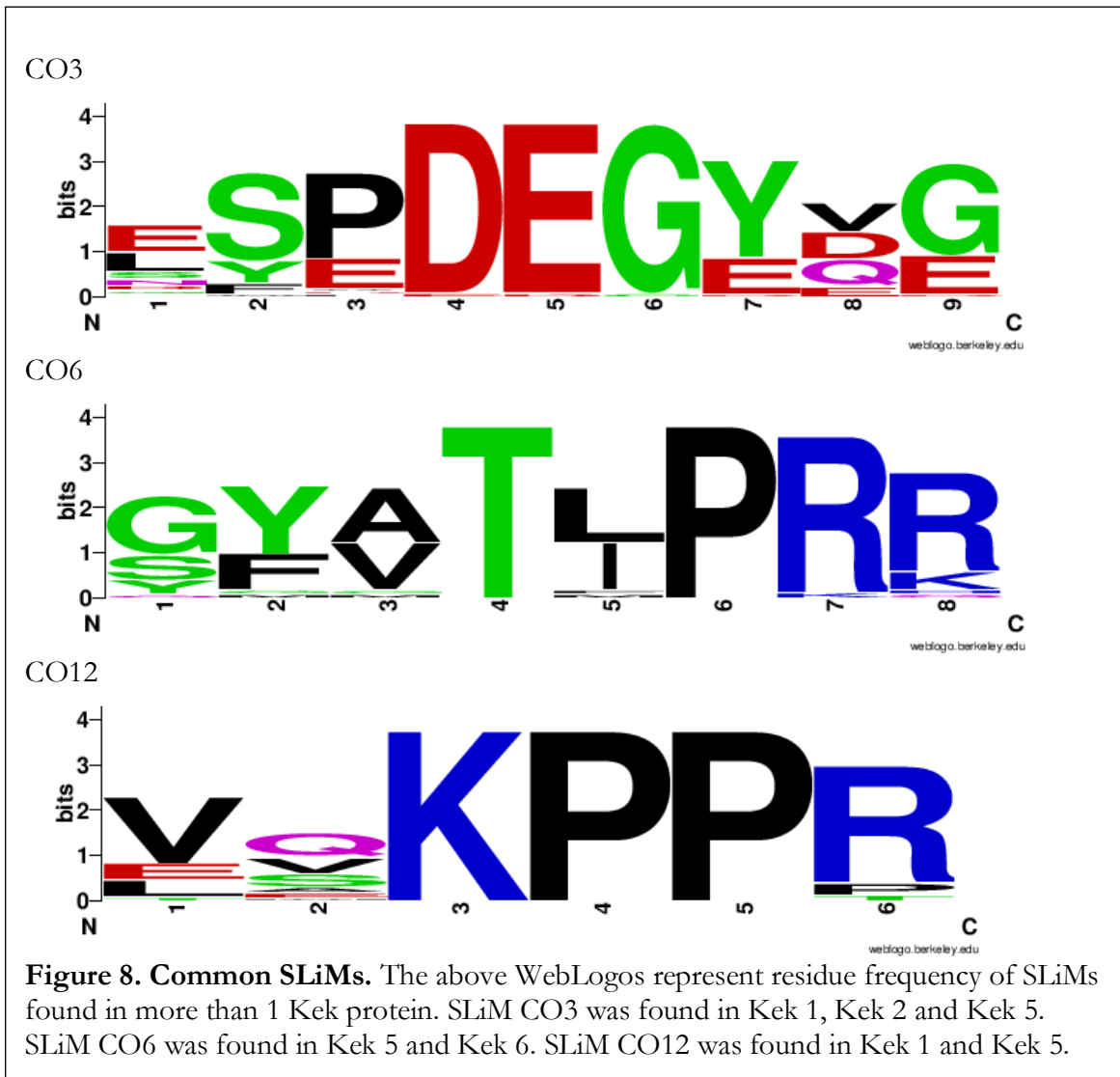
After all SLiMs, had been identified within a specific family member and its orthologs, the presence of these were then screened in all Kek family members. This allowed for the discovery of SLiMs in more than one Kek family member. Comparing SLiM sequences across the Kek family led to the identification of fingerprint motifs, submotifs within SLiMs that are conserved across members of the Kek family and across species.

The most well conserved SLiM was CO1, as shown in Table 7 and Figure 7; it appears in every member of the *Drosophila melanogaster* Kek family. In aligning CO1 across all Keks and orthologs, it became apparent that a PDL submotif is highly conserved across species and Kek family members. Thus, the PDL sequence represents a more highly conserved element, or fingerprint, within the CO1 motif. While all family members with the CO1 motif share this fingerprint, there are amino acid residues within the CO1 SLiM that are unique to specific family members. For example, the sequence of the CO1 SLiM in Kek1 is NPDL, while the same SLiM in Kek5 is PPDL.

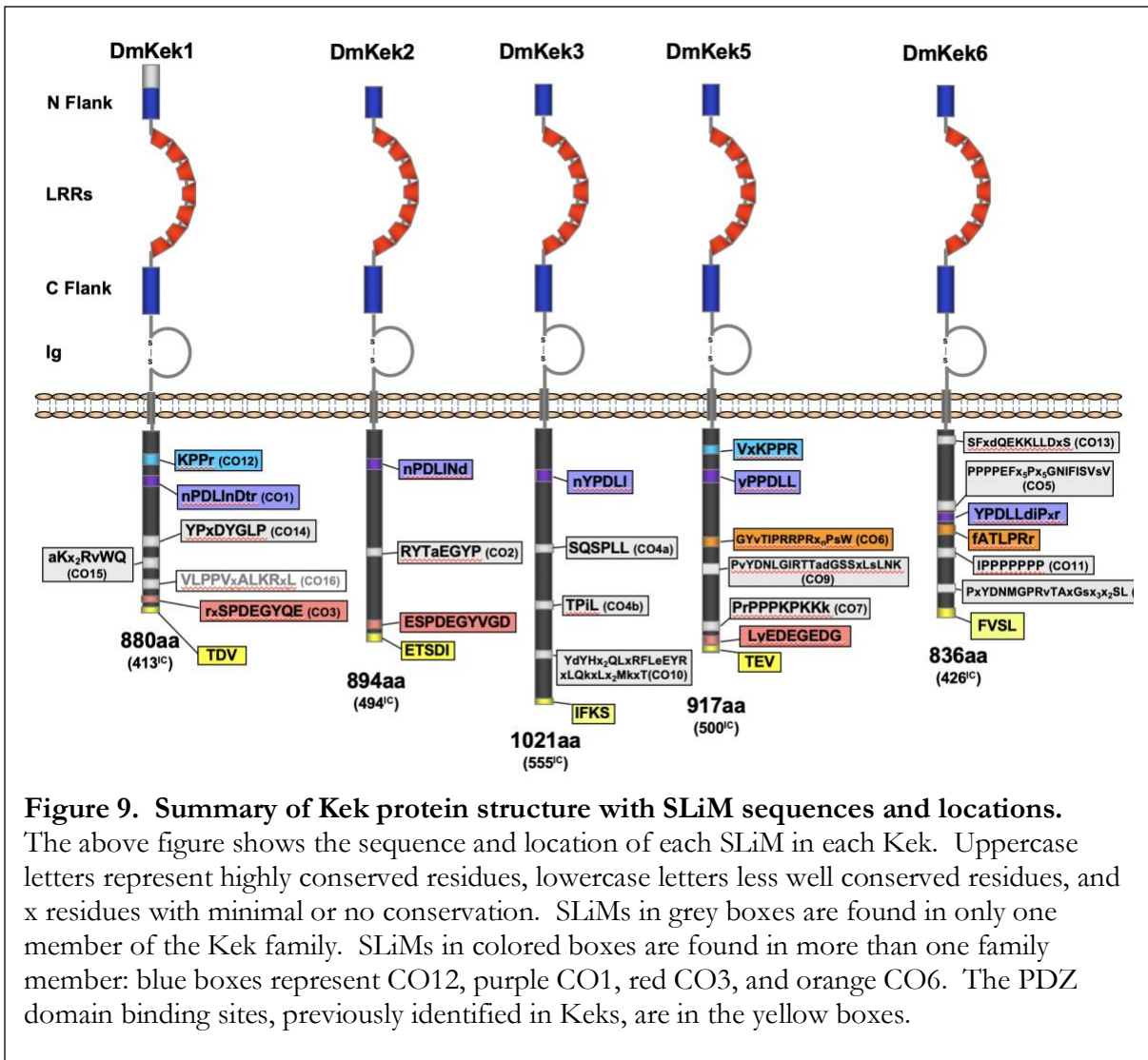


**Figure 7. CO1 is a universal SLiM.** CO1 was the only SLiM found in all five Keks. This image represents the frequency of the residues in all five Kek proteins. The most conserved residues, the SLiM fingerprint, was identified as PDL.

Three additional SLiMs were found to be conserved across family members. Again, each SLiM had a distinct fingerprint motif present. WebLogos for all three motifs are in Figure 8. CO3 was found in Kek1, Kek2, and Kek5 and the fingerprint motif was identified as SPDEGY. CO6 was found in Kek5 and Kek6 with TLP RR as a fingerprint motif. Finally, CO12 was found in Kek1 and Kek5 with a fingerprint motif of KPPR.



The identification of SLiMs revealed that not only is the SLiM conserved over time, but its relative position and order in the protein sequence is also conserved. For example, CO3 is consistently found just before the C-terminus, and CO12 maintains its position before CO1 in both Kek1 and Kek5. This is demarcated in the FASTA sequence documents in Appendix A; each SLiM is highlighted in a corresponding color, and it is evident that they are in the same relative position and order within the protein sequence. This positional conservation is more readily apparent in Figure 9, which is a graphic summary of all the SLiMs present in each Kek and the relative location of the SLiM



**Figure 9. Summary of Kek protein structure with SLiM sequences and locations.** The above figure shows the sequence and location of each SLiM in each Kek. Uppercase letters represent highly conserved residues, lowercase letters less well conserved residues, and x residues with minimal or no conservation. SLiMs in grey boxes are found in only one member of the Kek family. SLiMs in colored boxes are found in more than one family member: blue boxes represent CO12, purple CO1, red CO3, and orange CO6. The PDZ domain binding sites, previously identified in Keks, are in the yellow boxes.

## DISCUSSION

This project aimed to identify Kek orthologs in evolutionarily distant arthropods and to identify conserved short linear motifs, SLiMs, using a phylogenetic approach. Kek orthologs were identified in sixteen arthropods and then the intracellular domains were compared to identify highly conserved residues. The most highly conserved motifs were considered to be SLiMs. Finally, the SLiMs identified in individual Kek proteins were compared to the SLiMs identified in other members of the Kek family in an effort to identify submotifs, or fingerprint motifs, that were conserved across family members. The SLiMs identified in this project likely represent key motifs that play a role in Kek protein function.

### *Identification of Kek orthologs*

Generally speaking, the Kek family is very well conserved within arthropods. Every arthropod studied had at least Kek1, Kek2 and Kek6 orthologs. A Kek5 ortholog was found in every arthropod studied except *Acyrtosiphon pisum*. Kek3 was the least well conserved member of the Kek family, only eight of the sixteen studied arthropods had a Kek3 ortholog. While one would expect Kek3 is present in more closely related organisms, in actuality Kek3 was present in *Drosophila melanogaster*, appears to have been lost in some closely related species, but retained in *Diaphorina citri* – which is more evolutionarily distant, 358mya (Kumar et al, 2017). This suggests that Kek3's absence in the eight more closely related species is indicative of a less vital role for those species, hence its loss.

All five members of the Kek family were conserved over approximately 524 million years of evolution. For reference the evolutionary distance between *Homo sapiens* and *Pan troglodytes* (chimpanzee) is 6.4 million years (Kumar et al, 2017). The conservation of Kek family molecules in species across such a long span of time suggests that Kek proteins play a critical role that is essential for survival in those species.

### *Identification of SLiMs conserved in individual Kek family members*

When the intracellular domains of the Kek orthologs were compared, highly conserved motifs were considered to be putative SLiMs. These motifs have been conserved over approximately 524 million years of evolution, suggesting evolutionary selection to conserve these motifs thus maintaining protein functionality.

While the Kek proteins are members of the same family, it is likely each member of the Kek has a unique and specific function. This is supported by the presence of more than one member of the Kek family in the species studied. Unique SLiMs identified in individual members of the Kek family provide further support this model with those SLiMs likely mediating the specific function of that member of the Kek family.

### *Identification of SLiMs conserved across Kek family members*

While most of the SLiMs identified in this project were unique to a single member of the Kek family, four SLiMs were identified in more than one member of the Kek family. CO1 is arguably the most interesting SLiM discovered during this project, because it is so well conserved within arthropods and within the Kek family. The CO1 motif was found in every member of the Kek family with the PDL fingerprint motif and additional conserved residues that were unique to individual members of the Kek family. Because SLiMs have high specificity, it is unlikely that the CO1 SLiM serves a different function in each Kek; rather, the PDL motif likely has a similar function in each Kek, like a common binding partner, and the specific functions mediated by the unique conserved residues or other SLiMs.

The three other SLiMs conserved across specific Kek family members, CO3, CO6, CO12, also had identifiable fingerprint motifs SPDEGY, TLP RR, and KPPR, respectively. Like the PDL motif in CO1, SLiMs with the same fingerprint motif likely have similar functions with specificity determined by unique conserved residue or other SLiMs. SLiMs present in more than one member of the Kek family, but not all the members, are of interest because it supports the notion that members of the Kek family may have overlapping, in addition to unique, functions.

### *Kek Family Evolution*

The high specificity of SLiM interactions lends itself to both convergent and divergent evolution of SLiMs (Davey et al, 2012). Given the high conservation of the extracellular domain and the relative rarity of coexisting LRR domains and Ig domains, it is almost certain that the Kek family represents a group of proteins that diverged from a common ancestor, rather than a group of proteins that experienced convergent evolution due to a common binding partner.

Prior research into the evolution of Kek proteins suggest that Kek1, 2, and 3 form an intrafamilial clade, and Kek 4, 5, and 6 form another intrafamilial clade (Evans, 2006). The close relationship

between Kek5 and Kek6 is supported by the presence of the CO6 SLiM in both Kek5 and Kek6 and its absence from other members of the Kek family. This is further supported by the presence of a Kek5/6 protein in *Daphnia magna*. Kek5/6 protein in *Daphnia magna* is of particular interest, because it contains SLiMs that are unique to Kek5 and Kek6 in other organisms, suggesting that this single protein maybe able to perform the functions of both Kek5 and Kek6. Based on the presence of SLiMs alone, Kek5 may be more closely related to Kek1 than initially thought. The CO12 SLiM appears only in Kek1 and Kek5, and the CO3 SLiM appears in Kek1, Kek2, and Kek5. These common SLiMs between Kek1 and Kek5, suggest that perhaps the functions of Kek1 and Kek5 overlap more than initially thought.

This study has shown that Kek 1, 2, 3, 5, and 6 are well conserved within arthropods through identification of Kek orthologs in sixteen different arthropods that represent over .5 billion years of evolution. Additionally, this project has identified well conserved motifs, SLiMs, that represent key targets for revealing insights on Kek family mechanisms and functions. Future studies could examine the impact of SLiM deletions to determine which of these SLiMs are, in fact, functional and expand understanding of Kek protein mechanisms.

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## APPENDIX A: Demarcated ortholog FASTA sequences

### Key

|                                                                                                               |      |      |      |      |
|---------------------------------------------------------------------------------------------------------------|------|------|------|------|
| CO1                                                                                                           | CO2  | CO3  | CO4a | CO4b |
| CO5                                                                                                           | CO6  | CO7  | CO8  |      |
| CO9                                                                                                           | CO10 | CO11 | CO12 |      |
| CO13                                                                                                          | CO14 | CO15 | CO16 |      |
| <p>RED=Signal sequence</p> <p>BLUE=Transmembrane domain</p> <p>UNDERLINE=Continuation of overlapping SLiM</p> |      |      |      |      |

### Kek1 ortholog FASTA sequences

*Drosophila melanogaster* (Fruit fly)

>DmK1=CG12283

MHIREAVFLVLTLLPGMILGTRYNQHLHYANGGASSSGPGGYRPAPSSQNEVYSIADSQPMTEDGYMPPS  
 QHFPPTHSDLDPPAQQQSTCQTVCAKWKGGKQTVCEIDRHLIQIPEHIDPNTQVLDMSGNKLQTLSENEQ  
 FIRANLLNLQKLYLRNCKIGEIERETFKGLTNLVELDLSHNLLVTVPSLALGHIPSLRELTLASNHIHKI  
 ESQAFGNTPSLHKLDLSHCDIQTISAQAFGGLOGLTLLRLNGNKLSELLPKTIETLSRLHGIELHDNPWL  
 CDCRLRDTKLWLMKRNIPYPVAPVCSGGPERIIDRSFADLVHDEFACRPEMLPISHYVEAAMGENASITC  
 RARAVPAANINWYWNGRLLANNSAFTAYQRIHMLEQVEGGFEKRSKLVLTNAQETDSSEFYCVAENRAGM  
 AEANFTLHVSMRAAGMASLGSGQIVGLSAALVALIVFALGVIMCLLLRVKRQPYVDSKTPNHMEVITSVN  
 HQNSITNKTQPATGNGSIGGVVIANGAVANIIDGGVVQGGTLERKSSGRGGVPHGVHDQRSANPVQKPPR  
 LTDLPYSTQGYDNNGSVLSTASCFISPSGSTGNGGNNPDLINDTKRFGSDEFADLKIPPISGVGVGSGSE  
 YSRANGCDSLYPSGLWEHGAPVGTTSADDLFMKRYTDKTPIIDSTQLYDLHERTAATDYFSKTFPRSHLQ  
 QGMMTGGGGGTSTASTVTTNLSGGSSSGYPNDYGLPLVPGAHQHNLQMHPLQQQLTSTLNHQKQ  
 EGSSTGSSPHFSSRTLRLHEGSGGGSSRSPTPAISGGHANQAANPSTSSSSCSILPNGQPINAKTIR  
 VWQKGVPVLPVLTALKRALISSSRNSPDEGYQEGCGTDV

*Anopheles gambiae* (Mosquito)

>AgK1

MPVLLSLLLVLALLPALVSRGQVSGEPNCPSACQCKWKGGKQAVECLSGNLFITPENIDHSTQVLDVSGNN  
 LQIISNETFVRSNLLNLQKLYMRDCRIGQIDGAFAGLTNLVELDLINLLTAVPSAAFQHVSLRDLTL  
 ARNHIQKIESHAFRNVTALTKLDLSFCSIQTIAFQAFEGLSLHSLKLNQNLSELRPKTIETLSRLHGI  
 ELHGNPWVDCRLRAAKLWLTEHNIPYPIAPTCAGGPERVMDKTFGELQVDDFACKPEMLPVRRFIQSYS  
 GENATIECRSSAVPSATVNWYWNGKLLVNNSHFSAYQRVLVHEQGNFEKRSRLTLTNAQETDSSEFYCVV  
 ENRAGTAEANFTLHVAMRDVGFIENRQVIGLSAALVILILFILLIILFLLVRLRRIPMTETKTPNQVEV  
 ITSVSPSSNVNGKVATPINDCHSPDRAKAAGDLKCGPNPAANPLQKPPRLTDLPYSTSHYDGGGSLIASG  
 QCFVSPTHSLAGNNPDLINDTKRLGSGTDLTAATAAPGPAVPGGGVADPLAHLGQLQLQATSALSTALS  
 MDPVERPGSGEYSRAGCDSLYPSGLWETHSSNLAAATGLDHGGSHGPGPYSDKLPILGGGSGAGPAMLNL  
 DDETSSVDYLSRTFPRTHLTGGLSLSTTASSGSGYGHGVAATAATGGTTTTGSGGGYPADYGLPTVPG  
 AEQLHNKLASGQPAHHGSTGSMMPNKTTLRVWQKGVPVLPVLTALKRALSNSRNSPDEGYQEGCGTDV

*Plutella xylostella* (Diamondback moth)

&gt;PxK1

MKMRCLLVIMSVVVWNTTSA  
 GIAPPGSCPAVCACKWKGGKQTVECV  
 ERALITVPELVDPATQVLDLSGNN  
 LQILPQEAFA  
 RTGLVNLQRVYLRSCNIGQINERAFKGLTNLVELDL  
 SNNLLTQIPAH  
 SFKDAPFLRDL  
 SLAHNPVLKVHPDALS  
 NLGSVVKLDLSSCDIR  
 DIAPEAFRNMRSLES  
 SKLNGNRLRDLPISSLEKVEKLRAI  
 DLSDNPWTCDCRLRE  
 MKMWLAKRKL  
 LATPSCSAPGRLAGRP  
 FSELAIEEFACKPEILP  
 VSRHVEAAVGENATITCRTEAV  
 PSANINWYFNGRLMNGSNLNSHQ  
 KIFIFESGENKKKSSLVLTNTQ  
 QSDSAEFYCVAENKGGNSEANFTLHVT  
 MLAAGMASLGSAQIASLGAALFLVAVIVSLAVLIMFV  
 RFRNAPICESKTPSTLDRVVSGNEVHPASVDK  
 PCVAALGSRDELPGVSDPKCNPVQKPPRIGDIPYTTN  
 HYEGRGSVVTAGGPLMVSP  
 TMSVANDPDLINDTRPESAGRPGSGEYAREASDSL  
 YPSGLWDQMKRDQATSLARAVSSALPAYYTDRTPIME  
 SSSVEGSQEELGYMSRTFPRAHAAAAGGGAGSGDAP  
 YPADYGLPVGGARTLRVWQXXXXLPPVSALKRV  
 LATSRHSPDEGYQEGCATDV

*Tribolium castaneum* (Flour beetle)

&gt;TcKek1

MVLVVGVLVTLVLTPCLGGNCPS  
 PCTCKWKGGKQTVECTERGLITIPESVDPETQVLDLSGNNLQILPRE  
 TFVRSGLNLQRVFLRRCRIGQIDDLA  
 FRGLTNLIELDLSHNLLTAVPSGTFRDVPFLRDLV  
 LAYNPIQKIDSQAFKTIPGLIKDL  
 SNCEIQVIASKAFEGIEML  
 LESLKLNGNRLSELRLRTVETLNRLHGIEMHDNPW  
 HCDCLRAVKEWLVNNNIPYPISPICSGGPERLIDKTF  
 TELHIDDFACKPEILPVNRYIEATSGSNATILCRANA  
 IPVANINWYWNGRPLLNNSAFSSHQRIHVFE  
 EGKQEKRSVLVLTNVQEINSSEFYCVAENRAGNA  
 EANFTLHVSMRAAGITTLGSGQIAGLSVALIILII  
 FILLVIFVLLVRLRRIPFSESKTSGQIEVVTVVNG  
 TSKVEEPSHEHTKPTELNFCNPVQKPPRLSDSTIP  
 ASCFVSPSSASGNNPDLINDTKPSEDPEGLERPAS  
 GEYSRNADSLYPSGLWETDYSRQVNFYDDKTPIMD  
 GMSGGSLEELAFRAQGYPADYGLPIADKQQTLP  
 TNAKTLRVWQKGGVPVLPVLTALKRALTHSRNSP  
 DEGYQEGCGTDV

*Leptinotarsa decemlineata*

&gt;LdecK1

MDGLVCWLLSLVTLISVQATNSMG  
 GICPSPCMCKWKGGKQTVECMERGLITIPENIDTETQVLDLSANNL  
 QILPRETFIRSGLVNLQRVYLRSCRIGQIDSLA  
 FRGLTNLIELDLSQNLLTAIPSETFKDIPFLRDLIMS  
 NNPIQKVESRAFAQIHGLVKLDLSNCEIQNVAPKAF  
 EDIEMLESKLNGNRLSELRLRTVETLSRLHGVE  
 LHDNPWHCDCLRSVKEWLVKNNIPYPEDPVCSSG  
 GPERVHKTFSLEHVDDFACKPEILPVSRYIEAKSG  
 ENASIICRANAVPAAQVKWYWNGRQLINNSVFS  
 PNQMIHVHEEGKQEKRSNLILTNVQEVDSSEFYC  
 VAE NRAGSSEANFTLRVSLKPMGITSLGNGQIAGLSA  
 ALVFLILFILIVISILLTRLRRMPFAESKTPGQLE  
 V VTVINGGTLSNGKSASSQMS  
 SPVEPPAFTENKSPSELNFCNPVQKPPRLNDIPY  
 STAHYNGNGSIMSSSCFVSPSHSGNNPDLINDAK  
 VSEIEETIPDPNSSEVIFDKSVSGEYSRNTDSL  
 YPSGLWENDKVHIIRNAGFHYNDKTPIIIGDGT  
 STGGSAEELNFRLAQGTNRGATYPKDYGLPM  
 TETKLENQILTSATQVSLPANAKTLRVWQKGA  
 VPVLPVLTALKRVMNHN  
 RNSPDEGYQEGCGTDV

*Apis mellifera* (Honeybee)

&gt;AmKek1

MKILIFFLYVTTLGIVTSDKCAVECSCKWKS  
 GKRTVECVNRALTSIPEWVDPETQVLDTS  
 GNDIRTLPSNIFVRVRLTNLQRLYLRECRIDRID  
 SEALAGLTNLVELDLSHNLLTVVPTASFLDTPFL  
 RDLVLVSYNPLKRVHSHAFKSTPNLVKLDLSHTQ  
 LVEIEAKGFRGLDLLESKLNNQLSTLHPGT  
 FEPLNKLTSELHDNPWICDCHLREMKMWLVKHN  
 LPTLQAPLCRGPRLMNRTFTDLGIDDFACRPIL  
 LIASRYAEATIGENASIVCRVSAIPPAKVWY  
 WNGRLLTNHSAFSSYQKILIFEDGQFRKRSTL  
 VLTNAQEADSSEFYCVAENRAGTV EANFTLHV  
 SLRTAGMSTLGS  
 GHIAGISAALVVLILFILLVILVLFV  
 RFRMPVKDVKSAPV  
 AEGVSGDSAGGNNENNPSSATSTTRRKHEE  
 IETTSFGVESKPPPVSLT  
 LSYVQRPQAALLQ  
 TENEYGASIGRFDDHSQQPSVMVAPGACF  
 SSTSLMPIDNPDLIRDTRGSAEDITPYGGADY  
 SRMEVVDDAKILYSSCMWEARDTCRTTVPVST  
 YPSKETLAVVAPMVEQFP  
 PGAKQIRVWQKGPVLPVVSALKRVLGST  
 RSSPDEGYQEGTGTDV

*Habropoda laboriosa* (Southeastern blueberry bee)

