Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BZ92D6014

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Blast report description

Nucleotide Sequence (2521 letters)

RID <u>B8BZ92D6014</u> (Expires on 02-06 12:15 pm)

Query ID | |cl||Query_249449

Description None

Molecule type nucleic acid

Query Length 2521

Database Name nr

Description All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

excluding environmental samples from

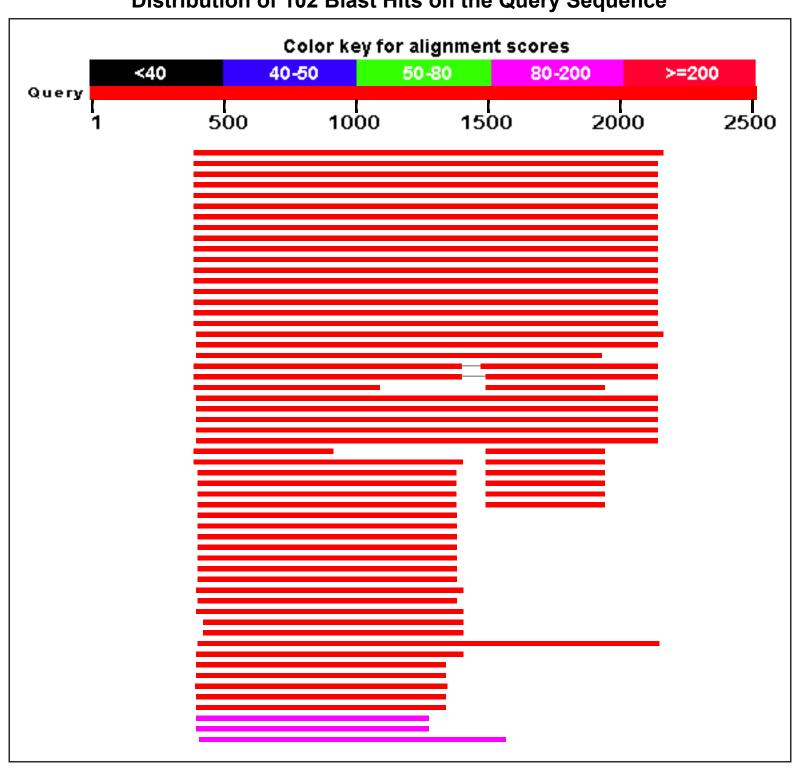
WGS projects

Program BLASTX 2.3.1+

□ Graphic Summary

No putative conserved domains have been detected

Distribution of 102 Blast Hits on the Query Sequence



$\begin{tabular}{ll} \hline \blacksquare \underline{Descriptions} \\ \hline \end{tabular}$

Sequences producing significant alignments:

| Description | Max score | Total score | Query cover | E value | Ident | Accession |
|--|--------------|-------------|----------------|------------|-------|----------------|
| spoonbill, isoform C [Drosophila melanogaster] | 1138 | 1138 | 70% | 0.0 | 100% | NP_726992.2 |
| spoonbill, isoform A [Drosophila melanogaster] | 1125 | 1125 | 69% | 0.0 | 100% | NP_572221.1 |
| GD16260 [Drosophila simulans] | 1075 | 1075 | 69% | 0.0 | 95% | XP_002106186.1 |
| uncharacterized protein Dyak_GE16815 [Drosophila yakuba] | 1066 | 1066 | 69% | 0.0 | 94% | XP_002100012.1 |
| uncharacterized protein Dere_GG18497 [Drosophila erecta] | 1053 | 1053 | 69% | 0.0 | 93% | XP_001976963.1 |
| GM12645 [Drosophila sechellia] | 1004 | 1004 | 69% | 0.0 | 90% | XP_002036917.1 |
| uncharacterized protein Dana_GF20944, isoform A [Drosophila ananassae] | 912 | 912 | 69% | 0.0 | 80% | XP_001964028.1 |
| GL14640 [Drosophila persimilis] | 880 | 880 | 69% | 0.0 | 77% | XP_002022659.1 |
| uncharacterized protein Dpse_GA28855, isoform A [Drosophila pseudoobscura pseudoobscura] | 879 | 879 | 69% | 0.0 | 76% | XP_002134418.1 |
| uncharacterized protein Dwil_GK25472 [Drosophila willistoni] | 871 | 871 | 69% | 0.0 | 78% | XP_002070853.1 |
| GH24358 [Drosophila grimshawi] | 800 | 800 | 69% | 0.0 | 69% | XP_001992176.1 |
| spoon [Drosophila busckii] | 788 | 788 | 69% | 0.0 | 68% | ALC48369.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Stomoxys calcitrans] | 723 | 723 | 69% | 0.0 | 63% | XP_013106377.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Musca domestica] | 709 | 709 | 69% | 0.0 | 60% | XP_005191355.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Bactrocera dorsalis] | 669 | 669 | 69% | 0.0 | 59% | XP_011203797.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Bactrocera oleae] | 662 | 662 | 69% | 0.0 | 59% | XP_014095002.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Bactrocera cucurbitae] | 658 | 658 | 69% | 0.0 | 60% | XP_011195171.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Ceratitis capitata] | 634 | 634 | 69% | 0.0 | 58% | XP_004520186.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Ceratitis capitata] | 624 | 624 | 69% | 0.0 | 57% | XP_004520187.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X3 [Ceratitis capitata] | 579 | 579 | 60% | 0.0 | 59% | XP_004520192.1 |
| uncharacterized protein Dvir_GJ14809 [Drosophila virilis] | 559 | 859 | 66% | 0.0 | 81% | XP_002059514.1 |
| uncharacterized protein Dmoj_GI11050, isoform A [Drosophila mojavensis] | 558 | 849 | 66% | 0.0 | 81% | XP_002011526.1 |
| LD28079p [Drosophila melanogaster] | 459 | 459 | 28% | 1e-152 | 100% | AAL28899.1 |
| a kinase anchor protein [Culex quinquefasciatus] | 434 | 434 | 69% | 6e-138 | 44% | XP_001869726.1 |
| AAEL008431-PA [Aedes aegypti] | 406 | 406 | 69% | 6e-127 | 43% | XP_001659213.1 |
| a kinase anchor protein [Anopheles | | | | | | |

| darlingi] | 339 | 339 | 69% | 2e-101 | 37% | ETN58422.1 |
|---|-----|-----|-----|--------|-----|----------------|
| AGAP002166-PA [Anopheles gambiae str. PEST] | 321 | 321 | 69% | 5e-95 | 38% | XP_308023.5 |
| AGAP002166-PA-like protein [Anopheles sinensis] | 305 | 305 | 69% | 5e-89 | 36% | KFB35785.1 |
| uncharacterized protein Dpse_GA28909 [Drosophila pseudoobscura pseudoobscura] | 285 | 285 | 21% | 7e-87 | 80% | XP_002134417.2 |
| A kinase anchor protein 1, mitochondrial [Zootermopsis nevadensis] | 281 | 281 | 40% | 5e-78 | 43% | KDR20045.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Bombyx mori] | 258 | 258 | 38% | 1e-71 | 43% | XP_004924818.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Papilio polytes] | 255 | 255 | 38% | 3e-71 | 41% | XP_013146233.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Papilio xuthus] | 257 | 257 | 38% | 5e-71 | 42% | XP_013182136.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Papilio polytes] | 256 | 256 | 38% | 9e-71 | 41% | XP_013146231.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Papilio machaon] | 256 | 256 | 38% | 1e-70 | 41% | XP_014370545.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Amyelois transitella] | 254 | 254 | 38% | 3e-70 | 41% | XP_013195864.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Plutella xylostella] | 254 | 254 | 38% | 4e-70 | 42% | XP_011553388.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Bombyx mori] | 254 | 254 | 38% | 5e-70 | 43% | XP_004924816.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X4 [Bombyx mori] | 254 | 254 | 38% | 6e-70 | 42% | XP_004924820.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Amyelois transitella] | 250 | 250 | 38% | 1e-68 | 41% | XP_013195867.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X3 [Bombyx mori] | 249 | 249 | 38% | 2e-68 | 42% | XP_004924819.1 |
| KH domain-containing protein C56G2.1, putative [Pediculus humanus corporis] | 251 | 251 | 39% | 4e-68 | 41% | XP_002426032.1 |
| putative a kinase anchor protein [Danaus plexippus] | 248 | 248 | 38% | 5e-68 | 41% | EHJ63868.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Tribolium castaneum] | 242 | 242 | 39% | 3e-66 | 41% | XP_971237.1 |
| GA16943 [Drosophila affinis] | 230 | 230 | 17% | 4e-66 | 83% | ADJ12817.1 |
| GA16943 [Drosophila miranda] | 228 | 228 | 17% | 2e-65 | 83% | ADJ12818.1 |
| GA16943 [Drosophila pseudoobscura] | 227 | 227 | 17% | 5e-65 | 81% | ADJ12838.1 |
| GA16943 [Drosophila pseudoobscura] | 227 | 227 | 17% | 6e-65 | 81% | ADJ12833.1 |
| GA16943 [Drosophila pseudoobscura] | 227 | 227 | 17% | 6e-65 | 81% | ADJ12832.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Cimex lectularius] | 239 | 239 | 39% | 3e-64 | 39% | XP_014252448.1 |
| PREDICTED: KH domain-containing protein C56G2.1-like [Halyomorpha halys] | 237 | 237 | 39% | 1e-63 | 39% | XP_014271999.1 |
| | | | | | | |

| GA16943 [Drosophila pseudoobscura] | 221 | 221 | 17% | 4e-63 | 80% | ADJ12839.1 |
|---|-----|-----|-----|-------|-----|----------------|
| GA16943 [Drosophila pseudoobscura] | 221 | 221 | 17% | 4e-63 | 80% | ADJ12840.1 |
| KH domain-containing protein [Operophtera brumata] | 227 | 227 | 69% | 1e-60 | 31% | KOB79527.1 |
| hypothetical protein D910_06197 [Dendroctonus ponderosae] | 217 | 217 | 40% | 5e-58 | 38% | ERL88815.1 |
| hypothetical protein YQE_07610 [Dendroctonus ponderosae] | 208 | 208 | 37% | 3e-56 | 39% | ENN75881.1 |
| PREDICTED: uncharacterized protein LOC106471261 [Limulus polyphemus] | 221 | 221 | 37% | 4e-56 | 39% | XP_013787306.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like [Limulus polyphemus] | 208 | 208 | 37% | 3e-55 | 36% | XP_013775508.1 |
| PREDICTED: uncharacterized protein LOC106806733 isoform X2 [Priapulus caudatus] | 208 | 208 | 37% | 4e-53 | 38% | XP_014664261.1 |
| PREDICTED: uncharacterized protein LOC106806733 isoform X1 [Priapulus caudatus] | 205 | 205 | 37% | 4e-52 | 38% | XP_014664258.1 |
| hypothetical protein DAPPUDRAFT_322467 [Daphnia pulex] | 192 | 192 | 34% | 2e-49 | 37% | EFX76340.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X2 [Lingula anatina] | 193 | 193 | 34% | 7e-49 | 37% | XP_013383304.1 |
| PREDICTED: LOW QUALITY PROTEIN: KH domain-containing protein C56G2.1 [Apis florea] | 192 | 192 | 46% | 8e-49 | 34% | XP_012339869.1 |
| PREDICTED: KH domain-containing protein C56G2.1-like isoform X1 [Apis mellifera] | 192 | 192 | 47% | 1e-48 | 34% | XP_006564454.1 |
| PREDICTED: KH domain-containing protein C56G2.1-like isoform X1 [Apis dorsata] | 192 | 192 | 46% | 1e-48 | 34% | XP_006623065.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X3 [Crassostrea gigas] | 194 | 194 | 39% | 1e-48 | 36% | XP_011449476.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Nasonia vitripennis] | 191 | 191 | 38% | 2e-48 | 36% | XP_001601576.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X2 [Crassostrea gigas] | 193 | 193 | 39% | 2e-48 | 36% | XP_011449475.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Athalia rosae] | 190 | 190 | 35% | 3e-48 | 37% | XP_012251572.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Bombus terrestris] | 188 | 188 | 46% | 2e-47 | 32% | XP_012169146.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X1 [Crassostrea gigas] | 190 | 190 | 39% | 3e-47 | 36% | XP_011449473.1 |
| K Homology domain containing protein [Oryctes borbonicus] | 187 | 187 | 60% | 3e-47 | 30% | KRT85600.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X1 [Lingula anatina] | 187 | 187 | 34% | 8e-47 | 35% | XP_013383303.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X2 [Aplysia californica] | 188 | 188 | 39% | 4e-46 | 36% | XP_005093022.2 |
| PREDICTED: KH domain-containing protein akap-1 [Diachasma alloeum] | 183 | 183 | 38% | 5e-46 | 35% | XP_015113342.1 |

| PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X1 [Aplysia californica] | 187 | 187 | 39% | 5e-46 | 36% | XP_012934994.1 |
|---|-----|-----|-----|-------|-----|----------------|
| PREDICTED: KH domain-containing protein C56G2.1 [Bombus impatiens] | 184 | 184 | 37% | 6e-46 | 35% | XP_003485511.1 |
| PREDICTED: KH domain-containing protein C56G2.1-like isoform X2 [Ceratosolen solmsi marchali] | 183 | 183 | 37% | 8e-46 | 35% | XP_011499408.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Fopius arisanus] | 182 | 182 | 38% | 9e-46 | 35% | XP_011312236.1 |
| PREDICTED: uncharacterized protein LOC106075240 [Biomphalaria glabrata] | 187 | 187 | 40% | 1e-45 | 36% | XP_013091637.1 |
| KH domain-containing protein C56G2.1 [Melipona quadrifasciata] | 184 | 184 | 38% | 3e-45 | 37% | KOX67995.1 |
| PREDICTED: KH domain-containing protein C56G2.1-like isoform X1 [Ceratosolen solmsi marchali] | 183 | 183 | 37% | 3e-45 | 35% | XP_011499407.1 |
| A-kinase anchor protein 1, mitochondrial [Stegodyphus mimosarum] | 182 | 182 | 31% | 5e-45 | 36% | KFM63633.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Megachile rotundata] | 180 | 180 | 67% | 1e-44 | 29% | XP_012135254.1 |
| KH domain-containing protein C56G2.1 [Habropoda laboriosa] | 179 | 179 | 37% | 2e-44 | 35% | KOC60170.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Strongylocentrotus purpuratus] | 179 | 179 | 41% | 6e-44 | 34% | XP_001199246.2 |
| PREDICTED: KH domain-containing protein C56G2.1 [Orussus abietinus] | 175 | 175 | 37% | 6e-43 | 34% | XP_012282550.1 |
| PREDICTED: KH domain-containing protein akap-1-like [Polistes canadensis] | 173 | 173 | 68% | 3e-42 | 27% | XP_014605983.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Copidosoma floridanum] | 173 | 173 | 35% | 4e-42 | 34% | XP_014214042.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Trichogramma pretiosum] | 173 | 173 | 36% | 5e-42 | 34% | XP_014232188.1 |
| PREDICTED: KH domain-containing protein C56G2.1 isoform X2 [Harpegnathos saltator] | 171 | 171 | 37% | 1e-41 | 35% | XP_011146583.1 |
| PREDICTED: KH domain-containing protein C56G2.1 isoform X1 [Harpegnathos saltator] | 170 | 170 | 37% | 3e-41 | 35% | XP_011146579.1 |
| A kinase anchor protein 1, mitochondrial [Crassostrea gigas] | 172 | 172 | 38% | 4e-41 | 35% | EKC18066.1 |
| A-kinase anchor protein 1, mitochondrial- like [Scleropages formosus] | 164 | 164 | 38% | 5e-41 | 31% | KPP61448.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Xiphophorus maculatus] | 171 | 171 | 39% | 1e-40 | 32% | XP_014327381.1 |
| PREDICTED: KH domain-containing protein akap-1 [Polistes dominula] | 168 | 168 | 37% | 1e-40 | 34% | XP_015175799.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial [Sarcophilus harrisii] | 171 | 171 | 37% | 2e-40 | 33% | XP_003768007.1 |
| PREDICTED: KH domain-containing protein C56G2.1 [Microplitis demolitor] | 168 | 168 | 38% | 2e-40 | 34% | XP_008550029.1 |
| PREDICTED: A-kinase anchor protein 1, mitochondrial-like [Salmo salar] | 169 | 169 | 40% | 9e-40 | 32% | XP_014018688.1 |

Alignments

spoonbill, isoform C [Drosophila melanogaster]

Sequence ID: ref|NP_726992.2| Length: 607 Number of Matches: 1

▶ See 2 more title(s) Range 1: 16 to 607

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|------------------------------|---------------|-----------|--------|
| 1138 bit | s(2943) | 0.0() Compositional matrix adjust. | 592/592(100%) | 592/592(100%) | 0/592(0%) | -2 |
| Features | s: | | | | | |
| Query | 2169 | IFQYSAKMVSGRPLLYLSLPGVAFIL | | | | |
| Sbjct | 16 | IFQYSAKMVSGRPLLYLSLPGVAFIL IFQYSAKMVSGRPLLYLSLPGVAFIL | | | | |
| Query | 1989 | ARKANGVLQNGKLPQQSASKSMNING | | | | |
| Sbjct | 76 | ARKANGVLQNGKLPQQSASKSMNING ARKANGVLQNGKLPQQSASKSMNING | | | | |
| Query | 1809 | SNGRTSNGKHQQQIDSEILKSKIQDA | | | | |
| Sbjct | 136 | SNGRTSNGKHQQQIDSEILKSKIQDA SNGRTSNGKHQQQIDSEILKSKIQDA | | | | |
| Query | 1629 | KATOKTVEPVVIKATRTPKISPENSF KATOKTVEPVVIKATRTPKISPENSF | | | | |
| Sbjct | 196 | KATOKTVEPVVIKATRIPKISPENSE | | | | |
| Query | 1449 | dqeQTVLKEEVVDSNGNQKRNVDAAS DQEQTVLKEEVVDSNGNQKRNVDAAS | | | | |
| Sbjct | 256 | DQEQTVLKEEVVDSNGNQKRNVDAAS | | | | |
| Query | 1269 | FPISLIGHLYGRKRAFINQIKAKTLA FPISLIGHLYGRKRAFINQIKAKTLA | | | | |
| Sbjct | 316 | FPISLIGHLYGRKRAFINQIKAKTLA FPISLIGHLYGRKRAFINQIKAKTLA | SVSVGKNP15GK SVSVGKNPYSGK | VRICTIEGTESI | EIDAALAMI | RQ 375 |
| Query | 1089 | RLPAKRYPNFTMQRIHFALPQTIVPL RLPAKRYPNFTMQRIHFALPQTIVPL | | | | |
| Sbjct | 376 | RLPAKRYPNFTMQRIHFALPQTIVPL | | | | |
| Query | 909 | hplhpshpslplLQKQLYDSYSTMEA HPLHPSHPSLPLLQKQLYDSYSTMEA | | | | |
| Sbjct | 436 | HPLHPSHPSLPLLQKQLYDSYSTMEA | | | | |
| Query | 729 | RCVIKFLDFGGYMNVGFNTLRQIRTD | | | | |
| Sbjct | 496 | RCVIKFLDFGGYMNVGFNTLRQIRTD RCVIKFLDFGGYMNVGFNTLRQIRTD | | | | |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFAS | | | | |
| Sbjct | 556 | TKGIVLQAQVAGYNSHNLPEIFLFAS TKGIVLQAQVAGYNSHNLPEIFLFAS | | | | |

spoonbill, isoform A [Drosophila melanogaster]