&gt;HlK1

MVPSSSFLETPFLRDLVLSNNPLKRIHSNAFKSTPNLVKLDLSHTQLIEIEVKGFRALELLESKLNNNQ  
 LSTLHPGTFEPLNKLTSIELHDNPWSCDCHLREMCMWLKHNLP TLQAPLCYGPQKLLNRTFTDLGIDDF  
 ACRPILLIPSRYAEATIGENASIVCRVSAIPPAKVWYNGRLLTNHSAFSSYQKILIFEQGFRKRSTL  
 VLTNAQEADSSEFYCVAENRAGSVEANFTLHVSLRTAGMSTLGSGQ IAGISAALVVLILLILLIILVLF  
 RLRRMPLKDVKSAPVPAEGVSADSTGANNENPPSATSTTRRKHEE IETTSFGVESKPPVSLNLSYVQRPQT  
 AGLQSENEYGSISRFDQNPQPSVMVAPGACFSSTSLMP IDNPD LIRDTRGSAEDITPYGGADYSRME  
 GVDDTKILYSSCMWEGRDTCRTTPVPST YPSKEALAVVAPMVEQFPPG AKQIRVWQ KGVFVLPVPSALKR  
 VLGSTRSSPDEGYQE GTGTDV

*Acromyrmex echinator* (New world ant)

&gt;AechinK1

MGVSVFLLYAVTSGTRDLTSIPEWIDPETQVLDMSGNNICHLPNNIFIHVRLTNLQRLYLRECRIDRIDS  
 EALAGLTNLVELDLSSNNMLAAVPSLSFTDTPFLRDLVLAYNPLKRIHSHAFKSTPNLVKLDLSHTQLVEI  
 EAKGFRGLEMLLESKLSSNNELSTLHQGTFEPLNKLTSIELHENPWICDCHLREMCMWLKHNLP TIVAPV  
 CHGPQQLLDRAFTDLGIDDFACRPILLIASRYAEATIGENASIVCHVRAPVPAADVWYNGRLLTNHSAF  
 SSYQKILIFEQGFRKRSTLILTNAQEADSSEFYCVAENPAGSVEANFTLHVSLRTAGMSTLGSGQ IAGI  
 SAALVVLILFILLIILVLF IRLRRMPLKDMKSSAPMEAASSDGVNGGSGGGGGGGGDDNNPSSATSTTR  
 RKHEE IETTSFALESKPPASLHLSYVQRPAAVMQDNEYSTISRFDQNPAMAAMPAGACFSSTSLMP  
 IDNPD LIRDTRGSTEDITPYGVTDYGRVEALDDAGKMLYTSCLWEARDSCGRTSAVSANV YPSKEQLAV  
 VAPVVEQFPPG AKQMRVWQ KGVFVLPVPSALKRVL GST RSSPDEGYQE GTGTDV

*Nasonia vitripennis* (Pteromalid parasitoid wasps)

&gt;NvitriK1

MSATCRLLLVCA LMLLVCCRTMA DKCTNVCVCKWKSGKQTVECRNRGLNGVPDGDIDPETQVLDASENAI  
 NFLTDGIFIKVRLTNLQRLYLRS CRIDRIEQNALAGLTNLVELDLSHNRLTSVPSQS FANAPFLRDLVLA  
 HNP I GKI PP HAFKDAPNLVKLDLSNCDLTDLA AKGFQGLDMLET LKLSHNRI STL LQHTFEPLNKLTSIE  
 LHENPWTC DCT LREMKS WLKHNLP TLIAPICORPEQLANRSFAELTADDFACRPVMAIVSRYAEATIGE  
 NASIVCTVTAIPPAKIKWIWNGKLYTNHSIVNSYQKILIYEEGKH FQKRSTLVLTNAQETDSSNFFCVAE  
 NQAGSVEANFTLHVSLRTAGMSTLGSGQ IAGISAALVVLILFILLITIMVLFVRLRRMPQKEVKSPAPGSD  
 NLPLDGCTSSNQDSGANNPQSATSTVSRRKLEEVETTSFNESLCAGKPAGGNAMPLNHSYAPRPVAASLL  
 PTESH DYLINRGYDDGSSSR TLHQSI LAAGPACYSSQASLMP VDNPD LIRDTRGSSDEAAIASYASGEY  
 SSSRLDMDEGKLLYSECLSWEATGSRALPSVSANPYKDLHQPHQQAQPQQQQQQQQQDSFPPG AKQI  
 RVWQKQGVFVLPVPSALKRVLST RSSPDEGYQE GTGTDV

*Linepithema humile* (Argentine ant)

&gt;LhumK1

MGVSVFLLYAVTVLGVAASGDKCADECCKWKSGKRTVECVDRGLTSIPEWIDPETQVLDMSGNDIRHLP  
 SNIFVRVQLTNLQRLYLRECRIDRIDSEALAGLANLVELDLSSNLLSTVPSASFTDTPFLRELVLAYNPL  
 KQIPSNFAFKSTPNLVKLDLSHTQLTEIESKGFGRGLELLESKLNNNR LERLQPGTFEQFKKLT SIELYDN  
 PWVCDCHLREMCMWLKHNLP TPVAPRCHGPPQLVDRAFTDLGIDDFACRPVLLIASRYAEATIGENASI  
 VCRVSAIPPAKIKWYNSRLLTNHSAFSSYQKILIFEQGFRKRSTLILTNAQEADSSEFYCVAENRAGS  
 VEANFTLHVSLRTAGMSTLGSGQ IAGISAALVVLILFILLIILVLF IRLRRMPLKDVKSAPLEAVSGEG  
 AGNGTGGGENNPPSATSTTRRKHEE IETTSFALESKPPASLHLSYVQRPQAAVMQENEYGTISRFDQSQ  
 SAVAAIPGAGCFSSTSLMP IDNPD LIRDTRGSTEDITPYGVADYGRVEAIDAGKMLYSSCLWEARDT  
 CGRTSAVTVNA YPSKEQLAAVAPVVEQFPPG AKQMRVWQ KGVFVLPVPSALKRVL GST RSSPDEGYQE GT  
 GTDV

## Diaphorina citri (Asian citrus psyllid)

&gt;DcK1 (a)

MYLVIVFFVLVSVSSCPSTCICKWKGGKQWMECRDKFLITIPAESELTQVLDMSGNNLQILPKEAFR  
 RAGLLNLQKLFLARCHIGQIDSGALDGLTNLIEIDLSNLLTSIPSLTFQSVRFLRDLNLARNPISKIEK  
 GAFQFVPGLVKLDMSERLEHISPEAFTGAKSLESIKLNGNRLSHFPVRSVEPLLKLMIELHDNPWVCD  
 CNMRSIKMWLADKKNVPVQPACTGPERLSGKVFSDLHADDFAKPEIRMDSTRYVEAVSSENATVVCVDS  
 IPPAAISWYWNGRLLNNTAFSSYQRFVIEQGEYERKSSVLVTNAQESDSGRFYCVAENRAGIADANFT  
 LQVTYRGVGLPFLGGGHINGISLALFFLIILILIIIIYLLIRMRTITYPNSKNPAQIEVMANGNAHAVVN  
 KTPSLTPVIETSSFTERKQFPPPSYHSTEMISPNGQLPNKTLHVINISNPDILINDTRKPEGLSPEPHND  
 DVLFQNNYWNQNIQPTNSELGFDSNDKTPIIDGVSIGGELDDNYPPDYGLPIVGGQGNELLPNNIHPNA  
 KTLRVWQRGVPVLPFVNALKRVLSRGSPEDEGYQEGSGTVDV

&gt;DcK1 (b)

MCHKFILSVFLLTLLASVTQASCPLGCSCWKAGKRTVECIDRNFYTIPEGIDLDTQVLDLSSNNINVLQ  
 KEIFLQMGITNIQKLYLRKCKLEFVDDRAFRGVTNMDLDELSDNLLSTVPSLIYIPYKLSINLAHNPIHQ  
 ISSYSFQSTPGIRYIDMSNCQIHTIYSEAFYGIDKIDTLKLNKNLASLKPRTVDKLPYIRNLDIYDNPW  
 LCDCKLREVKQFIDKYNIQFSFDPICISGPKKNIGQTFLELSINDFACVPEVELANNNEPVKEKVMVLP  
 SNLTLDRCVQSATPCRMWSINRKIYDHNWNSNKINIKEETVLSKDNSYLSVFSGGVDLAAASSPGGEN  
 IYDQKSTLTVFDELHTDDGNYVCIVENNAGRTEKAIIVEFSDAGFAAGSFQMRSLIIALFIIVLMIAFG  
 ILVIKLVNKNISNSIVKNSTSSVGSVTKNNSLSDTNYDNNTLPPARPPLPKDLDLHNAHVQCASDLDLV  
 SAARYNEWQQYSTPEHFNRSKSSSGFYDPHMLPIINLSSQASSSIQDFPPDFGLPVVNDYDKIPS  
 AKTLRVWQRGVPVLPQYTPGKRSIISFKNNQATDV

## Cimex lectularius (Bed bug)

&gt;ClK1

MIIFLFLVSVSFFGASLSGSGNCPPVCVCKWKGGKQTVECTDRALIMIEGVDSETQVLDMSGNNLQILP  
 REVFVRTGLLNLQRLYLRCRLGQIDDQALAGLTNLVELDLTNNLLTTIPSATFKDVPFLRDLVMARNPI  
 QKIESHAFKTVPGLVKLDLSNCALQMISPKAFEGVELLEALKLNGNQLHEIRPRTVETLSRLHGVELHDN  
 PWYCDCHLRAAKIWLMDNNIPYPIAPMCKGGPERIVHRTFAELDLDDFAKPEIRLDSRHVEATTGDNAT  
 IVCRAVASPEATISWYWNGRLLVNNSAFSSYQRVHIIENGTFDKKSTLIVTNAQEADSGDFYCIAENRAG  
 NAEANYTVHVSYRMAGMASLGSGQIAGLSAALVILILFILLVILVLLVRLRRVPFSESKTPGQLEVANG  
 NVTQKATTPVTETSTFVERKETANPVQKPPRPVESPVDYDGLGGVSNPVQFAAPISNPDILINDTREDGR  
 PGSGEYSRMNDGLYPASVWEEGYLGRTPSMDACDRTPIVEHVEDYPPDYGLPIPGGAPPPSAKTLRVWQ  
 GVPVLPFVNALKRVLTNRNSPDEGYQEGCGTVDV

## Halyomorpha halys (Brown marmorated stink bug)

&gt; HhK1

MLWAKHQKMVLIIIFVLFGVAYAWACPESCICKWKGGKQTIECVNKTLLITIPSNMDPGTQVLDFAAGNNLNK  
 LPKMRFENMGLINLQKIYLSRCRIKAIDRAFKGLTNLVELDLSENYITSVPTETFHDFPTLMRLALNGN  
 PIEVLRSAAFRLTYLTLELSNCKIKSIEDGAFEGLSLEWLKLDNNRIKIYIKGSNILPKDLHGIDLHH  
 NPWQCDCNLIDIRNWLLTYNIPHSIEPTCEFPARLQNKVKTLPLEDLACLDPVTPTTFYLEIAEGKNVS  
 LQCRVTAIPEARVSWWYQGEVLQNDSTVAPGLHLYYFLEEGTTEKRSELFIFNTNVDDNGTFVCIAENQA  
 GRSQSNYTIRIVLTKEPVVGLAVIPQAYVVALSAAIIVIGLLGVICIVLCFIQCRQRKRRKKKKDRSKVA  
 GIQNNQQMDKIPAPREDTITRVTASVAVPKPNGPVLNQEMMAFATGPGVLVIPNNLSYTSPPVPQTFQDK  
 NPDILINDTGSKEWNKESEEKEKIWAGGTLPRRDIFPKHLTADVHLSPGKFIDVDGYPVDYGLPKLPGPFP  
 VVMPPQAFYRTLPHKSRQGITARFSREAECIHYAPGDVRYTAEGYPSFQDPFISPPVGYRSDAASQWPES  
 GLDSLRTVSAQTSEVEPIPERQELTESPDEGYVGEEGDSSVN

## Acyrtosiphon pisum (Pea aphid)

&gt; ApK1 (a)

MARQWQLWLAAAVLAAAGATSVRADTCPEACQCKWKGGKQSVECRDKSLITVPTGIDAATQVLDVSGNNL  
 QILPESAFARLGLLNLQRVYMSRCRIGQIDGRALWGLTNAVEIDLNRNMLTAVPTATLADVPLLRDLSLA  
 GNPIQRVGPEAFRQCTGLVRLDLSGCELHEIAASAFVGIDRLETCLKLNDNRRLTELMAGTVATLHKVHGVE  
 LHENPWHCDCMRPVKVWLTDDNNVPTAVDPACASGPGRVANRTFSALAADDFAQCQPDILQQDDQTVQAAT  
 GDNASVSCRHSSPAKVSWYWNGRPLANNTAFGPFQRVFMTDDRTATGGGTGHSSLLLTNVQPSDSGQF  
 LCVAENRAGRAEANFTLVVTRLGGLAFLANGQVAGLSVFLVFLIVTILLVIVYLLVRIKRLPPSSSTRSDG  
 KPQHLVTTAASATSNGTAAVVVQVKQPVAGQATSPATTTVVSSMAVAVGGPYGGLDAGFDQATATEPVVG  
 GVRRPAKLTELSFATDHYDSGGFGHGGVLDAGRTVLYRSQPSNPDLIVDAPEQHSPPSQPPGAHSHHQ  
 QARRSASGEYRRTADDSLYSPGFWTPSDAAATDRTPPIIEKSPPLPAQSVAAVCSARETMVMAAAPDPKAA  
 SLRVWKHGVQVMPPLSALKRALNKGSPDEGYQE

&gt;ApK1 (b)

MWRFSGGRSARFLAAAALLALVVPASAVRSFEGCPAVCSCKWKGGRRRTVECADRALITVPTGVDADTQVLD  
 LSGNNLQILPNETFYKAGLANLQKAYLRNCRIGQIDESAFRGLTNLIELDLNNMLTSVPSYVFRDVPYL  
 RDLVAGNPIQKIEAHAFSGCPSVVKVDASNCGLSVAGLAFSGVVRLETLRINGNRRLTELSATVLES LN  
 KLRSIELHDNPWVCDCHLRPMKLWLAGNNVPYSQPALCSGGPDRLSGKPLTELDVEDFDCRPDVRAESRY  
 VEVTEGHNVTVRCRVEPGSMAHIAWYLNRRRLQGAGTPAVGYPGAASANPRMFVVDGVDEEDGGRRSEMT  
 LTDVRREDAGQYSCLAENRAGNSEANFTVYVTDSPVIMSTFGSAHVN

## Pediculus humanus corporis (Body louse)

&gt; PhumpK1

MAVISSSFPNWKTSKFIFIAIELCMLMPLQVVSCPSDCACKWKGGKQTVECPDKGLITIPNGIDAGTQVL  
 EFSGNNLKLPRERFERMGLLNLQRIYLSRCKILQIDDRAFRGLTNLVELDLNLFNTVPTETFDVPS  
 LMRLIVSGNPIRALQTASFRPLSFLTSELSNCQIESIEDGTFLGLDNLEWLKLDGNRLNFIIRGENILPD  
 AVHGVALDRNPWQCDCRLLEVHNWLLNYKIIHSTEPKCAGPERLVGEPIRNLEVGDACLDPVSPTTLYL  
 EIAEGKNISLLCRVSAIPEASVSWWFQGRILQNDTTLAPGFHFYFVEEGREEKRSELFIFNTNPDNGT  
 FVCAAENPAGKSLSNYTIIRIIVKEEPVVGIVFSREYLIAIFSVLTVFCFIIILVILAFLLIRCRQRKK  
 RKKERSKEMASQNKQKPLLRNEIITSPTETTGKSNGTVMSGQSNVSVFIPNIGGSNENESQSITSGVYIP  
 QNVFLTQONPDLINGTESAGNKFQIGESQIDGGQNLMSPPYADASRYIQTRGNCDLFIKQHYTADIHL  
 SPGRFFDGDGYPVDYGLPKVPLMVSLPTPDQQINYYRTLPNKRSKFSANPHLKFAAREAEFLSSSHSN  
 PYDYNPSNVRYTLEGYPCHQQQQQPQPPPPSNYSPSECEGTFIPSPPAAYKTDGISMIPPCDANNQWQCV  
 NAQQSRATDINADGIMQQQQQCSMSSKKTQAVLTESPDEGYVGD

*Daphnia magna* (Water flea)

>DmagnaK1

MASSTWDVTIGFKRWSAIWVIWTTLVTAGLVAMSAAGGAGACPGVKWKGGKQTVECRQRGLITLPSNIDP  
 QTQVLDLSGSNLQTLPREAFSRANLLNLQKIYLASCRIGQVDPTALRGLTNLIELDISDNLLTDVPSQAL  
 ADAVSLRELRLSSNPIQKIEQGAFDQAPGLVKLDLSDCQIETLAAGAFDGLDQLSHLRLGGNRLEELRPD  
 VVSSLPRRLHGLELQNNPWICDCRLRYLREWLQQHNVPSPATAACALPERLSGRALIELLVDDFACPPQV  
 IPFPAAPLLAGGGHPLHVEASAGENATLTCRMSGVPSPEITWLWRGKPMVNGSIPGEQEALPVGGAAEG  
 TGYPGDESESRVTILEEGKYEKTSYLILSPARETDSGEFVCVAANPAGLARVNLTLRVDIQAPVVGGLG  
 GAQIAGLGAGLFILLAAVVAILLLMLIRTRSSANSSGSSANKLDDIGKQSGQRPAMSLGQAHQGIQGSSS  
 SGPCVAKSPTLSALEYGQIAFVNPHSPNRVVVVTTAATASGLSDRPDLIHDA RNSSDHYGYDLGPPLDY  
 STLNRRYHHTHGQSADRDILAATSAGDYQSAQTDSFYPSALWDHILNPTSEEETSDGANNITIDQASSR  
 SSSGHMGSPHPLPHVPLTVMDRNGMPQIYVPYTSQGQVIQNPRDVLAAASYARDSEAGESAVSVDSYSLPR  
 RIPQQHSKESIGGQNFVPYPPDYGLPRQTQSPPTLAKPPTQHLLAAAGAATIERQPPAPTTEDPSTQQQQQQ  
 QQHNSSSSCYGSKANSSAESSPVATSSNTKGARFWQQRPGINNGKRSHHHFARDSPDEGYQENAPLTFEF  
 KYSIGLRLIENWLRKKHVPPAPLEHAEDHDIVSIVERKV

**Kek2 ortholog FASTA sequences***Drosophila melanogaster* (Fruit fly)

&gt;DmK2= CG4977

**MSGLPIWI PLLALLAITAAC**PPPEVCVCKWKGGKQTVECGGQQLSNLPEGMDPGTQVLNFSGNALQVLQSE  
 RFLRMDLLNLQKIYLSRNQLIRIHEKAFRGLTNLVELDLSENALQNPSETFQDYSSLMRLSLSGNPPIRE  
 LKTSAFRHLSFLTLELSNCQVERIENEAFVGMNDLEWLRLDGNRIGFIQGTHILPKSLHGISLHSNRWN  
 CDCRLLDIHFVLVNYNTPLAEEPCKMEPARLKGQVIKSLQREQLACLPEVSPQSSYTEVSEGRNMSITCL  
 VRAIPEPKVLWLFNGQVMSNDSLMDNLHMYYYIDETIGVSGAEKRS EIFIYNVGAEDNGTFSCVGQNI  
 GTTFSNYTLRVIIKEPPVVNEVSFPRD**YMNIVIVASSAGGGIIFVVLLCTIVVKCKKTSEPAKQRKKCDQV**  
 TSIAGGTDSSSTGSTQDTGMGMMKCASILNDGGDSMNGNPGLLLGDTLTPTKAANGAAGGGIILGNQMKQN  
 LLLYATPNSAQQLQLNVNLMGTGPGSPPLLLSNHGHLAAAYCSPPASLRNYQEK**NPDLVND**AESVKHKL  
 KTAVSLDGAGEYETQSDCGQYEGCYQLAAAPHPHQGHQHPHPGHPLMGRFAQAMTTLPRGMQLKPAPHQV  
 DVHLNPVCFLGQDGSFAYDYSSAHMVQQPPQQQQQQQQVQANNFYRTLPHNRLHKQQQFQAAAAAGGNV  
 GVGGNPTLRLYSLEAEFIQRGPTVSYEKYQLPNV**RFTAEGYP**QQQQQQQQQLQQQQQLQLQQQHQPSPPE  
 GYKSDLAVMPAPFQQWPSCLPGYRFAQSPTSLPAVATPPPAAVVATPPPPTS AVSTQSTATSTIPELDES  
 EASSPRLEEAAGSAAPPAGEEESSDTAKLKQLNGPLA**DSPDEGYVGDGQETSDI**

*Anopheles gambiae* (Mosquito)

&gt;AgK2

**MPYRWDTYALVLLALTVSWALPPATG**CPAEVCVCKWKGGKQTVECGGRFLNRLPDGMDPGTQVLNFSGN  
 SLTILQSERFRKMELINLQKIYLARNQLVKIHDRAFRGLTNLVELDLSDNTLSEVPTETFQDYAALMRLS  
 LSGNPICALRASAFKQLSYLTLELSNCQIELVEDEAFIGMDNLEWLRLDGNRIATIRGAHVLPELSHGI  
 NLQSNRWCHDCHLTDVYTWNLSFNVPQREEIKCSGPARLAGETVKTTLTDDLACL PVVTPETSYREIAEG  
 RNISLDCRIVATPEPTVAWLFGQVLLNDSFLSPNLHLYYFVDEL DGAHSELF IYNINADDNGTYSQVA  
 ENSAGRVQNTYTLHVIVKEEPVVEQVTFSEE**YFLAIVAASAATAVLLALLCCIVACK**CARARRASGSGAK  
 KSRGAKGATADGLGGVPAGQKQKASITHDLGEPLTAGKLNALGLGDGSDNPQDIVLYLNANPNGLDKAAL  
 NNMTAMAQFCSPPSARSYQDQ**NPDLINDA**ESGQHKARPRPDAIDSDLGEKDSDEQSSVQDGGSEVSFQQQ  
 QHQHQHQHQHQHQHQHQGGQGPYPYPPMVLRGPRFASSALSTLPRGGTAALGGKDL SAYQHQVDIHLSPGCFD  
 QNGYPVDLSLMAAPSGPPVNYRTLPHKKHQQLQQQQQQPGGPGKPIARYANDAEFINRTQSPAA YQMY  
 APTDV**RYTAEGYP**QHEHGQFPSPPDGYKEVHPVAYMSSAAAASAGFCVGPAPGPPQQWP TFLPGFHPQL  
 IPIMAPAGGALLASPMMPSPSGQQQQQQQQLSSPQTQPGSALKKCSVGAQTSEL DKDVIPEQREEEEE  
 EDEQDGGGGGSTVKLRHLTGPLA**DSPDEGYVGDSHETS**DI

*Plutella xylostella* (Diamondback moth)

&gt;PxK2

MQVLQKEIFQKLGLFDLQKIYLPKCRHKVDNYAFKGLANLVELDLNNYLTIVPSSNFVYFPSLMRLSL  
 NNNPITTIKTHCFQHLTFLNTLELSECKIEQIEVDAFAGLHHLEWLRLNGNRLSNMEGDNI FPDTLRGID  
 LENNRWNCDCQMKDLHNWLKFNMPHAVEPLCSTPERLRKRKIASVAAADLACAPKMSPTSVYLETNEGN  
 NVTLECVKAVPEAEISWWFQGQIIHNGSKDDYDLKTSYSLIGTTDKKSELFIFNVNQYDNGTYIC IADN  
 IAGRALANYTLKII IKEEPVIVVVSFPRK**HLVIIVTG VFLVIVLVIAIVAVVLLKF**KTDTKSRKKKDSGK  
 DVALRNQNNSSRNSDTSTFDTLQRKMNGSLITNAQTHHVHYTVQESTEDTYRQGSIKNFVDR**NPDIIND**  
 AETVTNNALNDNAIMSVYKTQNTNPENMEGESAFSLPPMMPRQVTWRDQQPPRGPHYHLYQHSADIHLNPG  
 CFLDNEGYPYDYGLPKMQCRGPPMHSNYAIVTPGYQTLPHKRPNVQKL GCKFAKDTEFNTTPCLNYVSG  
 NF**RHTLDGY**PVVNRVPFAGNGNMFIAQPGPLPEGYQVEPITLCCGAAQTESCSAAWGAAGTCAVMVPLD  
 VAEAGAAKCYHVETRCVDTQTGEGRGEARGAEARGGEARGAEAGEAPKPALRAGKYELEVCT**ESPDEGYVG**  
**DAVD**SADT

*Tribolium castaneum* (Flour beetle)

&gt;TcKeK2 (a)

MWVYWLVLGMLVERSLS CPVSCSCKWKNGKQTVICSGKSLTDIPDGLDPGTQVLD FSGNFLSNLRRELF  
 SNKQLINLQRIYLSNCQIKIINEKTFKGLSNLVELDL SRNLLETVP TSSFVDCPSLMRLTLSSNPLTVLK  
 RLAFNHLSYLSTLELDKCKIVEIEDGAFQGLHSLEWLLLEDNGLRTIRGELPRNLKGVELRGNPWECDC  
 IKELHVWLGRFNVPISEPTCSGPPRLASRVIKSIPVSELACLPDVSPTTFYLELAEGKNVSLQCHVHSI  
 PEASVSWWFRGQILQNNTIVSPGIHLIYFVEEGAENKRSELF IYNANSEDNGTFCNAENAAGTSQSNT  
 IKII IKEDPIVIVIVEFPFEC LLAAAIGAVVLALLIISGIIISIL RCKRRKEPLQ GKTEEDTNPKPTPDDD  
 TLYVCE DHPVPNHQSPTLLFQDQ NPD LINHRWLDSEGYPLDYGLPKLP TNY YRTLPSR PKRQSLQRPRYS  
 QEAEFLAYDHYHTDV RYTADGYPLPSNDGAPCCSIQWPVCVPANLHMVNNPNEMVYEP PPSGI IKRCVGA  
 QTEDEKIDSNEAGNEAMT ESPDEGYEGEPAVV

&gt;TcKeK2 (b)

MSWRGALVFLILSLTQCSGCPVFCSCWKWSGKQTV ECINKDLLVIPEGMDSS TQVLQFCGNNLQTLQRDK  
 FLKMDLINLQRIYLCRCRITSIDDR TFRGLTNLVELDL SGNLLETVPSETFLDCPSLMRLSLNANPIKTL  
 RRAAFNHLSFLNTIELSNCEISNVEQGA FQGLYSLEWLHLNGNKM TTLQGATYLPKSLKGVLQENPWEC  
 DCHILELHAWLRAFTMPHSVEPLCNGPTRLSRTIKSV PVGELACLPEVSPTMFYLEIGEGKNVTLQCQV  
 NAIPEARISWTFQGQLQNDSMIAPGVHLLYFIEEGAVEKRSELF IYNSNSDDNGTFICNAENAAGLVQA  
 NFTIRVIVKHDTTPV TNELPFE FILITLSAAAVSILLLL VVILLSI IKCHRNARLKKRNN SKAALSNTT  
 KDNLLQESVDDYSEKPPTQEEETMLYNTPPEDLPVSSI PPTLT PYQLEQ NPD LINGTESVGRFTPLKKRD  
 LYVYAPDVHLNPVGLLNSGSNCYKTL PYNRNKRSNAANPAGRFSREAEFLQRTMHPSYEHYS DRYTADG  
 YPVRTNEGAVEPCCSTTTTVSWPSCVPAS FVAKDCVKSVGAQTEDTNTKCEPIKETFT ESLDEGYEGEGA  
 EVHTNGEARYLPSCGSLNKLILPSPTCVLPY EYKFNR

*Apis mellifera* (Honeybee)

&gt;AmKeK2

MCSSMRAWWRGTL LGTMMLLSWTSSLVEG CPSMCTCKWKSGKEWVECANRDLKGLPQGAREETQVLDLS  
 NNHLVSLPPEC FHALGLINLQRLYLRSRSHISHIASRA FVGLVGLVELDLSEN LIEEIPSETFPSYSNLMK  
 LLLNGNPVREIHRGAFQHLVHLTNLELSQCRIENVEQGA FDLGHQLEWLRLDGNRLTRVPDLTLP LGGSL  
 RGLTLHNNPWLCD CRLQATQAWLKESAPAAPQESEPVCDSP PKLRGKQIKEVKLNELACL PQIELQDQIE  
 AYEGDNVTLKCDVYAVPA AKLTWWFNGELCELQ NENDSASSAYPRYVYRQRGGTNMSSALLYSVETLN  
 EGTYT CIAENGAGSAEANLSLRVLFQERITVEPPNDH SRSGYVVAVAAGALVGT LFALASLIGSIVFCVR  
 KRRRDRKRNSKALVSQNKSVMPITKDTT TSLPCRKGNGSLIGLEHQQMVS YTEREMSRAATLERREHRNV  
 EEPYCSPVSKYLT EPDLINEVPETTDVGYGQLYRHQP GERQILEYDSGYPLQPD LRPSNIPQLSYLDQDG  
 YPLNFGLPKIPFSAASTLPRLRQRM PVEGTAVAPPARYSREAEFLARSPGYDPVLPRTDT RYTAEGYP  
 AQQQQPQPIQPVEQPIQQQLPVSPVSPVAVFPEVPFIPSP PAAYRGETTPLSPRSLLSKTAREAAAAAA  
 RAEDLQPPHHP ESPDEGYVG DAMDV

*Habropoda laboriosa* (Southeastern blueberry bee)

&gt;H1K2

MCSSVRAWWRGALLGT MMLLSWTSTVVEG CPSMCTCXXXXXXXXWVECANRGLKGLPQGAREETQVFDVS  
 NNHLVSLPPEC FHALGLINLQRLYLARSNISRIASSAFMGLVGLVELDLSEN LIEEIPSETFPSYSNLMK  
 LLLNGNPVREIHRGAFQHLVHLTNLELSQCRIENIEQA AFDGLLLLEWLRLDGNRLTRVPDLTLP LGGSL  
 RGLTLHNNPWLCD CRLRATQAWLKESAPAAPQESEPVCDAPPRLRGKQIKDVKNELACL PQISLHHRLE  
 AYEGDNVTLKCDVYAVPA AKLTWWFNGELCELQ NENESLALLSTSI PRYAYRQRGGTNMSSLLIYSVES  
 QNEGIYTCTAENGAGSTEANLSLHVLFQERITVEPPNDH SRSGYVLAI IAGVLLGTLFAMGTLIGSIVFC  
 VRKRRRDRKRNSKALVSQNKSVMPITKDTT TSI PCRKGNGSLIGLEHQQMVS YTERELNRAATLERREHR  
 NLEEPYCSPVSKYLT EPDLINEVPETMDIGYGQLYRHQP GERQILEYDSGYPLQPD LRPSNIPQLSYLDQ  
 DGYPVNFGLPKIPFSAASTLPRLRQRM PVEGS AVAPPARYSREAEFLARSPGYDPVLPRTDT RYTAEGYP  
 YPVLQQQPIQPVEQPIQQQLPVSPVSPVAVFPEVPFIPSP PAAYRGETTPLSPRSLLSKTAREAAAAAA  
 RAEDLQPPHHP ESPDEGYVG DAMDV

Acromyrmex echinator (New world ant)

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>AechinK2 (a)
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MLLLLSWGTNAEEDCPSPMCACKWKGGKEWVECANRDLKGLPQGAREETQVLDLSGNHLVNLPAECFRALG  
LINLQRLYLKGSRINQIASEAFVGLVGLVELDLSENQIEQVPTDTFASYPMLRLILNGNPIREIRQSAE  
LRLVHLTNLEISKVIEIIIEQNAFEGLQSLEWLRLDGNRLTYVPDHTLPLGGNLRGLTLHNNPWQCDCL  
RIMQAWLKESAPAAPQESEPICDSPARLHGKQIKSLKINELACLPRIDLQDHLDIYEGGNITLRCDVHAI  
PTAKVTWWFNGEPCELQHENNSMASSISTFPRYIRQGGTNMSSTLFLYSVESLDEGTYSCIAENSAGSA  
VANLSLRVLFREKPTVEPPSDNPGSGYVAAIVAGALVGTLLALSCLVGSVIYCAKKRRRDRKRNSKALVT  
QSKSVLPITKDDTSSSSCRKNGSLIGGLEHQMVSYTEREINRAATLERREHTRNNHLDRDAYSVASPA  
KYLTEPDLINVPENSEVGYGQLYGRHHQRAGGVDRQVLEYDSGYPLQPDLRPPVLSQMNLYLDQDGYPL  
NFGLPKITFSTASTLPLRLRQRMTEPGSAAAPAARYSREAEFLARSPGYDPILPRTDARYTAEVSPVAVFP  
EVPFIPSPPAAYRGETTPLSPRSLLGKTAREAAAAAARAEEQLPPNHPESPDEGYVGDAMDV

>AechinK2 (b)

[illegible]

*Nasonia vitripennis* (Pteromalid parasitoid wasps)

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>Nvitrisk2
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MLPRLALLPPLPPLPPLLLLLLLLLLLRAAGRADACPSACSCWKAGKEWVECAARGLQGLPQGAREETQV  
LDLSGNQLFSLEAEGFLALRLVNLQRLYLARSRLRSVARLALSGLQGLVELDLADNELEQPPTESFASVP  
NLMRLGLAGNPLGELRREAFRQLAQLTFDLDSRCRLARLEAGAFAGLHALEWLKLQDNLLRQVPPATLPT  
SAGLHGLPLHGNPWLCDELAALRDWLVASQAQAPQDAEPSCQGPERLRARPVRLLKPQELACLPSVRLP  
ASPLDVYEGDNVTLLCEVQAVPQAAAGWLVNGRSLDLDAEPEPSELPRRVRSYVEQSSSENKISASLEIL  
EVESVDEGSYVCQAENAAGSARGNLTLRVLRERSTVEPPAESPGAGYAAAIAAGALLGTLLALGCLFLG  
IFLYARRLRSHSKSNLKQPSTAGSSVPPSILKKPSGDKPSKPACEPEGATSAYAPASAAAVLMPTASGR  
LEQPGYGPAAAELNEFGELSEVLYLQQRFT**EPDLINE**VPQVESGLPGGYLEPSYRRACLDAYSNCNCLDR  
DGYPLNFGPLKLGPVTPQQRGSATCSETLPRIRQRQQLMLSGSAAVPTIRLSREAEFLARAAGYPCPGNQ  
PVLEIGYAALVQPTPFIPSPPAAYRSEPAALSPRSLQAKTQLEGAVGGACPSNAPPALMQLPHPRHPQH  
QQHQPHQPHQAPLDPSENREGIEHP**ESPDEGYVGDAMDV**

*Linepithema humile* (Argentine ant)

&gt;LhumK2

MCSIASAAWRRRVLLGAMLLLLLSWVAGA AKDCPSMCACKWKGGKQWVECANRGLNGLPMGAQEETQVL  
 DLSDNQLMNLPAECFHKLGLTNLQRLYLSRSHISQIAAEAFVGLVGLVELDLSENLIEDVPTDTFAFCSN  
 LMRLILNGNRIRKIRQGAFRKLTQLTNLEISQCEIEEIERGAFEGLDSEWLRLNGNRLTRVPDYTLPLG  
 SNLRGLTLHNNPWQCDCRLRSMQGWLKDSASTAPQESEPVCGVPEKLQGRQIKSLKINDLACLPHIELQN  
 NLEVYEGENVTLKCEVYAVPTAKVTWSFNKVPCELQENENDSVTNDATTYSKYFYRQRGGTNMSSTLFLYS  
 VELLDEGTYGCVAENSAGFVEANLSLRVLFREKTTVEPPSDNPASGYVAAIAAGALVGTLLALGCLVGSV  
 IYCAKKRRRDRKRNSKALVTQSKSVMPI TKDTAGGGGGGTCTKGNGLIGLEHQQMVSYTEREINRAATL  
 ERREHSRNNPDRDAYRVASPVAKYLT E PDLIN E VPESTEVGYGQLYGRHHQRAGGVDRQILEYDSGYPLQ  
 PDLRPPVLPQMSYLDQDGYPLNFGLPKISFSTASTLPRLRTRMTPEGSAAAPAAARYSREAEFLARSPGY  
 DPVLSRTDAR YTAEGYPYPTHQHQQLQQQQPQQTMPSPIQPIQAIQPV EQPIQQQLPLQSPVSPIAVFPE  
 VPFI PSPPAAAYRGETTPLSPRSLLSKTAREAAAAAARAEELOPPNHP E SPDEGYVGDA MDV

*Diaphorina citri* (Asian citrus psyllid)

&gt;DcK2

MMYWIFLIATI IKIVSACPTSCICKWKGGKQTVECVNKSLITVVEGMDPNTQVLDYTGNNLKTLLHNEKFQ  
 KMGLVNLQKIYLSRCRISVIDSKAFRGLTNLVDLDFSHNVLQTVPSDTFPDYP SLMKLTLSGNPIKQIKT  
 GAFQPLSYLVTLELSKCGIEVIEDAAFGVGLDSLEWLKLDNNKITTISGSNLTPTGLHGIDLHNNPWTCDC  
 LLIGLRRWLESTKTPMAIDPICSVPRLSSVTIKQLSIDELACEPQITPSTFYLEIQEGKNVSLCKVSA  
 IPEAKITWLF DGVPIQNESMSASESHAVYSTEEGTEIKKSELLIYNSNIDNNGTFVCVAENQAGSTSSNY  
 TIRIVLKEENVEVVTVFPLEYVLIVSGIISVCSLVLIFLLVLCFLCFRRKKKKLKKKDESDKNVNGSNEN  
 VVKNLRESPKYTSVNATSATCMDKVNNGYI IADGHNDMMLYATDSGILVATNNMNTYPSYSISYQIEQNP  
 DLVND AESVDKDRRAQGGEDTQDTQDKASEAASVQYSDSGSQCEWGNVCYNRMQPMQHIVLNNVYNQPA  
 DIHLTPEKFMDRDGYPVDFGLPKVPPTHFPALVPATAYYRTLPHRRHTAANPNNRY SREAEFLSRSSQPAS  
 YEHYAPADV RYNI EGYPSASPTPYSSAPRVTFTEPLHILQGQPMQSNPPTETTTKNEQTWTESSADEQPS  
 TSNPEKSNENKSEGFQAKRHMIDSLLKNRDVKVGSHLHPRGLMLPPVLT E SPDEGYEGEGPE TTEM

*Cimex lectularius* (Bed bug)

&gt;C1K2

MLVVLLLLLGMVHVWACPSSCICKWKGGKQTVECINKSLITLPSGMDHGTQVLDFA GNNLDRLLRERFOR  
 MGLINLQKIFLSRCRIKHIEDRAFKGLTNLVELDLSDNSITSVP TETFYDYP SLMRLTLNGNPIKVLKTN  
 AFQPLSFLTNLLELSKCEMETIEDGAFDGLNMLEWLKLDNNNVKYISGKNILPRNLHGIDLHNNPWQDCN  
 LISLTQWLVKFSVPQSI EPACQTPERLKGKQIKTLSTNQLACL PDMKHVTPLILEISEGQNVSLCQVSA  
 IPEAKISWWYEGNVLQNDSTVAPGLHLYYFVEEGTVEKTSelfIFNTNVDDNGTFVCIAENSAGRSHSNY  
 TIRIILKEEPVIGLAVFPYEYFVVISAAVS VIALLGVICVTLCLIQCKRQKRRKRKKDRSKVAALPNQPI  
 SDKTPVVRDNDTITRIGSIVQAPKINGTAHQEMMAFASGPGVLVIPNNLKYTTAPMPQNYQE QNPDLIN  
 DTGSKEWKGPKEEQDIEKGWVAGTLPRRDVFPKHMTADVHLSPGKFIDQDGYPV DYG LPKMPGPFVVM P  
 SSSFYRTLPHKPRHAPAAKFSREAEFVTKPGSTASFEHFNPSDV RY TLEGYPCVQQLYPAFQDPFISPPA  
 GYKSDPKDAAAQWPESNLDTLRTQSVGAQTFECEQGSNAILEEPQALT E SPDEGYEGDVTE PAEN

**Halyomorpha halys (Brown marmorated stink bug)**

&gt;HhK2

MLWAKHQKMVLIIFVLFQVAYAWACPESCICKWKGGKQTIECVNKTLLITIPSNMDPGTQVLDFAFNNLNK  
 LPKMRFENMGLINLQKIYLSRCRIKAIDRAFKGLTNLVELDLSENYITSVPTETFHDFPTLMRLALNGN  
 PIEVLRSAAFRLTYLTLELSNCKIKSIEDGAFEGLSLEWLKLDNNRIKIYIKGSNILPKDLHGIDLHH  
 NPWQDCNLDIRNWLLTYNIPHSIEPTCEFPARLQNKVKTLPLEDLACLDPVTPTTFYLEIAEGKNVS  
 LQCRVTAIPEARVSWWYQGEVLQNDSTVAPGLHLYYFLEEGTTEKRSELFIFNTNVDDNGTFVCIENQA  
 GRSQSNYTIRIVLTKEFPVGLAVIPQAYVVALSAAIIVIGLLGVICIVLCFIQCRQKRRKKKKDRSKVA  
 GIONQQQMDKIAPREDTITRVTASVAVPKPNGPVLNQEMMAFATGPGVLVIPNNLSYTSPPVPQTFQDK  
 NPDILINDTGSKEWNKESEEKEKIWAGGTLPRRDIFPKHLTADVHLSPGKFIDVDGYPVDYGLPKLPGPFP  
 VVMPPQAFYRTLPHKSRQGITARFSREAECIHYAPGDVRYTAEGYPSFQDPFISPPVGYRSDAASQWPES  
 GLDSLRTVSAQTSEVEPIPERQELTESPDEGYVGEGGDSSVN

**Acyrtosiphon pisum (Pea aphid)**

&gt;ApK2 (a)

MYATDTPVRRRVAQTATMTTTTTTMI FVAAMMATMLAAAAGCPIGCMCKWKGGKQTVECVNRSLSAIP  
 NGMDVGTQVLDMSGNSMDALSRGRFMSAGLSNLQKIFMSRCRITYVDDAAFQGLSNLVELDLSDNGITDI  
 PTKSFDDYPQLMKLVLSGNAVTVVRTAAFKRLAYLTVLDLSRCRVSTIEPGAFLGLHSIEWLRDLHNQIV  
 RIESAGAVVLPLSLHGIEMHNPWTCDCRLRDVHRWLNNSAPHTVEPTCHGPDRLRGMVIRKLVAEELA  
 CAPVAAATSPEYVETDAGKNVTLACRVTPAGQSRVSWWFEGRQVANSTTSAGVELTVEDVGPADNGTYAC  
 VAENRAGWAACNFTVRVIQELSEVAAGSYPPDAPPPALLVIVLGGSVCFVAVAVVCAISCRLLVVKRRRH  
 RDHAGRPGGKSGGAGGGDAGPDDPSNSGQAAKTTSDIRQSDSVNLTVSSTVDGKLSSAEDVSVYGEYDTA  
 AGPGSSAGYEVHEVMHVGGGGGYDAYQQVHVAQGH PATATATTTLEANNPDILISDASTVIRDNGGGDYRDA  
 TDEVYKIAVPPPPSCGRDFWSTSGAVYPSGGGCGSYELQLSPGKLAAGEPYPADYGLPKLSSGQYPMPAP  
 PSLYRTLPHRRNAAKPQGRSCQEA EFVLLQHHHHHHHHHHQQQQQHHLNRYEPQNI RYNQQGYPPAS  
 AVAADAAYTTAAATFYEPPLSNASAQTLDDETMVM MMMMPPAPPPPLVTGAPALPAAGRQPQHLSAEH  
 AASQHKAVTAVQKQPATTESPDEGYVGEGPS

&gt;ApK2 (b)

MVLSTSTTTTAMMMMMMTTMTMTTISSSPGCPAGCACKWKNGKQTVECVDKKVTSVTLALGIDPATQV  
 LDISDNDLSAAGLPHDTFAAAGLSNLQRIHASRCNVYYVHRAFRGLTNLVDLDLSGNCLRQVPTGAFAE  
 CPSLMKLSLSGNPIGDLPARAFRHLGQLTALDLSGCGLTAVAAGAFDDL SGLDWLRLLDDNLLTHVPGPNT  
 LPARLHGVDLHRNDWQCDCRMVDMHRWLTASRPVTEEPVCSGPAAAYADVPVRRVSVAEALACAPAAYPAT  
 QPVQDVIEGVNVSFRCLVAAI PAATVEWLYGGVPVYRHNASELITVDGNTTAE LYVYNASVTDAGSYACV  
 AENRAGRARNFTVTVRPGRPF LAAGTVDDRSAPSQSSSATAGSGGTSGDGRPLLYVGCLAAGSVALSA  
 AA AVLVAIRCRRVKRSSTGVRAGDSSSTCKRRPTAPAADGYRTVSTTADKELSVPSAHRPASARTTATLV  
 TVTATGLDGAEDTTVATAESNPDVSDVKRTGWEIDFEQIVWAECP PATGYVSIQIPVQCGIECLGAYYA  
 TTAEAVAGSRCGGAGATLRRQRRRAAVLTAYDDTVQVVRTTAQGGYPTTTTGPGTIGIPAAAEPPTIV  
 EDPDDDVG GGVVGGVAPIISPPLPFRSGDEDGADKDDSI AL

## Pediculus humanus corporis (Body louse)

&gt;PhumpK2

MAVISSSFNWKTSKFIFIAIELCMLMPLQVVSCPSDCACKWKGGKQTVECPDKGLITIPNGIDAGTQVL  
 EFSGNNLKLPRERFERMGLNLQRIYLSRCKILQIDDRAFRGLTNLVELDLNLFNTVPTETTFVDYPS  
 LMRLIVSGNPIRALQTASFRPLSFLTSLELSNCQIESIEDGTFLGLDNLEWLKLDGNRLNFIRGENILPD  
 AVHGVALDRNPWQCDCRLLLEVHNWLLNYKIIHSTEPKCAGPERLVGEPINLEVGDLACLPDVSPTTLYL  
 EIAEGKNISLLCRVSAIPEASVSWWFQGRILQNDTTAPGFHFYFVEEGREEKRSELFIFNTNPDDNGT  
 FVCAAENPAGKSLSNYTIRIIVKEEPVVGLIVFSREYLIAIFSVLTVFCFIILVILAFLLIRCRQRKK  
 RKKERSKEMASQNQKPLLNEIITSPTETTGSNGTVVMMSGQSNVSVFIPNIGGSNENESQSITSGVYIP  
 QNVFLTDQNPDLINGTESAGNKFAQIGESQIDGGQNLSLMSSPYADASRYIQTRGNCDLFIKQHYTADIHL  
 SPGRFFDGDGYPVDYGLPKVPLMVSLPTPDQQINYYRTLPLNKRSKFSANPHLKFAAREAEFLSSSHSN  
 PYDYNPSNVRYTLEGYPCHQQQQQPQPPPSNYSPECEGTFIPSPPAAYKTDGISMIPPCDANNQWQCV  
 NAQQSRATDINADGIMQQQQQQCSMSSKKTQAVLTESPDEGYVGDTESGDI

## Daphnia magna (Water flea)

&gt;DmagK2

MALISLPLNGARTFLRLLVWSMLICCLTAACPDSCCKWKGGKQTVECVNKGIALPEGMDPETQVLDISG  
 STLQILHRTLFRQYGLVNLQRVYLARSRLGHLDDLTFQGLTNLVELDLSDNMLTSIPVAALSELPALMRL  
 SLARNPVRVSADSFRNLRYLITLELSQCQIEAVEAGAFDGLKALEWLKLDGNALANIGGSAVLPRSLHG  
 VTLHDNPWRCDQLSQLRSWLQFNIPLSMEPKCSQPERLASRLVKSLDPMDFACAPQISSSVTILEVSF  
 GDNVTLSCHVTGDPDPRVSWFHNGQKITATSSSTALYSSANETETVAETSFYTYTFIGVDGSDSQRSVLNIV  
 NATTKENGSYVCAAENRAGSARNNFTLLVLPLPTLPPPPGSIEYVITVGGVVAAIVITMVVIVIAVAVRC  
 CCCRRRSHRTRDKTANNIASIGGVGDSAKTKSNSSLSPELPPRP IQMLPSSSNIGNKGDNGYTMGVPLPG  
 GGRVGGAGREYHSTALDSSLDQSPDLINDTTATAKWKEQNAQAVSLDDGQFSPTLYASSAGSPSNVNASQ  
 YYPCSVPLSTISEAVLQQHQHGFYPAQCSTNVYNSSSSSLAVLNPAGYLVPMSMPGLPLVDAEGFPIDYG  
 LPRPSRPTRPTQTHVRFADPPSVSVRHYENYVVDGDNLQEATMENFLPDRKYPDSYDPLPSSPLNCSHHS  
 EIRYPSERYPQNFSPSSFPAGYNATGNYEEIIAAPPSPGYAGHQNHQHQQHQQEYMPPPGQMMKPNSSTS  
 IESSENSTLTLTGGAPSSPLDVSINDASSSSPGFLCSSTLQRQPHESPDEGYEDEGIDGTEI

## Kek3 ortholog FASTA sequences

*Drosophila melanogaster* (Fruit fly)

>DmK3

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MAAGRAAATLEAPGPPSGQDIASDNSAQRRTLATKVRKGRPRPQRRLLHPPLRPRLPLHLHLLWLLCCCS
QLGQLRAECPAVCECKWKSGKESVLCNANLTHIPQPLDAGTQLLDLSGNEIQLIIPDDSFATAQLNLQK
VYLARCHLRLIERHAFRKLINLVELDLSQNLLSAIPSLALYHVSELRELRLSGNPILRVPDDAFGHVPQL
VKLELSDCRLSHIAVRAFAGLESSLEWLKLDGNRLSEVRSGTITSLASLHGLELARNTWNCSCSLRPLRA
WMLQQNIPSGIPPTCESPPRLSGRAWDKLDVDDFACVPQIVATDTTAHGVEGRNITMSCYVEGVPPQPAVK
WLLKNRLIANLSAGGDGSDSEPRTAATQGRKTYVNMMLRNASNLITLTADMQDAGIYTCAAENKAGKV
EASVTLAVSRRPPEAPWGVRIILLGAVAALLLVGGSSFAAICLCSLQRRRKLRLWNSVPPVRRSESYEKI
EMTARTRPDLGGGASCGGGSATGAGLFHDAEEQGYLRAHTPLNDNDAGQAAAI VNPSAGSAQRRNGDYL
HVSTHCDDEEDDQQLHHHPQQQPASQHHHPNQQQHQQRKGSQGHVVSASGANN SAPLEETDLHIPRLID
IGGTDSASSSISSQVDAARLAGYAGHTWKTTPIATTKINSPHSPKVTSAAPSSLNTQATPYAHYGNHPA
DEMATSVCSEGESDLFDSNYPDLLDI AKYAVAQAQQEGRGQGYAQTTPNGGLCTLPRKLKTSKGYF
RNSSDSQSPLLADNSSKYGSSTLGDGSFLNEAMGLGRRYSAESSYANYSSSTATYTGGGQRANSFLNLVQS
GAHQGKLLPSHLGQKPSLPSSPVQHQRSLSSAATPLLD FSALASRAAGAANTSVAAYDYHAAQLERFLEE
YRNLQDQLCKMKETCDTIRKKETPLRVAIGSAAQLADPVMYSAASHSPKPPATSNLKT KTLLPGQPPDP
PPYWLHRNAMLKRLNGDGSAGTNGSGGSPASPQPRQDIFKS
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*Tribolium castaneum* (Flour beetle)

>TcKeK3

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MIPPAHTMPSLHFHLALIIGFCTQMIVADCPR LCECKWKSGKESVSCPNANLSSIP LHLEAGTQVLDVSK
NNLVNLKHDEFKAGLLNLQKVYLSQCRLKNLERYAFRKLINLVELDL SHNLLSSVPSHSFDSIPELREL
KLNDNPIQRILNDAFINVPQLIRLELSECRISTIEPRAFHGLESSLEWLKLDYNKLTEVLSSSFTILENL
HGLELAGNPWNCTCPLRPLRLWMLQKNVPFGIPPICQSPKRLRSKTWDKLDLDEFACIPEIFAYESKTKG
VEGKNVTMTCRITGIPEPSVRWLLKNKVIANLSGSSYSNGKKLYMVHLSNNSSDLTIFSADLQDAGVYVC
AAENKAGRAEASVTLAVIRKPPETA FN NKILIASVITGIALVLASCLIALCVYSVRKKQMLTWRTRCRR
EDNYEKIEMNHKVAGNSNGGAVQAEI AVVATKKNGEYRVVPVADNEEVEEEEEESNVEAAAKRIWQDTAIE
KRWNSPEHLLDPEDLHIPRRTLQEARD DIRKGFSSSTSGIYSGYEQPSTLSQS VAPHLLRRQISGGHATT
YNSELSSLMEDEADKKYPDLIENSSYKFGNKANSEGGSVADITDLFCTLPRKRTLIQSARYKSSDSQSPL
LPESRYGSSGGESSCGSQESGLRRLSDCPKYPAGNLNKNRVNKNISNSYLNLTREEELTS TPLL DVTGLES
RVGLTPNANSYDYHAAQLERFLEEYRSLQQLTKMKETCDNLCQDHLQAGSSQVTPSTSNDDVVRNPNVS
PNSNQSLSDSIDFRNFESELTKYLLAKSSPSPKTFTNNSGVFNN
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*Diaphorina citri* (Asian citrus psyllid)