Sequence ID: ref|NP_572221.1| Length: 585 Number of Matches: 1

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|-----------------|-----------------|----------------|-------|
| 1125 bit | s(2910) | 0.0() Compositional matrix adjus | t. 585/585(100° | %) 585/585(100% | %) 0/585(0%) - | -2 |
| Feature | s: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFR MVSGRPLLYLSLPGVAFILGVFWFR | | | | |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFR | | | | |
| Query | 1968 | LQNGKLPQQSASKSMNINGTLVNgs LQNGKLPQQSASKSMNINGTLVNGS | | | | |
| Sbjct | 61 | LÕNGKLPÕÕSASKSMNINGTLVNGS | | | | |
| Query | 1788 | GKHQQQIDSEILKSKIQDAEHKTLC GKHQQQIDSEILKSKIQDAEHKTLC | | | | |
| Sbjct | 121 | GKHQQQIDSEILKSKIQDAEHKTLC | | | | |

| Query | 1608 | EPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPKEEPSKKEAdqeeleqdqeQTVL | 1429 |
|-------|------|--|------|
| Sbjct | 181 | EPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPKEEPSKKEADQEELEQDQEQTVL EPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPKEEPSKKEADQEELEQDQEQTVL | 240 |
| Query | 1428 | KEEVVDSNGNQKRNVDAASPSLSICSVQSGDSGKGSSLPRSEATRVKTTYEFLFPISLIG | 1249 |
| Sbjct | 241 | KEEVVDSNGNQKRNVDAASPSLSICSVQSGDSGKGSSLPRSEATRVKTTYEFLFPISLIG KEEVVDSNGNQKRNVDAASPSLSICSVQSGDSGKGSSLPRSEATRVKTTYEFLFPISLIG | 300 |
| Query | 1248 | HLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALAMIRQRLPAKRY | 1069 |
| Sbjct | 301 | HLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALAMIRQRLPAKRY HLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALAMIRQRLPAKRY | 360 |
| Query | 1068 | PNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSHIFIQhplhpsh | 889 |
| Sbjct | 361 | PNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSHIFIQHPLHPSH PNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSHIFIQHPLHPSH | 420 |
| Query | 888 | pslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFL | 709 |
| Sbjct | 421 | PSLPLLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFL PSLPLLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFL | 480 |
| Query | 708 | DFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTKGIVLQ | 529 |
| Sbjct | 481 | DFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTKGIVLQ DFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTKGIVLQ | 540 |
| Query | 528 | AQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD 394 | |
| Sbjct | 541 | AQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD AQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD 585 | |

GD16260 [Drosophila simulans]

Sequence ID: ref|XP_002106186.1| Length: 593 Number of Matches: 1

▶ See 2 more title(s) Range 1: 1 to 593

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|------------------------------|------------------------------|---------------------|---------|
| 1075 bit | s(2781) | 0.0() Compositional matrix adjust. | 568/595(95%) | 576/595(96%) | 12/595(2%) | -2 |
| Features | s: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRRF MVSGRPLLYLSLPGVAFILGVFWFRRF | | | | |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFRRF | | | | |
| Query | 1968 | LQNGKLPQQSASKSMNINGTLVNgsgs LONGKLPOO ASKSMNI+GTLVNGSGS | | SPTTMLYGKSAE SPTTMLYGKSAE | | |
| Sbjct | 61 | LQNGKLPQQPASKSMNIDGTLVNGSGS | | | | |
| Query | 1788 | GKHQQQIDSEILKSKIQDAEHKTLCSI GKHQQQIDSEILKSKIQDAEHKTLCSI | | | | |
| Sbjct | 119 | GKHQQQIDSEILKSKIQDAEHKTLCSI | | | | |
| Query | 1608 | EPVVIKATRTPKISPENSFLDTNYTNK EPVVIKATRTPKISPENSFLDTNYTNK | | | PSKKEAdq SKKEADO | |
| Sbjct | 179 | EPVVIKATRTPKISPENSFLDTNYTNK | KECEONNNCEPK KECEONNNCEPK | KEEPAKEEPAKE | | |
| Query | 1458 | leqdqeQTVLKEEVVDSNGNQKRNVDA LEQDQEQTVLKEEVVD+NGNQKRNVDA | ASPSLSICSVO |)SGDSGKGSSLE | PRSEATRVKT | TY 1279 |
| Sbjct | 239 | LEQDQEQTVLKEEVVDNNGNQKRNVDA | | | | |
| Query | 1278 | EFLFPISLIGHLYGRKRAFINQIKAKT EFLFPISLIGHLYGRKRAFINOIKAKT | | | | |
| Sbjct | 299 | EFLFPISLIGHLYGRKRAFINQIKAKI | | | | |
| Query | 1098 | IRQRLPAKRYPNFTMQRIHFALPQTIV IRQRLPAKRYPNFTMQRIHFALPQTIV | | | | |
| Sbjct | 359 | IRQRLPAKRYPNFTMQRIHFALPQTIV | PLSTESLYNLQ | LKLIEGINNDV | VVSAVLSGS | HI 418 |
| Query | 918 | FIQhplhpshpslplLQKQLYDSYSTM FIQHPLHPSHPSLPLLQKQLYDSYSTM | | | | |
| Sbjct | 419 | FIQHPLHPSHPSLPLLQKQLYDSYSTM | | | | |
| Query | 738 | DEERCVIKFLDFGGYMNVGFNTLRQIF DEERCVIKFLDFGGYMNVGFNTLRQIF | | | | |
| Sbjct | 479 | DEERCVIKFLDFGGYMNVGFNTLRQIF | | | | |
| Query | 558 | NKLTKGIVLQAQVAGYNSHNLPEIFLF N+LTKGIVLOAOVAGYNSHN+PEIFLF | | | | 94 |
| Sbjct | 539 | NOLTKGIVLQAQVAGYNSHNIPEIFLF | | | | 93 |

uncharacterized protein Dyak_GE16815 [Drosophila yakuba]

Sequence ID: ref|XP_002100012.1| Length: 590 Number of Matches: 1

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|---------|----------------|--|--------------|--------------|------------------------|----------|
| 1066 bit | s(2756) | 0.0() | Compositional matrix adjust. | 552/590(94%) | 573/590(97%) | 5/590(0%) | -2 |
| Features | s: | | | | | | |
| Query | 2148 | | RPLLYLSLPGVAFILGVFWFRRF RPLLYLSLPGVAFILGVFWFRRF | | | | |
| Sbjct | 1 | | RPLLYLSLPGVAFILGVFWFRRF | | | | |
| Query | 1968 | LONGK | KLPQQSASKSMNINGTLVNgsgs KLPQQ ASKSMNINGT+VNGSGS | gsgssSDEKDS | PTTMLYGKSAP | IKIOSNGRT | 'SN 1789 |
| Sbjct | 61 | | KLPQQ ABKBHNINGI VNGBGE KLPQQPASKSMNINGTIVNGSGS | | | | |
| Query | 1788 | | QOIDSEILKSKIQDAEHKTLCSI QOIDSE+LKSKIQDAEHK LCSI | | | | |
| Sbjct | 121 | | QQIDSEMLKSKIQDAEHKKLCSI | | | | |
| Query | 1608 | | KATRTPKISPENSFLDTNYTN KATRTPKISPENSFLDTNYT K | | | EAdqeeleq EADQEEL+C | |
| Sbjct | 181 | | KATRTPKISPENSFLDTNYTTK | | | | |
| Query | 1443 | | .KEEVVDSNGNQKRNVDAASPSI .KEEVVDSNGNQKRNVDAASPSI | | | | |
| Sbjct | 241 | | LKEEVVDSNGNQKRNVDAASPSI | | | | |
| Query | 1263 | | SHLYGRKRAFINQIKAKTLASVS SHLYGRKRAFINQIKAKTLASV+ | | | | |
| Sbjct | 301 | | GHLYGRKRAFINQIKAKTLASVA | | | | |
| Query | 1083 | | ZPNFTMQRIHFALPQTIVPLSTE ZPNFTMQRIHFALPQTIVPLS E | | | | |
| Sbjct | 361 | | PNFTMQRIHFALPQTIVPLSNE | | | | |
| Query | 903 | | npslplLQKQLYDSYSTMEAPLI IPSLP+LQKQLYDSYSTMEAPLI | | | | |
| Sbjct | 421 | | IPSLPMLQKQLYDSYSTMEAPLI | | | | |
| Query | 723 | VIKFI ++KFI | DFGGYMNVGFNTLRQIRTDFMN DFGGYMNVGF+TLRQIRTDFMN | VPFOSTECILS | NIEPIGGTWSII | EAAEILNKI EAAETIN+T | TK 544 |
| Sbjct | 481 | | LDFGGYMNVGFSTLRQIRTDFMN | | | | |
| Query | 543 | | QAQVAGYNSHNLPEIFLFASLGE QAQVAGYNSHN+PEI+LFASLGE | | | | |
| Sbjct | 541 | | AQVAGYNSHNIPEIYLFASLGE | | | | |

uncharacterized protein Dere_GG18497 [Drosophila erecta]

Sequence ID: ref|XP_001976963.1| Length: 588 Number of Matches: 1

| Score | | Expect | Method | | Identities | Positives | Gaps F | rame |
|-----------|------------|--------|--------------------------------|---------------|------------------------------|--------------|--------------------------|------|
| 1053 bits | s(2722) | 0.0() | Compositional m | atrix adjust. | 547/590(93%) | 568/590(96%) | 7/590(1%) -2 | 2 |
| Features |) : | | | | | | | |
| Query | 2148 | | PLLYLSLPGVAFI PLLYLSLPGVAFI | | | | | |
| Sbjct | 1 | | PLLYLSLPGVAF1 | | | | | |
| Query | 1968 | | LPQQSASKSMNIN LPQQ ASKSMNIN | | gsgssSDEKDS GSGSSSDEKDS | | | |
| Sbjct | 61 | | LPQQPASKSMNIN | | | | | |
| Query | 1788 | | QIDSEILKSKIQI QIDSE+LKSKIQI | | | | | |
| Sbjct | 119 | | QIDSEMLKSKIÕD | | | | | |
| Query | 1608 | | KATRTPKISPENS KATRTPKISPENS | | ECEONNNCEPKI ECEONNNCEPKI | | EAdqeeleqdo EADOE L+O | |
| Sbjct | 179 | | KATRTPKISPENS | | | | | |
| Query | 1443 | | KEEVVDSNGNQKF KEEVVDSNGNQKF | | | | | |
| Sbjct | 239 | | KEEVVDSNGNÕKF | | | | | |
| Query | 1263 | | HLYGRKRAFINQI HLYGRKRAFINQI | | | | | |
| Sbjct | 299 | | HLYGRKRAFINÕI | | | | | |
| Query | 1083 | | PNFTMQRIHFALE PNFTMQRIHFALE | | | | | |
| Sbjct | 359 | | PNFTMQRIHFALE | | | | | |
| Query | 903 | | pslplLQKQLYDS PSLP+LQKQLYDS | | | | | |
| Sbjct | 419 | | PSLPMLQKQLYDS | | | | | |

| Query Sbjct | 723 479 | VIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTK ++KFLDFGGYMNVGF+TLRQIRTDFMNVPFQ+TECILSNIEPIGGTWSIEAAEILN+LTK LVKFLDFGGYMNVGFSTLRQIRTDFMNVPFQATECILSNIEPIGGTWSIEAAEILNQLTK | 544 538 |
|----------------|------------|--|------------|
| ~ 1 | 543 539 | GIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD 394 GIVLQAQVAGYNSHN+PEI+LFASLGPNNVIFINKELV R LAKWVEM D GIVLQAQVAGYNSHNIPEIYLFASLGPNNVIFINKELVARNLAKWVEMRD 588 | |

GM12645 [Drosophila sechellia]

Sequence ID: ref|XP_002036917.1| Length: 573 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 573

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|----------|--------|--|--------------|----------------------------|--------------|---------|
| 1004 bit | ts(2596) | 0.0() | Compositional matrix adjust. | 542/600(90%) | 550/600(91% |) 42/600(7%) | -2 |
| Feature | s: | | | | | | |
| Query | 2148 | | RPLLYLSLPGVAFILGVFWFRRI RPLLYLSLPGVAFILGVFWFRRI | | | | |
| Sbjct | 1 | | RPLLYLSLPGVAFILGVFWFRRI | | | | |
| Query | 1968 | | TLPQQSASKSMNINGTLVNgsg TLPQQ ASKSMNI+GTLVNGSG | | SPTTMLYGKSA SPTTMLYGKSA | | |
| Sbjct | 61 | | LPQQ ASKSMNITGILVNGSG. LPQQPASKSMNIDGTLVNGSG. | | | | |
| Query | 1788 | | QIDSEILKSKIQDAEHKTLCS QIDSEILKSKIQDAEHKTLCS | | | | |
| Sbjct | 119 | | QIDSEILKSKIQDAEHKTLCS: | | | | |
| Query | 1608 | | KATRTPKISPENSFLDTNYTNI KATRTPKISPENSFLDTNYTNI | | | | KE 1474 |
| Sbjct | 179 | EPVVI | KATRTPKISPENSFLDTNYTNI | KECEQNNNCEP! | KEEPAKEEPAK | | |
| Query | 1473 | | eleqdqeQTVLKEEVVDSNGNQI CLEQDQEQTVLKEEVVD+NGNQI | | | KGSSLPRSEA | TR 1294 |
| Sbjct | 239 | | LEQDQEQTVLKEEVVD+NGNQI | | | | 279 |
| Query | 1293 | VKTTY | EFLFPISLIGHLYGRKRAFING FLFPISLIGHLYGRKRAFING | | | | |
| Sbjct | 280 | | -FLFPISLIGHLYGRKRAFING | | | | |
| Query | 1113 | | IIRQRLPAKRYPNFTMQRIHFA IIRQRLPAKRYPNFTMQRIHFA | | | | |
| Sbjct | 334 | | IIRQRLPAKRYPNFTMQRIHFAI IIRQRLPAKRYPNFTMQRIHFAI | | | | |
| Query | 933 | SGSHI | FIQhplhpshpslplLQKQLYI FIQHPLHPSHPSLPLLQKQLYI | OSYSTMEAPLLE | PSLELSAVCVI | PINDVWYRVO | IV 754 |
| Sbjct | 394 | | FIQHPLHPSHPSLPLLQKQLYI | | | | |
| Query | 753 | | DEERCVIKFLDFGGYMNVGFN | | | | |
| Sbjct | 454 | | DEERCVIKFLDFGGYMNVGFN DEERCVIKFLDFGGYMNVGFN | | | | |
| Query | 573 | | NKLTKGIVLQAQVAGYNSHNLI | | | | |
| Sbjct | 514 | | N+LTKGIVLQAQVAGYNSHN+1 NQLTKGIVLQAQVAGYNSHNII | | | | |
| | | | | | | | |

uncharacterized protein Dana_GF20944, isoform A [Drosophila ananassae] Sequence ID: **ref|XP_001964028.1|** Length: 610 Number of Matches: 1

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|--------|--|--------------|--------------|-------------------------|-------|
| 912 bits | (2358) | 0.0() Compositional matrix adjust. | 486/611(80%) | 525/611(85%) | 27/611(4%) | -2 |
| Features | s: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRR MVSGRPLLYLSLPGVAFILGVFWFRR | | | SIEPTV-QAR +E TV + R | |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFRR | • | | | |
| Query | 1977 | NGVLQNGKLPQQSASKSMNINGTLVN NGVLONGKLPO A+KSMNINGT+ N | | | TMLYGKSAP TMLYGKSAP | |
| Sbjct | 61 | NGVLQNGKLPQ-PATKSMNINGTIAN | | | | |
| Query | 1815 | IQSNGRTSNGKHQQQIDSEILKSKIQ IQSNGRT GKHQQQIDSE+LKSKIQ | | | | |
| Sbjct | 120 | IQSNGRTPPGKHQQQIDSEHLKSKIQ | | | | |

| Query | 1635 | NRKATQKTVEPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPKEEPRKKKTVEPVVIKATRTPKISPENSFLDTNYECEQNNNCEPKEPP | 1486 |
|-------|------|--|------|
| Sbjct | 180 | KRKTNSKTVEPVVIKATRTPKISPENSFLDTNYTTTAPTTAGSECEQNNNCEPKSEVVVP | 239 |
| Query | 1485 | SKKEAdqeeleqdqeQTVLKEEVVDSNGNQKRNVDAASPSLSICSVQSGDSGK +KKE + ++ ++ +++ VDSNGN QKRNVDAASPSLSICSVQSGDSGK | 1327 |
| Sbjct | 240 | AKKEEQLAQQKEQVDEQQQQQQQTELDVDSNGNTNQKRNVDAASPSLSICSVQSGDSGK | 299 |
| Query | 1326 | GSSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRI GSSLPRSEATR KT+YEFLFP SLIG LYGRKR FINQIK+KTLA+V + KNPYS KVRI | 1147 |
| Sbjct | 300 | GSSLPRSEATRAKTSYEFLFPNSLIGQLYGRKRMFINQIKSKTLANVVLSKNPYSAKVRI | 359 |
| Query | 1146 | CTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEG CTIEGT+SEIDAALAMIRQRLP+KRYPNFTMQRIHFALPQTIVPLSTESL NLQLKLIEG | 967 |
| Sbjct | 360 | CTIEGT+SEIDAALAMIRQRLPSKRYPNFTMQRIHFALPQTIVPLSTESLNNLQLKLIEG | 419 |
| Query | 966 | INNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPINNDVVVSAVLSGSH F+QHPLHPSHPSLP+LQKQLYDSYSTMEAP LPSLE+SAVCVIP | 787 |
| Sbjct | 420 | INNDVVVSAVLSGSHFFVQHPLHPSHPSLPMLQKQLYDSYSTMEAPPLPSLEISAVCVIP | 479 |
| Query | 786 | INDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSN IN VWYRVQIVD DPEDEERCV++FLDFGGYMNVGF+ LRQIR DFM+VPFQ+TECILSN | 607 |
| Sbjct | 480 | INGVWYRVQIVDVDPEDEERCVVRFLDFGGYMNVGFSLLRQIRADFMSVPFQATECILSN | 539 |
| Query | 606 | IEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVG +EPIG WSIEAAEILN+LTKGIVLQAQVAGYNSHN+PE++LFASLGPNNVIFINKELV | 427 |
| Sbjct | 540 | VEPIGDNWSIEAAEILNQLTKGIVLQAQVAGYNSHNIPEVYLFASLGPNNVIFINKELVA | 599 |
| Query | 426 | RKLAKWVEMSD 394 R LAKWVE+ D | |
| Sbjct | 600 | RNLAKWVEIRD 610 | |
| | | | |