>DcK3

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MDHDECADDVMMIYEWVYIMVLVCTGCLQVFAECPSTCECKWKGGKETVLC KAKNFTTIP EQLDVGTQV
LDLSDNLFVEMTKDLFQETFQELGLVN LQKIYLNKNKIKSLDRYTFRKLINLVELDLSYNQIQFVPSHIL
DSILELRELKLSGNPIQKITHEAFINVPKLMRLEISDCKIIFIESRAFAGLESSLEWLKVDRNKIVNVRP
VTFTSLHSLKGIELYGNPWNCSCYLRPLREWLLRN NIPVGVPVCKYPNHMSGKSWDRNLNLEDFACSPNI
RPITPDVTAEENENVTLSCRATGSPVPKIKWIFKEKIIANISSGLANMKNRQYIIKTINSLSNLTIVAVT
MSDSGIYTCRAKNGAGEVFTNISLNVIKVETAVAQPD PVYLVASLTTVVTIILTACFVVL CII LLKAKRK
RYADVNRRYLEDKCESNHQQSKPLTVNKM DRPPVPSAVPAVPLVPPHPPRNEYSSVPLSDTTTRGPEPR
DKIDHEENIDKDASVYYNCNIGDVALGHHVLRKEVLPAGGGSLYTTASPGYPDLL ENYSSSNSNKSATDY
ILSKNSSKYPKVSDS QSPLL PSSRYGSSGGESSGESPOSVRQSISSLTIK
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*Cimex lectularius* (Bed bug)

&gt;ClK3

MLVEILVILVVLPRIPGDCPPQCECKWKNGKESVICVNGNLTRIPGQLEAGTQLDLTGNILISIAKDAF  
 KNAGLLNLQKIYIAKCRIRTMDKYAFRKIINLVELDLSYNSLNTVPSHIFDSISKRELKLNNGNPIQKIG  
 NDAFSSVPLVKLEISDCKLASLDPNFAAGLENSLEWLKVDRNRLKEIQPTTLTSLLSLHGLELSSNPWNC  
 SCVLRPLRQWMLNNNIPTSVPLCKYPSRIESKSWDKLSVDEFACSPDISPVRPSVKTEEGTNVSLSCTV  
 TGNPLPSVKWVWKNKPLDNSSAHANNKKVYTLRLVNKKSTLIVHSTESSDAGVYFCVATNKAGRVEGNVT  
 LSVTKKIPETKISGKMLFGCSVVGFLLL VATCLLLCLLGQPRKESRATKAESYEKIEMDKKGDCINDISV  
 SNKIHTPMGEYRSIPTFEQGEQDDENGSPNSNHSDAPRPANRQTRELASASKLYCQLGGVQPHILRKEVL  
 PTASLYTTAISEERNYPDLVTYPPTSNTAQCSATLPRSKIWYPMVSSSQSPLLAGSRCGSSAGESSGSRN  
 RFSAESRSSSNYRLPGKSCERSVSSLNLCIEPEISCSQTRQKSWHHPSLPTSPVRYHMAHKYDSNADTSE  
 TPILNLLGSAVYDYHAAQLERFLEEYRSLQDELNRMKETCEGLKEKSIIEKPALSDFFSYRYTSNSIYNDL  
 FRN

*Halyomorpha halys* (Brown marmorated stink bug)

&gt;HhK3

MRVVALIVFLLRECLGCPPTCDCKWKSGKESAI CVRNNLTHIPKGIDSSTQLDLTGNRISAI DRDAFDK  
 AGLFNLQKIYLA CKGLRDMDFAFRRLTNLVELDLSYNSITVPSHIFDSISELRELKLTGNLIQKVSNE  
 AFINVRQLVKLELSECRIVLLEPRAFSGLEKSLEWLKLDKNRLVEVRPGTFTNLSNLHGLELAGNPWNCS  
 CRLRPLRQWMSIQNVPSSTPASC SHPHRLRGKTWDRLQDNEFACTPVMHRTRNTVVQAVEGNTVTLSCLV  
 NGNPTPTVRWLWKNRPIANVSGIPNHRKLYILHYNGSRSTLTVYSAEIADAGVYFCVASNKAGRVQGNVT  
 LAISRREPESKLTGKVL MVGAAMAFLLFVVS GF LFCIFGQPRKPPRVNQAENYEKIE MEKKGESCLPENQ  
 PNNRIHPTLCEYRGVPVEDIEEETTQPS PMLVPNASSNTPRTHLQ LSEDLIGVQQHILRKEILPTTSLYT  
 TAAPDDSSIPDVVTNPASIVSAAATLPRFRSKDWYPNVSSSQSPLLAGSASGSSPGEMSISRYSIESRA  
 SARYSSRPRRCERSASSLDLFEPEHKSQWRPSLPSPTRFNPHRSFQVSETPILNLLDSANHYDYHATQL  
 DRFLDEYRTLQKEINRMKETCQELRGSTTAELFPYTYRV

*Acyrtosiphon pisum* (Pea aphid)

&gt;ApK3

MPSSPAPASAAAMAGGGLIVLLVLSACVVRGARADCPVACECKWRSGKESAICASANMTAVPRHLDYGT  
 QLDDLNDNPLYRLGKDAFADADLLNLQKLFLSRCRIKALDRYAFRKLNNLVELDLSHNSIPVVP SAVLES  
 VP ELRELRLNGNPIMKVPNGAFTHVPRLVRLDVSGCRVALLESTAFAGLENSLEWLRLDNNQLRDVKPST  
 VVSLARLHGVLNDNPWNCCKLRPLREWMARRNV PFGAPPVCKTPVRLARTPWDKLELDDFACEPHSV  
 VSAVVVTEGDNATVSCRMYGVPI PSSRWTRNDRPLSQTGH SVPVTEGRYTNLTIVSVVAQDGGSYACEL  
 ENRSGSSRSNVTVVVVKRSPQLVLGADRYALPGLIVGVILVLSFCLIFLCGLAIRSKGSPTGSRGVPVSG  
 PLDSAVANIDADPFDRYEKIEMDRDDNNKSMQHRHLHQFPASSSDMNGRPDP PGYAESAATSSGLLHHRHD  
 EHEDYDGLPPIDEPPSSTAPSITDRPTARPSHPTTNVPHRPRILPDDPKDGKKKTYLECNLGEVTLHHV  
 LHKESLPAGHLYTTAAGRQELFNTKNVPDLLDTLVPTKGRRISQTLPRSGISSNSRRNTVYTTPRPSQS  
 PLLLGSRSSGGSNTSRSQLSFDSSISSDHPRLTAGQKSSSYLNLSTASC GGGGDYSGGSSGGYHHQHHP  
 SYYWTPPSLPSSPARERRLPAIPVGRGAGLPTAAAE TPILDPLSSRRRTYSGTGGGGGHHYHNHNSNGGSG  
 NQMHNQLTGSNHSLLMSDGASVTYDYHTAQ LDMFLDEYKTLRKELTKMQRTCDTLRLSNASLASSVAAP  
 DAVDHRSKPEPLAAPAASSSSSSRTTPKSILKNKNQATYVYRPVGERRNSYHQLNPAPDDIYLS

## Pediculus humanus corporis (Body louse)

&gt;PhumpK3

MNALMTFTMMFLLNVIKTGDCPRYCECKWKSGKESVLCTNANMTEIPKQLDSGTQLLDLTGNALLTIGS  
 DEFFNASLLNLQKIFLSKCLRFLEKSSFRKIINLVELDLSYNELHSVPSHTFEFITELELRLNGNP  
 RVLNNAFKMVPRLTKLDLSECRIGYVEIKAFQGLETSLEWLKLDKNKIMNIKPYALVTGNLHGLELSGN  
 PWNCSGLRTLREWMLRQNPYSIPPVCKHPSRLSEKNWDKLDLDEFACVPRIEAESEYKNGEETNVTL  
 SCIVHGIPEPKVRWLKKNHPIANLSTSGGIDGKPKLYSVEIGRETSNLTIHADSQDNGVYVCRAENKAG  
 KSEANITLTVVIKPIVRIWSSRMIAAVGVVSLLEFIIVVGLLTFCAWSSRKRKFDHRTVGGREYDSGYE  
 MNHKKPINYNKIVDYGNHCRSNSTSKTYKITVFNNP

## Daphnia magna (Water flea)

&gt;DmagnaK3

MLESKLARKMRLPCGIKKLAVFYVVLGAWVGSIRCTTVEQSNTCLKPCVCKWKGGKESVSCHQAGWTEVP  
 SSGLESTIQVLDLSGNPLSQLVANEFRRLGLTHLQRVILQRCALRHIDPTAFAGLTNLVELDLSHNVLSS  
 IPTQAFLEHFPRELKLNGLNPLIRLAGHTFASASKLIRLEVANCQLNHIDHKAFHGLELLEWLRLDGNLI  
 EVLPTATLGPLRTLRLGIDLHNPWNCTCPLRPLRSWLAARNMPFSVPPLCLSPGRLRGQSWNRMPLEELA  
 CPPKIHPVDSLQVQVAGQAANLTCHVASNPEASVLWFFADRLIVNLTTPEESPPTVNQVYYLREASDRID  
 RTDKTSTLMLASAREQDSGFYVCQATNRAEKVSANITLLVKSNGIDLAAGQLSRGLTAGLILAI FGMLIL  
 VLLVCCCLCSLKRARMHASLRHRRPSMVMGVPSMNGNSAGGMFDKLDQTDNFLRRQSTASDNYKNHNGSL  
 YKTEDNAEGAGSSHPHEAKVETRFQDKQWLVSQPSKPCLDIKLATNDAEVMTEPIVDGHRQIAMYQNKV  
 KFNAEETNTPRPILKSEKVSSPSPTRNYPDLVDLLPSADYSDSSDVTSNQDEMEILQLKRERSSPPIYPT  
 SRYLQTARQQETTFPGRAVVAVPGNHNRRRLSDWEVNELDDQEHHSMPFYQTQHPVASRRESYDSEL  
 DTAQTELI RRHHSEEFDEDFHRRYAYHTGQLNRFLLEYRALQKRLAQMQDTWGRCLDDIDRSVRHHHRH  
 HHHSNHQPNAQRPLRPILKNRLTLPRQTRRWSCDEQEPEIDILEPELQGSNYEVSSAVDELYYS

## Kek5 ortholog FASTA sequences

### *Drosophila melanogaster* (Fruit fly)

>DmK5

```
MMGNRTERSGRRLGMILLLLGVLVVLMALPPPTAGTTDWMQSCGTCHCQWNSGKKSADCKNKALTKIPQD
MSNEMQVLDFAHNQIPELRREEFLLAGLPNVHKIFLRNCTIQEVHREAFKGLHILIELDLSGNRIRELHP
GTFAGLEKLRNVIINNNEIEVLPNHLFVNLSFLSRIEFRNNRLRQVQLHVFAGTMALS AISLEQNRLSHL
HKETFKDLQKLMHLSLQNAWNCSCELQDFRDFAI SKRLYTPPTDCQEPPLRGKLVSEVPSENFACRPR
ILGSVRSFIEANHDNISLPCRIVGSPRPVNTWVYNKRPLQQYDPRVRVLT SVEQMPEQPSQVLTSELRIV
GVRASDKGAYTCVADNRGGRAEAEFQLLVSGDYAGAVSASDGMGMGAIGAPTIDPQTNMFLIICLIITTL
LLLLLVAVLTTLFWYCRRIKTYQKDDTMMSGDGLISSKMDKTHNGSMLEGSVIMEMQKSLLEVNPFVEKPP
RRTDIESVDGGDDVLEIKKTLDDTVYVANHSRDEEAVSVAMSDTTTTPRSRHTYVDDAYANS LPPDLLA
FPARVPPTSPSMQSSQSNIPDQVIYGIRSPPSLTSPVYTHMTPHGIYGTKTMTAPHNGFMTLQHPKSRNL
ALIATTNSSRQHQHHLHQLQQQQQHHLHHLHQLQQQQQQQQQHPLATTSPFLPAPVVYSPATGVVMKQGYMTI
PRKPRAPSWAPSTSGAAGHGS IQLSEFQSPTSPNPSETGTATTAE LQAE PVYDNLGLRRTTAGGNSTLNLT
KIAGSQGGAGQQYSMRDRPLPATPSLT SVSSATNASKIYEP IHELIQQQQQLQQQQQQQLRGSMDETP
LYGVRQQGITILPGSSISGAGLGHAAYLSPGSGAAVSPSHASSSGDSPKAAKIP PRPPPKPKKKMSVTTT
RSGQGSTSQ LFDDEGEDGTEV
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### *Anopheles gambiae* (Mosquito)

>AgK5

```
MSAWRSTDDTVPLSTKPMPTGRRKPSSWKVGVLVLTLLAMQLLVSPAHTTESDFTKQCSNCKCSWKSGR
KSADCTNQRLPVVPQELSNE LQILDLSHNQIDELPAKTFEAAHQTNLQKLYLRHNSMKRVDRDAFRNLTI
LIELDMANNNLTALEAGVFDDLTKIRV IILNNNQIERIDKNLFYGLQYLT KVHLRSNRLVRIALNSFVNV
PNLSQIELDYNELQALRKESFSGLEKLTSLSLTNNPWNCSTLRSFAEYVLAKNLYTSPTACSVPKALAG
RQWTEIELDDFACPPAIVENRMQFPGAGENATFICKVTGLPLPKIDWLFQKRSFSRHDQRLRVTEAVRTS
PRDQSEVLVSELTIVGVRPSDRGTYVCKATNRGGIDESEQFFDLKADPHPITSATRSKDILQIVLIVVV
VLLFVILSWVLVYCICCRKRRFKKNSAMRENGQMNTKMDKSQNESILDGGSVMVDMQKSLLTEVNPVEK
PPRRADIDAGEKPGSGGGQSSVGGDYDEKHEAKRTLLEETGFVAQDEETASVALSDSNPRSRATFVDDGC
GTNLPPDLLAFPARFPQSPSIQSSMSNIHDGRIYGKSPLASPIYQTGPGTSLGGGASAQMPAGFRTLQHP
KTGRTIAIAAARSNSPFTPAPLIYPPLALKHQGYVTIPRKQRTPSWTPSMSSAVTAELLPAGSAGHSGAT
SPTSPIDLSLGE PVYDNLGLRRTTASGNSTLKLNTGLRGTPLGSTAAGTALTSTPMAKYSMKDRPLPATP
GGQTATPNSSLLGHGGGNYEAIPEALPYGAGQSMVAGGLSGFDLDQSSIYGPVVGTTTNRSKVP PRPPPK
PKKKVVLPAAGGIVTTGDDQSSAPSCQMATAGGDSSGINTSTTNTSTSP LVAEDCDDGTEV
```

### *Plutella xylostella* (Diamondback moth)

>PxK5

```
MAHKYRKKWLKFALLPLALLSTACADFTECQRPCDCRWQSGNKAAICANSSLRAVPANLSNDIQILDLS
NNNLQQLHQEAFKKVGLSNLKKLFLKDCSIESVHKSFTTLAIMIELDLSKNKIQYLHPDTRFGTEKLRL
INLNNNFIDKLEDGLFRNLKYLQKVEVSNNRIVRIGTKAFANLPQLKILRFDGNNLSHMKPETLMGLSNL
SGLDLHNNRWRDCNLQTFRNWVISHNLYTAPTACSEPASLRDKLWNELDSSNFACRPTILEPLPDATVK
SYEENVTLTCKVVGNPTEPVVWRFN SKTIEMRAFGEIRYVISDNTVDLIRWVNLTVLHARYSDRGNYTCI
AENPGGRDEKTLTLYLSKYGSYGTIMGMDTDS FAILVGCLSAFLIIFGSITAVCYYSQRNETKKLIKDD
TRTNGEALIEGSLGSELEKGYPAEVNPLSKPPRKHEAPPSLTSAATEMSELNRTLLDNDSTLASSGENRA
QDAEPLPKMSQETLLVDRLAQEHQTYPPDLLSFPLRGSTQISPAGVDRPKSTQTTNSPIKSPGYGV TALN
PNLNFNRIQLPSTSQGSYSKGGYVTLPRRPRMPNWLPEGNYPQVFSTLNGVI PYDNFGMKLFGNGSNYYSL
NKSELDVMTGSSRGVNPVNPYSVPQGV EACDEIEPAPSPAPGTPHATIPRSSISSPNIHNQLLALQAMSMNH
GRGTRVPMSSSEPRPLKVILTPPENESLIKNTSRELRRMGNGNVTGTLGRKTV PKPPPKPRKRSSNEMKE
PFLNLSGETATQV
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**Tribolium castaneum (Flour beetle)**

&gt;TcKeK5

MRADTHTFYMKMAHRLIVLMVLSLASANNDDWEKKCNKCKCVWSNGKRTADCTNRDFSEIPKDLSEIR  
 EIDFSNNPLHYLGREVFVNAELRDIHKLRFVNCSISAMDDTAFKGLVLLIELDLSRNSIGLLTSKIFEEN  
 RKLRLSLSHNKVKRLDQGLFYNMTHLQRLSLDHNEIEYINDSAFFLLPALQHLNLAYNKLTVMSSDFLD  
 NFPKIVSLNLESNPWICDRLQEFNRQTKRANLITTQTQCAEPPLKGRWLTDNIVFACVPQIVEPLPS  
 THIEATTSNITLTCTRVLGDPQPDVDWVSNRIIDRDPRLNTQRFITSKRKVG DYTWNNLTITNVNYRDKG  
 EYKCVAKNPGGSDEKNVSLIVSSIGGIGGGGGLAFGATLPLVIALSIGGVIALVVILILVCCCCRKSTHG  
 MATKRRDLQDSSDECIRLHGQPDMEKALITDVNPMKPPRICSVPPSVNSGGTEVSEAKKNLLDSDSVFA  
 GDDESRSFDFDMPPYRKSQTLLPEPDYRGNHTYPPDLLPFPPRMCQVSPAGSSASTVADTSRLPAHHGPQS  
 PLHSPLYDSNTLYRTL PYRSQS PFVGP PARVPRQGYVTIPRRPRQRWSTDTPTTSDVEEPLYDNLGLRT  
 TVDGSSALSLNKLG EATTPKSI RLFPMSPSSCDPIAENEPPPAAPKLSPSSTQWAKANAEALRSPDNRN  
 SLPDGGKVKVAPVPPPKPKKRTSTGPLFEDEGEDGTEV

**Apis mellifera (Honeybee)**

&gt;AmKeK5

MELRTAKLLLYSTLMVVVCWSQEYWTAQCASSCKCRWISGKKAAECIRQNL SQIPVGLSPEIQNF DLTGN  
 RITYLMHESFSRVHLVNLQKLVLRKCEIELIHTDAFNGLKIVIEIDL SANNIGTLYPGT FEETQRLRVLL  
 LNDNKLKVL ENGLFHN LKYLQKVELSNNELE RIDDKTFRNLPELRS LTL DANNLSALKVQS FETLPKLG S  
 LELHNNPWNCNCR LKRFRDWTIEKKLYTKPTTCQQPESLAGKMWDEISSDEFACRPEIFTIGPSVRVEVG  
 KGNVTFWCRASGIPRPQLSWVHRSRVINNHTRRHNGEKIYILKSNHEWLNLTIPDVAHSDKGDYVCLAKS  
 PGGNTEKNVT LTIAGDALGGKDNIISLPLALGLGV TALLLLIVTVTLCVCYCRRRRIRHDEKSLEAASME  
 HHGLGEQEKS LITTINPVVKPPRRYEAPSVTSHGTEMTELNRTLLDND SVFADGIGGGV GSGVIGGVGDD  
 EREERATPELESGTGTL CRGGGGSYRQYPPDLLAFSGGRGASPTSQASTAPDNTRLPSQHATPATAAFGS  
 PSNNQYPAAFKTLPHNRSVTPYGITSS TIAPVMPRHGYVTIPRRPRAPSWSSGPPTSPTDGLEPVYDNLG  
 LRTTADGSSVLSLNK SPEPLSTMRNRPLPGTPGSHYGTIQRSTPNILTSSPLDRSAPEGAAEWPSKIAD E  
 STDSTNQLLGQQTQQQQQQQQQQQQSGSSSTLN RKVPPRPPPKPKKKSTNGPLYEDEGEDGTEV

**Habropoda laboriosa (Southeastern blueberry bee)**

&gt;H1K5

MELRTANLLLYSALVVVCWSQEDWTAQCSSSCKCRWISGKKTAECINQNLTEIPSSLSQEIQNF DLQGN  
 RIKHLTHDSFSAVSLVNLQRLVLRKCEIESIHT EAFNGLKIVIEIDLSSNNIRTLYPGTFAETQRLRMLV  
 LNDNKLKVL ENGLFRDLVFLQTVKLAN NRLEKIQNKT FVNLPGLKVLTL DGNNLSTLGVS FESLPMLGS  
 LELRNNPWNCNCH LKRFRDWTIERKLYTHPTTCQQPLSLVGKMWDEVHSDEFACRPEIFTIGPDVKVEVG  
 KGNVTLWCKASGVPRPQLYWVHRSRILNNHTRRHNGEKNYVLRLSHDWLNLTIPDATPSDKGDYVCVAKS  
 PGGNTEKNVT LVIAGDVIGGNDNMFPLQIVLLLGLSALLVTIFAATLCVCYCRRRRTRHDEKSLEAATME  
 HHGLGEQEKS LITAINPVVKPPRRYEAPSVTSHGTEMTELNRTLLDND SVFADGIGGGV GGVIGGVGDD  
 EREERATPELESGTGTL CRGGTGSYRQYPPDLLAFSGGRGASPTSQASTAPDNTRLPSQHATPTTAAGS  
 PSNQYPAAQFKTLPHNRSVTPYGIASSTIAPVMPRHGYVTIPRRPRAPSWSSGPPTSPTDGLEPVYDNLG  
 LRTTADGSSVLSLNK SPEPLSSMRNRPLPGTPNSHYGTIQRSTPNILTSSPLDRAAPEGAAEWPTKLAD E  
 STTDSNHLLSQQQQPQQQSSASNSNTLGRKVP PRPPPKPKKKSTNGPLYEDEGEDGTEV

**Acromyrmex echinator (New world ants)**

&gt;AechinK5 (a)

MQCLSTCKCKWVSGKKTAECIKQDLTQVPGDLSPEIQSLDLTGNRITHLARNAFSRVNLVNLHKLRLDC  
 GIELINKDAFSDLKIIIEIDLSGNNIHSLSHPSVFYETQKLRVLLLNQNKLVLDNGLFFNLTFQKVTLS  
 DNRLERIEEQAFRNLPNLHSLALDGNFSTLQQLQSFESLPKLGSLQNNPWNCNCHLKKFRDWAIQRKL  
 YTQPTTCQQPLHMIGKMWDEVSSDDFACRPKITNIEPSNKIEAAKGDVTISCRATGIPRPELSWTYRNL  
 ITNSSKHGNDKNYLLLENHDWNLNTIIDALPADKGDYICHAKSPGGEAEKNVTVSIMGDALSGRENFISL  
 PLAIGLGTALCLLIVTVVLCVCYCRRRHTRHDEKGLEAASLEHHGLGEQEKS LITINPVVKPPRRYE  
 PSVTSHTDGVGSGVVGGVGGVGDDEKEHERATPELDGSGNGGVVGGGGGTLPRGGAGYHHRQYPPDLIA  
 FSGGRGASPTSQASTAPDSTRLPSQQMIAPAAAATTAATASSYGSPPSGQYHPAAFKTLPHSRSATPYSL  
 GPSSSSSPLAPVLPRLHGYVTIPRRPRAPSWSSAPPTSPTDALEPVYDNLGLRTTADGSSMSLNLKSPESV  
 ASSMRGRPLPGTPGGSHYGSIQRSTPNILTSNPLDRVAPEGA AEWPLKLTDESMDGGHLLLTQQQQQQQA  
 AASNTLGRKVP PRPPPKPKKK SANGPT LYEDEGEDGTEV

&gt;AechinK5 (b)

MIPRTASRWLLCVALTVALCQQEDWMQCLSTCKCKWVSGKKTAECIKQDLTQVPGDLSPEIQSLDLTGN  
 RITHLARNAFSRVNLVNLHKLRLDCGIELINKDAFSDLKIIIEIDLSGNNIHSLSHPSVFYETQKLRVLL  
 LNQNKLVLDNGLFFNLTFQKVTLS DNRLERIEEQAFRNLPNLHSLALDGNFSTLQQLQSFESLPKLG  
 LELQNNPWNCNCHLKKFRDWAIQRKLYTQPTTCQQPLHMIGKMWDEVSSDDFACRPKITNIEPSNKIEAA  
 KGDVTISCRATGIPRPELSWTYRNLITNSSKHGNDKNYLLLENHDWNLNTIIDALPADKGDYICHAKSP  
 GGEAEKNVTVSIMGDALSGRENFISL PLAIGLGTALCLLIVTVVLCVCYCRRRHTRHDEKGLEAASLEH  
 HGLGEQEKS LITINPVVKPPRRYEAPSVTSHSTXLLDNDVSFADGVGSGVVGGVGGVGDDEKEHERAT  
 PELDGSNGGVVGGGGGTLPRGGAGYHHRQYPPDLIAFSGGRGASPTSQASTAPDSTRLPSQQMIAPAAA  
 ATTAATASSYGSPPSGQYHPAAFKTLPHSRSATPYSLGPSSSSSPLAPVLPRLHGYVTIPRRPRAPSWSSA  
 PPTSPTDALEPVYDNLGLRTTADGSSMSLNLKSPESVASSMRGRPLPGTPGGSHYGSIQRSTPNILTSN  
 PLDRVAPEGA AEWPLKLTDESMDGGHLLLTQQQQQQQAAASNTLGRKVP PRPPPKPKKK SANGPT LYEDEG  
 EDGTEV

**Nasonia vitripennis (Pteromalid parasitoid wasps)**

&gt;NvitriK5

MSRMRGKPRTLQLVLSLALLASNCVGQEDWNCVPSCCKI WVSGKKTAECKRQNLTEIPESLSMEIQHLD  
 LTGNFISHLPERAFTRVSLDNLQKLVLRECGIKAVNVEAFSGLRIVIEIDMSANRIRQLHRGT FNQTERL  
 RVLLLNQNRLERLDDEL FHNLFQKVELSDNHLMRVGLSTFHNLPGLLT LTLDGNNLQHLNLKSF DNLT  
 KLSSLELRKNPWNCCHLQEFRDWT LN RKLYTRPTSCEQPQALAGRMWDEIESEEFACAPRIESIGAMQL  
 GDAGSGRAQLWCRAQAKPRPQISWVHRQ RVLGNGTKRHTSSDKSYILQVADDWANLTIPELLLSDKGEYI  
 CIAKNFGGSVERNVSLLVLGEGGSRGEGMLGLPLAIGLGIIAFLFLLVALTFCLCYCRRQRSHHDEKSAE  
 AASLDHHGLGEQEKS LITAINPVVKPPRRYEAPSVTSHGTEMTELNRTLLDNESVFADGVGSVVGVLANG  
 LNDEERGRATPELEAVMSGHNVANSVHATPGGNMGGVSGLSNQAGSVISGLGTLSRNTTPYRQYPPDL  
 LAFSGGRNSSPTSQASTAPDSSRLPSQHPPPHQVQLGFGSPSSPVATGLVIAAYTPIGFKTLPHPARASS  
 ATPYSLGHHHPSMARHGYGTIPRRPRAPSWSSGPPTSPTEREIQEPVYDNLGLRTTADGSSALS LNKSP  
 PKGFSMRGRPLPATPSSPSPLSNGQLTLPRAPRGPPALAHQLNRSAPEGAPEWPLDLVAEHESQPTSPS  
 ARKVP PRPPPKPKKK NPNGP LYEDEGEDGTEV

**Linepithema humile (Argentine ant)**

&gt;LhumK5

MGEGERGFLAMGPRTASRWLLCAALMVALCQGQEDWDGGHCQPMCKCKWVSGKKTAECKQNLTEVPKNL  
 SSEIQYLDLTGNRITHLIYKAFNNSNVTLVNLHKLSLRECGIESIHTGAFKDLKIIIEIDLSNNNIRTLO  
 PGTFHDTQRLRVLLLNQNKLELQNGLFFNLTLFQKVSLSDNILERIGERVFRELPGLHSLALNGNNFTT  
 LQLHSFESLPKLGSLLELQNNPWNCNCHLKRFRDWTIERKLYTKPTTCQKPTTMAGKMWDEVTSDEFACRP  
 KIVAIGPASKIEMGKGDVTLTCKASGIPRPQLAWGHRARLINSITKRPNSDRGYILTSQDWLNLITIVDL  
 TPSDKGDYVCHAKSTGGESERNVTTLTVG DALGGRDNFISLP **IAIGLGVSA**CLLLIVT**VALCV**CYCRHR  
 TRDDEKGLEAASLEHHGEQEKS LITINP **VVKPPRR**YEAPSVTSHGTEMTELNRTLNDNSVFADGVVGS  
 GVVGGVGGSIGDDEKDERATPELGRGSGTLPRGTTGYHHRQYPXDLLAFSGGRGASPTSQASTAPDNT  
 RLPNQHASAMTPAATSLYGSPSSQFHPAAFKTLPHSRSATPYGLGPSSSSSPIAPVLP RHGYVTI **PRRP**  
**RAPSW**SSGPPTSPTVELE **PVYDNLGLRTTADGSSKLSLNK**SPEPALSMRGRPLPSTPGTSHYGTIQRSTP  
 NILAGSPLDRAAPEGAAEWPIKLADQSLDDGHSLLAQPPQPPQASASNTLGRKIP **PRPPPKPKK**SANGP  
**LYEDEGEDGTEV**

**Cimex lectularius (Bed bug)**

&gt;C1K5

**MSPI**SFIGLAT**FLIFTTETHSTA**SDWTSTCLKCKCKWVSGKKTADCSYSHHTAVPSLSSEVQHLDLNGNK  
 IHSLSDFSFKSVGLVHLHKLYLKNCGIQELHKDAFKGLQILIELDLSENKIHILHPGTFQGNRYRLRIYM  
 SRNPIQRLEDGLFTNLTLFQTVDMSQCLISHISSKTFVNVSNLHTFILNGNRLSHMKLSVVDKLYKLRSL  
 ELKNNPWRCDCHLKAFRDWVVDHKLYSQPTFCHEPQSLENKIWTDIESEAFACKPQILYPNVGTTVVADG  
 DEVLSLSCRVTGNPTPEVHWVYNARIITNNTRTKYGDLYLRSSGEINRWVNVTVTRVRPQDRGEFTCVA  
 KSFGGVDERNITLIVKSSNGGYIGSAGIANS **WP**IVIGLTTGLTAVFLIVII **LCCCC**CRKRKNLLPGKKSP  
 VNGVSPNGDITHHIGAAEQEKSLLAVNP **VQKPPRR**YEVQISPTAGTEMSELNRKLLDDGSVIAHSILGDE  
 DRSSSEIETTPQRLRDKLESET **YPPDLI**AFQGRGHTASPAGSSTSTALDPASRHTLHLGHQSPLHSPIYN  
 GFGMLPYRSRQSPFSPAAPIILPCQGYVTIPRRPRIPSWSSAPTSLLEDPLSPIKAE **PVYDNLGPRTTV**  
**DGSSILSLN**KAGTDTNPRRKTPSIPSSFSPEEKEGGILRPLPSPLSPDDKRYWRNRSGDGILKRVGSAD  
 MPIETISKAKVA **PKPPPKPKSNVP** **LYEDEGEDGTEV**

**Halyomorpha halys (Brown marmorated stink bug)**

&gt;HhK5

**MSDIAKTAVFIVFLGVAVVQP**DDWTLCPPGCKCKWVSGRKTADCKKADLRKIPETFKSEIQSLDLSENKL  
 DHLPDEAFKSVGLVNLHKVFLRECNIEIHKDTFKGLGILVEVDLSANRIHVLHPGTFRDNVRLRIIFYFN  
 GNPIERIEANLFVNLLHLQTVEMGDCKITEIDDKAFRNVSNLLNLKLNANKLTHLKLSTFTDLLKLRSLV  
 LQDNPWNCNCHLRDFRNWVIERNLYAVPTSCTQPEHLRGKMWNVINAKDFACKPKILWPPIGTSVSADNR  
 DVSLGCKVTGNPMPEVHWVHNSKIIISDNTKVKYSVNRYTIKTSLVDSSEESDRWVNLTVNQVSLQDKGQF  
 QCVAKSPGGLDERNVTLVYADNDGFIGVGSVND **WPLI**IGLCTGMAALLII **ILLCCWYCC**RHKQSQSK  
 KSSSAMPANGDVMHRITPSNEQEKSLLTVNP **VQKPPRR**YEAQINNDAVEISELNRKLLDESSLQGNCTCPT  
 EEDNSVECLDIRQEGANVEKPVSEA **HPPDLL**SFPSRSHNISPASSSTSNGFDNLSRASLYPAMQQSILNP  
 SVHYNCGTLPYRSRSHSPFSPTAPIVLPRQGYVTIPRRPRVPSWSSAPTSLDDPLSPIKAE **PVYDNLGP**  
**RTTADGSSVLSLNK**SFSENPRGRNSSSNVPNYFHFEGGLRPSPLSPERENRADGILKRTCSADGDIGP  
 IRSKVA **PKPPPKPKKDGP** **LFEDEGEDGTEV**

**Acyrtosiphon pisum (Pea aphid)**

&gt;ApK5

MIGLYTLIALLLWAPIASHSA SELDWVTVCNQOTCRCKWVSGQKMAECINSSLT SIPKTL SNEVQVLDLT  
 NNKILEINKDAFREVG LINLHKLIARNCSI ELVDKDAFRGLEILIELDLSNNNIHVLHPTTFRDPFRLRK  
 IYLNHNLIQRLRNGLF SNMSFLQTVELNSCLITDIEPKTFYNITKFNSLELSGNQLANMKAEVLYSVPSL  
 MNLGITNNPWRCDCKLRPFMNLVMNKNLYIKTASCTEPPRLNKLWGD IKPDDFACQPIIEYPAQSSTFQ  
 LDDDELMTIGCKINGEPMPSVQWVFNNRPI SNYSHGDYKFTVYESVDNTMAKWINLTVSRSLIGKSEFK  
 CIAQNPAGLEERKITVIVQSGTKGILGSTVSVKESLP I I IGLVAGIFI I I ILLIIVCCLCCYRRRPASGG  
 VLSKKSHANGFSNGDVPNHNNHVTSLVSEPSEQQK SLLAVVNPVQKPPRRYESSPTGTEMTELKRNLDE  
 TSVSGDADEQFYGESGDELANI IDSSGISNGVGNRSYRKGT HPPDLLAFPRGSGGGGGHSSPAGSVVST  
 VPSFQSPLHSPIYSGTLPYNRSQSPFSSRPAQPPA GYVTIPRRPRVPSWASSTGVGGTSASTPTAGHVDD  
 PLGVGRICE PVYDNLGPRTTADGSSVLSLTKAVADSAAVHRPKPQYSQTLPHKTKLHSGHRPRFTADDAQ  
 DARRVPSPAPRSPDKTLP SQVSGLPQHNALPPNYSPLVEMDARNRSSWAPSRVGTPESGVLKPASQTSVK  
 RKVP PKPPPKPKMKGGP LFEDEGEDGTEV

**Pediculus humanus corporis (Body louse)**

&gt;PhumpK5

MDFHLNII FTTFLVVFAGSDWTTNCPPPCKCIWSYGKKTAECDAGFNSVPNTLSPELQVININNNNL  
 HILPSQAFKSVNLFNLHKVFMKNCSI ELIDKNALSGMVVLEIDLSNNNIKNLHRDLFRECEKVVREVRFS  
 NNPIQKLDDGLFSNLEFLQTVDFTGCKLHEIGSQVFWNVPALTTLELKRNFYTLQLSSVEHLHKLKNFG  
 LTDNPWNCNCKLRPLRNWVIQRNLYAIPTSCKEPLQMKDVLWNEVNDPNEFACKPKIISLTREPHGILAC  
 LVEGDPMPVTVTWSFNKLVNTNYSFLASDFVQESTVNGELKWSNLT LRNTRGGKDNGEYKCVAKSYGGST  
 ELGREVKYDPYLDGDSYGGSSDGTYDN WLLLAGSIIGALLLIAIVLFVKCYVCKRYTRKNNRNKKDKESV  
 NGSVTHVIDSEEKNLINVINPLQKPPRTANASANSSETEFHESNVSQYNDKGSSD

**Daphnia magna (Water flea)**

&gt;DmagnaK5/6

MATMTIMLKAVLMLFFCLLAMLAGPVTA DWTATCTAGCTCKWADGKKVAECPGAGFTTIPENLSPEIQVL  
 DLRGNLGLVLNRAFSSVGLLNLQRIFLRNCSLT LVEKD AFHDLNIMVEVDLSHNQLHRFHPETFTNNEK  
 LRSLSLSHNPLEKLEAHQFPPLPNLRSLELVKCQLEMVDKKA FMHLSKLET LKLSANKFTNLKPEVFLPL  
 NKLKSLDLQDNPWNCDCRLLALRDYLSEANLNSTLTLC TEPEHLKGKPWSRLAAEDFACKPLIDVNEPHV  
 EGR LGFDVTFSCRVS GNPPPTIWWVLQNRQIVNTTASQSEQFVIRQSTHPTKINPSIASLHAEPQQPEF  
 EYWSNLTLRRISEQDAGQYRCIARNKGGQVDANVSLQTPPAPVTILIEGETGLMSYTTAITLAVVGALVL  
 LVGLVLLIVCLVRRVPKRKQPQPRDGSAAKLNGSAKTVNGNGSIAAVSEQEKSLLDIEMDQHTSLQNAST  
 DGYHAVSQTDIDAQQHMQLQLRHQQLOQQQQQQQMRMMHGSNTYIPGDRYDTSRVPESLTRHLMMLDG  
 CQVQQNPDGSFY PDLLDIPHRGARGGGSPSTHSGASNETANQQQQHMMSTLSAAQLAGHPSYGVIGLHP  
 PLQFTDSSSTTSSTAVLLPVGARPGYVTLPRRPRPRMP SWASSPPPMSSSSPGPGSLPAEEPQQ PLYDTI  
 GPRVTADGSSTSALS LNKIAGLTPNPSSGLSPRMQSSTLSRGHKISLPAYYVPIEEVDIPPPSPLVQQR  
 DHQQSTPNILSNGQYEDHHHHHHRMGREPVLYGFNNNNNSSTPIRRADDSETQHLLNDSSTPTSANTSYS  
 NAAPEVISPIPDFRTAGSRASVSSLSSNTGLRRKIAPAVPPKPPGSIVVARPASVVPYHDDVASPAKVAP  
 KPPPKPKRLSTTGDSVKLEDLENGGDSGGQAAYEDEGEDGTEV

## Kek6 ortholog FASTA sequences

*Drosophila melanogaster* (Fruit fly)

>DmK6

MHRSMDRRRSRTPRTLPCWILLCLVAWTVADDWSLSCASNCTCKWTNGKKSALCSSLQLTTIPNTLSTELQVLVLNDNHI PYLNREEFSTLGLNLQRIYLLKKSEVQYIHKESFRNLKILVEIDLSDNKLMLDKDTFMGNDRLRILYLN GNPLKRLAAYQFPILPHLR TLDMDCLISYIDPMSLANLNLLEFLNLKNNLLESLS EYVFQHMANLKTLSLEENPWQCNCCKLRKFRGWYVNSRLSSVSLVCKGPPAQKDRTWDSVDDELFGC PPRVEIFNNEEVQNIDIGSNTTF SCLVYGDPLPEVAWELNGKILDNDNVLFESIASDKLWSNLT VFNVTSLDAGTYACTGSNSIGSMTQNI SIYLSEIVQH VLEKTPETFWYFGLIMGIFGT VFL LISISFVVC LCKRTRQHRHANKAGVKSSVSFNDQEKLLDSSVT TTTNDRGDSYGIDNQPTSIGMNKGDSAGMGFNQIEIHAVESH RHGSM LVQQQPQQQVAGGGGMRQQLMQVKDSTCGMMSVPTSMAGHAHSHPAQISEEFPLNVGVFP PPFECFSNIVPNPAFGGNI F IRVSVTQDMLD GADLNMYPDLLNIPKRMQDVQESGAGAVAVPEGQFATLPRHTARRGILKKDTS LQQQQQQHQQQHQHQQQQQQIQQQQHQQ LQQQHQP SGLYTHDEIVTYNLEASGYDPHQSGYHSNAMELPPPPPPAVTAVVQCHHPSPNNCASCINNAPPPSACQSPPEVTPMRPLDSSAYPKYDNMGR RITASGGLGGSNLSLHDEERYENETLFGQAESQTKGMPEQSQDLHQPEVTQGDQKGGGPGEFVSL

*Anopheles gambiae* (Mosquito)

>AgK6

MPLLQRTKPLKMIQLYCTVLFLLLSTALCADWSASCPQNCTCKWSNGKKSALCNGADLSAVPSNLSTEIQVLVLNDN NIPYLNREEFTTLGLVNLQKIHLKHSRVKYLHREAFKNL KILVEVDLSENEIETLDKQTFAGN NRLRIINLYDNPIKMLVAEQFPVLPYLRNIDLHGCQLRYVAETA FSNLDLLEFLDLSKNRLES LPHHVFNHMKNLKT LILEENWWNC DCHLRDFRNWYLNSSLNRRSLICQRPYALKGLSWEYLETEQFGC MPTVEIYRD EYEIEDLGTNITYKCAVSGDPEPNVRWDMNGKDVDQDNAI IETERHVAFDGSVTLWSNLTILNVTNNDSGFYTCTAQNRI GLASKNFSLVLP EVVERV I I KTPETFWYFGLILGIFGTIFGLLALS VVVC L V KRKLRMRRRRKTIKNSVSFNDQEKLLDLSITTNERQEFASDVVTPSTKTDSTIAMEPVQITIESIATSKREEYPLNVGVFP PPFECTQM IANPTISNIYISVSVTQDPLEGGPADVNMYPDLLNIPNRHQKGPPKMPVSVTSYATLPRKTATVGGGPRCSITSGHSSSSGGSSGAGKPSVGIGPPQVGSPLSCTPSLLAAAEIPLTEGIVNYAT TALRDDSGCEMSSSSPVPSMCAECSKVLKASGGTFAPKYGTTSR TLPGLGGDLATSGPSSSNSSGSKCEKPLACLKYDNMGRRYTASGNSTLSLPDELKPAGGPGPAGAA FVIKQQDIETIVEQDDQPGGAPDGTEAPLPQQPPPPSAVVAGGTS DQEAQRGLYVVGNDFVSL

*Plutella xylostella* (Diamondback moth)

>PxK6

MSMRAAWARWYVIVVLSSCAARTASDWLDCAQIPACRCKWSSGKKTASCASADLRRPPALASDIQVLDLHDNPLRTL PQEVFSTIGLLNLQRVNLRGTKLRSIHPDAFLELRILIEVDLADNDLSNIPKDI FRGNERLRLVVL SNNPLTTLVADQFP SPLPHLRMLLLDGCR LKLIHTNALRN LKALETIDLRRNQLTFLRLITFALPALKT LSLSGNPWRDCRLREFKDWFLDSTLGTEDLVCEPSTKSGSKWRSVPSESMVCAPEVRSSTLVIRTEVGMPTTFGCWVHGVPKPQVTWLFEGVDVHNSTLDS DLEEA ESEVDIDDS EDKVP GSVRWNVTVLNV TSSAAGEWTCIAKSSAGEARAVISLVLP RYQTATARTDPGIPQVIGVVF GALGVLATL GFLGAVACWHMRRRTVPASRSFTDQEKRLLDASVVVSCDRSIAEMASPCDFEMTERSISEEPRGCGFDPVHITIEGTPGAFPPPPAEFAVPVPYGNIFISVQVAGHGEGPGGKYPDLLSGGATLPRRSRTCCA PVYDNMGP RVTATGSSTWSLPGA GAEGVDNTETPVLTLPPPPPEFVSL

*Tribolium castaneum* (Flour beetle)

&gt;TcKeK6

MAAVILLLV~~TA~~MALAAAPDWTDCPSPCRCKWSSGKKTAVCKGGGFSAPVDTLDGEMQVLDLSGNYISRLGN  
 DAFKSVGLLNLQRI~~FL~~ATAGIQEVHKDAFRDLTILVEVDLSHNQIKSLHPETFHGNERLRVLYLNGNPLR  
 RL~~VQEQFPQLPHLRILELDGCQLEYVHKNAFVHLSVLETLSLRQNLLRNLSEEVFMNFAHLKTLVLEGNP~~  
 WKCDCELGRGFRDWFLLSKLSNSVSLTCTQPERLEGK~~LWENVLSEEFACPPRVSVFPQSQVQAEAGGNVSFG~~  
 CHVTGDPEPQVSWLYEGYPINHTWLVIQAE~~EGLLDKWANISVYNVSDTDTGVYTCTARNILDSVSLNVTL~~  
 VLPEVVTATTVSKSEGG~~FLWWGLLVALVTLGSVGLGASIAVCCLRGRKTQKRMKASVSFTEQEKKLLDVS~~  
~~IATTT~~DRGTGSCEVLGPEMELDPPVHITIESEPLPLA~~VFPPPPPEFGNVVPSAYGNIFISVSVSRDPSDAS~~  
 RCPDLLDLPHRAKPVYHGMATLPRR~~P~~CAAPHYDNMGPRVTAAGSSTLSLPGVPPPPPPPPPPQLTPEFVS  
 L

*Apis mellifera* (Honeybee)

&gt;AmKeK6

MIGTRHHPLRGRILLALF~~FLLGTLALLSKAAA~~FDPDWTDCPAVCRCKWTS~~GKKSALCPDAGLTSLPASLDP~~  
 DMQVLDLSGNKIPALQSEIFKRSGLLNLQRVFLRNAGIH~~KIHADSFRDMRILVEIDLSDNHVEMLEPDTF~~  
 LGNERLRILILSGNPLTRLRSHQF~~PLLQHLRNLELQRC~~SLSEIHGEAFVYLTGLESRLDKNVLEYLDVS  
 VISNLPRLKTLTLDGNRWSCDCRLRDFRTWLI~~PNGPSKLYSVPQACSSPMRLEGRKWEDVKPVEFACEPE~~  
 VFVLASSIQEETNGNLSLACLATGDPEPEV~~VWQLNGGPNATKLTEQIYTGTYVAYATSDVDTISSYNER~~  
 SSPGRLVDRWNNLTVYNASDGDAGEYSCFAKNIAGLARDTVSVAIPRVYTAPTLSQSDN~~WLLWVSLAGGG~~  
 AAALCASISAVLLALCVCGGTR~~ROTAREKVKLQSSTSFGDQEKKLLDLSVTTTT~~TPGNSNDRGSGHGSIV  
 EGCSTGDLELAERGSICDPMSAATVTVERLRPEMSGGPAMRTVPCV~~FPPPPPEFTSGVLPPGIFGNIFIS~~  
 VAVPQDASDRCY~~PDLLDIPVH~~ATGGAAGKTALPPASSV~~SSFATLPRRALRSSDLC~~SPYDNMGPRVTANGS  
 SAFSLTDV~~DLRLSPPPPP~~RRIQPPHEFVSL

*Habropoda laboriosa* (Southeastern blueberry bee)

&gt;HlK6

MIGIRHHPLRGRVLLALF~~FLLGTFALLSRAAA~~FDPDWTDCPAVCRCKWTS~~GKKSALCPDAGLTSLPASLDP~~  
 DMQVLDLSGNKIPALQSEIFKRSGLLNLQRVFLRNAGIH~~QIHADSFRDMRILVEIDLSDNHVKALEPGTF~~  
 LGNERLRILILSGNPLNSLRTHQF~~PVLQHLRNLELQRC~~SLTKIHGEAFVHLNGLESRLDQNELEYLEVS  
 VISSVPRLKTLTLDGNQWSCDCRLRDFRSWLIPSRPSKLYSVPQVCSSPLRLEGRKWEDVKPVEFACEPE  
 VFVLANSIQEETNGNLSLACLATGDPEPEV~~VWQLNGGPNATKLT~~DQTYSGTYVAYATSDMTYNERSTSS  
 SRLIDRWNNLTVYNASDGDAGEYSCFAKNIAGLARDTVNVAIPRVYTAPTLSQSDN~~WLLWMSLAGGGAAA~~  
 LCASISAVLLALCVCGGT~~RRHSAREKVKLQNSTSFGDQEKKLLDLSVTTTT~~PGNSNDRGSGHGSIVEACS  
 TGDLELAERGSICDPMAAATVTVERLRPEVSSSSISAMRSVPCAAI~~FPPPPPEFTSGVLPA~~GIFGNIFIS  
 VSV~~PQDSSDRCY~~~~PDLLDIPVH~~GTSGVLNKTTSALPAASSV~~SSFATLPRRALRSSDLC~~SPYDNMGPRVTAN  
 GSSAFSLTDV~~DLRLSPPPPP~~RRIQPPHEFVSL

*Acromyrmex echinator* (New world ant)

&gt;AechinK6

MLVTRPHPLGGRILLALF~~LTTGCFALLSRAAA~~FDPDWTDCPAVCRCKWTS~~GKKSALCPDAGLTSLPASLDP~~  
 DMQVLDLSGNKIPALKEEIFKLAGLVNLQRVFLRNAGIY~~NIHANSFKDMRILIEIDLSDNHVTVLKPD~~TF  
 LGNERLRILILSGNPLGTLRNLQF~~PVLQHLRNLELQRC~~SLTEVHGQAFARLTGLEFLKLDTNQLEYLESS  
 VISGLSRLKTLTLDGNQWRCDCRLRDFRTWLI~~P~~DPVPSKLYSVPQICSGPPRLEGRRWEDVKPTEFACEPK  
 VFVLASSIQEETNGNLSLACRTSGDPEPEV~~VWQLNGGPNATKSTDQPYMGTLVIYATSEAGIP~~SNDKSA  
 SRTVGD~~WSNLTVYNASDS~~DAGEYACFAKNIAGLARDTVSVAIPRVYTAPTLSQSDN~~WLLWVSLAGGGAA~~  
 AACASISAVLLVLCLCGGN~~RRHSKREKVKLQSSSSFGDQEKKLLDLSVTTTT~~TPGNSNDRGSGHGSIGEA  
 CSTGDLELAERSSICDPMAAAAVTVERLRPADNSVNTIRAVPCTATATAGI~~FPPPPPEFTTGVLPA~~GIFG  
 NIFISVSLPQDASSERCY~~PDLLDIPVH~~AVSGATTVTSTGGKTAALPSAAAINV~~SSFATLPRRALR~~STEVA  
 AGSPYDNMGPRITANGSSAFSLTDMTMDMLRLSPPPPPRRIQPPHEFVSL

*Nasonia vitripennis* (Pteromalid parasitoid wasps)

&gt;NvitrK6

MTRSQRVLALFVLVASWRALLSRAAAFPDWTDCPAVCRCRWTSKGKSAFCPDAGLTSLPASLDPDMQVLD  
 LSGNQIPDLQAETFKHAGLLNLQRVFLRNAGIRKIHADAFKDMRILIEVDLSDNHVLSLEPHTFTGNERL  
 KLLVLSGNPLGQLKPSQFPKLQHLKNLELQRCALKRVHALAFQWLPALETLSLDNNELEYLEATTLPAPLK  
 HLKTLGLDNNPWSCDCHLRDFSRLLVTNMSRLYSVSQSCISPALKQGRRWEDVAPKEFACLPKLPANA  
 IQEEMNGNVSLACFVTGDPAPEVSWHLNGVPINGTKRIGDDVGPQGGLWVWSDSIKTKNNLVERWRNLTI  
 YNASDVDAGEYTCHAENIAGLVRDVTVSI PRVFTAPTLSQADNWLLWLSLAGGGTVALCVSASAVLLAM  
 CLCGGARRRSRRAKVKLQASASFGDQEKLLDLSVTTTATTTTSQQHSQHNQSQSRQQQAPAPIQADLNHC  
 QPEFELELEPRLIEEQRLVGQSSASVTIERLRLOPDACGSPPPSSNSSSVICPVAVAAAAAARAQLPA  
 NIYISVSLGNGAPNQEAAPVAVAAAAASLQAAELQVHERCYPDLLDIGLSSFATLPRRCRRPGELGSPYDN  
 MGPRVTATGSSTFSLVEQPEPSIAVAAPLIQPPPEFVSL

*Linepithema humile* (Argentine ant)

&gt;LhumK6

MLVTRPHPLGGRILLALFLLTGC FALLSRAAAFPDWTDCPAVCRCKWTSKGXSALCPDAGLTSLPASLDP  
 DMQVLDLSGNKIPELQAEIFKRAGLVNLQRVFLRNAGIYSIHADSFKDMRILIEIDLSDNHVTSLEPDTF  
 LGNERLRILILSGNPLGLTRNTQFPALQHLRNLELQRCSLTEIHGQAFSRLTGLEFLKLDGNHLEYLEAS  
 VISNLSRLKTLTLEGNQWRDCRLRGFRTWLIPEAPSKLYSVPQICSGPQRLEGRRWEDVKPVEFACEPE  
 VFVLASSIQEETNGNLSLACLATGDPEPEVWQQLNGGPVNVTKSTDQSYTGTLVVYTTSEIGSVTSDKSA  
 SSKIVPDRWSNMTVYNASDSDAGEYVCFARNIAGVARDAVNVAIPRVYTAPTLSQSDNWLLWVSLAGGA  
 AAACASISAVMLALCLCGGSRHRSKREKIKLQGSSEFGDQEKLLDLSVTTTTPGNSNDRGSGHGSGLGEA  
 CSTGDLELAERGSICDPMAAA V TVERLRPAESAVNAIRTVPCASTPAGVFPPPPPEFTTGVLPA G IFGN  
 IFISVSLPQDASSERCYPDLLDIPVHAVSGAATGVVTTGSKAILPATSTVNVSSFATLPRRALRTSEIAI  
 GSPYDNMGPRITANGSSAFSLTMDLRLSPPPPPRIIQPPPEFVSL