GL14640 [Drosophila persimilis]

Sequence ID: ref|XP_002022659.1| Length: 605 Number of Matches: 1

| Score | | Expect Method | | Identities | Positives | Gaps | Frame |
|----------|----------|----------------------------|--------------------------------------|-------------------------------|----------------------------|----------------------------|--------------|
| 880 bits | (2275) (| 0.0() Compos | sitional matrix adjust. | 466/609(77%) | 508/609(83%) | 28/609(4%) | -2 |
| Features | s: | | | | | | |
| Query | 2148 | | SLPGVAFILGVFWFRR | | | | |
| Sbjct | 1 | | SLPGVAFILGVFWFRR SLPGVAFILGVFWFRR | | | + V+AR AI VVSHVEARTAI | |
| Query | 1971 | VLQNGKLPQ LONGKLP | QSASKSMNINGTL Q A+KSMNINGT | | SDEKDSPTTML SDEK+SP TML | | |
| Sbjct | 61 | | FLLQQATKSMNINGTD | | | | |
| Query | 1803 | | QIDSEILKSKIQDAEH QIDSE+LKSKIQDAEH | | | | |
| Sbjct | 121 | | ÕIDSEMLKSKIÕDAEH | | | | |
| Query | 1623 | | KATRTPKISPENSFLD KATRTPKISPENSFL+ | | | | 1477 |
| Sbjct | 180 | | KATRTPKISPENSFLE | | | KVAVVEEKPKI | PK 236 |
| Query | 1476 | EA | dqeeleqdqeQTVLKE QT +KE | | NVDAASPSLSI NVDAASPSLSI | | |
| Sbjct | 237 | PNPNPNPKEA | AVVGYHDCDIÕTDIKE | TDTDNNGNQKR | NVDAASPSLSI | CSVÕSGDSGK | GS 296 |
| Query | 1320 | | KTTYEFLFPISLIGHL K +YEF+FP+SLIG I | | | | |
| Sbjct | 297 | SLPRSEATRV | KVSYEFVFPVSLIGQL | YGRKRAFINQI: | KAKTQANVLLS | KNPCTNKLRI | CV 356 |
| Query | 1140 | | ALAMIRQRLPAKRYPN ALAMIRQRLP KRYPN | | | | |
| Sbjct | 357 | | ALAMIRÕRLPVKRYPN | | | | |
| Query | 960 | NDVVVSAVLSO NDVVVSAVLSO | GSHIFIQhplhpshps GSH+F+ HPLHPSHP+ | lplLQKQLYDS | YSTMEAPLLPS YS MEAPLLP | LELSAVCVIP: +E+SAVCV+P- | IN 781 +N |
| Sbjct | 417 | | GSHLFVNHPLHPSHPA | | | | |
| Query | 780 | DVWYRVQIVD' +WYRVÕIVD | IDPEDEERCVIKFLDF D +DEERCV+KFLDF | 'GGYMNVGFNTL' 'GGYMNV + L' | RQIRTDFMNVP ROIRTDFM VP | FOSTECILSNI FO+TECILSNI | IE 601 IE |
| Sbjct | 477 | | LDEDDEERCVVKFLDF | | | | |
| Query | 600 | | AEILNKLTKGIVLQAQ ++L+KLTKGIVLQAQ | | | | |
| Sbjct | 537 | | IDVLSKLTKGIVLÕAÕ | | | | |
| Query | 420 | LAKWVEMSD LAKWVEM D | 394 | | | | |
| Sbjct | 597 | LAKWVEMRD | 605 | | | | |
| | | | | | | | |

uncharacterized protein Dpse_GA28855, isoform A [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_002134418.1**| Length: 605 Number of Matches: 1

See 3 more title(s)

Range 1: 1 to 605

| Score | Expect | Method | Identities | Positives | Gaps F | rame |
|--------------|----------------|--|------------------|----------------|--------------------------------|-------|
| 879 bits(227 | 2) 0.0() | Compositional matrix adju | ıst. 466/611(76% | 6) 508/611(83% | 5) 32/611(5%) -2 | 2 |
| Features: | | | | | | |
| Query 21 | | RPLLYLSLPGVAFILGVFWI | | | | |
| Sbjct 1 | | RPLLYLSLPGVAFILGVFWI RPLLYLSLPGVAFILGVFWI | | | + V+AR ANG GVVSHVEARTANG | |
| Query 19 | ~ | GKLPQQSASKSMNING GKLP QQ A+KSMNING | | | LYGKSAPIKIQSI LYGKSAPIKIQSI | |
| Sbjct 61 | | GKLPTSFLQQQATKSMNING | | | | |
| Query 18 | 03 GRTS GRT | NGKHQQQIDSEILKSKIQDA G QQQIDSE+LKSKIQDA | | | | A 162 |
| Sbjct 12 | | PGV-QQQIDSEMLKSKIQDA | | | | г 179 |
| Query 16 | | VEPVVIKATRTPKISPENSI VEPVVIKATRTPKISPENSI | | | КК кк | - 147 |
| Sbjct 18 | | VEPVVIKATRTPKISPENSI | | | | 236 |
| Query 14 | 76 | EAdqeeleqdqeQ | | | LSICSVQSGDSG LSICSVQSGDSG | |
| Sbjct 23 | 7 PKPN | PSPNPKEAAVVGHHDCDIQ | | | | |
| Query 13 | | PRSEATRVKTTYEFLFPISI PRSEATRVK +YEF+FP+SI | | | | |
| Sbjct 29 | | PRSEATRVKVSYEFVFPVSI | | | | |
| Query 11 | | GTESEIDAALAMIRQRLPAI GTESEIDAALAMIRQRLP I | | | | |
| Sbjct 35 | | GTESEIDAALAMIRÕRLPVI | | | | |
| Query 96 | | VVVSAVLSGSHIFIQhplhr VVVSAVLSGSH+F+ HPLHI | | | | |
| Sbjct 41 | | VVVSAVLSGSHLFVNHPLHI | | | | |
| Query 78 | | WYRVQIVDTDPEDEERCVII WYRVQIVD D +DEERCV+I | | | | |
| Sbjct 47 | 5 VNGI | WYRVÕIVDLDEDDEERCVVI | KFLDFGGYMNVNL | SVLRÕIRTDFM | VVPFÕATECILSI | 534 |
| Query 60 | | GGTWSIEAAEILNKLTKGIV GTWS+EA ++L+KLTKGIV | | | | G 427 |
| Sbjct 53 | | NGTWSLEAIDVLSKLTKGIV | | | | A 594 |
| Query 42 | | KWVEMSD 394 KWVEM D | | | | |
| Sbjct 59 | | KWVEMRD 605 | | | | |

uncharacterized protein Dwil_GK25472 [Drosophila willistoni]

Sequence ID: ref|XP_002070853.1| Length: 595 Number of Matches: 1

| Score | | Expect | Method | | | Identities | Positives | Gaps | Frame |
|-----------|------------|-------------|-------------------|------------|-------------|------------------------------|----------------------------|------------------------|----------|
| 871 bits(| (2251) (| 0.0() | Composi | tional mat | rix adjust. | 470/606(78%) | 516/606(85%) | 32/606(5%) | -2 |
| Features | 5 : | | | | | | | | |
| Query | 2148 | | | | | RYKNCLDKPDD RR KN LDKPDD | | | XAN 1975 |
| Sbjct | 1 | | | | | RNKNRLDKPDD | | | |
| Query | 1974 | | NGKLPQQ NGKLPQ | | | 'NgsgsgsgssS 'NG+ | | | |
| Sbjct | 61 | | | | | NGN | | | |
| Query | 1803 | GRTS GR+ | | | | LKSKIQDAEHK LKSKIQDAEHK | | | |
| Sbjct | 112 | | | | | LKSKIQDAEHK | | | |
| Query | 1653 | | FYNRKA- FYNRK+ | | | ATRTPKISPENS ATRTPKISPENS | | -CEQNNNCEP EONNNC P | |
| Sbjct | 171 | | | | | TRIPKISPENS | | | |
| Query | 1491 | EPSK E + | | | | DSNGNQKRNVD. KR VD. | AASPSLSICSV AASPSLSICS+ | | |

| Sbjct | 230 | EVEEEVILNQQQQQEQQTVVTDVQQQQQQQQPKRQVDAASPSLSICSIQSGDSGKGSSLP | 289 |
|-------|------|--|------|
| Query | 1311 | RSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEG | 1132 |
| Sbjct | 290 | RSEATR+KT YEFLFPISLIG LYGRKRAFINQIK KTLASVS+GKNPYSGKVRICTIEG RSEATRIKTKYEFLFPISLIGQLYGRKRAFINQIKTKTLASVSLGKNPYSGKVRICTIEG | 349 |
| Query | 1131 | TESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDV | 952 |
| Sbjct | 350 | TESEIDAAL+MIRQRLP+KRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDV TESEIDAALSMIRQRLPSKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDV | 409 |
| Query | 951 | VVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVW | 772 |
| Sbjct | 410 | VVSAVLSGSH+F+QHPLHPSHPSLP+LQK LYDSY+TM+APLLPS+E+SAVCV+PIN++W VVSAVLSGSHVFVQHPLHPSHPSLPMLQKGLYDSYTTMDAPLLPSIEISAVCVMPINEIW | 469 |
| Query | 771 | YRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIG | 592 |
| Sbjct | 470 | YRVQIVDTDPED ERC++KFLDFGGYMNV F LRQIRTDFM+VPFQ+TECILSNIEPI YRVQIVDTDPEDSERCLVKFLDFGGYMNVNFGLLRQIRTDFMSVPFQATECILSNIEPID | 529 |
| Query | 591 | GTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAK | 412 |
| Sbjct | 530 | TWS+EAAEILNKLTKGIVLQAQVAGYNSHN+PEI+LFASLGPNNVIFINKELVGR LAK KTWSVEAAEILNKLTKGIVLQAQVAGYNSHNVPEIYLFASLGPNNVIFINKELVGRNLAK | 589 |
| Query | 411 | WVEMSD 394 | |
| Sbjct | 590 | WVEM D WVEMRD 595 | |

GH24358 [Drosophila grimshawi]

Sequence ID: ref|XP_001992176.1| Length: 627 Number of Matches: 1

| Score | i | Expect Method | Identities | Positives | Gaps I | Frame |
|----------|----------|--|------------------------------|--------------------|------------------------------|--------|
| 800 bits | (2066) C | 0.0() Compositional matrix adjus | st. 442/640(69% |) 497/640(77% |) 68/640(10%) - | 2 |
| Features | s: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWF | | | | _ |
| Sbjct | 1 | MVSGRPLL+LSLPGVAFILGVFWF: MVSGRPLLFLSLPGVAFILGVFWF: | | | | - |
| Query | 1977 | NGVL-QNGKLPQQSASKSM NG+ QNGKLP + +KSM | | | EKDSPTTMLYGK E DSP TMLYGK | |
| Sbjct | 58 | NGLQSQNGKLPNNAVGGGATTKSM | | | | |
| Query | 1827 | APIKIQSNGRTSNGKHQQQ API IQ NGR S GKHQ Q | | | DEDFENLSSPRD DEDFENLSSPRD | |
| Sbjct | 109 | APITIQ-NGRASPGKHQHQQQQQQQ | | | | |
| Query | 1668 | PDSV-NTRVSFYNRKATQKTVEPV PDS+ N RV FYNRK OK EPV | VIKATRTPKISP VIKAT TPKISP | | | |
| Sbjct | 168 | PDSISNNRVLFYNRKINQKGEEPV | | | | |
| Query | 1494 | EEPSKKE+ +E + + | Adqeel A+ E+ | eqdqeQTVL EOT++ | KEEVVD E | S 1408 |
| Sbjct | 228 | KEMKETKTAPATAPTPALTPIAGV | | | | |
| Query | 1407 | NGNQKRNVDAASPSLSICSVQSGD NGNQKRNVDAASPSLSICSVQSGD | | | | |
| Sbjct | 288 | NGNQKRNVDAASPSLSICSVQSGD | | | | |
| Query | 1230 | RAFINQIKAKTLASVSVGKNPYS- R FINQIKAKTLA+V + K YS | | | | |
| Sbjct | 348 | RTFINQIKAKTLANVVLSKTRYSS | GKLRICTIEGTE | NEIDAALAMIR | QRLPARRYPNFT | M 407 |
| Query | 1053 | QRIHFALPQTIVPLSTESLYNLQL QRIH+ALPQT+VPLSTESLYNLQL | | | | 1 874 |
| Sbjct | 408 | QRIHYALPQTVVPLSTESLYNLQL | | | | IA 467 |
| Query | 873 | LQKQLYDSYSTMEAPLLPSLELSA LQK +YDSYSTM+APLLP++E+SA | VCVIPINDVWYR | VOIVDTDPEDE | ERCVIKFLDFGG | Y 694 |
| Sbjct | 468 | LQKAMYDSYSTMDAPLLPNIEISA | VCVMPINGIWYR | VÕIVDTDADDV | ERCLIKFLDFGG | Y 527 |
| Query | 693 | MNVGFNTLRQIRTDFMNVPFQSTE MNV F+ LRQIRTDFM +PFQ+TE | | | | |
| Sbjct | 528 | MNVSFSALRQIRTDFMALPFQATE | | | | |
| Query | 513 | YNSHNLPEIFLFASLGPNNVIFIN | | | | |
| Sbjct | 588 | YNSHN+PEI+LFASLGPNN+IFIN YNSHNIPEIYLFASLGPNNIIFIN | | | | |

| 788 bits | (2036) (| 0.0() Compositional matrix adjust. 417/612(68%) 479/612(78%) 27/612(4%) -2 | |
|----------|----------|--|------|
| Features | S: | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRRRYKNCLDKPDDEDSSAINDSSIEPTVQARK MVSGRPLLYLSLPGVAFILGVFWFRRR KN LDK DD+ ++ + +++ T + | 1981 |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFRRRNKNRLDKSDDDANADASAKTVKEVNDCTQRTVT | 60 |
| Query | 1980 | ANGVLQNGKLPQQSASKSMNINGTLVNgsgsgsgsSDEKDSPTTMLYGKSAPIKIQSNG ANG L NG S ++ ++ S S +G +SDEK+SP T+L+GKSAPI IQSNG | 1801 |
| Sbjct | 61 | ANGKLPNGNANAASTKVPPTVSKSMNISSSSNNGDNSDEKESPNTILFGKSAPITIÕSNG | 120 |
| Query | 1800 | RTSNGKHQQQIDSEILKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRVSFYNRKAT R S GKHQQQIDSE+LKSKIQDAEHK LCSIDEDFENLSSPRDLPDS+N RV+FYNRK | 1621 |
| Sbjct | 121 | RASPGKHÕÕÕIDSEMLKSKIÕDAEHKKLCSIDEDFENLSSPRDLPDSLNNRVTFYNRKTN | 180 |
| Query | 1620 | QKTVEPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPKEEPSKKEAdqeeleqdqe Q+ EPVVIKATRTPKISPENSFL++ Y +E NN + | 1441 |
| Sbjct | 181 | QRAEEPVVIKATRTPKISPENSFLESKYAKQEQNNNNTNNNNSNNKEASPTPVAATVTAS | 240 |
| Query | 1440 | QTVLKEEVVDSNGNQKRNVDAASPSLSICSVQSGDSGKG T +E +D NGN KRNVDAASPSLS+CSVQSGDSGKG | 1324 |
| Sbjct | 241 | ATSTTDEALDDTVKQTMLTKAEESNMQDADAVNGNPKRNVDAASPSLSLCSVQSGDSGKG | 300 |
| Query | 1323 | SSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVR SSLPRSEAT R+K YEF FP SL+G LYGR+RAF+NQIK+KT A+V + K YSGKVR | 1150 |
| Sbjct | 301 | SSLPRSEATTTRIKAKYEFYFPNSLVGQLYGRRRAFLNQIKSKTQATVMLSKIKYSGKVR | 360 |
| Query | 1149 | ICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIE ICT+EG+++EI+AALAMIRQRLPAKRYPNFTMQRIH+ALPQT+VPLSTESLYNL+LKLIE | 970 |
| Sbjct | 361 | ICTLEGSDNEIEAALAMIRQRLPAKRYPNFTMQRIHYALPQTVVPLSTESLYNLELKLIE | 420 |
| Query | 969 | GINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVI GINNDVVVSAVLSG+H+ +QHPLHPSHP+L +LQ +Y+SYS M+APLLPS+ELSAVCV+ | 790 |
| Sbjct | 421 | GINNDVVVSAVLSGNHVVVQHPLHPSHPTLHVLQNAMYESYSAMDAPLLPSIELSAVCVM | 480 |
| Query | 789 | PINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILS PIN VWYR QIVD D D ERC++KFLDFGGYMNV F LRQIRTDFM VPFQ+TECILS | 610 |
| Sbjct | 481 | PINGVWYRAQIVDIDASDAERCLVKFLDFGGYMNVSFKLLRQIRTDFMTVPFQATECILS | 540 |
| Query | 609 | NIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELV NIEPI G+WS+EAA+IL+KLTKG+VLQAQVAGYNSHNLPEI+LFASLGPNNVIFINKELV | 430 |
| Sbjct | 541 | NIEPIDGSWSVEAADILSKLTKGVVLQAQVAGYNSHNLPEIYLFASLGPNNVIFINKELV | 600 |
| Query | 429 | GRKLAKWVEMSD 394 R LAKWVEMSD | |
| Sbjct | 601 | ARNLAKWVEMSD 612 | |

Identities

Positives

Gaps

Frame

PREDICTED: A-kinase anchor protein 1, mitochondrial [Stomoxys calcitrans] Sequence ID: **ref|XP_013106377.1**| Length: 586 Number of Matches: 1

Expect Method

Score

| Score | I | Expect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|--------------|----------------------------|------------|---------|
| 723 bits | (1867) (| 0.0() Compositional matrix adjust. | 386/616(63%) | 454/616(73% | 61/616(9%) | -2 |
| Features | S: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRR | | | ~ | 1984 |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFRR MVSGRPLLYLSLPGVAFILGVFWFRR | | | | LT 58 |
| Query | 1983 | KANGVLQNGKLPQQSASKSMNINGTL | | | | |
| Sbjct | 59 | K+ N P S +KSMNINGT+ KSTSNSNNKAKPTSSPTKSMNINGTV | | PIDDDNPANRL | FGKSAPIKIV | QN 107 |
| Query | 1803 | GRTSNGKHQQQIDSEILKSKIQDA GR + + QQQIDSE+LK+KIQDA | EHKTLCSIDED | FENLSSPRDLP | DSVNTRVSFY | NR 1630 |
| Sbjct | 108 | GRGPSPVKQTQQQIDSEVLKTKIQDA | EHKLLRSIEED: | FENLSSP DEF FENLSSPVDLP | DSINNRMSFY | SR 167 |
| Query | 1629 | KATQKTVEPVVIKATRTPKISPENSF K +PVVI AT TPKISPENSF | LDTNYT | | NK | |
| Sbjct | 168 | NVDIKKDKPVVIMATTTPKISPENSF | | NNNVEENSSRK | | _ |
| Query | 1521 | EQNNNCEPKEEPSKKEAdqeeleqdq N E K+ P++ E Q | | | | |
| Sbjct | 228 | N E K+ P++ E Q VSKTNVEMKKCPAENEIAQT | EDV | NDKRNVEA | ASPSLSLCSV | QS 270 |
| Query | 1341 | GDSGKGSSLPRSEATRVKTTYEFLFP GDSGKGSSLPRSEATR KTTYEF P | | | | YS 1162 |
| Sbjct | 271 | GDSGKGSSLPRSEATRAKTTYEFFLP | | | | YP 330 |
| Query | 1161 | GKVRICTIEGTESEIDAALAMIRQRL GK+R+C I+GTESEI AALAMIRQRL | | | | |
| Sbjct | 331 | GKLRVCAIDGTESEIQAALAMIRQRL | | | | |

| Query | 981 | KLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSA LIEGINNDVVVSAV+SG+HIF+Q PLHP+HPSL +LQK L++SYST + PLLP +EL+A | 802 |
|-------|-----|--|-----|
| Sbjct | 391 | NLIEGINNDVVVSAVISGAHIFVQQPLHPTHPSLAVLQKCLFESYSTADTPLLPGVELNA | 450 |
| Query | 801 | VCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTE | 622 |
| Sbjct | 451 | VCV+P+N +WYRVQIV+ D ED ERC++KFLDFGGYMNV FN LRQIR+DFM VPFQ+TE VCVMPVNGIWYRVQIVNGDIEDAERCIVKFLDFGGYMNVHFNELRQIRSDFMTVPFQATE | 510 |
| Query | 621 | CILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFIN | 442 |
| Sbjct | 511 | CILSN+EPI WS E+A+IL +LTKGIVLQAQ+AGYNSHN+PEIFLFA LGPNNVIFIN CILSNVEPIDTCWSPESADILCRLTKGIVLQAQIAGYNSHNIPEIFLFACLGPNNVIFIN | 570 |
| Query | 441 | KELVGRKLAKWVEMSD 394 | |
| Sbict | 571 | KELV R LAKWV++ D KELVARNLAKWVDIRD 586 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Musca domestica] Sequence ID: **ref|XP_005191355.1**| Length: 610 Number of Matches: 1

▶ See 2 more title(s) Range 1: 1 to 610

| Score | İ | Expect Method | Identities | Positives | Gaps | Frame |
|----------|------------|--|-----------------------------|---------------------------|--------------------------|------------|
| 709 bits | (1830) (| 0.0() Compositional matrix adjust. | 377/626(60%) | 452/626(72%) | 57/626(9%) | -2 |
| Features | 3 : | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRR | | | EPTVQARKAN | |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFRR: MVSGRPLLYLSLPGVAFILGVFWFRR: | | D+ + + +I NDTKKLGNGTI' | TSDKDLPSQT | V EV 56 |
| Query | 1968 | LQNGKLPQQSASKS | MNINGTLVNgs MNINGT+ | | DSPTTMLYGK ++P ++GK | |
| Sbjct | 57 | TEDLITKTNTTCNNNSSKPTSTPTKS | | | | |
| Query | 1824 | PIKIQSNGRTSNGKHQQQIDSEI PIKI NGR + OOO+DSE+ | LKSKIQDAEHK' LK+KIQDAEHK | | | |
| Sbjct | 106 | PIKIVQNGRGPSPVKQTAQQQLDSEV | LKTKIÕDAEHKI | LLRSIEEDFEN | LSSPVDLPDS | IN 165 |
| Query | 1653 | TRVSFYNRKATQKTVEPVVIKATRTP | | | | 1489 |
| Sbjct | 166 | NRTSFYSRNVDIKKDKPVVIMATTTP | | | | EK 224 |
| Query | 1488 | PSKKE. PS+K | Adqeeleqdqe(| QTVLKEEVVDS + + | | |
| Sbjct | 225 | DNNTTSSSVGGSNGNGEKSISPSEKV | | | | |
| Query | 1371 | PSLSICSVQSGDSGKGSSLPRSEATR PSLS+CSVQSGDSGKGSSLPRSEATR | | | | |
| Sbjct | 285 | PSLSLCSVQSGDSGKGSSLPRSEATR. | | | | |
| Query | 1191 | SVSVGKNPYSGKVRICTIEGTESEID +V + K Y GK+R+C +EGT+SEI | | | IHFALPQTIV IHFALPQ++V | |
| Sbjct | 345 | TVVLRKKMYPGKLRVCVVEGTDSEIQ | | | | |
| Query | 1011 | STESLYNLQLKLIEGINNDVVVSAVL S ESL NLQL LIEGINNDVVVSA++ | | | | |
| Sbjct | 405 | SNESLLNLQLNLIEGINNDVVVSAII | | | | |
| Query | 831 | PLLPSLELSAVCVIPINDVWYRVQIVIPLLP +EL+AVCV+P+N +WYRVQIVI | | | | |
| Sbjct | 465 | PLLPGVELNAVCVMPVNAIWYRVÕIV | DGDVEDPERCV | VKFLDFGGYMN | VHLSELRÕIR | SD 524 |
| Query | 651 | FMNVPFQSTECILSNIEPIGGTWSIE. FM VPFO+TECILSNIEPI W+ E | AAEILNKLTKG: A+IL +LTKG: | | | |
| Sbjct | 525 | FMTVPFQATECILSNIEPIDSCWTPE | | | | |
| Query | 471 | LGPNNVIFINKELVGRKLAKWVEMSD LGPNNVIFINKELV R LAKWV++ D | 394 | | | |
| Sbjct | 585 | LGPNNVIFINKELVARNLAKWVDIRD | 610 | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Bactrocera dorsalis] Sequence ID: **ref|XP_011203797.1|** Length: 595 Number of Matches: 1

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|--------|------------------------------|--------------|--------------|------------|-------|
| 669 bits(1726) | 0.0() | Compositional matrix adjust. | 362/613(59%) | 443/613(72%) | 46/613(7%) | -2 |
| Features: | | | | | | |

| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRRRYKNCLDKPDDEDSSAINDSSIEPTVQARKANGV MVSGRPLLYLSLPGV FILGV+W+RRR KN D + N ++ + NG | 1969 |
|-------|------|---|------|
| Sbjct | 1 | MVSGRPLLYLSLPGVVFILGVYWYRRRNKN-RSNGDTTEKEQENLNTHNSKESKHQINGS | 59 |
| Query | 1968 | LQNGKLPQQSASKSMNINGTLVNgsgsgsgssSDEKDSPTTMLYGKSAPIKIQSNGR K LP S S+NIN ++ ++SPT L+GKSAPIKI N R | 1798 |
| Sbjct | 60 | K LP S S+NIN ++ ++SPT L+GKSAPIKI N R FMQKKSHPLPSDSVNINNKNEGEESPTVRLFGKSAPIKIVQNCR | 103 |
| Query | 1797 | TSNGKHQQQIDSEILKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRVSFYNRKATQ S K QQ +DSE+LK+KIQ AE+K L SIDEDFENLSSP DLPDSV+ R++FY+R | 1618 |
| Sbjct | 104 | GSPVKQQQVVDSEVLKNKIQSAENKVLRSIDEDFENLSSPVDLPDSVDNRIAFYSRNVNC | 163 |
| Query | 1617 | KTVEPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPKEEPSKKE K+ PVVI+ATRTPKISPENSFL+ YT KEC + N+N ++ + | 1474 |
| Sbjct | 164 | KSDAPVVIRATRTPKISPENSFLENKYT-KECEENNNLNLIENVKNNSNARNQQGHPIQS | 222 |
| Query | 1473 | AdqeeleqdqeQTVLKEEVVDSNGNQKRNVDAASPSLSICSVQSGDSG + L+ ++ +L++ VD N KRNVDAASPSLS+CSVQSGDSG | 1330 |
| Sbjct | 223 | STNITLKTTEQSPILEDNFNKENAMNISCQDVDITENGKRNVDAASPSLSLCSVQSGDSG | 282 |
| Query | 1329 | KGSSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGK-V KGSSLPRSEA RVK+TYEF PSIGHLYG+K FINQIK KT A+V + K Y+GK V | 1153 |
| Sbjct | 283 | KGSSLPRSEANRVKSTYEFFLPNSFIGHLYGKKHFFINQIKVKTSANVLIRKTNYAGKLV | 342 |
| Query | 1152 | RICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLI IC IEG+ESEI+AAL MIRORLP KR+PNFTM +I A POT+VPLS +SL NLOLKLI | 973 |
| Sbjct | 343 | CICIIEGSESEIEAALTMIRQRLPTKRFPNFTMNKIQSASPQTVVPLSADSLLNLQLKLI | 402 |
| Query | 972 | EGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCV E INNDV+V+AV++G+H+F+QHPLHPSHPSL +LQK LYDSY+ EAPLLP +E++AVCV | 793 |
| Sbjct | 403 | ENINNDVIVTAVVNGAHMFVQHPLHPSHPSLTVLQKCLYDSYTLSEAPLLPGIEINAVCV | 462 |
| Query | 792 | IPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECIL +P+ +WYRVQIV+ D ED++RCV+KFLDFGGYMNV FN LRQIR+DFM+VPFQ+TEC+L | 613 |
| Sbjct | 463 | LPVKGIWYRVQIV+DED++RCV+RFLDFGGIMNVFN LRQIR+DFM+VFFQ+TEC+L | 522 |
| Query | 612 | SNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKEL SN+EPI WS EA ++L +LT+GIVLQAQVAGYNSHN+PEI+L+A LGP N+IFIN+EL | 433 |
| Sbjct | 523 | SNVEPIDSMWSSEAVDVLCQLTRGIVLQAQVAGYNSHNIPEIYLYAYLGPGNIIFINREL | 582 |
| Query | 432 | VGRKLAKWVEMSD 394 R LAKWVE+ D | |
| Sbjct | 583 | EARNLAKWVELRD 595 | |
| | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Bactrocera oleae] Sequence ID: **ref|XP_014095002.1**| Length: 595 Number of Matches: 1 Range 1: 1 to 595

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|--------|-------------|--|---------------------------|--------------------------|------------------------------|--------------|
| 662 bits | (1708) | 0.0() | Compositional matrix adjust. | 362/612(59%) | 438/612(71% | o) 44/612(7%) | -2 |
| Feature | s: | | | | | | |
| Query | 2148 | | RPLLYLSLPGVAFILGVFWFRF RPLLYLSLPGV FILGV+W+R | | DDEDSSAINDS + E + | SSIEPTVQARKA S E T | AN 1975 N |
| Sbjct | 1 | | RPLLYLSLPGVVFILGVYWYRI | | | | |
| Query | 1974 | GVLQ +O | NGKLPQQSASKSMNINGTLVNG N P S S+NIN | | | KSAPIKIQSNGI KSAPIKI N | |
| Sbjct | 61 | | NKSNPLPSDSVNIN | YKNEG | EESPTGRLFG | KSAPIKIVQNCI | |
| Query | 1794 | SNGK S K | HQQQIDSEILKSKIQDAEHKTI CQQQ+DSE+LK+KIQ AE+K I | CSIDEDFENLS | SPRDLPDSVN' | TRVSFYNRKAT(| QK 1615 K |
| Sbjct | 106 | | K-QQQVDSEVLKNKIQSAENKVI | | | | |
| Query | 1614 | | VVIKATRTPKISPENSFLDTN) V+I+ATRTPKISPENSFL+ \ | TNKECEQNNN- T K CE+NNN | | | 1507 |
| Sbjct | 165 | | VIIRATRTPKISPENSFLENKY | | DLIENVKIKSI | OTGNQQGHPTQ8 | SS 223 |
| Query | 1506 | CEPK C | EEPSKKEAdqeeleqdqeQTVI +P ++ E+ + | | | LSICSVQSGDS0 LS+CSVQSGDS0 | |
| Sbjct | 224 | | 'HKPIEQSPILEQNFNKETVMNI | | | | |
| Query | 1326 | | PRSEATRVKTTYEFLFPISLIC | | QIKAKTLASV: IK KT A+V | | |
| Sbjct | 284 | | PRSEANRAKSTYEFFLPNSFIC | | | | |
| Query | 1149 | | EGTESEIDAALAMIRQRLPAKF EG+ESEI+AALAMIRQRLP KF | | | | |
| Sbjct | 344 | | EGSESEIEAALAMIRQRLPTKE | | | | |
| Query | 969 | | IDVVVSAVLSGSHIFIQhplhps IDV+V+AV++G+H+F+QHPLHPS | | | | |
| Sbjct | 404 | | IDVIVTAVVNGAHMFVQHPLHPS | | | | |
| Query | 789 | PIND P+ | VWYRVQIVDTDPEDEERCVIKE +WYRVQIV+ D ED++RCV+KE | LDFGGYMNVGF | NTLRQIRTDFI | MNVPFQSTECI | LS 610 |
| Sbjct | 464 | | IWYRVQIVE D EDFFRCVFKE SIWYRVQIVEQDVEDKQRCVVKE | | | | |
| Query | 609 | NIEP | PIGGTWSIEAAEILNKLTKGIVI | LQAQVAGYNSHN | LPEIFLFASL | GPNNVIFINKE | LV 430 |

N+EPI WS EA ++L +LT+GIVLQAQVAGYNS N+PEI+L+A LGP N+IFIN+EL NVEPIDSMWSSEAVDVLCQLTRGIVLQAQVAGYNSQNIPEIYLYAYLGPGNIIFINRELE 583 Query 429 GRKLAKWVEMSD 394 R LAKWVE+ D Sbjct 584 ARNLAKWVELRD 595

PREDICTED: A-kinase anchor protein 1, mitochondrial [Bactrocera cucurbitae]

Sequence ID: ref|XP_011195171.1| Length: 579 Number of Matches: 1

Range 1: 1 to 579

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|--------|---|--|---------------------------|--------------|--------------------------|---------------|
| 658 bits | (1697) | 0.0() | Compositional matrix adjust. | 357/597(60%) | 435/597(72%) | 30/597(5%) | -2 |
| Features | 3: | | | | | | |
| Query | 2148 | | RPLLYLSLPGVAFILGVFWFRR | | | SIEPTVQARK S E T Õ | AN 1975 N |
| Sbjct | 1 | | RPLLYLSLPGVVFILGVYWYRR | | | | |
| Query | 1974 | G-VL G ++ | QNGKLPQQSASKSMNINGTLVN QN P S S+NIN | gsgsgsgssSD: ++ | | | GR 1798 GR |
| Sbjct | 59 | | QNKSNPLPSDSVNINNK | • • | | | |
| Query | 1797 | | KHQQQIDSEILKSKIQDAEHKT K QQQ+DSE+LK+KIQ+AE+K | | | | TQ 1618 |
| Sbjct | 105 | | K-QQQVDSEVLKNKIQNAENKA | | | | NC 163 |
| Query | 1617 | | PVVIKATRTPKISPENSFLDTN PVVI+ATRTPKISPENSFL+ | | | | eQ 1438 |
| Sbjct | 164 | | PVVIRATRTPKISPENSFLENK | | | • | • |
| Query | 1437 | | EEVVDSNGNQKRNV ++ VD N KRNV | DAASPSLSICS | | | |
| Sbjct | 223 | • | KDGAMNIQCPDVDITENGKRNV | | | | |
| Query | 1281 | $egin{array}{c} 	ext{YEFL} \ 	ext{YEF} \end{array}$ | FPISLIGHLYGRKRAFINQIKA P + IGHLYGRK FINOIK | KTLASVSVGKN KT A+V + K | | IEGTESEIDA IEG+ESEI A | |
| Sbjct | 283 | | LPSNFIGHLYGRKHFFINÕIKV | | | | |
| Query | 1104 | | QRLPAKRYPNFTMQRIHFALPQ ORLP+KR+PNFTM +I A P+ | | | NDVVVSAVLS NDV ++AV++ | |
| Sbjct | 343 | | QRLPSKRFPNFTMDKIQPASPE | | | | |
| Query | 924 | | QhplhpshpslplLQKQLYDSY Q P HPS PSL LQ+ +YDSY | | | DVWYRVQIVD WYRVÕIV+ | |
| Sbjct | 403 | | QQPCHPSKPSLDNLQRCMYDSY | | | | |
| Query | 744 | | ERCVIKFLDFGGYMNVGFNTLR ERCVIKFLDFGGYM+V F+ LR | | | | AE 565 AE |
| Sbjct | 463 | | ERCVIKFLDFGGYMDVHFHELR | | | | |
| Query | 564 | | LTKGIVLQAQVAGYNSHNLPEI LT+GIVLQAQVAGYNSHN+PEI | | | LAKWVEMSD LAKWV++ D | 394 |
| Sbjct | 523 | | LTRGIVLQAQVAGYNSHNIPEI | | | | 579 |
| | | | | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Ceratitis capitata]