*Diaphorina citri* (Asian citrus psyllid)

&gt;DcK6

MLAVVVILLAACLGTGSPDWTDCPDTCRCKWTLGKKSALCKDANFTALPSTLDSIDIQVLDLNNNKISYL  
 TKEAFKSIGLLNLQRIYLNKSGIREVHRDTFKYLTILVEVDLSDNQIAWLHQDTFLGNDRLKVLYLNGNP  
 ITELRAQQFPKLPYLKTIELQHCQIHSVHKDALIHLTALESNLNNGNRLKHLSESVFPTPNLKTLSLDG  
 NPWCCDCHLRSFRNWLLKSKLYSHPLSCTEPGMLQTKHWDVKAQEFACPPNVTIKESMVIREAGGNVTM  
 SCYVYGDPEPTILWLLNGQVLHNSSFLLLEEEEGDALFEKSVSITLNFVTDLDAGEYTCYAENIRGNASG  
 EISLDLPEINLATTLSKTD SWYMLVLGISVCVSVIVSIGMSFCVCRAHEHKNKRKRKGKMKQSVSFND  
 QEKLLDVSITTTDRHTGSCEALGSQPDMEIEQSLAMEQPPVHITIESHAVDPQVS VFPPPPPEFSSNHL  
 PTSTYGNIFISVSVSQEPGSDPPKYPDLIDMPHRSVSVGTGPGTNPAYFATLPRRPRSKVIEPSSLVRV  
 GPKYDNMGPRVTAGGASILSLPDATSTEDIPSPPPPTLCTPLGVEYVSL

*Cimex lectularius* (Bed bug)

&gt;ClK6

MMWAVRVLLLGVCREVLAAPDWTDCPSTCCKWTSKGKSALCRYAGFTAIPTDLDSDMQVLDLTGNEIP  
 FLTKDAFKSVGLNLQRIFLKGAGVRELHSDAFKKLTILVEVDLSDNLIATLHQNTFAGNDRLKVLYLNG  
 NPITELKPTQFPHLPHLKTLEMQHCQITEVNRDAFLHLPALLEYLNLNNGNRLKKIAETVFLPLSKLKSLSL  
 DGNPWKCDCLRGFKNWLLSSNLYSHPLVCTEPSALVSKHWQDIKPLEFACPPPEVSVSDSMLQEETGMNV  
 TLKCRVRGDPEPHVSWLFGHSIGNGTLNQDQILLIEEDGEVKAEKWSSLSIINVSEADAGEYTCVAK  
 NIRGQAATNVSLLLPEVVIATTVSKNENWFVWIVWATSCAVLIVTAAIASCIVIRVRHNNARFRKNNLK  
 TTTSYTEQDKLLDVSITTTDRQTGSCEGLGSQTDMEFLEHLSQSIPVEMCDQPVHITIESHSAEPAVS  
 YQPPPEFSRSILPAGAFGNIFISVSVSQEPTVESPRYPDLLDLPHRKTVAVATDNSYFATLPRQPRIKET  
 EPVLRVR PQYDNMGPRVTAAGSSTISLPDSANAEDIPPPPPPNCTPLTVEYVSL

## Halyomorpha halys (Brown marmorated stink bug)

&gt;HhK6

MWVVQLLLLGVASCIVLAAPDWTDCPSACSKWTSKGKSAFCTHADFTTIPSSLNSDMQVLDLSDGNKIIPY  
LNKEAFKSVGLLNLQRIFLRGSGVHELHSEAFKELTILVEVDLSDNLISILHKDTFAGNDRCLKVLYLNGN  
PLTELQAAQFPHLPYLKTLEMQHCQIARIHKDAFKHLPSELELLNLNGNRLKQISESVFLPVTKLKSLSLD  
GNPWKCDCELRGFRNWLLSSNLYSHPLTCTEPASLSSQQWEDIQPLEFSCSPSVHVEETMIQEEPPGNIT  
LKCRILGDPEPEVIWLFNGRVLGNSTMDQILLRQEEDGDVKPEKWTTLNIMNVSEDDAGEYTCSAKNIGG  
QAAINVSLILPEVIIATTLSKSDTWFMWAVWAGSGSGGVIFITLAVCLICRFRGGSSRYVRQGKIKQSES  
YTDQDKKLLDVSITTTTDRQTGSCEGLGSQADIELLEHSLQSIPLVCDPVQITIESHSAEPVS VYQPPP  
EFSTSILPPGAFGNIFISVSVSQEPPDAPRYPDLLDLPHRKS SVS VATE PYFATLPKRQPATRLKETEPVL  
RVGPQYDNMGPRVTACGSSTISLPDSTSADDIPPPPPPNCTPLTVEYVSL

## Acyrthosiphon pisum (Pea aphid)

&gt;ApK6

MPGGQPVQLIVMVLVYCGTTFGDWADCPTPCQCKWSSGKKTALCKDADFTDIPLSLDADMQVLDLSSNNL  
RHLPEDAFKKVGLLNLQRVFLRGCGIHNHVKDAFRELKILVELDLSDNLIGSLHQETFQGNERLRVLYLN  
GNPLTEIKEVQFPVLQHLRTLELQHCQIKRIHRDAFLHLSSLESINLNGNLLKWLSETVFLPI SKLKTLS  
LDGNPWVCDCHLRSFRNWFVSSNLYSHPLSCIEPNVLSGSRWENIKPPEFACPPVVKIDRNSVLEDAGNI  
TFTCKVTGDPEPEVSWYFNGHSIDNYTDRMDENRTWLDNNRMWSALHIFNVSDV VAGEFTCEARN SRGQM  
SANVSLALPEVAVATTLSKSKSMYLVIVCVAASATVLLFVIGLTCCVCQVKKSGGRD SKTNFKGSTSFS  
DADKRLLDASISTTQAGSCEMLGGSSCQDLELIEQSLQNIPLAAVCDQQPVHITIESHDPNSSLSLYPPP  
PEFSTSILPSVSGFGNIFISVSVSQEPPDPESRYPDLLDMKHRQKQSVSVGTSSTHHIPPASSYYATMPR  
KKRIIDHQSIKSVMPHYDNMGPRITATGSCTNLSSLSN SGESSDDIPPPPPPLCTGHTDYVAL

## Pediculus humanus corporis (Body louse)

&gt;PhumpK6

MAGGVIASLLVLAAAWSVASPDWMDCPGPCRCKWSSGKKSACFRDAGLTTVPTLNADIQVLDLTRNIIPF  
LSKDLFKSIGLLNLQRIFLRNISLKEIHPDAFRNLSILVEIDLSENKIDKIHPNTFYGNDRLRFLNLSGN  
PLTELVGNQFPPLKYLKTIELQNCYLNYINKDAFVNLPLETLNLNSNQLNNVTENVFKLIKKLTKLKD  
NNPWKCDALRDFRTWLLQSNLYSVPLTCMDPPSLSGLHWNDVSTEEFACSPKVTVTEVMIQEEVGNNVT  
FKCHVTGDPEPDVMWLYNGKPVNGTANDQMYEEKDGGLEKVVMSIYNVSELDAGEYSCLAKNLRGSSI  
GNLTLMLPEVISATTLSKTESWLLIAGLIAGGVATFFSITLTLVFTFCFCGRKR RRRKRGRRKTELKGSVS  
FTEQEKKLLDVSITTTTDRPSNSESVEQLNQPDMMEMESASIPLELCEPVHITIESHGTNNTNMVPLSVP  
LTVFPPPPPEFSTSVLPAGAFGNIFISVSVSQEPSSDTVIRYPDLLDIPHRSKNSSARVSVGGGGGGVGPS  
EGGSLTTSQSYATFPRRPRPKSVTESNEPQVRLGPMYDNMGPRVTAGGSSTLSLPEVEESEIPPPPPPP  
PPLPPSLCLPLSVDYISL

*Daphnia magna*

>DmagnaK5/6

>MATMTIMLKAVLMLEFFCLLAMLAGPVTA DWTATCTAGCTCKWADGKKVAECPGAGFTTIPENLSPEIQV  
 LDLRGNQLGVLVNRAFSSVGLLNLRIFLRNCSLTLEKDAFHDLNIMVEVDLSHNQLHRFHPETFTNNE  
 KLRSLSLSHNPLEKLEAHQFPPLPNLRSLELVKQCQLEMVDKKAFMHLSKLETCLKSANKFTNLKPEVFLP  
 LNKLKSLDLQDNPNWNCDCRLLALRDYLSEANLNSTLTCTEPEHLKGKPWSRLAAEDFACKPLIDVNEPH  
 VEGRLGFDVTFSCRVSIGNPPPTIWWVLQNRQIVNTTTASQSEQFVIRQSTHPTKINPSIASLHAEPQQPE  
 FEYWSNLTLLRISEQDAGQYRCIARNKGGQVDANVSLQTPPAPVTILIEGETGLMSYTTAITLAVVGALV  
 LLVGLVLLIVCLVRRVPKRKQPQPRDGSAKLNLSAKTVNGNGSIAAVSEQEKSLLDIEMDQHTSLQNAS  
 TDGYHVSQTDIDAQQHMQMQLQLRHQQLOQQOQQOQMRMMHGSNTYIPGDRYDTSRVPESLTRHLMMLD  
 GCQVQQNPDGSFYPDLLDIPHRGARGGGSPSTHSGASNETANQQQHHMMSTLSAAQLAGHPSYGVIGLH  
 PPLQFTDSSSTTSSTAVLLPVGARPGYVTLPRRPRPRMPSWASSPPPMSSSSPGPGSLPAEEPQQPLYDT  
 IGPRVTADGSSTSALS LNKIAGLTPNPSSGLSPRMQSSTLSRGHKISLPAYYVPIEEVDIPPPSPLVQQR  
 RDHQQSTPNILSNGQYEDHHHHHHRMGREPVLYGFNNNNNSSTPIRRADDSETQHLLNDSSTPTSANTSY  
 SNAAPEVISPIPDFRTAGSRASVSSLSSNTGLRRKIAPAVPPKPPGSIVVARPASVVPYHDDVASPAKVA  
 PKPPPKPKKRLSTTGDSVKLEDLENGGGDSGGQAAYEDEGEDGTEV

## APPENDIX B: BoxShade Outputs

### Kek1 BoxShade Outputs

>Fraction of Sequence: 1.0

```
DmK1      1  RVKRQPYVDSKTPNHMEVITSVNHQNSITNKTQPATGNGSIGGVVIANGAVANIIDGGVV
AgK1      1  RLRRIPMTETKTPNQVEVITSVSPSSNVNGKVATPI-----NDCHS
PxK1      1  RFRNAPICESKTPSTLDRVVSNGEVHP--ASVD-----KPCVA
consensus 1  R k  P  dsKTP  me i S
```

```
DmK1      61  QGGTLERKSSGRGGVPHGVHDQRSANPVQKPPRLTDLPYSTQGYDNNGSVLSTASCFISP
AgK1      42  -----PDRAKAAGDLKC--GPNPAANPLQKPPRLTDLPYSTSHYDGGSLIASQCFVSP
PxK1      37  -----ALGSRDELPG--VSDPKCNPVQKPPRIGDIPYTTNHYEGRGSVVTAGGPLMVS
consensus 61  v          NPvQKPPRL DLPYsT Yd GSvl a i
```

```
DmK1      121  SGSTGNGGNNPDLINDTKRFGSDEFADL-----
AgK1      95  THS--LAGNNPDLINDTKRLGSGTDLTAATAAPGPAVPGGGVADPLAHLGQLQLQATSAL
PxK1      88  PTM--SVANDPDLINDTRP-----
consensus 121  gN PDLINDTk
```

```
DmK1      149  --KIPPISGVGVGGSGEYSRANGCDSLYPSGLWEHGAPVGT---TSADDLFMKRYTDKT
AgK1      153  STALSMLDPVERPFGSGEYSRA-GCDSLYPSGLWETHSSNLAATGLDHGGSHGPGPYSDKL
PxK1      105  -----ESAGRPGSGGEYARE-ASDSLYPSGLWDQMKRDQATSLARAVSSALPAYYTDRT
consensus 181  GSGEY R g DSLYPSGLWe YtDk
```

```
DmK1      203  PIIIDST-----QLYDLHERTAATDYFSKTFPRSHLQQGMMTG-----GGGGTST----
AgK1      212  PIILGGGGSGAGPAMLNLDDETSSVDYLSRTFPRTHLTGGLSLSTTASSGGSYGHGVAAAA
PxK1      157  PIMESSS-----VEGSQEELGYMSRTFPAHAAAA-----GGG-----
consensus 241  PII l Y SkTFPR H g G
```

```
DmK1      247  ASTVTTNLSGGSSSGYPNDYGLPLVPGAEHQHNHQLQMHPLQQLQQQLTSTLNHQKQEGS
AgK1      272  AAATGGTTTTTSGGGYPADYGLPIVPGAELHNKLASGQPAH-----
PxK1      190  -----AGSGDAPYPADYGLPVG-----
consensus 301  YP DYGLPl
```

```
DmK1      307  STGSSPHFSSRTLPRLHEGSGGGGSSRSSPTPAISGGHANQAANPSTSSSSCSILPNGQP
AgK1      314  -----H-----GSTGSMP
PxK1      207  -----
consensus 361
```

```
DmK1      367  INAKTIRVWQKGGVPVLPPVTALKRALISSSRNSPDEGYQEGCGTDV
AgK1      322  MNAKTIRVWQKGGVPVLPPVTALKRAL-SNSRNSPDEGYQEGCGTDV
PxK1      207  -GARTLRVWQXXX-XXLPPVSALKRVL-ATSRHSPDEGYQEGCATDV
consensus 421  AkTiRVWQ LPPVtALKR L SR SPDEGYQEGCgTDV
```

&gt;Fraction of Sequence: 0.7

```

DmagnaK1      1  RTRSSA-----N-----SSGSSANKLDDIGK
PhumpK1       1  RCRRQRRKKRKK-----
DmK1          1  RVKRQPYVDSKTPNHMEVITSVNHQNSITNKTQPATGNGSIGGVVIANGAVANIIDGGVV
AmKek1        1  -----
LhumK1        1  -----
consensus     1

```

```

DmagnaK1      22  QSGQRPA--MSLGQAHQGIQGSSSSGPCVAKSPTLS---ALEYGQIAFV----NPHSP
PhumpK1       13  -----ERSKEM-ASQNQK-PLLRNEIITSPTETTGS-NGTVVMSGQ
DmK1          61  QGGTLERKSSGRGGVPHGVHDQRS-ANPVQKPPRIIT---DLPYSTQGYDNNGSVLSTA-
AmKek1        1  -----RFR---RMPVKDKVSA---VPAEG-
LhumK1        1  -----RLR---RMPLKDKVSS---APLEA-
consensus     61  1      lp      g

```

```

DmagnaK1      71  NRVVVVTTTAAATASGLSDRFDLIHDA-RNSSDHYGYDLGPPLDYSTLNRRYHTHGQSADR
PhumpK1       52  SNVSVFIPNIG--GSNENESQSITSGVYIPQNVFLTDQNPDLING-----
DmK1          115 ---SCFISPSGSTGNGGNNPDLINDTKRFGSDEFADLKIPPI-SG-----
AmKek1        19  ---VSGDSAG---GNNENNPPSATSTTRKHHEEIIETTSF-----
LhumK1        19  ---VSGEGAGNGTGGGENNPPSATSTTRKHHEEIIETTSF-----
consensus     121  g  n p      r  d

```

```

DmagnaK1      130 DILAATSAGDY-QSAQTDSFYPSALWDHILNPTSEEETSDGANNITIDQASSRSSSGH
PhumpK1       95  --TESAGN-----KFQIGES---QIDGGQN-----LSL-----
DmK1          156 --VGVGSGSEYSRANGCDSLYPSGLWEHGAPVGTTS-----DDL-----
AmKek1        52  -----GVESKPPPV-----
LhumK1        55  -----ALESKP-PAS-----
consensus     181  al  h

```

```

DmagnaK1      189 MGSPHILPHVPLTVMDRNGMPQIYVPYTSG---QVIQNPRDVLAAASYADRDSEAGESAVS
PhumpK1       118 -----MSSPYADA--SRYIQTRGN-----
DmK1          194 -----FMKRYTDK--TPIIDSTQL-----YDL-----HERTAA
AmKek1        62  -----LTLSYVQRPQAALLQTENE-----YG-----AS
LhumK1        64  -----LHLSYVQRPQAAMQ-ENE-----YG-----T
consensus     241  i  Y      viq      y

```

```

DmagnaK1      246 VDSYSLPRRIPQOH-----SKESIGGQNFVPYPPDYGLPRTQSPPT
PhumpK1       135 CD-----LFIKQHYTADIHLSPGR-----FFDGDGYPDYGLPKVPLMVS
DmK1          220 TDY--FSKTFRPSHLQQ-GMMTGSGGGTSTASTVTTNLSGGSSSGYPNDYGLPLVPGAEH
AmKek1        85  IG-----RFDHDSQQPSVMVAPGACFSSTTSL-----
LhumK1        85  IS-----RFDQSQSAAVAIPGAGCFSSTTSL-----
consensus     301  f      l  g

```

```

DmagnaK1      287 LAKPPTQ-----HLAAA-----GAATIERQ
PhumpK1       175 LPTPDQQINYRTP-----NKRSAKFSAANPHLKFAFREAEFLSSSHS-NPYDYN
DmK1          277 QHNHQLQMHPLQQLQQLTSTLNHQKQEGSSTGSSPH--FSSRTLPRLHEGSGGGSSRS

```

|           |     |                                                          |
|-----------|-----|----------------------------------------------------------|
| AmKek1    | 112 | -----MPIDN-----PDLIRDTRRGSAEDITP---YGGADYSRMEVVDD-AKILYS |
| LhumK1    | 112 | -----MPIDN-----PDLIRDTRRGSTEDITP---YGVADYGRVEAIDDAKMLYS  |
| consensus | 361 | a p f l a                                                |

|           |     |                                                             |
|-----------|-----|-------------------------------------------------------------|
| DmagnaK1  | 307 | PPAPTT---EDPSIQQQQQQQQH---NSSSSCYGSKANSSAESSPVATSSNTKGARFWQ |
| PhumpK1   | 225 | PSNVRYTLEGYPCHQQQQQPQPPFPSNYSPSECEG-----TFIPSP-----PAAYK    |
| DmK1      | 335 | --SPT---PAISGGH--ANQAANPST-SSSSCSI-----LPNGQPINAKTIRVWQ     |
| AmKek1    | 154 | --SCMWEA-RDTCRTT--VPVSTYPSKETLAVVAP-----MVEQFPFGAKQIRVWQ    |
| LhumK1    | 155 | --SCLWEA-RDTCGRTSAVTVNAYPSKEQLAAVAP-----VVEQFPFGAKQMRVWQ    |
| consensus | 421 | ps s p k r wq                                               |

|           |     |                                                              |
|-----------|-----|--------------------------------------------------------------|
| DmagnaK1  | 360 | QR----PGI-----NNGKRSHHHFARDSPDEG                             |
| PhumpK1   | 271 | TDGISMIPPCDANNQWQCVNAQQSRATDINADGIMQQQQQQCSMSSKKTQAVLTESPDEG |
| DmK1      | 377 | KGVPVLPVPTALKRAL-----ISSSRNSPDEG                             |
| AmKek1    | 200 | K-GVPVLPVVSALKRVL-----GSTRSSPDEG                             |
| LhumK1    | 203 | K-GVPVLPVVSALKRVL-----GSTRSSPDEG                             |
| consensus | 481 | gi miPpi a r SPDEG                                           |

|           |     |                                                    |
|-----------|-----|----------------------------------------------------|
| DmagnaK1  | 383 | YQENAPLTFEFKYSIGLRLIENWLRKKHVPPAPLEHAEDHDIVSIVERKV |
| PhumpK1   | 331 | YVGDTTESGDI-----                                   |
| DmK1      | 405 | YQEGCGTDV-----                                     |
| AmKek1    | 226 | YQEGTGTDV-----                                     |
| LhumK1    | 229 | YQEGTGTDV-----                                     |
| consensus | 541 | Yqe                                                |

## Kek2 BoxShade Outputs

&gt;Fraction of sequences: 1.0

```

PxK2      1 ---KT--DTKSRKKK-----DSGKDVALRNQN-----NSS
DmK2      1 KCKKTSEPAKQRKKCDQVTSIAGG-TDSST-----GSTQDTGMGMMKCASILNDGGDS
AgK2      1 -----KCARARRASGSGAKKSRGAKGATADGLGGVPAGQQKCASITHDLGEP
consensus 1                      K

```

```

PxK2      26 RNSD-----TSTFDTLQRKMNGSLITNAQ--THHVHYTVQE-----
DmK2      53 MNGNPGLLLGDTLTPTKAANGAAGGGIILGNQ-MKQNLLLYATPNSAQQLQLNVNLMGT
AgK2      48 LTAG-----KLNGAIGLDGSGNPQDIVLYLNANPN-----
consensus 61                      G l          vv Y

```

```

PxK2      61 -----STEDTYRQSGSIKNFVDRNPDIINDAETVTNNALNDNAIMS----V
DmK2     112 GPGSPPLLLSNHGHLAAAYCSPASLRNYQEKNPDLVNDAESVKHKLKTAVSLDG--AGE
AgK2      78 ---GLDKAALNNMTAMAQFCSP-SARSYQDQNPDLINDAESGQHKARPRPDAIDSGLGE
consensus 121                      S k f d NPDiiNDAAEt

```

```

PxK2     102 YKTQNTNPENMEGESA-----FSLPPMMPRQVTWR---DQQ
DmK2     170 YETQSD-CGQYEGCYQLAAAPHPHQGHQHP---H-----PGHP---LM-GRF-AQAMTT
AgK2     134 KDSDEQ-SSVDGGSEVSFQQQQHQHQHQHQHQHQHQHQGQGQGPYYPPMVLRGPRFASSALST
consensus 181 t          eG                      P          w

```

```

PxK2     135 PPR-----GPYHLYQHSAADIHLNPGCFLDNEGYPY-DYGLPKMQCRGPPMHSNYA--
DmK2     215 LPR-----GMQLKPAPHQVDVHLNPVCFLGQDGSFAYDYSSAHMVQPPQQQQQQQQV
AgK2     193 LPRGGTAALGGKDL SAYQHQVDIHLSPGCFLDQNGYPV-DLSL-----MAAPS
consensus 241 PR                      H DiHL P CFL n G D

```

```

PxK2     184 -IVTPGYQTLPHKRPNVQKL-----GCKFAKDTEFNTTPP----CLNY
DmK2     268 QPANNFYRTLPHNRLHKQQQFQAAAAAGGNVGVGNPTLRYSLAEFIQRGP-TVSYEKY
AgK2     240 GPPVNYRYRTLPHKKHQQLQQQQQ-----QPGGPGKPIARYANAEFINRTQSPAAYQMY
consensus 301          Y TLPH r Q                      kf d EF          Y

```

```

PxK2     222 VSGNFRHTLDGYPVVNRVPVFA--GNGNMFIAQP---GPLPEGYQVEPIT-----
DmK2     327 QLPNVRFTAEGYPQQQQQQQQQLQQQQQLQLQQQHQFSPPEGYKSDLA-----
AgK2     295 APTDVRYTAEGYPQHE-----HGQFSPPDGYKGEVHPVAYMSSAAAA
consensus 361          R T dGYP                      PeGY e

```

```

PxK2     267 ---LCCGAAQ-----TESCSAAWGAK-----GTCA-VMVPLDVAEAGAAKCY-
DmK2     376 -----VMPAPFQQWPSCLPGYRFAQSPTSLPAVATPPPAVVATPPPPTSAVSTQ---
AgK2     338 SAGFCVGPAPGPPQQWPTFLPGFHPQLIPIMAPAGG-----ALLASPMMPSPSGQQQQQQ
consensus 421                      s aw                      A v P

```

```

PxK2     305 -----HVETRCVDTQTG-----EGRGEARGAEARGGEARGAEGEAPKPALRAG
DmK2     426 -----STATSTIPELDESEASSPRLEEAAGSAAPPAGEEESD TAK-L

```

```

AgK2      393 QQLSSPQTQPGSALKKCSVGAQTSELDKDVPEQREEEEE--EEDEQDGGGGGSTVK-L
consensus 481                                     R  E                               r

```

```

PxK2      348 KYELEVCTESPDEGYVGDAVDSADT
DmK2      468 KQLNGPLADSPDEGYVGDGQETSDI
AgK2      450 RHLTGPLADSPDEGYVGDSHETSDI
consensus 541 k          eSPDEGYVG D  ds D

```

>Fraction of sequences: 1.0

```

PhumpK2    1 RCRRQRKKRKKERSKEMASQ-----NQKPLLRN-E--IITSPTE
DmagK2     1 CCRRRSHRTRDKT-ANNIASIGGVGDSAKT---KSNSSL-----PELPP-RPIQM-----
ApK2 (a)   1 -VKRRRHRDHAG---RPGGKSGGAGGGDAGPDDPSNSGQAAKTTSDIRQSDSVNLTVSST
consensus  1  rR  rk r          a                               l          i

```

```

PhumpK2    38 TTGKSNGTVVMSGQSNVSVF-----IPN---IGGSN---ENESQS
DmagK2     47 -----LPSSN-----IGNKGDNGYTMGVPLPGGGRVGGAGR--EYHS--
ApK2 (a)   57 VD GK-----LSSAEDVSVYGEYDTAAGPGSSAGYEVHEVMH---VGGGGGYDAYQQVH
consensus  61                      m                               i          iGG

```

```

PhumpK2    72 ITSGVY-IPQNVFLTQNPDLINGTESAGNKFQIGE--SQID-----GGQNLS
DmagK2     83 -----TALDSSLQSPDLINDTTATAKWKEQNAQAVSLDDGQFSPTLYASSAGSPSN
ApK2 (a)   107 VAQGH PATATATTTLEANPDLISDASTVIRD-----NGGGDYR
consensus  121                      d  PDLI                               gG

```

```

PhumpK2    117 LMSS-----P-----YADASRYIQTRGNCDLFIKQHYTADTHLS
DmagK2     135 VNASQYYPCSVLPQLSTISEAVLQQHQHFYPAQCSTNVYNSSSSLAVLNPA GYLVPMSMP
ApK2 (a)   145 DATDEVYKIAVP-----PPPSGRDFWSTSGAVYPSGGGCGSYELQLS
consensus  181                      P                               t          i  l