Sequence ID: ref|XP_004520186.1| Length: 608 Number of Matches: 1

Range 1: 22 to 608

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|--------------|-----------------------------|-------------------------|----------------|
| 634 bits | (1635) (| 0.0() Compositional matrix adjust. | 348/605(58%) | 426/605(70%) | 35/605(5%) | -2 |
| Feature | s: | | | | | |
| Query | 2166 | FOYSAKMVSGRPLLYLSLPGVAFILG | | | AINDSSIEPT' IN + + | VQ 1990 |
| Sbjct | 22 | FQYS KMVSGRPLLY+SLPGV FILGY FQYSTKMVSGRPLLYMSLPGVVFILGY | | | | ST 81 |
| Query | 1989 | ARKANGVLQNGKLPQQSASKSMNING | | | MLYGKSAPIK L+GKSAPIK | |
| Sbjct | 82 | + + P QS SMNIN PHAGVNYMLSKSEPLQSDSMNINNI | | | | |
| Query | 1809 | SNGRTSNGKHQQQIDSEILKSKIQDAI N R S K QQ+DSE+LKSKIQ+AI | | | | |
| Sbjct | 128 | QNSRGSPVKQQVDSEVLKSKIQNAI | | | | |
| Query | 1629 | KATQKTVEPVVIKATRTPKISPENSFI K PVV++ATRTPKISPENSFI | | | | KE 1474 +E |
| Sbjct | 186 | NVNCKNDAPVVVRATRTPKISPENSFI | _ | | | · - |
| Query | 1473 | AdqeeleqdqeQTVLKEEVVDSNC A E E + K+ EV+D | | DAASPSLSICS\ DAASPSLS CS | | |

| Sbjct | 245 | AKISENHIIIENSFNKQNAIEVIDQGNTVLENEERNVDAASPSLSSCSDQSGDSGKGSSL | 304 |
|-------|------|--|------|
| Query | 1314 | PRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVR-ICTI PRSEA R KT YEF P S +G LYGRK FIN IK KT A V V K Y G V IC I | 1138 |
| Sbjct | 305 | PRSEANRAKTKYEFFIPNSFVGQLYGRKHTFINHIKVKTSADVDVRKTYYGGIVVCICRI | 364 |
| Query | 1137 | EGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINN EG++SEI AALAMIRQRLP KRYPNFTMQ+I FA P+T+VPLS E++ NLQLKLIEGINN | 958 |
| Sbjct | 365 | EGSDSEIKAALAMIRQRLPIKRYPNFTMQKIIFAPPETVVPLSIENIQNLQLKLIEGINN | 424 |
| Query | 957 | DVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPIND DV VS +++ H+F+Q PLHP+ P L +L K + DSY TM P LP +EL+A+CV+P N | 778 |
| Sbjct | 425 | DV VS 111 HTF O FEMALE F L 1 K 1 DSI IM F LF 1 EL A 1 CV 1 N DVRVSTIINAGHMFVQQPLHPTAPKLDVLNKCISDSYETMVTPPLPRVELNAICVMPANG | 484 |
| Query | 777 | VWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEP +W RVQIVD +D + C++K LD GGY+ F+ LRQIR+DF+ VPFQ+TEC+LSN+EP | 598 |
| Sbjct | 485 | LWLRVQIVDQH-DDGKHCLVKLLDCGGYVTAEFSQLRQIRSDFLTVPFQATECVLSNVEP | 543 |
| Query | 597 | IGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKL I WS EAAE+L LT GI+LQAQ+AGYNS N+PE++LFA+LGPNN+IFINKELV R L | 418 |
| Sbjct | 544 | IDSIWSQEAAEVLGYLTGGIILQAQIAGYNSLNIPEVYLFANLGPNNIIFINKELVARNL | 603 |
| Query | 417 | AKWVE 403 AKWV+ | |
| Sbict | 604 | AKWVD 608 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Ceratitis capitata]

Sequence ID: ref|XP_004520187.1| Length: 581 Number of Matches: 1

▶ See 2 more title(s) Range 1: 1 to 581

| Score | | Expect Method | Identities | Positives | Gaps F | rame |
|-----------|--------|--|------------------------------|-----------------------------|--------------------|--------|
| 624 bits(| (1610) | 0.0() Compositional matrix adjust. | 343/599(57%) | 421/599(70%) | 35/599(5%) -2 | 2 |
| Features | S: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRR MVSGRPLLY+SLPGV FILGVFW+RR | | DEDSSAINDSSI E+ IN | EPTVQARKAN | G 1972 |
| Sbjct | 1 | MVSGRPLLITSLPGV FILGVFW+RR | | | | N 60 |
| Query | 1971 | VLQNGKLPQQSASKSMNINGTLVNgs ++ P QS SMNIN + | | OSPTTMLYGKSA +SPT L+GKSA | | |
| Sbjct | 61 | YMLSKSEPLQSDSMNINNKNI | | | | |
| Query | 1791 | NGKHQQQIDSEILKSKIQDAEHKTLC K QQ+DSE+LKSKIQ+AE K L | | | | г 1612 |
| Sbjct | 107 | PVKQQVDSEVLKSKIQNAEDKVLR | | | | N 164 |
| Query | 1611 | VEPVVIKATRTPKISPENSFLDTNYT PVV++ATRTPKISPENSFL++ Y | | | KKEAdqee K+EA E | 1456 |
| Sbjct | 165 | DAPVVVRATRTPKISPENSFLESKYI | | | | N 223 |
| Query | 1455 | eqdqeQTVLKEEVVDSNGN E + K+ EV+D N | QKRNVDAASPSI ++RNVDAASPSI | | | г 1297 |
| Sbjct | 224 | HIIIENSFNKQNAIEVIDQGNTVLEN | EERNVDAASPS | LSSCSDÕSGDS | GKGSSLPRSEA | N 283 |
| Query | 1296 | RVKTTYEFLFPISLIGHLYGRKRAFI R KT YEF P S +G LYGRK FI | | | | |
| Sbjct | 284 | RAKTKYEFFIPNSFVGQLYGRKHTFI | | | | |
| Query | 1119 | IDAALAMIRQRLPAKRYPNFTMQRIH I AALAMIRORLP KRYPNFTMQ+I | | | | A 940 |
| Sbjct | 344 | IKAALAMIRÕRLPIKRYPNFTMÕKII | | | | Г 403 |
| Query | 939 | VLSGSHIFIQhplhpshpslplLQKQ +++ H+F+Q PLHP+ P L +L K | | | | |
| Sbjct | 404 | IINAGHMFVÕQPLHPTAPKLDVLNKC | | | | |
| Query | 759 | IVDTDPEDEERCVIKFLDFGGYMNVG IVD +D + C++K LD GGY+ | FNTLRQIRTDF1 F+ LRQIR+DF- | | | |
| Sbjct | 464 | IVDQH-DDGKHCLVKLLDCGGYVTAE | | | | |
| Query | 579 | IEAAEILNKLTKGIVLQAQVAGYNSH EAAE+L LT GI+LQAQ+AGYNS | | | | 403 |
| Sbjct | 523 | QEAAEVLGYLTGGIILQAQIAGYNSL | | | | 581 |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X3 [Ceratitis capitata]

Sequence ID: ref|XP_004520192.1| Length: 549 Number of Matches: 1

| Score | Expect Method | Identities | Positives | Gaps | Frame |
|-------|---------------|------------|-----------|------|-------|

| 579 bits | (1492) (| 0.0() Compositional matrix adjust. 313/527(59%) 381/527(72%) 32/527(6%) -2 | |
|----------|------------|---|------|
| Features | S : | | |
| Query | 1935 | SKSMNINGTLVNgsgsgsgssSDEKDSPTTMLYGKSAPIKIQSNGRTSNGKHQQQIDSEI S SMNIN + +++SPT L+GKSAPIKI N R S K OO+DSE+ | 1756 |
| Sbjct | 39 | S SMNIN + +++SPT L+GKSAPIKI N R S K QQ+DSE+ SDSMNINNKNIDEESPTGRLFGKSAPIKIVQNSRGSPVKQQVDSEV | 84 |
| Query | 1755 | LKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRVSFYNRKATQKTVEPVVIKATRTP LKSKIQ+AE K L SIDEDFENLSSP DLPDS++ R++FY+R K PVV++ATRTP | 1576 |
| Sbjct | 85 | LKSKIQNAEDKVLRSIDEDFENLSSPIDLPDSIDNRITFYSRNVNCKNDAPVVVRATRTP | 144 |
| Query | 1575 | KISPENSFLDTNYTNKECEQNNNCEPKEEPSKKEAdqeeleqdqeQTVLKE- KISPENSFL++ Y K+CE+NNN EP + + K+EA E E + K+ | 1423 |
| Sbjct | 145 | KISPENSFLESKYI-KDCEENNNSEPMTKTTTEKIDVNQKEEAKISENHIIIENSFNKQN | 203 |
| Query | 1422 | EVVDSNGNQKRNVDAASPSLSICSVQSGDSGKGSSLPRSEATRVKTTYEFLFPI EV+D N++RNVDAASPSLS CS QSGDSGKGSSLPRSEA R KT YEF P | 1261 |
| Sbjct | 204 | AIEVIDQGNTVLENEERNVDAASPSLSSCSDQSGDSGKGSSLPRSEANRAKTKYEFFIPN | 263 |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVR-ICTIEGTESEIDAALAMIRQRL S +G LYGRK FIN IK KT A V V K Y G V IC IEG++SEI AALAMIRQRL | 1084 |
| Sbjct | 264 | SFVGQLYGRKHTFINHIKVKTSADVDVRKTYYGGIVVCICRIEGSDSEIKAALAMIRQRL | 323 |
| Query | 1083 | PAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSHIFIQhp P KRYPNFTMQ+I FA P+T+VPLS E++ NLQLKLIEGINNDV VS +++ H+F+Q P | 904 |
| Sbjct | 324 | PIKRYPNFTMQKIIFAPPETVVPLSIENIQNLQLKLIEGINNDVRVSTIINAGHMFVQQP | 383 |
| Query | 903 | lhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDPEDEERC LHP+ P L +L K + DSY TM P LP +EL+A+CV+P N +W RVQIVD +D + C | 724 |
| Sbjct | 384 | LHPTAPKLDVLNKCISDSYETMVTPPLPRVELNAICVMPANGLWLRVQIVDQH-DDGKHC | 442 |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTK ++K LD GGY+ F+ LRQIR+DF+ VPFQ+TEC+LSN+EPI WS EAAE+L LT | 544 |
| Sbjct | 443 | LVKLLDCGGYVTAEFSQLRQIRSDFLTVPFQATECVLSNVEPIDSIWSQEAAEVLGYLTG | 502 |
| Query | 543 | GIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVE 403 GI+LQAQ+AGYNS N+PE++LFA+LGPNN+IFINKELV R LAKWV+ | |
| Sbjct | 503 | GIILQAQIAGYNSLNIPEVYLFANLGPNNIIFINKELV K LAKWV+ | |
| | | | |

uncharacterized protein Dvir_GJ14809 [Drosophila virilis]

Sequence ID: ref|XP_002059514.1| Length: 655 Number of Matches: 2

| Score | | Expect | Method | | Identities | Positives | Gaps | Frame |
|----------|--------|--------|-------------|------------------|------------------------------|----------------------------------|------------|---------|
| 559 bits | (1441) | 0.0() | Composition | nal matrix adjus | st. 276/340(81 | %) 309/340(90%) | 2/340(0%) | -2 |
| Features | s: | | | | | | | |
| Query | 1407 | | | | | AT-RVKTTYEFLFI | | |
| Sbjct | 316 | | | | | AT R+KT+Y F FI ATTRMKTSYRFFFI | | |
| Query | 1230 | | | | | ESEIDAALAMIRQF ESEIDAALAMIRQF | | |
| Sbjct | 376 | | | | | ESEIDAALAMIRQE | | |
| Query | 1053 | QRIH | FALPOTIVPI | LSTESLYNLQLE | KLIEGINNDVVV | /SAVLSGSHIFIQI /SAVLSG H+F+QI | nplhpshpsl | Lpl 874 |
| Sbjct | 436 | | | | | /SAVLSG HYFYQI /SAVLSGDHVFVQI | | |
| Query | 873 | | | | | RVQIVDTDPEDEEF RVQI D+D +DE+F | | |
| Sbjct | 496 | | | | | RVÕICDSDADDEQF | | |
| Query | 693 | | | | | WSIEAAEILNKLI WS +AA+ILNKLI | | |
| Sbjct | 556 | | | | | WSADAADILNKLI | | |
| Query | 513 | | | | KELVGRKLAKWV KELV R LAKWV | | | |
| Sbjct | 616 | | - | | KELV K LAKWV KELVARNLAKWV | | | |
| | | | | | | | | |

Range 2: 1 to 234

| Score | E | xpect | Method | Identities | Positives | Gaps | Frame | |
|----------|----------|-------|--|--------------|--------------|------------|-------|----|
| 299 bits | (766) 6e | -86() | Compositional matrix adjust. | 164/235(70%) | 181/235(77%) | 13/235(5%) | -2 | |
| Features | S: | | | | | | | |
| Query | 2148 | | RPLLYLSLPGVAFILGVFWFRF RPLLYLSLPGVAFILGVFWFRF | | | | RK 19 | 81 |

| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFRRRNKNRVDKNDDDANAVANGKPVKEAAEPGLTQRK | 60 |
|-------|------|--|------|
| Query | 1980 | ANGVLQ-NGKLPQQSASKSMNINGTLVNgsgsgsgssSDEKDSPTTMLYGKSAP NGV NGKLP + A+KSMNI+ G G GS ++ DEK+SP TMLYGKSAP | 1822 |
| Sbjct | 61 | VNGVQSLNGKLPTGNGNGTVNATKSMNISVGGGGGGGGGSMNNIDEKESPNTMLYGKSAP | 120 |
| Query | 1821 | IKIQSNGRTSNGKHQQQ-IDSEILKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRV I IQSNGR S GKHQQQ IDSE+LKSKIQDAEHK LCSIDEDFENLSSPRDLPDSVN RV | 1645 |
| Sbjct | 121 | ITIQSNGRASPGKHQQQQIDSEMLKSKIQDAEHKKLCSIDEDFENLSSPRDLPDSVNNRV | 180 |
| Query | 1644 | SFYNRKATOKTVEPVVIKATRTPKISPENSFLDTNYTNKECEONNNCEPKEEPSK 1480 | |
| Sbjct | 181 | SFYNRKA +K EPVVIKATRTPKISPENSFL++ YT KECE NNNCEP +K SFYNRKANKKAEEPVVIKATRTPKISPENSFLESKYT-KECEPNNNCEPSNADNK 234 | |

uncharacterized protein Dmoj_GI11050, isoform A [Drosophila mojavensis] Sequence ID: **ref|XP_002011526.1**| Length: 681 Number of Matches: 2

▶ See 3 more title(s) Range 1: 341 to 681

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|------------|--|--------------|--------------|-----------|-------|
| 558 bits | (1437) | 0.0() Compositional matrix adjust. | 276/341(81%) | 312/341(91%) | 3/341(0%) | -2 |
| Features | S : | | | | | |
| Query | 1407 | NGNOKRNVDAASPSLSICSVOSGDSGK NGNOKRNVDAASPSLSICSVOSGDSGK | | | | |
| Sbjct | 341 | NGNQKRNVDAASPSLSICSVQSGDSGK NGNQKRNVDAASPSLSICSVQSGDSGK | | | | |
| Query | 1230 | RAFINQIKAKTLASVSVGKNPYS-GKV R FIN+IK+KTLA+VS+ KN YS GK+ | | | | |
| Sbjct | 401 | RTFINKIKSKTLANVSLSKNRYSSGKL | | | | |
| Query | 1053 | QRIHFALPQTIVPLSTESLYNLQLKLI QRIH+ALPQ+IVPLSTESL++LQL LI | | | | |
| Sbjct | 461 | QRIHYALPQSIVPLSTESLHSLQLNLI | | | | |
| Query | 873 | LQKQLYDSYSTMEAPLLPSLELSAVCV LQK + DSYS+MEAP LPS+E+SAVCV | | | | |
| Sbjct | 521 | LÕKNMLDSYSSMEAPKLPSIEISAVCV | | | | |
| Query | 696 | YMNVGFNTLRQIRTDFMNVPFQSTECI YMNV F+ LRQIRTDFM +PFQ+TECI | | | | |
| Sbjct | 581 | YMNVSFSVLRÖIRTDFMTLPFÖATECI | | | | |
| Query | 516 | GYNSHNLPEIFLFASLGPNNVIFINKE GYNSHN+PEI+LFASLGPNN+IFINKE | | | | |
| Sbjct | 641 | GYNSHNIPEIYLFASLGPNNIIFINKE | | | | |

Range 2: 1 to 229

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|----------------------------|-----------------------|----------------------|---------------|
| 291 bits | (744) 1e | e-82() Compositional matrix adjust. | 159/237(67%) | 178/237(75%) | 28/237(11%) | -2 |
| Features | S: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFR | | | _ | • |
| Sbjct | 1 | MVSGRPLLYLSLPGVAFILGVFWFR MVSGRPLLYLSLPGVAFILGVFWFR | | | |) + PRK 60 |
| Query | 1983 | KANGVL-QNGKLPQQS ANG+ QNGKLP | | GTLVNgsgsgsg G+++N | gssSDEKDSPT +K+SP | |
| Sbjct | 61 | TANGIQSQNGKLPAGNGNGAVPGTG | | | | |
| Query | 1842 | LYGKSAPIKIQSNGRTSNGKHQQQ- LYGKSAPI IQSNGR S GKHQQQ | | | | |
| Sbjct | 114 | LYGKSAPITIQSNGRASPGKHQQQQ | | | | |
| Query | 1665 | DSVN-TRVSFYNRKATOKTVEPVVI | | | | 1498 |
| Sbjct | 174 | DS++ RVSFYNR +QK EPVVI DSISKNRVSFYNRNTSQKKEEPVVI | KATRTPKISPE KATRTPKISPE | | | 229 |

LD28079p [Drosophila melanogaster]

Sequence ID: gb|AAL28899.1| Length: 236 Number of Matches: 1

Range 1: 1 to 236

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|----------|-----------------------------|---------------|---------------|-----------|-------|
| 459 hits(1182) | 1e-152() | Compositional matrix adjust | 236/236(100%) | 236/236(100%) | 0/236(0%) | -2 |

Features: Query 1101 MIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSH 922 MIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSH

Sbjct 1 MIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSH 60
Query 921 IFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDP 742

Query 921 IFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDP 742 IFIQHPLHPSHPSLPLLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDP

Sbjct 61 IFIQHPLHPSHPSLPLLQKQLYDSYSTMEAPLLPSLELSAVCVIPINDVWYRVQIVDTDP 120

Query 741 EDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEI 562 EDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEI Sbjct 121 EDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEI 180

LNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD

236

Query 561 LNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD 394
LNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMSD

a kinase anchor protein [Culex quinquefasciatus]

Sequence ID: ref|XP_001869726.1| Length: 589 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 581

181

Sbjct

| Score | E | xpect | Method | Identities | Positives | Gaps | Frame |
|----------|------------|---------------|--|------------------------------|------------------------------|--------------------------|---------|
| 434 bits | (1117) 6 | e-138() | Compositional matrix adjust. | 258/591(44%) | 368/591(62%) | 19/591(3%) | -2 |
| Features | S : | | | | | | |
| Query | 2148 | | RPLLYLSLPGVAFILGVFWFRR | | | ~ | GV 1969 |
| Sbjct | 1 | | RPLLYLSLPG+A I+G+ WFRR RPLLYLSLPGLALIIGLVWFRR | | S +S STSEGGAESVA | R TTDDSERTCE | AE 60 |
| Query | 1968 | LONGI Q+G | KLPQQSASKSMNINGTLVNgsg +O+S++L+SG | | | PIKIQSNGRT PI I SN R+ | |
| Sbjct | 61 | | OFGKÕTESLPITPSANLKHDSG | | | | |
| Query | 1788 | | QQIDSEILKSKIQDAEHKTLCS QQ+D+E+LK KI++++ + L | | SPRDLPDSVNT: SP +LP +V+ : | | |
| Sbjct | 117 | | ŽÕLDAELLKLKIEESDIRNLRL | | | | |
| Query | 1620 | | EPVVIKATRTPKISPENSFLDT EPVVIKA+ T KISP+NSF | NYTNKECEQNNI +KE E N- | | EAdqeeleqd + + + | qe 1441 |
| Sbjct | 176 | | EPVVIKASMTAKISPQNSFATE | | | | |
| Query | 1440 | QTVLI + | KEEVVDSNGNQKRNVDAA +VD +NG + + + | SPSLSICSVQS(SP+LSICS++S(| | | |
| Sbjct | 236 | | NNNIVDEPQAANGEEIGSH | | | | _ |
| Query | 1272 | | SLIGHLYGRKRAFINQIKAKTL L+ + GRK F+ IKAKT | | GKVRICTIEGT: K +ICT+EGT | | |
| Sbjct | 292 | | YLVSKMLGRKAGFVQLIKAKTG | | | | |
| Query | 1092 | QRLPZ ++ P | AKRYPNFTMQRIHFALPQTIVP KR+ T+OR+H A + +VP | | KLIEGINNDVV +L+EGINNDV | | |
| Sbjct | 352 | KKFPI | EKRFSALTLÕRVHIAPTENVVP | | | | |
| Query | 912 | | npshpslplLQKQLYDSYSTME HPS PSL LO+ L SY+ E | | | RVQIVDTDPE RVÕIV PE | |
| Sbjct | 412 | | HPSFPSLNTLQQCLNQSYNMTE | | | ~ | |
| Query | 732 | | IKFLDFGGYMNVGFNTLRQIRT +K+LD+GGY NV +LROIRT | DFMNVPFQSTEO | | | |
| Sbjct | 471 | | VKYLDYGGYANVPVTSLRÕIRT | DFMAVPFÕSIE | CVLSNVKPSGD | SGWTPGASEA | |
| Query | 555 | | GIVLQAQVAGYNSHNLPEIFLF G++LOAOVAGY + LPEI+L+ | | | | |
| Sbjct | 531 | | GLILQAQVAGYTAEGLPEIYLY | | | — | |