```

```

PhumpK2    151 PGRFFDGDGYFVDYGLPKVPLMVSLPTPD-----QQINYYRTLPNKRS-----A
DmagK2     195 GLPLVDAEGFPIDYGLPRPSRPTR-PTQTHVRFADPPSVSV--RHYEN-YVVDGDNLQEA
ApK2 (a)   188 PGKLAAGEPYPADYGLPKLSSGQY-PMPA-----PPSLYRTLPHRRNAAKPQGRSCQEA
consensus  241          gd yP DYGLPk          P                               A

```

```

PhumpK2    195 KFSAANPHLKFFASREAEFLSSSHSNPYDYNPSNVRYTLEGYPCHQQQQQPQPPPPSNYSP
DmagK2     251 TMENFLPDRKYP---DSYDPLSSPLNCSHHSEIRYPSE RYPQNFSPSS---F-PAGYNA
ApK2 (a)   241 E FVLLQQHHHHHHHHHHQQQQQHHLNRYEPQNI RYNQQGYYPASAVA---A-DAAYYT
consensus  301          k                               vRY          YP          Y

```

```

PhumpK2    255 SECEGTFIPSPPAAYKTD-----GISMIPPCDANNQ-----WQCVN
DmagK2     304 TGN YEEIIAAPP SGY-AGHQNHQHQQHQQEYMYPPPGQMMKPNSSSTSI ESENSTLTGTG
ApK2 (a)   297 TAA--ATFYEPPSLSNASAQTLDDETMVMMPMPA-----PP-----PPLVT
consensus  361 s          PP                               M  PP

```

```

PhumpK2    291 A-----QSRATDINADGIMQQQQQCSMSSKKTQAVLTESPDEGYVGDTTESGDI
DmagK2     363 GAPSSP-----LDVSINDAS--SSSPGFLCSSTLQRQPHE SPDEGYEDEGIDGTEI
ApK2 (a)   338 GAPALPAAGRQPQHLSAEHAA--S-QHKAVTAVQKQPATTE SPDEGYVGEGPDS---

```

```

consensus  421 a          i          m      Q      ESPDEGY  d  e

>Fraction of sequences: 1.0
DmagK2      1  CCRRRSHRT-RDKTANNIASIGGVGDSAKTKSNSSLSPELPPRP IQMLPSSSNI-----
DmK2        1  KCKKTSEPAKQRKKCDQVTSIAGGTDSTGSTQD-----TGMGMMKCASILNDGGDS
HlK2        1  -RKR--RRD--RKR--NSKALVSQNKS-----VMP-----
DcK2        1  RRKK--KKLKKKDE--SDKNVNGSNEN-----VVKN-----
consensus   1    rr          i          ml

DmagK2      54  -----GNKGDNGYTMGVPL-----PGGG
DmK2        53  MNGNPGLLLGDTLTPTKAANGAAGGGIILGNQMKQNLLLYATPNSAQQLQLNVNLMGTG
HlK2        24  -----ITKDTT-SIPCR--KGNGSLIGLEH-QQMVSYTERELNRAAT-----
DcK2        28  LRESPK-YTSVNAT-SATCMDKVNGGYI IADGH-NDMMLYATDSGILVAT-----
consensus   61          G  mg

DmagK2      72  R-----VGGAG--REYHS--TALDSSLDQS PDLINDTTATAKWKEQNAQAVSLDDGQF
DmK2       113  PGSPPLLLSNGHGLAAAYCSPPASLRNYQEKNPDLVNDAESVKHKLK---TAVSLDGAGE
HlK2        63  -----LERREHRNLEEPYCS----PVSKYLTEPDLINEVPE-----
DcK2        75  -----N---NMNTY-PSYS----ISYQIEQN PDLVNDAESVDKDRR---AQGGEDTQDT
consensus  121          S          PDLiNd

DmagK2     121  SPTL--YASSAGSPSNVNASQYYP-CSVPQLSTISEAVLQQHQ--HFYPAQCSTNVYN-
DmK2       170  -----YETQSDCGQYEG-CYQ--L---AAAPHPHQGHQHPHPGHPLMGRFAQ
HlK2        95  -----TMDI-----GYGQL--Y--R---H-----QPGERQI-----
DcK2       118  QDKASEAASVQYSDSGSQCEWGNVCYN--R---M-----QPMQHIV-----
consensus  181          y          P

DmagK2     175  ---SSSSLAVLNPAGYLVPMSPMGLPLVDAEGFP-IDYGLPRPSRPTRPTQTHVRFADP-
DmK2       211  AMTTLPRGMQLKPAPHQVDVHINPVCFLGQDGSFAYDYSSAHMVQPPQQQQQQQVQPA
HlK2       114  ----LEYDSGYPLQPDLRPSNIPQLSYLDQDGYP-VNFGL-----PKIPFSAASTLPR
DcK2       155  ----LN--NVYNQP---ADIHLTPEKFMDRDGYP-VD FGL-----PKVPTHFPALVPA
consensus  241          m      v  eG      y          P

DmagK2     230  -----PSVSVRH---YENYVVDGDN-----LQEATMENFLPDRKYPDSYDPLPSS
DmK2       271  NNFYRTLPHNRLHKQQQFQAAAAAGGNVGVGGNPTLRYSLAEFFIQRGPT-VSYEKYQ--
HlK2       162  LRQ--RMP-VE-----GSAVAPPARYSREAEFLARSPGYD--PVL P--
DcK2       198  TAYYRTLPHRR-----HTAANPNNRY SREAEFLSRSSQPASYEHYA--
consensus  301          P          F1

DmagK2     272  PLNCSSHSEIRYPSERYPQNFS PSS--FPAGYNATGNYEEIIAAPPSGYAGHQNHQHQHQ
DmK2       328  -----LPNVRFTAEGYPQQQQQQQQQLQQQQQLQLQQHQFSPPEGYKSDLAVMPAP-
HlK2       198  -----RTDTRYTAEGYPYPVLQQQPIQPVEQPIQQQLPVSPVSP-----VAV-----
DcK2       239  -----PADVRYNIEGYPSASPTYSSAP-----RVTFTEP-----LHI-----
consensus  361          Ry  E  YP          P

DmagK2     330  QQEYMYPPPGQMMKPNS-----TSIESSENSTLT-L
DmK2       381  FQQWPSCLPGYRFAQSPTSLPAVATPPPA-AVVATPPPPTSA---VSTQSTATSTIPEL
HlK2       240  -----FPEVPFIPSPPAAYRGET-----TPLS-----

```

## APPENDIX B: BoxShade

|           |     |                                                            |
|-----------|-----|------------------------------------------------------------|
| DcK2      | 272 | -----LQGQPMQSNPPTETTTKNEQTWTESSADEQPSTSNPEKSNENKSEGFQAKRHM |
| consensus | 421 |                                                            |
|           |     |                                                            |
| DmagK2    | 361 | TGGAPSSP-LDVSINDAS-----SSSPGFLCSSTLQRQPHESPDEGYEDEGIDGTEI  |
| DmK2      | 436 | DESEASSPRLEEAAGSAAPPAGEEESSDTAKLKQLNGPLADSPDEGYVGDGQETSDI  |
| HlK2      | 262 | PRLLS-KTA-REAAAAAAAA-----RAEDLQPPHHPESPDEGYVGDAMDV---      |
| DcK2      | 325 | IDSLLK-NRD-VKVGSHLHP-----HRGLMLPPVLTESPDEGYEGEGPETTEM      |
| consensus | 481 | eSPDEGY eg d                                               |

## Kek3 BoxShade Outputs

&gt;Fraction of sequences: 1.0

```

DmagnaK3      1  -----KRAR-----
TcKeK3        1  -RKKQMLTWRT-RECRREDNYEKIEMNHKVAGNSNGGAVQAEI-----
ApK3          1  -----RSKGSPTGSRGV---PVSG--
ClK3          1  -----
DmK3          1  QRRRKLRLWNSVPPVRRSESYEKIEMTARTRPDLGGGASCGGSATGAGLFHDAEEQGYL
consensus     1

```

```

DmagnaK3      5  -----MHA---
TcKeK3       42  -----AVVATKKNGEYRVVPVADNEEEVEEEESNVEAAAKRIW
ApK3        17  -----PLDS-----AVANIDA----DPFDREYEKIEMDRD--DNN-----KSMQHRLH
ClK3         1  -----
DmK3        61  RAAHTPLNDNDAGQAAAIVNPSAGSAQRRNGDYLHVSTHCDDEED-----QQLHHHPQ
consensus    61

```

```

DmagnaK3      8  -----SLRHRRPMSVMGVPSMNNGNSAG
TcKeK3       80  QDTAIEK-----RWNSPEHLLDPEDLHIPRRTLQEAR
ApK3        53  QFPASSSDMNGRPDPGGY-----AESAAATSSGLLHHRHDEHEDYDGLPIPIDEPPSS-
ClK3         1  -QPRKE----SRATKAESYEKIEMDKKGDCINDISVSNKIHPTMGEYRSIPTFEQGEGDD
DmK3       115  QQPASQ---HHPHPNQQQHQQRKGSQGHVVSASG-ANNSAPLEETDLHIPRLIDIGGTD
consensus   121

```

```

DmagnaK3     31  GMFDKLDQTDNFLRRQSTASDNYKNHNGSLYKTEDNAEGAGSSHPEAKV-----ETRF
TcKeK3     113  DIRKG-----FS-----STSGIY-SGYEQPSTLSQ-----
ApK3      104  -----TAPSI---TDRPTARPSHP---TTNV
ClK3       56  EN-----GSPNSNH--SDAPRPANR
DmK3     170  SASSS-----ISSQVDAAARLAGYAGHTWKTTPIAT-TKINSPHSKPVTSAAPSSLNT
consensus  181

```

```

DmagnaK3     85  QDKQWLVSNQPSKPCLDIKLATNDAEVMTEPIVDGHRQIAMYQNKVKFNAEETNTPRPIL
TcKeK3     138  -----SVAPHLL
ApK3     124  PHRPRIIPDDPKDGKKKTYLE-----CNLGEVTLHHHVL
ClK3      74  Q-----TTRELSASKLY-----CQLGGV--QPHIL
DmK3     222  QATPYAHYGNHPADEMATSVF-----CSEGQE--SD---
consensus  241

```

```

DmagnaK3    145  KSE-----KVSSPSPTRNYPDLVDLLPSADYSDSSDV-----
TcKeK3     145  RRQI-SGGHATTYNSELSSLMEDEADKKYPDLIENSSYKFGNKANSEGGs-----VADIT
ApK3     158  HKESLPAGHLYTTA---AGRQELFNTKNVPDLLDTLVPTK-----GR--R--ISQTLPR
ClK3      97  RKEVLPTASLYTTA---I-----SEERNYPDLVYTPP-----TSN
DmK3     251  -----LFDSNYPDLLDI AKYAVAQAQQEGRGQGYAQAATTPN
consensus  301

```

```

DmagnaK3  177  -----TSNQDEMELIQLKRERSSPPIYPTSRYLQTA-----RQQE-----
TcKeK3    199  DLFCTLPRKRTLISARYKSSDSQSPLLPESRYGSSGGESSCGSQES-----GLRRL
ApK3      205  SG---ISSNSRRNTVYTTPRPSESQSPLLLGSRSSTG--SNTSRSQLSFDSSISSDHPRL
ClK3      129  TAQC--SATLPRSKIWYPMVSSSQSPLLAGSRC-----GSSAGESSG--SNRRF
DmK3      288  GGLCTLPRKLKTSWKYFRNSSDSQSPLLADNSSKYG--SSTLGDGSFLNEAMG--LGRRY
consensus 361  S Pi

```

```

DmagnaK3  212  -----TTFPGRRVAVPGNHNRRRLSDWEVNEL-----DDD-QEHHSMPFYQTQHVPV
TcKeK3    251  SDCPK-----YPAGNLNKNRVNKISNSYLNLTR-----
ApK3      260  TAGQKSSSYLNLSTASCGGGGD-----YS-GGSSGGYHHQHHPYWTTPPSLPS
ClK3      174  SAESRSSS-----NYRLPGKSC---ERSVSSLNLCIEPEISCSQTRQKSWHHPSLPT
DmK3      344  SAESSYANYSSSTA--TYTGGGQ-----RANSFLNLVQSGAHQGLLPShLGQKPSLPS
consensus 421

```

```

DmagnaK3  260  ASRRESYDS-----ELDTAQTELIRR-----
TcKeK3    279  -----EEELTSTPLLDVTGLESRVG-----
ApK3      308  SPARERRLPAIPVGRGAGLPTAAETPIILDPLSSRRRTYSGTGGGGGHHYHNHSGGSGN
ClK3      223  SPVRYHMAHKYDS-----NADTSETPII-----
DmK3      395  SPVQHQRSL-----SSAATPLLDLSALASRA-----
consensus 481  T li

```

```

DmagnaK3  281  -----HHSEEFDEDFHRRYAYHTGQLNRFLLEYRALQKRLAQMQDTWGRCLDDDI
TcKeK3    299  -----LTPNANSYDYHAAQLERFLEEYRSLQKQLTKMKETCDNLCQDHL
ApK3      368  QMHNQLTGSNHSLLSMSDGASVTYDYHTAQLDMFLDEYKTLRKELTKMQRTCDTLRLSNA
ClK3      246  -----NLLGSAVYDYHAAQLERFLEEYRSLQDELNRMKETCEGLKEKSI
DmK3      421  -----AGAANTSVAAYDYHAAQLERFLEEYRNLQDQLCKMKETCDTIRKKET
consensus 541  Y YH gQL FL EYr L L M T

```

```

DmagnaK3  331  DRSVRHHHR---HHHHSNHQPNAQRPLRPI-----LKNRLTLPRQ---TRRW
TcKeK3    343  QAGSSQVTPSTSNDDVVRNNPVSPNS-NQSLEDSIDFRNFESELT KYLLAKSSPSPKTFT
ApK3      428  SLASSVAAPDAVDHR-SKPEPLAAPAASSSSSR-----TTPKSILKNKNQ--ATY-
ClK3      290  EKPALSDFSSYR-----YTSNSIYNDLFRN-----
DmK3      468  PLRVAIGQSAAQ-----LADPVMYSAASHSPKPPATSNLKTLLPGQPDPDPY
consensus 601

```

```

DmagnaK3  372  SCDEQEPEDILE---PELQGSNYEV--SSAVDELYYS
TcKeK3    402  N-NSGVFNN-----
ApK3      476  V-----YRPVGERR-----NSYHQLNPAP-DDIYLS
ClK3      -----
DmK3      519  LHRNAMLKRLNGDGSAGTNGSGGSPASPQPRQDIFKS
consensus 661

```

## Kek5 BoxShade Outputs

&gt;Fraction of sequences: 1.0

```

DmK5      1  CRRIKTYQKDTTMMSGDGLISSKMDKTHNGSMLE-GSVIMEMQKSLLNTEVNPVEKPPRRT
AgK5      1  CRK-RRFKNSAMRENGQVNTKMKDKSQNESILDGGSVMVDMQKSLLTEVNPVEKPPRRA
PxK5      1  -----TSQRNETKKL--IKDDTRTNGEALIEGSLGSEIEKGYPAFVNPLSKPPRKH
TcKeK5    1  -----RKSTHGMA TKRRDLQDSSDECIRLHGQPDMEKALITDVNPPMKPPRIC
consensus 1  1 D em K eVNPv KPPR

```

```

DmK5      60  DIESVDGGD-----DVLEIKRTLLD DTVYVANHSRDEEAVSVAMSDTTTTPR
AgK5      60  DIDAGEKPGSGGQSSVGGDYDEKHEAKRTLLDETGFVAQ---DEETASVALS--DSNPR
PxK5      50  EAPPSL-----TSAATEMSELNRTLLDNDSTLASSGENR---AQDAE--PLPKM
TcKeK5    49  SVPPSV-----NSGGTEVSEAKNLLSDSVFAGDDESR---SDFDF--MPPYR
consensus 61  d E k LLd A

```

```

DmK5      107 SRHT-YVDDA--YANSLPPDLLAFPARVPPTSPSMQSSQSNIPDQVIYGI--RSPPSLTSL
AgK5      115 SRAT-FVDDG--CGTNLPPDLLAFPARFP-QSPSIQSSMSNIHDGRIYK--SP---LAS
PxK5      94  SQETLLVDRLAQEHQTYPPDLLSFPLRGSTQISPAGVDRPK-----STQTTNSPIKS
TcKeK5    93  KSQT-LLEPDYRGNHTYPPDLLFFPPRMC-QVSPAGSSASTVADTSRLPAHHGQPSPHLS
consensus 121 T vd PPDLL FP R 1 S

```

```

DmK5      162 FVYTHMTPHGIYGTCTMTAPHNGFMTLQHPKSRNLALIATTNSSRQHQHHLQLOQQQHH
AgK5      166 PIYQTGPGTS-LGGGASAQMPAGFRTLQHPKTGRTIAIA-----
PxK5      146 PGYGV-----
TcKeK5    151 PLYDSN-----
consensus 181 P Y

```

```

DmK5      222 HHHQLOQQQQQQQOHLPLATTSPFLPAPVVYSPATGVVMKQGYMTIPRKPRAPSMAWSTSG
AgK5      204 -----AARSNSPFTPAPLIYPPLA--LKHQGYMTIPRKQRTPSWTPSMSS
PxK5      152 -----ALNPNL-FNRIQLPS-TSQGSYSKQGYMTIPRRPRMPNWLPEGNY
TcKeK5    157 -----TLYRTLPIYRSQSPPFVGPPARVPKQCYMTIPRRPRQR-WSTDTPT
consensus 241 f k GYmTiPRk R W

```

```

DmK5      282 AAGHGSIQ-----SEFQSPTSPNPSETGTATTAELQAEVYDNLGLRRTTAGCNSTLNLT
AgK5      247 AVTAELLPAGSAGHSGATSPTS-----PIDLSLGEVYDNLGLRRTTASCNSTLKLN
PxK5      195 PQ-----VFSTLNGVIPYDNFGMKLFGNGSNYYSLN
TcKeK5    201 T-----SDVEEPLYDNLGLRRTTVDGSSALS LN
consensus 301 YDN Glr G L

```

```

DmK5      337 KIAGSQ-----GG--AGQQYSMRDRPLPATPSLTSVSSATN---ASKIY
AgK5      298 KTGLRGTPLGSTAAGTALT--ST--PMAKYSMKDRPLPATPGGQTATPNSSLLGHGGNY
PxK5      226 KSELDVMTGSSRGVNPYNYSVPQGVACDEIEPAPSPAPGTPHATIPRSSIS-----S
TcKeK5    228 KLGEATTPKS-----IRLFMPSPSSCDPIAENEP-PAPAPKL-----SPS-----S
consensus 361 K P Pa P

```

```

DmK5      376 EPIHELIQQQQQLQQQQQQQQRLGSMDEPLYGVRQQGITILPGSSISGAGLGHAAYLS
AgK5      354 EAIPEAL-----PYGAGQ---SMV-AGGLSGFDLDQSSI--
PxK5      278 PNIHNQLLALQAMSMNHGR-GTRV-PMSSEP---RPLKVILTPPEN-----ESLIK
TcKeK5    268 TQ-----WAK
consensus 421

```

```

DmK5      436 PGSGAAVSPSHASSSGDSPKAAKIPPRPPPKPKKKMSVTTRSGQ-----
AgK5      384 -----YGPVVGTTTNRSKVPPRPPPKPKKKVVLPAAAGGIVTTGDDQSSAPSCQMA
PxK5      324 NTSRELRRMGNG-NVTGTLGRKTVPKPPPKPKKRSSN-----
TcKeK5    273 ANAEALRSPDNRRNSLPDGGKVKVAPVPPPKPKKRSTST-----
consensus 481          K  P  PPPKPkKk

```

```

DmK5      481 -----GSTSQLFDDEGEDGTEV
AgK5      434 TAGGDSSGINTSTTNTSTSPVAEDCDDGTEV
PxK5      361 -----EMKEPFLNSGETATQV
TcKeK5    311 -----GPLFEDEGEDGTEV
consensus 541          e gT V

```

>Fraction of sequences: 1.0

```

DmagnaK5_6 1 RRVPPKRKQPQPRDGSAAKLNGSAKTVNGNGSTA-----AVSE-GEKSLLDIEMD
HhK5       1 RPK----QSQ-----SKKSSSAM--PANGDV-----MH-RITPSNEGEKSLITVNPV
ApK5       1 RRPASGGVL-----SKKSHANG--FSNGDVPNHHNHVTSLVSEPSGEQKSLAVNPV
consensus  1 Rr          K          NG i          S  Q  L  i

```

```

DmagnaK5_6 49 QHTSLQNASTDGYHAVSQTDIDIAQHHMQMQLQLRHQQLQQQQQQQMRMMHGSNTYIPGD
HhK5       41 QKPP-----RRYEAQINN--DAVEISE-----LNRKLLD-----ESSLQGN
ApK5       53 QKPP-----RRYESSPT--GTEMTE-----LKRNLDD-----ETSVSGD
consensus  61 Qh          Y          a          L h  L          t i G

```

```

DmagnaK5_6 109 RY----DTS--RVPESLTRHLMMLDGCQVQNPDGsfYPDLLDIPHRGARGGGSPSTHSG
HhK5       75 TCPTEEDN-----SVECLDIRQEGANVEKPVSEAHPPDLLSFPSRSHNISPASSSTSN
ApK5       85 ADEQFYGESGDELANIIDSSTGNSGVNGRSYRKGTHTPPDLLAFPRGSGGGGGHSSPAG-
consensus 121          l  m  q          PDLL  P          S

```

```

DmagnaK5_6 163 ASNETANQQQQHMMMSLTSAAQLAGH-PSYGVIGLHPPLOHTDSSSTTSSTAVLLPVGAR
HhK5       128 GFDNL-----SRASLYPAMQQSILNPSVHY--NCGTLPYSRSHSPFSPTA--PIVLPR
ApK5       144 -----SVVSTVPVSFQSPLH---SPI--YSGTLPYNRSQSPFSRPFSSRP---AQPP
consensus 181          S  Q          L f  S  S  S

```

```

DmagnaK5_6 222 PGYVTIPRRPRPRMPSWASSPPPMSSSSP--GPG----SLPAEEPQQPLDYDTIGPRVTAD
HhK5       177 QGYVTIPRRP--RVPSWSSAP-----TPSLDDPLSP- IKAEPYDNLGPRTTAD
ApK5       183 AGYVTIPRRP--RVPSWASSSTGVGGTSASTPTAGHVDDPLGVGRLCEPYDNLGPRTTAD
consensus 241  GYVTlPRRP  RmPSW S          L          pLYD iGPR TAD

```

```

DmagnaK5_6 276 GSSTALSLSLNKIAGLTPNPSSGLSPRMQ--SST-----LSRGHKISLPAYYVPIEEVDIP
HhK5       224 GSSVLSLN--KSFSENPR---GRNS-----SSNVPNYFHFEGGLR-----P
ApK5       241 GSSVLSLT--KAVADSAA---VHRPKPQYSQTLPHKTKLHSGHPRFTADD-AQDARRVP
consensus 301 GSS  L  K          S          G k          P

```

```

DmagnaK5_6 329 PPSPLVQQPRDHQQSTPNILSNGQYEDHHHHHHHRMGREPVLGYFNNNNNSSTPIRRADDS
HhK5       260 SPSPLSPEENR-----A-----
ApK5       295 SPAPRSPDPTLPSQ-----V-----
consensus 361  P  P  r

```

```

DmagnaK5_6 389 ETQHLLNDSSTPTSANTSYSNAAPEVISPIPDFRTAGSRASVSSLSSNTGLRRKIAPAVP
HhK5       273 -----DGI-----

```

```

ApK5      310 -----SGLPQHNALPPNYSPLVEMDARN-----RSSWAPSR-
consensus 421

DmagnaK5_6 449 PKPPGSIVVARPASVVPYHDDVASPAKVAPKPPPKPKKELSTTGDSVKLEDLENGGGDSG
HhK5      276 -----LKRTCSADGDIGPIRSKVAPKPPPKPKK-----
ApK5      341 ---VGT----PESGVLKPASQTSVKRKVPKPPPKPKMK-----
consensus 481          KV PKPPPKPK r

DmagnaK5_6 509 GQAAYEDEGEDGTEV
HhK5      304 DGPLEDEDEGEDGTEV
ApK5      373 GGPLEDEDEGEDGTEV
consensus 541      yEDEGEDGTEV

>Fraction of sequences: 1.0
DmagnaK5_6 1 -RRVPRKQPPQPRD-GSAAKLNGSAKTVNNGS-IAAVSEQEKSLIDIEMD-----
DmK5      1 CRRIKTYQKDTTMMSGDGLISSKMDKTHNGSMLEGSVIMEMQKSLINEVNPVEKPPRRTD
LhumK5    1 -RRHRT-----RD-----DEKGLEASLEHHG--EQEKSLITTINPVVKPPRRYE
AechinK5 (a) 1 -RRRHT-----RH-----DEKGLEASLEHHGLGEQEKSLITTINPVVKPPRRYE
consensus 1  RR          K  g          E  KSLI

DmagnaK5_6 49 -----QHTSLQNASTDGYHAVSQ--TDI--DAQQHMQMQLQLRHQ
DmK5      61 IESVDG-GDDVLEIKKTLDDTVYVANHSR-DEEAVSV-----
LhumK5    43 APSVTSHGTEMTELNRTLLDNDVSFADGVV-GSGVVGVGGSIGDDEKDERATPELGR-
AechinK5 (a) 45 APSVTSHTD-----GV-GSGVVGVGVGVDDEKEHERATPELDGS
consensus 61          V

DmagnaK5_6 85 QLQQQQQQQMMRMMHGSNTYIPGDRYDTSRVPESLTRHLMMLDGCQVQQNPDGsfYPDLL
DmK5      97 -----AMSD-TTTPRSR-----HT-----YVDDAYANSLPDDL
LhumK5    101 -----GG-SGTLPRGT-----TG-----YH-----HRQYFXDLL
AechinK5 (a) 85 -----GNGGV-VGGG-GGTLPRGG-----AG-----YH-----HRQYPPDLL
consensus 121          P          DLL

DmagnaK5_6 145 DIPHRGARGGGSPSTHSGASNETANQQQCHMM-----STLSAAQLAGHPSYGV--
DmK5      126 AFPAV--PPTSPSMQS---SQSN-IPDQVIYGIRSPPSLTSPVYTHMT--PHGIYGTKT
LhumK5    124 AFSGGR--GASPTSQASTAPDNTR-LPNCHASA-----MTPAATSLYGSPP
AechinK5 (a) 115 AFSGGR--GASPTSQASTAPDSTR-LPSQOMIA-----PAAAATTAATASSYGSPP
consensus 181          S  S  t  Q          YG

DmagnaK5_6 194 -----
DmK5      178 MTAPH-NGFMTLQHPKSRNLALIATTNSSRQHQHHLQLQQQQQHHLHHHQQQQQQQQQH
LhumK5    167 SSQFHPAAFKTLPHS-----
AechinK5 (a) 163 SGQYHPAAFKTLPHS-----
consensus 241

DmagnaK5_6 194 -IGLHPPLQFTDSSSTTSSTAVLLPVGARPGYVTLPRPRPRMPSWASSPPPMSSSS---
DmK5      237 PLATTSPF-LP----APVYSPATGVVMQGYMTIPRKP--RAPSWAPSTSGAAGHGSIQ
LhumK5    182 -R-SATPYGLG---PSSSSSPIAPVLPKHGYVTIPRKP--RAPSWSSGPP-----
AechinK5 (a) 178 -R-SATPYSLG---PSSSSSPLAPVLPKHGYVTIPRKP--RAPSWSSAPP-----
consensus 301      P          V  r  GYvTlPRrP  R  PSW

DmagnaK5_6 250 -----PGP----GSLPAEEPQQPYDITIGPRVTADGSSSTSALSLNKIAGLTPNPSS
DmK5      290 LSEFQSPTSPNPSETGTATTAELQAEPVYDNLGLRRTTAGCNST--LNLTKIAGSQGGAGQ
LhumK5    225 -----TSPTVELEPVYDNLGLRRTTAGGSSK--LSLNKSPPEP-----
AechinK5 (a) 221 -----TSPTDALEPVYDNLGLRRTTAGGSSM--LSLNKSPES-----V