AAEL008431-PA [Aedes aegypti]

Sequence ID: ref|XP_001659213.1| Length: 588 Number of Matches: 1

See 1 more title(s)

Range 1: 1 to 588

| S | core | Expect | Method | Identities | Positives | Gaps | Frame | - |
|----|--------------|-------------|--|--------------|--------------------------|-----------------------|-------|----|
| 40 | 06 bits(1043 | 3) 6e-127() | Compositional matrix adjust. | 261/610(43%) | 378/610(61%) | 50/610(8%) | -2 | |
| Fe | eatures: | | | | | | | |
| Qι | uery 214 | | RPLLYLSLPGVAFILGVFWFRRI RPLLYLSLP +A I+G+ WFRR- | | XPDDEDSSAIND P +E S + | SSIEPTVQA + + TV A | | 81 |

| Sbjct | 1 | MVSGRPLLYLSLPSLAIIIGLVWFRRKKFIGFDSGGKTPAEEKSEGVETADKTVHAED | 58 |
|-------|------|---|------|
| Query | 1980 | ANGVLQNGKLPQQSASKSMNINGTLVNgsgsgsgssSDEKDSPTTMLYGKSAPIKIQSNG + ++S+ IN + SS ++ S ++ GKSAPI I SN | 1801 |
| Sbjct | 59 | ECRAIDLKHTESLPINPSPNDKDESSKNQSSSSSSSSSSGKSAPIDIVSNT | 108 |
| Query | 1800 | RTSNGKHQQQIDSEILKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRVSFYNR- R+ OO+D+E+LK KI++++ + L I+E DF + SP +LP +V+ R +N+ | 1630 |
| Sbjct | 109 | RSPPKFSDQQLDAELLKLKIEESDIRNLRLIEEQDDFSSFESPVNLPGTVD-RFQNFNKF | 167 |
| Query | 1629 | -KATQKTVEPVVIKATRTPKISPENSFLDTNYTNKECEQNNNCEPK K+ + +EPVV+KA+ T KISP+NSF ++ E ++ NN + | 1495 |
| Sbjct | 168 | DKSFEPQMEPVVVKASMTAKISPKNSFATELSSSTESPESCNGTVEDAHTQDMVNNNSAR | 227 |
| Query | 1494 | EEPSKKEAdqeeleqdqeQTVLKEEVVDSNGNQKRNVDAASPSLSICSVQSGDSG EE + E + E + V++N + N + ASP LS+CS+ SGDSG | 1330 |
| Sbjct | 228 | EEAVEHETETVRATHNEDTVNNNAMNEENGEEPHSPVASPPLSVCSMHSGDSG | 280 |
| Query | 1329 | KGSSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVR KGSS P+SE V T+Y+FL P+ L+ L GRK F+ IKAKT +V + +NP + K + | 1150 |
| Sbjct | 281 | KGSSPPQSECAPV-TSYDFLLPVYLVSKLLGRKAGFVQLIKAKTGVNVLIKRNPETHKTK | 339 |
| Query | 1149 | ICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIE IC++EGT++EID ALA+IR++ P KR+ T+OR+H + +VPL L+L+E | 970 |
| Sbjct | 340 | ICSLEGTQAEIDNALALIRRKFPEKRFSALTLQRVHVGQTENVVPLPLIDTTCFNLQLVE | 399 |
| Query | 969 | GINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVI GINNDV V ++++G H+F+O PLHPS+PSL +O+ + SY+T+EAP LP + +++CV | 790 |
| Sbjct | 400 | GINNDVTVCSIVNGGHVFLQQPLHPSYPSLNTMQQCMNQSYNTIEAPQLPEITENSICVA | 459 |
| Query | 789 | PINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILS + D WYRVQIV + ED + C++K+LD+GGY +V LRQIRTDFM VPFQS EC+LS | 610 |
| Sbjct | 460 | VVQDSWYRVQIVSHNAED-QYCLVKYLDYGGYASVPVTNLRQIRTDFMGVPFQSIECVLS | 518 |
| Query | 609 | NIEPIGGT-WSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKEL N++P G + W+ EA+E L LTKG++LQAQVAGY + LPE++LFASL +NVIFINKEL | 433 |
| Sbjct | 519 | NVKPNGDSGWTPEASEALCSLTKGLILQAQVAGYTAEGLPEVYLFASLARDNVIFINKEL | 578 |
| Query | 432 | VGRKLAKWVE 403 R+LA W E | |
| Sbjct | 579 | AARQLAVWEE 588 | |
| | | | |

a kinase anchor protein [Anopheles darlingi]

Sequence ID: **gb|ETN58422.1|** Length: 592 Number of Matches: 1 Range 1: 1 to 592

| Score | Ex | rpect Method | Identities | Positives | Gaps | Frame |
|---|------------|--|----------------------------|---------------------------|--------------------------|--------------|
| 339 bits(869) 2e-101() Compositional matrix adjust. 228/617(37%) 333/617(53%) 60/617(9%) -2 | | | | | | |
| Features | S : | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFRF | | | ~ | G- 1972 |
| Sbjct | 1 | M++GRPLL+LSLPG+A I+G+ W+RF MIAGRPLLFLSLPGLALIVGLVWYRF | | | E TV + ESTVGGASCH | AE 58 |
| Query | 1971 | VLQNGKLPQQSASKSMNINGTI V Q+ LP QS S NG + | | SDEKDSPTTML | | SN 1804 N |
| Sbjct | 59 | LEPDVRÕSSSLPIÕSVGSSNGAM | | | | |
| Query | 1803 | GRTSNGKHQQQIDSEILKSKIQDAEH S G D H | | | | |
| Sbjct | 109 | KSPSKGGDAGLCDPFGH | | | | |
| Query | 1623 | TQKTVEPVVIKATRTPKI-SPEN O K EPV+I+ T+ + S + | ISFLDTNYTNKE D N + | CEQNNNCEPKE + +PK | | |
| Sbjct | 158 | NÕMLEKAQEPVIIRPTKPASLQSCQE | | | | |
| Query | 1455 | eqdqeQTVLKEEVVDSNGN + +Q K++ S NGN | QKRNV KRN | D + | AASPSLSICS ASP LSICS | VQ 1345 |
| Sbjct | 218 | QTQSQQQPQKQQQTASDKANGNTVT | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYEFLE S DSGKGSS P S + YEFL | | KRAFINQIKAK + F+ ÕIK K | | |
| Sbjct | 278 | SEDSGKGSSPPHS-VGHANSIYEFLI | | | | |
| Query | 1164 | SGKVRICTIEGTESEIDAALAMIRQF + +ICT++G+ +I AL MIRO+ | | | VPLSTESLYN] +P+S + | LQ 985 |
| Sbjct | 337 | THTSKICTLQGSPDDIQTALKMIRQK | | | | SS 396 |
| Query | 984 | LKLIEGINNDVVVSAVLSGSHIFIQL L L+EGINNDV VS ++S H+F+ | plhpshpslpl PLHP++ L | | MEAPLLPSLEI EAP LP + | LS 805 |
| Sbjct | 397 | LPLVEGINNDVAVSCIVSVGHLFVHQ | | | | PN 456 |
| Query | 804 | AVCVIPINDVWYRVQIVDTDPEDEEF AVCV + WYR Q++ E ++ | CVIKFLDFGGY ++K+LD+GGY | | RTDFMNVPFQ R DF+ VPFQ | |
| Sbjct | 457 | AVCVACVAGNWYRAQVMQHVTETDQ- | | | | |
| Query | 624 | ECILSNIEPIGGTWSIEAAEILN EC+LSNI+PI +WS +A ++ | KLTKGIVLQAQ +LT G+V+QAQ | | | NV 454 NV |
| Sbjct | 516 | ECVLSNIQPIDESQNSWSEDATDLFF | | | | |

Query 453 IFINKELVGRKLAKWVE 403 +FIN+E+V R A+W++ Sbjct 576 VFINQEMVARGFARWID 592

AGAP002166-PA [Anopheles gambiae str. PEST]

Sequence ID: ref|XP_308023.5| Length: 576 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 576

| Score | E | xpect Method | Identities | Positives | Gaps F | rame |
|----------|----------|--|------------------------------|-----------------------------|-----------------------------|------------|
| 321 bits | (823) 56 | e-95() Compositional matrix adjust. | 229/601(38% |) 324/601(53%) | 44/601(7%) -2 | 2 |
| Feature | s: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFF M++GRPLL LSLP +A I+G+ W+F | | | | V 196 |
| Sbjct | 1 | MIAGRPLLLLSLPSLAIIVGLVWYF | | | | т 55 |
| Query | 1968 | LQNGKLPQQSASKSMNINGTLVNgs L + P S S+ I G | gsgsgssSDEK + | | APIKIQSNGRTS API I N S | |
| Sbjct | 56 | LAEHE-PDMRQSSSLPIQQQSGGGG | | | | |
| Query | 1788 | GKHQQQIDSEILKSKIQDAEHKTLO | SIDEDFENLS- | SPR-DLPDSVN | TRVSFYNRKATO | - 161 |
| Sbjct | 115 | D + +S + DDLLGRSHL | -LEHDNEELSF | SPSIDLPGSVV | SRYPQNLRKFNÕ | M 157 |
| Query | 1617 | KTVEPVVIKATRTPKI-SPENSF T EPVVI+ T+ + S | LDTNYTNKECE D N | QNNNCEPKEE-I + PK++ I | | q 145 |
| Sbjct | 158 | MEPTKEPVVIRPTKAASLQSGHFRV | | | | D 217 |
| Query | 1449 | dqeQTVLKEEVVDSNGN- + E +V D | | SLSICSVQSGDS LSICSV+S DS | | т 129 |
| Sbjct | 218 | RLNGNCVPEPDAATIDDVFDPKPES | | | | P 277 |
| Query | 1296 | RVKTTYEFLFPISLIGHLYGRKRAF V TTYEFL P L+ + G++ F | TINQIKAKTLAS T+ OTK KT A+ | VSVGKNPYSGKV | VRICTIEGTESE +ICT+EG++ E | |
| Sbjct | 278 | SV-TTYEFLVPAFLVAGMLGKQGTF | | | | |
| Query | 1116 | DAALAMIRQRLPAKRYPNFTMQRIF ALA+IR++ P KR+P T+ORI | IFALPQTIVPLS + +T++PLS | | IEGINNDVVVSA +EGINNDV VS | |
| Sbjct | 337 | QDALAVIRKKFPQKRFPGLTLQRIE | | | | |
| Query | 936 | LSGSHIFIQhplhpshpslplLQKQ ++ H+F+ PLHP+H +L +Q | | | | |
| Sbjct | 397 | INVGHLFVHQPLHPTHLTLNSMQNS | | | | |
| Query | 756 | VDTDPEDEERCVIKFLDFGGYMNVG V E ++K+LD+GGY + | | | | т 586 т |
| Sbjct | 457 | VQNVTES-NLVLVKYLDYGGYSMLF | PQNLRQIRTDF | 'ISVPFÕSIECVI | LSNIQPIDESQN | |
| Query | 585 | WSIEAAEILNKLTKGIVLQAQVAGY WS EA E+ +LT ++OAOVAGY | NSHNLPEIFLF + +PEI+LF | | NKELVGRKLAKW N+E+V R A+W | |
| Sbjct | 516 | WSEEATELFRRLTSNAIMQAQVAGY | | | | |
| Query | 405 | E 403 | | | | |
| Sbjct | 576 | D 576 | | | | |
| | | | | | | |

AGAP002166-PA-like protein [Anopheles sinensis]

Sequence ID: gb|KFB35785.1| Length: 588 Number of Matches: 1

Range 1: 1 to 588

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|--------------|--------------|-------------------------|---------|
| 305 bits | (782) 5 | e-89() Compositional matrix adjust. | 223/618(36%) | 331/618(53%) | 66/618(10%) | -2 |
| Feature | s: | | | | | |
| Query | 2148 | MVSGRPLLYLSLPGVAFILGVFWFF M++GRPLL+LSLP +A I+G+ W+F | | | EPTVQARKAN E + +R | 1975 |
| Sbjct | 1 | MIAGRPLLFLSLPSLALIVGLVWYF | | _ | | TA 55 |
| Query | 1974 | GVLQNGKLPQQSASKSMNING V Q LP Q + + N | | | MLYGKSAPIKI +SAPI I | ~ |
| Sbjct | 56 | DLEPDVKÕTSSLPIÕQSGNNNNGAE | | | | |
| Query | 1806 | NGRTSNGKHQQQIDSEILKSKIQDA N S G + + +S + | | | LPDSVNTRVSF LP +V +R | YN 1633 |
| Sbjct | 106 | NKSPSKGDDMNNLLGRSHM | | ~ ~- | | NL 152 |
| Query | 1632 | RKATQKTVEPVVIKATRTP | KISPENS | FLDT1 | NYTNKECEQNN | NC 1504 |

| Sbjct | 153 | K Q EPV+I+ T+T ++ EN+ E + + MKFNQMMEPVKEPVIIRPTKTASLQSGYFRVPDENAKTTTQQQQPSPPPIQPEMKTHQQL | 212 |
|-------|------|--|------|
| Query | 1503 | EPKEEPSKKEAdqeeleqdqeQTVLKE-EVVDSNGNQKRNVDAASPSLSICSV | 1348 |
| Sbjct | 213 | + +P ++ ++ E D+ N K R SP LSICS+ QSSSQPPAEQNERLTESDSTNNNNNTSCEGNDAAFNGKPEETFDERAEQTGSPPLSICSM | 272 |
| Query | 1347 | QSGDSGKGSSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNP | 1168 |
| Sbjct | 273 | +S DSGKGSS P S + TTYEFL P L+ + G++ F+ +K +T A+V + +NP RSEDSGKGSSPPHSVGPSL-TTYEFLVPAFLVAGMLGKQGVFVKHVKKETGANVIIKRNP | 331 |
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNL | 988 |
| Sbjct | 332 | + +ICT+EG++ EI ALA+IR++ P +R+P T++RI + + ++P+S DTHNSKICTLEGSQQEIKDALALIRKKFPQRRFPALTLKRIEISRVEAVIPISLMKDTCS | 391 |
| Query | 987 | QLKLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPSLEL | 808 |
| Sbjct | 392 | L L+EGINNDV VS +++ H+F+ PLHP++ SL +QK L +SY+ EAP +P + SLPLVEGINNDVAVSCIINVGHMFVHQPLHPTYLSLSSMQKSLNESYTKSEAPHMPEIVP | 451 |
| Query | 807 | SAVCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQS | 628 |
| Sbjct | 452 | +AVCV+ VWYR QIV D +D ++K+LD+GG+ + LRQIRTDF+ VPFQS NAVCVVFAAGVWYRAQIVQLD-QDSNMVLVKYLDYGGFSLLPPQNLRQIRTDFITVPFQS | 510 |
| Query | 627 | TECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNN | 457 |
| Sbjct | 511 | EC+LSNI+P+ TWS EA E+ +LT ++QAQVAGY + +PEI+LF+S+ +N VECVLSNIQPVDESQNTWSEEATELFRRLTSNTMMQAQVAGYTAEGIPEIYLFSSIAKDN | 570 |
| Query | 456 | VIFINKELVGRKLAKWVE 403 | |
| Sbjct | 571 | V+FINKE+V R A+WV+ VVFINKEMVARGYARWVD 588 | |

uncharacterized protein Dpse_GA28909, partial [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_002134417.2**| Length: 177 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 177

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|-------|--|--------------|--------------|-----------|-------|
| 285 bits | (730) | 7e-87() Compositional matrix adjust. | 142/177(80%) | 162/177(91%) | 0/177(0%) | -2 |
| Features | s: | | | | | |
| Query | 924 | HIFIQhplhpshpslplLQKQLYDSYS H+F+ HPLHPSHP+LP+LQKQL+DSYS | | | | |
| Sbjct | 1 | HLFVNHPLHPSHPALPMLQKQLFDSYS | | | | |
| Query | 744 | PEDEERCVIKFLDFGGYMNVGFNTLRC +DEERCV+KFLDFGGYMNV + LRC | | | | |
| Sbjct | 61 | EDDEERCVVKFLDFGGYMNVNLSVLRQ | | | | |
| Query | 564 | ILNKLTKGIVLQAQVAGYNSHNLPEIF +L+KLTKGIVLQAQVAGYNSHN+PEIF | | | | 394 |
| Sbjct | 121 | VLSKLTKGIVLQAQVAGINSHNIPEIF | | | | 177 |

A kinase anchor protein 1, mitochondrial [Zootermopsis nevadensis] Sequence ID: **gb|KDR20045.1|** Length: 817 Number of Matches: 1 Range 1: 461 to 816

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|------------------------------|---------------------------|-----------------------|---------|
| 281 bits | (719) 5 | e-78() Compositional matrix adjust. | 154/361(43%) | 229/361(63%) | 26/361(7%) | -2 |
| Feature | s: | | | | | |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSVQ DS + +V ASPS+S CS | | LPRSEATR + +R | | KT 1285 |
| Sbjct | 461 | DSANHSPADVMLASPSISSCSDAQS: | | | | |
| Query | 1284 | TYEFLFPISLIGHLYGRKRAFINQI YEF+ P L+G L GR F++OI | KAKTLASVSVGI K KT AS+ + - | | | |
| Sbjct | 521 | VYEFVLPQHLVGRLIGRHGCFVHQI | | | | |
| Query | 1104 | AMIRQRLPAKRYPNFTMQRIHFALP MIRQR P KRYPN +++++ F P | | NLQLKLIEGIN LQL L+EG+N | | |
| Sbjct | 581 | EMIRÕRFPPKRYPNVSLEQVSFLPP | | | | |
| Query | 924 | HIFIQhplhpshpslplLQKQLYDS H F+O P HP+ P+L + | | | NDVWYRVQIV WYR Ö+V | |
| Sbjct | 638 | HFFLQQPTHPTFPALIRQDACMNVC | | | | |
| Query | 747 | DPEDEERCVIKFLDFGGYMNVGFNT D E + C IKF+D+GGY+ V + | | | | SI 577 |
| Sbjct | 698 | DSET-DACDIKFVDYGGYVTVTSSV | | | | |

| Query | 576 | EAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMS EA + + +LT+G VLOAOV GY ++P ++L+A G + V+ IN+ELV + LA+WVE + | 397 |
|-------|-----|--|-----|
| Sbjct | 757 | EAVDSMEELTQGQVLQAQVCGYAEDSMPLVYLYAIHG-SQVVLINQELVSQGLAEWVESA | 815 |
| Query | 396 | D 394 | |
| Sbjct | 816 | E 816 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Bombyx mori]

Sequence ID: ref|XP_004924818.1| Length: 600 Number of Matches: 1

Range 1: 257 to 594

| Score | E | xpect Method | Identities | Positives | Gaps F | rame |
|----------|------------|--|-------------|----------------|------------------------|------|
| 258 bits | (660) 1e | e-71() Compositional matrix adjust. | 146/342(43% |) 215/342(62%) | 20/342(5%) -2 | 2 |
| Features | S : | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSG VD S S+C S S DSG | | | | |
| Sbjct | 257 | VD S S+C S S DSG: VDPLLASPSMCNFSDNHSEGSSDSG: | | | ++F+ +L RIHQFVLSQNL | |
| Query | 1251 | GHLYGRKRAFINQIKAKTLASVSVG G L G+ +F+ QIKAKT ASV V | | | | |
| Sbjct | 317 | GLLIGKHGSFVTÕIKAKTGASVYVR | | | | |
| Query | 1071 | YPNFTMQRIHFALPQTIVPLSTESL' +PNF++Q I L Q + PL E L | | | | |
| Sbjct | 377 | FPNFSLÕEISAELYÕKLTPLIPEFL | | | | |
| Query | 891 | hpslplLQKQLYDSYSTMEAPLLPS- PSL +L + + +Y + P LP | | | | |
| Sbjct | 434 | FPSLHVLHRLMAATYQNPDVPSLPR | | | | |
| Query | 714 | FLDFGGYMNVGFNTLRQIRTDFMNV +DFGGY+ V + L+QIR+DFM + | | | | |
| Sbjct | 493 | LVDFGGYLTVDNDQLKQIRSDFMTL | | | | |
| Query | 534 | LQAQVAGYNSHNLPEIFLFASLGPNI L AOVAGY+ LP + L+ +L P | | | | |
| Sbjct | 553 | LHAQVAGYDETGLPLVHLYLTLHPQ | • | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X2 [Papilio polytes]

Sequence ID: ref|XP_013146233.1| Length: 531 Number of Matches: 1

Range 1: 186 to 525

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|--------------|--------------|--------------------------|--------|
| 255 bits | (652) 3e | e-71() Compositional matrix adjust. | 144/347(41%) | 214/347(61%) | 28/347(8%) | -2 |
| Features | 3: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSG VD S S+C S S DSG | | | RVKTTYEFLFI R+ ++F+] | |
| Sbjct | 186 | VD S S+C S S DSG. VDPLLASPSMCHFSDSHSEGSSDSG: | | | | |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASV +L+G L G+ +F+NQIKAKT ASV | | | | |
| Sbjct | 243 | TLVGLLIGKHGSFVNQIKAKTGASV | | | | |
| Query | 1080 | AKRYPNFTMQRIHFALPQTIVPLST KR+PNF++Q I L Q + P | | | | |
| Sbjct | 303 | EKRFPNFSIQEISAELYQRLAPFIP | | | | |
| Query | 900 | hpshpslplLQKQLYDSYSTMEAPL HP+ PSL L + + +Y + P | LPS-LELSAVCV | /IPINDVWYRVO | IVDTDPEDEE | RC 724 |
| Sbjct | 360 | HPTFPSLHALHRLMAATYQNPDVPS | | | | rs 418 |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDF V+K +DFGGY+ V + L+QIR+DF | | | WSIEAAEILNI WS EA I+ | KL 550 |
| Sbjct | 419 | VVKLVDFGGYLTVDNDQLKQIRSDF | | | | GL 478 |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFA T G +L AQVAGY+ LP + L+ | | | 409 | |
| Sbjct | 479 | TAGQLLHAQVAGYDEAGLPLVHLYL | | | 525 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Papilio xuthus] Sequence ID: **ref|XP_013182136.1|** Length: 607 Number of Matches: 1

▶ See 2 more title(s) Range 1: 262 to 601

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|----------------------------|------------------------------|------------------------|---------|
| 257 bits | (656) 56 | e-71() Compositional matrix adjust. | 145/347(42%) | 214/347(61%) | 28/347(8%) | -2 |
| Features | s: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSG VD S S+C S S DSG | | | RVKTTYEFLF | |
| Sbjct | 262 | VDPLLASPSMCHFSDSHSEGSSDSG | | · - | | _ |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASV +L+G L G+ +F+NQIKAKT ASV | | | | |
| Sbjct | 319 | NLVGLLIGKHGSFVNÕIKAKTGASV | | | | |
| Query | 1080 | AKRYPNFTMQRIHFALPQTIVPLST KR+PNF++O I L O + P | | EGINNDVVVSAV E +NND +++ + | | |
| Sbjct | 379 | EKRFPNFSIÕEISPELYÕRLAPFIP | | | | |
| Query | 900 | hpshpslplLQKQLYDSYSTMEAPL | | VIPINDVWYRVÇ P + WYR Ĉ | | |
| Sbjct | 436 | HPTFPSLHALHRLMAATYQNPDVPS | | | | |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDF V+K +DFGGY+ V + L+QIR+DF | | | WSIEAAEILN WS EA I+ | IKL 550 |
| Sbjct | 495 | VVKLVDFGGYLTVDNDQLKQIRSDF | | | | GL 554 |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFA T G +L AQVAGY+ LP + L+ | SLGPNNVIFINI +L P VIF+N | | 409 | |
| Sbjct | 555 | TAGQLLHAQVAGYDEAGLPLVHLYL | | | 601 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Papilio polytes]

Sequence ID: ref|XP_013146231.1| Length: 609 Number of Matches: 1

▶ See 1 more title(s) Range 1: 264 to 603

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|---------------------------|--------------------|-------------------------|--------|
| 256 bits | (654) 96 | e-71() Compositional matrix adjust. | 144/347(41%) | 214/347(61%) | 28/347(8%) | -2 |
| Feature | s: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSG | | | | |
| Sbjct | 264 | VD S S+C S S DSG VDPLLASPSMCHFSDSHSEGSSDSG | | +P ANLNMVPSDSGI | R+ ++F+ SRIHQFII | _ |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASV +L+G L G+ +F+NQIKAKT ASV | | | | |
| Sbjct | 321 | TLVGLLIGKHGSFVNQIKAKTGASV | | | | |
| Query | 1080 | AKRYPNFTMQRIHFALPQTIVPLST KR+PNF++Q I L Q + P | | | | |
| Sbjct | 381 | EKRFPNFSIQEISAELYQRLAPFIP | | | | |
| Query | 900 | hpshpslplLQKQLYDSYSTMEAPL HP+ PSL L + + +Y + P | LPS-LELSAVCV LP ++ ++C | | | |
| Sbjct | 438 | HPTFPSLHALHRLMAATYQNPDVPS | | | | |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDF V+K +DFGGY+ V + L+QIR+DF | | | -WSIEAAEILN WS EA I+ | KL 550 |
| Sbjct | 497 | VVKLVDFGGYLTVDNDQLKQIRSDF | | | | GL 556 |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFA T G +L AQVAGY+ LP + L+ | | | 409 | |
| Sbjct | 557 | TAGQLLHAQVAGYDEAGLPLVHLYL | | | 603 | |
| | | | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Papilio machaon] Sequence ID: **ref|XP_014370545.1|** Length: 609 Number of Matches: 1

| Score | Expect | Method | Identities | Positives | Gaps | Frame | _ |
|--------------|-----------|------------------------------|--------------|--------------|------------|--------|-----|
| 256 bits(654 |) 1e-70() | Compositional matrix adjust. | 144/347(41%) | 214/347(61%) | 28/347(8%) | -2 | • |
| Features: | | | | | | | |
| Query 13 | 36 VDA | ASPSLSICSVQSGDSG | KGSS | LPRSEAT | RVKTTYEFLF | 'PI 12 | 261 |

| | | VD S S+C S S DSGKG S +P R+ ++F+ P | |
|-------|------|--|------|
| Sbjct | 264 | VDPLLASPSMCHFSDSHSEGSSDSGKGCSEAASPPPANLNMVPSDSGLRIHQFVIPQ | 320 |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALAMIRQRLP +L+G L G+ +F+NQIKAKT ASV V ++P S K +IC +EGT++EI+AA+ MI+++ P | 1081 |
| Sbjct | 321 | NLVGLLIGKHGSFVNQIKAKTGASVYVRRHPDSVKQKICAVEGTQNEIEAAIDMIKEKFP | 380 |
| Query | 1080 | AKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSHIFIQhpl KR+PNF++Q I L Q + P E LQL+L+E +NND +++ ++S H F+Q PL | 901 |
| Sbjct | 381 | EKRFPNFSIQEISAELYQRLAPFIPEFLQLQLVESVNNDTIMTCLVSAGHFFLQQPL | 437 |
| Query | 900 | hpshpslplLQKQLYDSYSTMEAPLLPS-LELSAVCVIPINDVWYRVQIVDTDPEDEERC | 724 |
| Sbjct | 438 | $ar{	ext{HP}}+ar{	ext{PSL}}\ ar{	ext{L}}++++Y++P\ ar{	ext{LP}}++++C\ ar{	ext{P}}+WYR\ ar{	ext{Q}}++\ ar{	ext{T}}\ ar{	ext{E}}++HPTFPSLHALHRLMAATYQNPDVPSLPRPVKEGSICAAPTENNWYRAQVISTS-EENDTS$ | 496 |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKL | 550 |
| Sbjct | 497 | V+K +DFGGY+ V + L+QIR+DFM +PFQ+TE +L+ ++P WS EA I+ L $VVKLVDFGGYLTVDNDQLKQIRSDFMTLPFQATEALLAFVKPANNEEDWSSEALRIMAGL VVFT$ | 556 |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKW 409 | |
| Sbjct | 557 | T G +L AQVAGY+ LP + L+ +L P VIF+N+ELV R LA+W TAGQLLHAQVAGYDEAGLPLVHLYLTLNPQQVIFLNRELVERGLAEW 603 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Amyelois transitella]

Sequence ID: ref|XP_013195864.1| Length: 597 Number of Matches: 1

▶ See 1 more title(s) Range 1: 252 to 591

| Score | Ex | cpect Method | Identities | Positives | Gaps | Frame |
|-----------|------------|---|-----------------------------|--------------|-------------------|--------------|
| 254 bits(| (650) 3e | e-70() Compositional matrix adjust. | 144/347(41%) | 213/347(61%) | 28/347(8%) | -2 |
| Features | S : | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSGIVD S S+C S S DSGI | | | RVKTTYEFLER+ ++F+ | |
| Sbjct | 252 | VDPMLASPSMCHFSDNHSEGSSDSG | | - | | _ |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASV | | | | |
| Sbjct | 309 | +L+G L G+ +F+ QIKAKT ASV TLVGLLIGKHGSFVAQIKAKTGASV | | | | |
| Query | 1080 | AKRYPNFTMORIHFALPOTIVPLSTI KR+PNF++O I L O + PL | ESLYNLOLKLIE | GINNDVVVSAV | LSGSHIFIO | pl 901 |
| Sbjct | 369 | EKRFPNFSLQEISAELYQRLAPLVP | | | | |
| Query | 900 | hpshpslplLQKQLYDSYSTMEAPLI HP+ PSL L + + +Y + P I | | | | |
| Sbjct | 426 | HPTFPSLHALHRLMAATYQNPDVPA | | | | |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDF | | | | |
| Sbjct | 485 | V+K +DFGGY+ V + L+QIR+DFI VVKLVDFGGYLTVDNDQLKQIRSDFI | | | | L MGL 544 |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFA | | | 409 | |
| Sbjct | 545 | T G +L AQVAGY+ LP + L+ TAGQLLHAQVAGYDETGLPLVHLYL | +L P VI++N+ TLSPQQVIYLNF | | 591 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Plutella xylostella] Sequence ID: **ref|XP_011553388.1**| Length: 590 Number of Matches: 1

Range 1: 248 to 584

| Score | Ex | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------------|--------------|------------|--------------|
| 254 bits | (649) 4e | e-70() Compositional matrix adjust. | 145/346(42%) | 213/346(61%) | 29/346(8%) | -2 |
| Features | S: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSG VD S S+C S S DSG | | | | |
| Sbjct | 248 | VD S S+C S S DSG: VDPLLASPSMCHFSDNHSEGSSDSG: | | | | |
| Query | 1257 | LIGHLYGRKRAFINQIKAKTLASVS | VGKNPYSGKVRI V ++P S K +1 | | | |
| Sbjct | 305 | LVGLLIGKHGSFVTLIKGKTGASVY | | | | |
| Query | 1077 | KRYPNFTMQRIHFALPQTIVPLSTE KR+PNFT++ I L Q ++PL E | | | | |
| Sbjct | 365 | KRFPNFTLEEISPELYQKLMPLVPE | | | | |
| Query | 897 | pshpslplLQKQLYDSYSTMEAPLL P+ PSL L + + +YS + P L | | | | RCV 721 V |
| Sbjct | 420 | PTFPSLHALHRLMAATYSQPDVPPL | | | | |

| Query | 720 | IKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLT +K +DFGGY+ + + L+QIR+DFM +PFQ+TE +L+ ++P TWS EA I+ LT | 547 |
|-------|-----|---|-----|
| Sbjct | 479 | VKLVDFGGYLTLDADQLKQIRSDFMTLPFQATEALLAFVKPANNESTWSGEALRIMAGLT | 538 |
| Query | 546 | KGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKW 409 G +L AQVAGY+ LP + L+ +LGP VIF+N+ELV R A+W | |
| Sbjct | 539 | AGQLLHAQVAGYDEAGLPLVHLYLTLGPQQVIFLNRELVERGFAEW 584 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X1 [Bombyx mori]

Sequence ID: ref|XP_004924816.1| Length: 601 Number of Matches: 1

▶ See 2 more title(s) Range 1: 257 to 595

| E | rpect Method | Identities | Positives | Gaps F | rame | |
|--|--|---|--|---|---|--|
| 254 bits(648) 5e-70() Compositional matrix adjust. 146/343(43%) 215/343(62%) 21/343(6%) -2 | | | | | | |
| 3: | | | | | | |
| 1386 | | | | | | |
| 257 | | | | | | |
| 1251 | | | | | | |
| 317 | | | | | | |
| 1071 | | | | | | |
| 377 | | | | | | |
| 891 | | | | | | |
| 434 | | | | | | |
| 714 | | | | | I 538 | |
| 493 | | | | | Q 552 | |
| 537 | | | | | | |
| 553 | ~ | | | | | |
| | (648) 5e s: 1386 257 1251 317 1071 377 891 434 714 493 537 | 1386 VDAASPSLSICSVQSGDSGI VD S S+C S S DSGI 257 VDPLLASPSMCNFSDNHSEGSSDSGI 1251 GHLYGRKRAFINQIKAKTLASVSVGI G L G+ +F+ QIKAKT ASV V 317 GLLIGKHGSFVTQIKAKTGASVYVRI 1071 YPNFTMQRIHFALPQTIVPLSTESLI +PNF++Q I L Q + PL E 377 FPNFSLQEISAELYQKLTPLIPEF 891 hpslpllQKQLYDSYSTMEAPLLPS PSL +L + + +Y + P LP 434 FPSLHVLHRLMAATYQNPDVPSLPRI 714 FLDFGGYMNVGFNTLRQIRTDFMNVI +DFGGY+ V + L+QIR+DFM +I 493 LVDFGGYLTVDNDQLKQIRSDFMTLI 537 VLQAQVAGYNSHNLPEIFLFASLGPI +L AQVAGY+ LP + L+ +L P | (648) 5e-70() Compositional matrix adjust. 146/343(43%) S: 1386 VDAASPSLSICSVQSGDSGKGSSLPRS VD S S+C S DSGKG +S P + 257 VDPLLASPSMCNFSDNHSEGSSDSGKGCSEAASPPPA 1251 GHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICT G L G+ +F+ QIKAKT ASV V ++P S K +IC 317 GLLIGKHGSFVTQIKAKTGASVYVRRHPESSKQKICA 1071 YPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGIN +PNF++Q I L Q + PL E LQL+L+E +N 377 FPNFSLQEISAELYQKLTPLIPEFLQLQLVESVN 891 hpslplLQKQLYDSYSTMEAPLLPS-LELSAVCVIPT PSL +L + + +Y + P LP ++ A+C P 434 FPSLHVLHRLMAATYQNPDVPSLPRPVKEGAICAAPT 714 FLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNI +DFGGY+ V + L+QIR+DFM +PFQ+TE +L+ + 493 LVDFGGYLTVDNDQLKQIRSDFMTLPFQATEALLAFV 537 VLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVG +L AQVAGY+ LP + L+ +L P VIF+N+ELV | (648) 5e-70() Compositional matrix adjust. 146/343(43%) 215/343(62%) 1386 VDAASPSLSICSVQSGDSGKGSSLPRSEATRVKT VD S S+C S S DSGKG +S P + V T 257 VDPLLASPSMCNFSDNHSEGSSDSGKGCSEAASPPPASLNIVPTETDL 1251 GHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAA G L G+ +F+ QIKAKT ASV V ++P S K +IC +EGT+SEI+AA 317 GLLIGKHGSFVTQIKAKTGASVYVRRHPESSKQKICAVEGTQSEIEAA 1071 YPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSG +PNF++Q I L Q + PL E LQL+L+E +NND +++ ++S 377 FPNFSLQEISAELYQKLTPLIPEFLQLQLVESVNNDTILTCLVSA 891 hpslplLQKQLYDSYSTMEAPLLPS-LELSAVCVIPINDVWYRVQIVD PSL +L + + +Y + P LP ++ A+C P + WYR Q++ 434 FPSLHVLHRLMAATYQNPDVPSLPRPVKEGAICAAPTENNWYRAQVIS 714 FLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGT-WSIE +DFGGY+ V + L+QIR+DFM +PFQ+TE +L+ ++P WS E 493 LVDFGGYLTVDNDQLKQIRSDFMTLPFQATEALLAFVKPANNVEWSGE | (648) 5e-70() Compositional matrix adjust. 146/343(43%) 215/343(62%) 21/343(6%) -268: 1386 VDAASPSLSICSVQSGDSGKGSSLPRSEATRVKTTYEFLFPISL VD S S+C S S DSGKG +S P + V T ++F+ +L 257 VDPLLASPSMCNFSDNHSEGSSDSGKGCSEAASPPPASLNIVPTETDLRIHQFVLSQNL 1251 GHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALAMIRQRLPAK G L G+ +F+ QIKAKT ASV V ++P S K +IC +EGT+SEI+AAL MI+++ P K 317 GLLIGKHGSFVTQIKAKTGASVYVRRHPESSKQKICAVEGTQSEIEAALDMIKEKFPEK 1071 YPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSHIFIQhplhp +PNF++Q I L Q + PL E LQL+L+E +NND +++ ++S H F+Q PLHP 377 FPNFSLQEISAELYQKLTPLIPEFLQLQLVESVNNDTILTCLVSAGHFFLQQPLHP 891 hpslplLQKQLYDSYSTMEAPLLPS-LELSAVCVIPINDVWYRVQIVDTDPEDEERCVI PSL +L + + +Y + P LP ++ A+C P + WYR Q++ T E+ + V + 434 FPSLHVLHRLMAATYQNPDVPSLPRPVKEGAICAAPTENNWYRQVISTS-EENDTSVV 714 FLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGT-WSIEAAEILNKLTKG +DFGGY+ V + L+QIR+DFM +PFQ+TE +L+ ++P WS EA I+ LT G 493 LVDFGGYLTVDNDQLKQIRSDFMTLPFQATEALLAFVKPANNVEWSGEALRIMAGLTAG 537 VLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKW 409 +L AQVAGY+ LP + L+ + LP VIF+N+ELV R LA+W | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X4 [Bombyx mori]