```

```

consensus      361      PLYD iG R TA G S    L L K

DmagnaK5_6     297 GLSPRMQSSTLS-----RGHKISLPAYYVPIEEVDIPPPSPLVQQRRDHQQSTPNILS
DmK5           348 QYS--MRDRPLPATPSLTSVSSATNASKIYEPIHEI-----IQQQQQLQQQQQ-----
LhumK5         259 ALS--MRGRPLPSTPGTSHYGTIQRSTPN-----I-----
AechinK5 (a)   256 ASS--MRGRPLPGTPGGSHYGSIQRSTPN-----I-----
consensus      421      S  M    L                      v

DmagnaK5_6     350 NGQYEDHHHHHHRMGREPVLGYFNNNNNSSTPIRRADDSETQHLLNDSSTPTSANTSYSN
DmK5           394 -----QQQQLGSMDEPLVGV-----
LhumK5         287 -----LAGSPIDRA-----
AechinK5 (a)   284 -----LTSNPIDRV-----
consensus      481                      m    Pv

DmagnaK5_6     410 AAPEVISPIEDFRTAGSRASVSSLSSNTGLRRKIAPAVPPKPPGSIVVARPASVVPYHDD
DmK5           411 -RQQGITILP-----GSSIS-----GAGLGHAAY-----LSPGSGAAVSP-SHASSSGD
LhumK5         296 -APEGAAEWPI-KLADQSLD-----D---GHSL-----AQQP-QQPQASAS
AechinK5 (a)   293 -APEGAAEWEL-KLTDESMD-----G---GHLL-----TQQQ-QQQQAAAS
consensus      541                      P                      r

```

## Kek6 BoxShade Outputs

&gt;Fraction of sequences: 1.0

```

DmK6      1 CKRTTRQHRHANKAGVKSSVSFNDQEKKLLDSSVTTTTTNDRGDSYGIDNQPTSIGMNKGD
PxK6      1 -----HMRRRTVPASRSFTDQEKRLLDASVVVSCDRSIAEMA---SPCDFE-----
AgK6      1 -KRK--LRMRRRRKTIKNSVSFNDQEKKLLDLSITTNERQEFS-----SDVV-----
TcKeK6    1 -----RGRKTQKRMKASVSFTEQEKKLLDVSIAATTTDRGTGS-----CEVL-----
consensus 1          h      v  S  SF dQEKkLLD Sv

```

```

DmK6      61 SAGMGFNQIEIHAVESHHRGSMVLVQQQPQQQQVAGGGGMRQQLMQVKDSTCGMMSVPTSM
PxK6      44 -----MTERSISEEPRGCGFDPVHITI
AgK6      46 -----TPS---TKTDSTIAMEPVQITI
TcKeK6    42 -----GPE---MELDP-----PVHIT-
consensus 61                                     V  s

```

```

DmK6      121 AGHAHSHPAQISEEFPLNVGVFPPPPPEFCSNIVPNPAFGGNIFIRVSVTQDMLDG--ADL
PxK6      66 EGT-----PGAFPPPPAEF---AVVPY-GNIFISVQVAGHGE---GPG
AgK6      65 ESIA---TSKREEYPLNVGVFPPPPPEFCTQMIANPTI-SNIYISVSVTQDPLEGGPADV
TcKeK6    55 -----IESEPLPLAVFPPPPPEFGNVV--PSAY-GNIFISVSVSRDPS-----DA
consensus 121          g FPPPP          Nifi V V

```

```

DmK6      179 NMYPDLLNIPKRMQDVQESGAGAVAVPEGQFATLPRHTARRGILKKDTSLQQQQQQHQQQ
PxK6      103 GKYPDLLSG-----GATLPRRSRTCCAPVYDNMGPR-----
AgK6      120 NMYPDLLNIPNRHQKGPPK---MPPVSVTSYATLPR--KTATV---GGGPR-----
TcKeK6    96 SRCPDLLDLPHRAKPVYHG-----MATLPR--RPCAAPHYDNMGPR-----
consensus 181      PDLL          ATLPR

```

```

DmK6      239 HQHQHQHQHQHQIQQQQHQQLQQQHQPSSGLYTHDEIVTYNLEASGYDPHQSGYHSNAMELP
PxK6      134 -----VTATGSSTWSLPGAGAEGVDNTETP
AgK6      163 -----CSITSGHSSSSGGSSGAGKPSVGIG
TcKeK6    135 -----VT-----AAGSSTLSLPGVPPP
consensus 241                                     t

```

```

DmK6      299 PPP--P---PPAVTAV-----VQCHHPSPNNCASCINNAP
PxK6      159 VLTLP--PPPEFVSL-----
AgK6      188 PPQVGSPLSCTPSLLAAAEIPLTEGIVNYATTALRDDSGCEMSSSSPVPSMCAECSKVLK
TcKeK6    152 PPP-PPPPQLTPEFVSL-----
consensus 301          P

```

```

DmK6      329 PPPSACQ-----SPP--VEVTPMRPLDSSAYPKYDNMGRRITASG
PxK6      -----
AgK6      248 ASGGTFAPKYGTTSRTLPGLGGGDLATSGPSSSNSSGSKCEKPLACLKYDNMGRRYTASG
TcKeK6    -----
consensus 361

```

```

DmK6      367 GLGGSNLSLHDEERYENETLFGQAESQTKGMPEQSQDLHQPQEVTTQGQDKGGGPG-----
PxK6      -----
AgK6      308 NS---TSLSPDELKPAGGP--GPA---GAAFVIKQQDIE--TIVEQDDQPGGAPDGTEAP
TcKeK6    -----
consensus 421

```

```

DmK6      422 -----EFVSL
PxK6      -----
AgK6      358 LPQQPPPPSAVVAGGTSDQEAARGLYVVGNDVFSL
TcKeK6    -----
consensus 481

```

>Fraction of sequences: 1.0

```

ApK6      1  -KKS GGRD SKTNFKGSTSFSDADKRLLDASISTTQ---AGSCEMLGGSSCQDIELIEQS
PhumpK6   1  RKRRRKRGRRKTELKGSVSFTEQEKLLDVSITTTTDRPSNSESVEQLNQPDMEEMME--
HhK6      1  -RGGSSRYVRQGKIKQSESYTDQDKLLDVSITTTTDRQTGSCE--GLGSQADIELLEHS
ClK6      1  -RHNNARFRRKNNLKTITTSYTEQDKLLDVSITT--TDRQTGSCE--GLGSQTDMEFLEHS
consensus 1  kk  gRyrrktnlKgstSftdqKkLLDvSItTttdrqtgScem glgsq DmElleHs

```

```

ApK6      57  LQNIPLAAVCDQQPVHITIESHDPNS-----SLSLYPPPPEFSTSILPVSVSGFGNIF
PhumpK6   58  SASIPLEL-C-E-PVHITIESHGTTNNTNMVPLSVPLTVFPPPEFSTSILPA-GAFGNIF
HhK6      58  LQSIPLEV-C-D-PVQITIESHSAEP-----VSVYQPPPEFSTSILPP-GAFGNIF
ClK6      57  LQSIPVEM-C-DQPVHITIESHSAEP-----AVSVYQPPPEFSRSILPA-GAFGNIF
consensus 61  lqsIPlel C dqPVhITIESHsa p          lsvy PPPEFStSiLPa gaFGNIF

```

```

ApK6      109 ISVSVSQEPP-DPESRYPDLLDMKHROKQSVSV---GTSST-----HHIPPASSYYATM
PhumpK6   114 ISVSVSQEPSSDTVIRYPDLLDIPHRSKNSSARVSVGGGGGGVGPSEGGSLTTSQSYATF
HhK6      105 ISVSVSQEPP-D-APRYPDLLDLPHRKSVS VAT-----E-PYFATL
ClK6      106 ISVSVSQEPTVE-SPRYPDLLDLPHRKTVA VAT-----DNSYFATL
consensus 121 ISVSVSQEPp d pRYPDLLDlpHRkkvsvat g          essyyATl

```

```

ApK6      159 PRK----KRIIDHQSIKSVMPHYDNMGPRITATGSCNTLSLSNSNGESSDDIPPPPP---
PhumpK6   174 PRRPRPKSVTESNEPQVRLGPMYDNMGPRVTAGGSSTL--SLPEVEESEIPPPPPPPPP
HhK6      143 PKR-QPATRLKETEPVLRVGPQYDNMGPRVTAGGSSTI--SLPDSTSA-DDIPPPPP---
ClK6      146 PRQ----PRIKETEPVLRVRPQYDNMGPRVTAGGSSTI--SLPDSANAEEDIPPPPP---
consensus 181 Prr p sriketepvlrvGPQYDNMGPRvTAgGSSTi SLpdsge eddiPPPP

```

```

ApK6      212 --PPLCTGH-TDYVAL
PhumpK6   232 LPPSLCLPLSVDYISL
HhK6      196 --PPNCTPLTVEYVSL
ClK6      197 --PPNCTPLTVEYVSL
consensus 241  Pp CtpltvdYvsL

```

>Fraction of sequences: 1.0

```

DmK6      1  CKRTTRQHRHANKAGVKS SVSFNDQEKLLDSSVTTTTTNDRGDSYGIDNQPTSIGMNKGD
PhumpK6   1  --RKRRRKRGRRKTELKGSVSFTEQEKLLDVSITTTTDRPSNSESVEQLNQPD
LhumK6    1  -CGGSRRHSKREKIKLQSSSFQDQEKLLDLSVTTTTTPGNSNDRGSGHSLGEACSTGD

```

|           |     |                   |                             |                    |              |                        |
|-----------|-----|-------------------|-----------------------------|--------------------|--------------|------------------------|
| HlK6      | 1   | -CGGT             | RRHSAREKVKIQNST             | SFGDQEKLLDL        | SVTTTT       | PGNSNDRGSGHGSIVEACSTGD |
| consensus | 1   |                   | R h K v S SF dQEKLLD SvTTTT |                    |              | D                      |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 61  | SAGMGFNQIEIHAVESH | HRHGSMLVQQQPQQQQV           | VAGGGGMRQQLMQVKDST | CGMMSVPTSM   |                        |
| PhumpK6   | 53  | MEMMESASIPLE      | -----                       | -----              | -----        | LCEPVHITI--            |
| LhumK6    | 60  | LELAERGS          | -----                       | -----              | -----        | ICDPMAAAATVT           |
| HlK6      | 60  | LELAERGS          | -----                       | -----              | -----        | ICDPMNAATVT            |
| consensus | 61  |                   |                             |                    |              | C m                    |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 121 | A----             | GHAHSHP--AQISEEF            | PLNVGVF-PPPPEF     | CSNIVPNPAFGG | NIFIRVSVTQDM           |
| PhumpK6   | 74  | -E-----           | SHGTNNTNMVP-LSV             | PLTVF-PPPPEF       | STSVLPAGAF-  | GNIFISVSVSQEP          |
| LhumK6    | 79  | VERLRPAES--       | AVNAIRTVPCAST               | PAGVFP             | PPPPEFTTGVL  | PAGIF-GNIFISVSLPQDA    |
| HlK6      | 79  | VERLRPEVSSSS      | SISAMRSVPCA---              | AIFP               | PPPPEFTSGVL  | PAGIF-GNIFISVSVSQDS    |
| consensus | 121 |                   |                             | vF PPPPEF s ivP    | F GNIFI      | VSv Qd                 |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 173 | LDGADLNMYPDLLNI   | PKRMQDVQES----              | GAGA-----          | VAVPEGQFATL  | PRHTARRG               |
| PhumpK6   | 123 | SS-DTVIRYPDLLD    | IPHRSKNSSARVSV              | GGGGGGVGPSEGG      | SLTTSQSYATF  | PRRPRPKS               |
| LhumK6    | 136 | SS-ER--CYPDLLD    | IPVHAVSGAATGV               | VTTGSKAILPA--      | TSTVNVSSFATL | PRRALR--               |
| HlK6      | 134 | -S-DR--CYPDLLD    | IPVHGTSGVLNKT               | T-----SALP---      | AASSVSSFATL  | PRRALR--               |
| consensus | 181 |                   | YPDLL IP r                  |                    |              | fAT PRh                |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 221 | ILKKDTSLQQQQQQH   | QQQQHQQQQQQQQQ              | IQQQQHQQQLQQQH     | QPSGLYTHDEI  | VTYNLEA                |
| PhumpK6   | 182 | VTESNEPQVRL-      | -----                       | -----              | GPMYDN--     | MGPRVTA                |
| LhumK6    | 189 | -----TSEIAI-      | -----                       | -----              | GSPYDN--     | MGPRITA                |
| HlK6      | 179 | -----SSDL-        | -----                       | -----              | CSPYDN--     | MGPRVTA                |
| consensus | 241 |                   |                             |                    | Y v l A      |                        |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 281 | SGYDPHQSGYHSN--   | AMELP                       | PPPPPP             | PAVTAVVQCHHP | SPNNCASCINNAPP         |
| PhumpK6   | 206 | GGS---            | STLSLPEVEESEI               | PPPPPPPPP          | -----        | PLPPSLCLPLS            |
| LhumK6    | 208 | NGS---            | SAFSLTDMDLRLS               | PPPPPRIIQ          | -----        | PPHE----               |
| HlK6      | 196 | NGS---            | SAFSLTDVDLRLS               | PPPPPRIIQ          | -----        | PPHE----               |
| consensus | 301 | G S               |                             | PPPPP              |              | PP                     |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 339 | VEVTPMRPLDSSAY    | PKYDNMGRRITAS               | GGLGGSNLSLHDE      | ERYENETLFGQ  | AESEQTKGMP             |
| PhumpK6   | 242 | VDYISL            | -----                       | -----              | -----        | -----                  |
| LhumK6    | 237 | --FVSL            | -----                       | -----              | -----        | -----                  |
| HlK6      | 225 | --FVSL            | -----                       | -----              | -----        | -----                  |
| consensus | 361 |                   | m                           |                    |              |                        |
|           |     |                   |                             |                    |              |                        |
| DmK6      | 399 | EQSQDLHQPQEVT     | QGQDKGGGPGEFVSL             |                    |              |                        |
| PhumpK6   |     | -----             | -----                       |                    |              |                        |
| LhumK6    |     | -----             | -----                       |                    |              |                        |
| HlK6      |     | -----             | -----                       |                    |              |                        |
| consensus | 421 |                   |                             |                    |              |                        |

## APPENDIX C: SLiM Weblogos

## Kek1 Weblogos

CO12



CO1



CO6



CO9



CO7

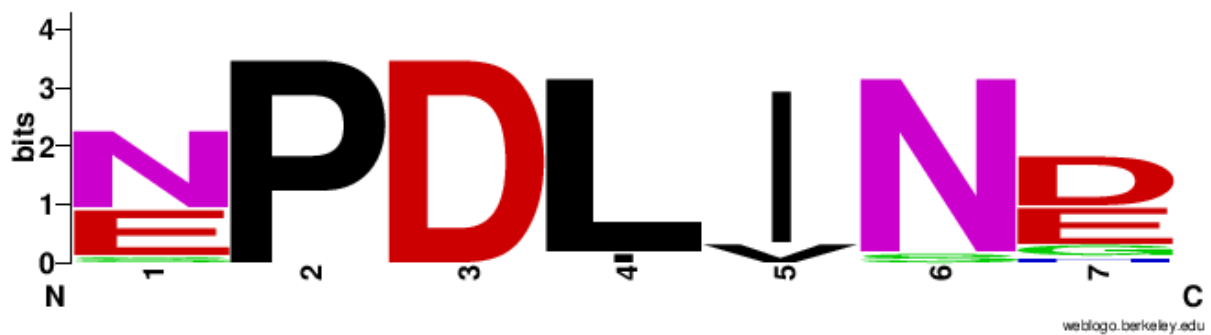


CO3

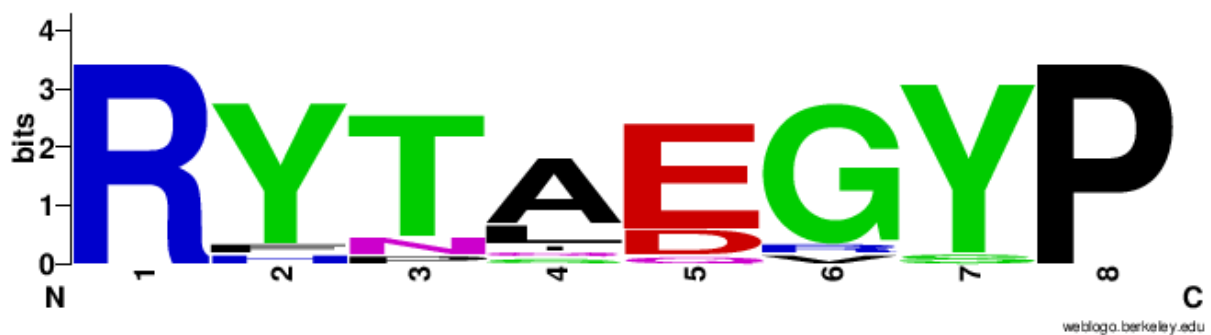


Kek2 Weblogos

CO1



CO2



CO3



Kek3 Weblogos

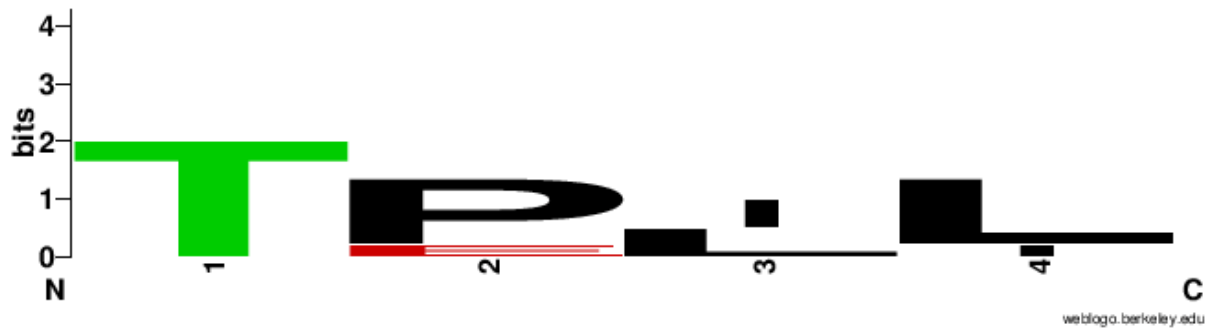
CO1



CO4a



CO4b



CO10



Kek5 Weblogos

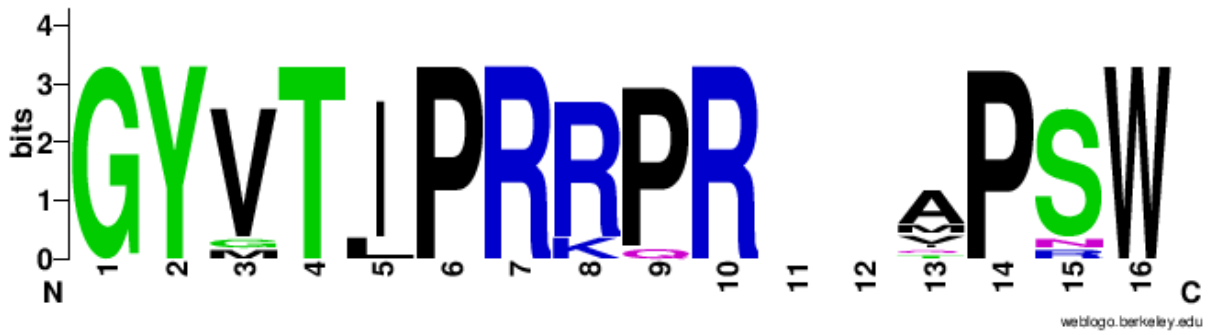
CO12



CO1



CO6



CO9



CO7



CO3



Kek6 Weblogos

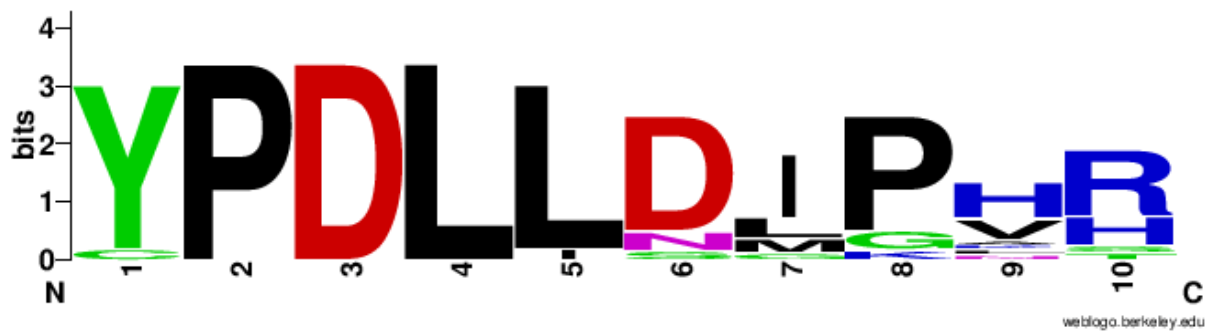
CO13



CO5



CO1



CO6



CO8



CO11



### Composite Weblogos

CO1 (Kek1, 2, 3, 5, and 6)



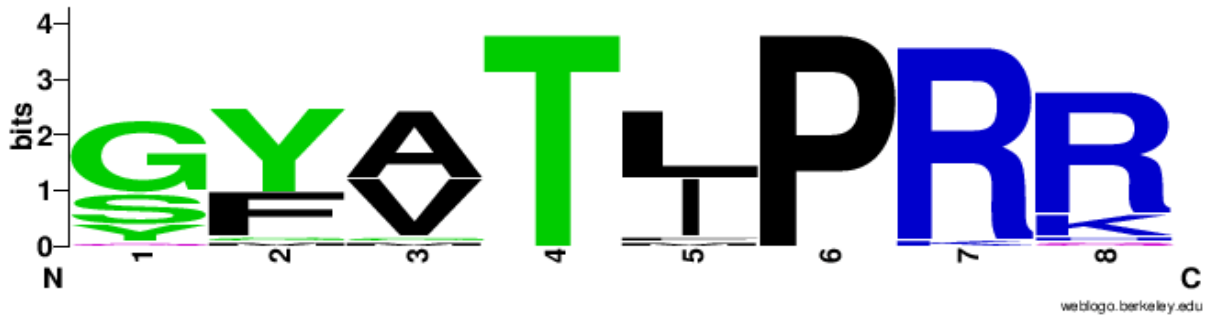
CO3 (Kek 1, 2, and 5)



CO4 (Kek3)



CO6 (Kek 5 and 6)



CO12 (Kek1 and 5)



## APPENDIX D: Summary of SLiM presence in Kek orthologs

| Protein   | C01 | C02 | C03 | C04 | C05 | C06 | C07 | C08 | C09 | C010 | C011 | C012 | C013 | C014 | C015 | C016 |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|
| DmK1      | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| AgK1      | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| PxK1      | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| TcKek1    | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| AmK1      | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| HlK1      | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| AechinK1  | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| NvitriK1  | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | +    | +    | +    |
| LhumK1    | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| DcK1 (a)  | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | +    | +    | +    |
| DcK1 (b)  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | +    | -    |
| ClK1      | +   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | +    |
| HhK1      | +   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | +    | -    | +    |
| ApK1 (a)  | +   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | +    |
| ApK1 (b)  | +   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | -    |
| PhumpK1   | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | +    | +    | -    |
| DmagK1    | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | +    | +    | -    |
| DmK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| AgK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| PxK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| TcKek2a   | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| TcKek2b   | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| AmK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| HlK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| AechinK2a | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| AechinK2b | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| NvitriK2  | +   | -   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| LhumK2    | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| DcK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| ClK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| HhK2      | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| ApK2 (a)  | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| ApK2 (b)  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| PhumpK2   | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| DmagK2    | +   | +   | +   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| DmK3      | +   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| TcKek3    | +   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| DcK3      | +   | -   | -   | +   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| ClK3      | +   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| HhK3      | -   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| ApK3      | +   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| PhumpK3   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | -    | -    | -    | -    | -    |
| DmagK3    | +   | -   | -   | +   | -   | -   | -   | -   | -   | +    | -    | -    | -    | -    | -    | -    |
| DmK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| AgK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| PxK5      | +   | -   | -   | -   | -   | +   | +   | -   | +   | -    | -    | -    | -    | -    | -    | -    |
| TcKek5    | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| AmK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| HlK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| AechinK5a | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| AechinK5b | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| NvitriK5  | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| LhumK5    | -   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| ClK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| HhK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| ApK5      | +   | -   | +   | -   | -   | +   | +   | -   | +   | -    | -    | +    | -    | -    | -    | -    |
| PhumpK5   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -    | -    | +    | -    | -    | -    | -    |
| DmK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| AgK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| PxK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| TcKek6    | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| AmKek6    | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| HlK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| AechinK6  | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| NvitriK6  | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| LhumK6    | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| DcK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| ClK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| HhK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| ApK6      | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| PhumpK6   | +   | -   | -   | -   | +   | +   | -   | +   | -   | -    | +    | -    | +    | -    | -    | -    |
| DmagK5/6  | +   | -   | +   | -   | -   | +   | +   | +   | +   | -    | -    | -    | +    | -    | -    | -    |