Sequence ID: **ref|XP_004924820.1|** Length: 598 Number of Matches: 1 Range 1: 257 to 592

| Score | Ex | rpect Method | Identities | Positives | Gaps Fr | ame |
|----------|----------|--|--------------------------|--------------|----------------------------|-----|
| 254 bits | (648) 6e | e-70() Compositional matrix adjust. | 144/342(42%) | 213/342(62%) | 22/342(6%) -2 | |
| Features | 3: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSGIVD S S+C S S DSGI | | | -TYEFLFPISLI | |
| Sbjct | 257 | VD 5 5+C 5 5 DSG. VDPLLASPSMCNFSDNHSEGSSDSG. | | | | |
| Query | 1251 | GHLYGRKRAFINQIKAKTLASVSVG G L G+ +F+ QIKAKT ASV V | | | | |
| Sbjct | 317 | GLLIGKHGSFVTQIKAKTGASVYVR | | | | |
| Query | 1071 | YPNFTMQRIHFALPQTIVPLSTESLY +PNF++Q I L Q + PL E L | | | | |
| Sbjct | 377 | FPNFSLÕEISAELYÕKLTPLIPEFL | | | | |
| Query | 891 | hpslplLQKQLYDSYSTMEAPLLPS- PSL +L + + + + P LP | -LELSAVCVIPI ++ A+C P | NDVWYRVQIVD | TDPEDEERCVIK T E+ + V+K | 715 |
| Sbjct | 432 | FPSLHVLHRLMAATYQNPDVPSLPR | | | | |
| Query | 714 | FLDFGGYMNVGFNTLRQIRTDFMNV +DFGGY+ V + L+QIR+DFM + | | | | |
| Sbjct | 491 | LVDFGGYLTVDNDQLKQIRSDFMTL | | | | |
| Query | 534 | LQAQVAGYNSHNLPEIFLFASLGPNI L AOVAGY+ LP + L+ +L P | | | | |
| Sbjct | 551 | LHAQVAGYDETGLPLVHLYLTLHPQ | | | | |
| | | | | | | |

Sequence ID: ref|XP_013195867.1| Length: 595 Number of Matches: 1

Range 1: 252 to 589

| Score | Е | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|---------------------|---------------|------------------------|-------|
| 250 bits | (639) 16 | e-68() Compositional matrix adjust. | 142/347(41%) |) 211/347(60% |) 30/347(8%) |) -2 |
| Feature | s: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSGI | | | | |
| Sbjct | 252 | VD S S+C S S DSGI VDPMLASPSMCHFSDNHSEGSSDSGI | KG S KGCSEAASPPP | | R+ ++F+ LRIHQFI | _ |
| Query | 1260 | SLIGHLYGRKRAFINQIKAKTLASV +L+G L G+ +F+ QIKAKT ASV | | | | |
| Sbjct | 309 | TLVGLLIGKHGSFVAQIKAKTGASV | | | | |
| Query | 1080 | AKRYPNFTMQRIHFALPQTIVPLSTI KR+PNF++Q I L Q + PL I | | | | |
| Sbjct | 369 | EKRFPNFSLÕEISAELYÕRLAPLVP | | | | |
| Query | 900 | hpshpslplLQKQLYDSYSTMEAPLI HP+ PSL L + + +Y + P I | | VIPINDVWYRV | QIVDTDPEDE 2++ T E+ | |
| Sbjct | 424 | HPTFPSLHALHRLMAATYQNPDVPA | | | | |
| Query | 723 | VIKFLDFGGYMNVGFNTLRQIRTDFI V+K +DFGGY+ V + L+QIR+DFI | | | TWSIEAAEIL WS EA I+ | |
| Sbjct | 483 | VVKLVDFGGYLTVDNDQLKQIRSDFI | | | | _ |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFA T G +L AQVAGY+ LP + L+ - | | | 409 | |
| Sbjct | 543 | TAGQLLHAQVAGYDETGLPLVHLYL | | | 589 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial isoform X3 [Bombyx mori]

Sequence ID: ref|XP_004924819.1| Length: 599 Number of Matches: 1

Range 1: 257 to 593

| Score | E | xpect Method | Identities | Positives | Gaps | Frame | |
|-----------|----------|--|--------------|--------------|-----------------------|----------------|--|
| 249 bits | (637) 2e | e-68() Compositional matrix adjust. | 144/343(42%) | 213/343(62%) | 23/343(6%) | -2 | |
| Features: | | | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSG | | | | | |
| Sbjct | 257 | VD S S+C S S DSG VDPLLASPSMCNFSDNHSEGSSDSG | | | | -L+ ILV 316 | |
| Query | 1251 | GHLYGRKRAFINQIKAKTLASVSVG G L G+ +F+ QIKAKT ASV V | | | | | |
| Sbjct | 317 | GLLIGKHGSFVTQIKAKTGASVYVR | | | | | |
| Query | 1071 | YPNFTMQRIHFALPQTIVPLSTESL +PNF++Q I L Q + PL E | | | | | |
| Sbjct | 377 | FPNFSLQEISAELYQKLTPLIPEF- | | | | | |
| Query | 891 | hpslplLQKQLYDSYSTMEAPLLPS PSL +L + + +Y + P LP | | | | | |
| Sbjct | 432 | FPSLHVLHRLMAATYQNPDVPSLPR | | | | | |
| Query | 714 | FLDFGGYMNVGFNTLRQIRTDFMNV +DFGGY+ V + L+QIR+DFM + | | | AAEILNKLTK A I+ LT | | |
| Sbjct | 491 | LVDFGGYLTVDNDQLKQIRSDFMTL | | | | | |
| Query | 537 | VLQAQVAGYNSHNLPEIFLFASLGP +L AQVAGY+ LP + L+ +L P | | | | | |
| Sbjct | 551 | LLHAQVAGYDETGLPLVHLYLTLHP | | | | | |

KH domain-containing protein C56G2.1, putative [Pediculus humanus corporis] Sequence ID: **ref|XP_002426032.1|** Length: 714 Number of Matches: 1

| Score | E | xpect | Method | Identities | Positives | Gaps | Frame | <u>) </u> |
|----------|----------|--------|-------------------------------------|--------------------------|--------------|------------|-------|--|
| 251 bits | (642) 4e | e-68() | Compositional matrix adjust. | 145/355(41%) | 219/355(61%) | 24/355(6%) | -2 | _ |
| Features | s: | | | | | | | |
| Query | 1413 | DSNG | GNQKRNVDAASPSLSICSV N V ASPS+S S | QSGDSGKGSSL S DSGKG S | PRSEATR | VK | | 282 |
| Sbjct | 331 | DSAN | NSPSEVMLASPSVSGYSDTHSE | | | v | • | 90 |

| Query | 1281 | YEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALA YEF+ P L+G L GR +++N+IK T AS+ + ++P + K++IC +EGT+ +I++AL | 1102 |
|-------|------|--|------|
| Sbjct | 391 | YEFVIPQHLVGRLIGRYGSYVNEIKETTHASIYIKRHPDTSKLKICAVEGTQMDIESALD | 450 |
| Query | 1101 | MIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSH MIRO+ P KRYPN T++++ + ++P+ +ES +OL LIEGINNDV++S+++S H | 922 |
| Sbjct | 451 | MIRQKFPKKRYPNVTLEQVVISPEPQMIPIISESMQLYLIEGINNDVLLSSLVSAGH | 507 |
| Query | 921 | IFIQhplhpshpslplLQKQLYDSYSTMEAPLLP-SLELSAVCVIPINDVWYRVQIVDTD F+Q P HP++ SL L + YS + PL+P + +C P+++ WYR QIV D | 745 |
| Sbjct | 508 | FFLQQPTHPTYLSLNRLNTCMNYCYSEPDQPLIPDGVGAGILCAAPVHNGWYRAQIVSMD | 567 |
| Query | 744 | PEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEA ED + C +KF+D+GGYM + + LRQIR DF+N+PFQ+ EC L++++P W + | 571 |
| Sbjct | 568 | -EDSKICDVKFVDYGGYMTMPVSLLRQIRFDFVNLPFQAAECYLASVKPSNEENVWCENS | 626 |
| Query | 570 | AEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWV 406 ++ KLT G VLQAQV GY +P I+L+ + + VI +N+ELV LA+W+ | |
| Sbjct | 627 | KSLVEKLTFGKVLQAQVYGYAEDGIPLIYLYTVVD-DKVILVNEELVNHGLAEWI 680 | |

putative a kinase anchor protein [Danaus plexippus]

Sequence ID: gb|EHJ63868.1| Length: 597 Number of Matches: 1

Range 1: 252 to 591

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|--------------|-------------------|----------------------|---------|
| 248 bits | (634) 56 | e-68() Compositional matrix adjust. | 141/344(41%) | 211/344(61%) | 22/344(6%) | -2 |
| Features | s: | | | | | |
| Query | 1386 | VDAASPSLSICSVQSGDSGI | | | | |
| Sbjct | 252 | VD S S+C S S DSGI VDPMLASPSMCHFSDNHSEGSSDSGI | | A 'NINIVSAEAGI | ++F+ P RIHQFIIPQT | |
| Query | 1251 | GHLYGRKRAFINQIKAKTLASVSVG G L G+ +F+ +IKAKT A+V V | KNPYSGKVRICT | TIEGTESEIDAA | LAMIRORLPA | KR 1072 |
| Sbjct | 312 | GLLIGKCGSFVTKIKAKTGATVYVRI | _ | | | |
| Query | 1071 | YPNFTMQRIHFALPQTIVPLSTESLY +P+F++Q I L Q + P+ E | | | | |
| Sbjct | 372 | FPHFSIQEISAELYQRLTPVVPEF- | | | | |
| Query | 891 | hpslplLQKQLYDSYSTMEAPLLPS- PSL L + + + Y + + P LP | | | | |
| Sbjct | 429 | FPSLHALHRLMAATYQSPDVPALPKI | | | | |
| Query | 714 | FLDFGGYMNVGFNTLRQIRTDFMNVI +DFGGY+ V + L+QIR+DFM +1 | | | | |
| Sbjct | 488 | LVDFGGYLTVDNDQLKQIRSDFMTL | | | | |
| Query | 540 | IVLQAQVAGYNSHNLPEIFLFASLG +L AQVAGY+ LP + L+ +L 1 | | |)9 | |
| Sbjct | 548 | QLLHAQVAGYDERGLPLVHLYLTLS | | | 91 | |

PREDICTED: KH domain-containing protein C56G2.1 [Tribolium castaneum]

Sequence ID: ref|XP_971237.1| Length: 536 Number of Matches: 1

| Score | Ex | xpect Method | Identities | Positives | Gaps | Frame |
|-----------|----------|---|------------------------------------|---------------------|------------|-----------------|
| 242 bits(| (617) 3e | e-66() Compositional matrix adjust. | 143/350(41%) | 217/350(62%) | 18/350(5%) | -2 |
| Features | S: | | | | | |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSVQ DS + +V ASPSLS S | | | | EFL 1270 EF+ |
| Sbjct | 179 | DS + +V ASPSLS S DSANHSPADVMLASPSLSSISDNHS | | PS+ EVVTPPPSRSLV | | |
| Query | 1269 | FPISLIGHLYGRKRAFINQIKAKTL P SL+G L G+ + ++ IK KT | | | | |
| Sbjct | 239 | IPQSLVGKLIGKHGSSVSNIKDKTG | | | | |
| Query | 1089 | RLPAKRYPNFTMQRIHFALPQTIVP: + P KR+P T++++ F LP+ + P- | | | | |
| Sbjct | 299 | KFPLKRFPEVTLEQVSF-LPE-VSP | | | | |
| Query | 909 | hplhpshpslplLQKQLYDSYSTME P HPS P+L +L + YS + | APLLPS-LELS <i>P</i> +P+LP+ + + | | | |
| Sbjct | 356 | QPAHPSFPNLNILTGYMNVCYSEAD | | | | |
| Query | 732 | ERCVIKFLDFGGYMNVGFNTLRQIR | TDFMNVPFQSTE | ECILSNIEPIGG | T-WSIEAAEI | ILN 556 |

+KFLDFGGY + + LRQIR DFM++PFQ+ EC L+N++P+ T W EA + ATAYVKFLDFGGYSYIEISKLRQIRGDFMSLPFQAAECFLANVKPVEETGWRDEAFSAVV Sbjct 415 474 KLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWV ++TKG ++ Q+ Y +P ++ + LGP V+F+N+ELV + A+W+ EMTKGAIIYTQIVDYTEEGIPLVYCYLILGPRQVVFLNQELVNQGHAEWL Query 555 Sbjct 475 524

GA16943, partial [Drosophila affinis]

Sequence ID: gb|ADJ12817.1| Length: 186 Number of Matches: 1

Range 1: 4 to 148

| Score | E | expect Method | Identities | Positives | Gaps | Frame |
|-----------|---------|--|--------------|--------------|------------------------|-------|
| 230 bits | (586) 4 | e-66() Compositional matrix adjust. | 123/149(83%) | 131/149(87%) | 4/149(2%) | -2 |
| Features: | | | | | | |
| Query | 1944 | QSASKSMNINGTLVNgsgsgsgssSI | | | | |
| Sbjct | 4 | Q A+KSMNINGT + + +G+GS SI QQATKSMNINGTDATENGNGSGSI | | | | |
| Query | 1764 | SEILKSKIQDAEHKTLCSIDEDFENI SE+LKSKIQDAEHK LCSIDEDFENI | | | KTVEPVVIK K VEPVVIK | |
| Sbjct | 61 | SEMLKSKI QDAEHKKLCSIDEDFENI | | | | |
| Query | 1584 | RTPKISPENSFLDTNYTNKECEQNNI RTPKISPENSFL+ YT KECEONNI | | | | |
| Sbjct | 121 | RTPKISPENSFLEATYT-KECEQNNI | | | | |

GA16943, partial [Drosophila miranda]

Sequence ID: gb|ADJ12818.1| Length: 188 Number of Matches: 1

▶ See 13 more title(s) Range 1: 4 to 150

| Score | E | expect Method | Identities | Positives | Gaps | Frame | |
|-----------|---------|--|--------------|------------------------------|------------------------|-------|--|
| 228 bits | (581) 2 | e-65() Compositional matrix adjust. | 123/149(83%) | 130/149(87%) | 2/149(1%) | -2 | |
| Features: | | | | | | | |
| Query | 1944 | QSASKSMNINGTLVNgsgsgsgssSD Q A+KSMNINGT +G+GSGS SD | | KSAPIKIQSNGR KSAPIKIQSNGR | | · | |
| Sbjct | 4 | QQATKSMNINGTDATENGNGSGSGSD | | | | , — — | |
| Query | 1764 | SEILKSKIQDAEHKTLCSIDEDFENL SE+LKSKIODAEHK LCSIDEDFENL | | | KTVEPVVIK K VEPVVIK | | |
| Sbjct | 63 | SEMLKSKIQDAEHKKLCSIDEDFENL | | | | | |
| Query | 1584 | RTPKISPENSFLDTNYTNKECEQNNN RTPKISPENSFL+ YT KECEONNN | | | | | |
| Sbjct | 123 | RTPKISPENSFLEATYT-KECEQNNN | | | | | |

GA16943, partial [Drosophila pseudoobscura]

Sequence ID: gb|ADJ12838.1| Length: 190 Number of Matches: 1

Range 1: 3 to 150

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|--------------|--------------|-----------------------|-------------------|
| 227 bits | (578) 5 | e-65() Compositional matrix adjust. | 122/150(81%) | 130/150(86%) | 2/150(1%) | -2 |
| Features | s: | | | | | |
| Query | 1947 | QQSASKSMNINGTLVNgsgsgsgssS QQ A+KSMNINGT +G+GSGS S | | | | - |
| Sbjct | 3 | QQQATKSMNINGT +G+GSGS S QQQATKSMNINGTDATENGNGSGSGS | | | | , z. – |
| Query | 1767 | DSEILKSKIQDAEHKTLCSIDEDFEN DSE+LKSKIQDAEHK LCSIDEDFEN | | | QKTVEPVVI K VEPVVI | |
| Sbjct | 62 | DSEMLKSKIQDAEHKKLCSIDEDFEN | | | | |
| Query | 1587 | TRTPKISPENSFLDTNYTNKECEQNN TRTPKISPENSFL+ YT KECEQNN | | | | |
| Sbjct | 122 | TRTPKISPENSFLEATYT-KECEQNN | | | | |

GA16943, partial [Drosophila pseudoobscura]

Sequence ID: gb|ADJ12833.1| Length: 190 Number of Matches: 1

▶ See 4 more title(s) Range 1: 3 to 150

| Score | E | Expect Method | Identities | Positives | Gaps | Frame | |
|---|------|--|------------|-----------|-----------------------|-----------------|--|
| 227 bits(578) 6e-65() Compositional matrix adjust. 122/150(81%) 130/150(86%) 2/150(1%) -2 | | | | | | | |
| Features: | | | | | | | |
| Query | 1947 | QQSASKSMNINGTLVNgsgsgsgssS OO A+KSMNINGT +G+GSGS S | | | | QQI 1768 OOI | |
| Sbjct | 3 | QQQATKSMNINGT +G+GSGS S QQQATKSMNINGTDATENGNGSGSGS | | | | · ~ | |
| Query | 1767 | DSEILKSKIQDAEHKTLCSIDEDFEN DSE+LKSKIODAEHK LCSIDEDFEN | | | QKTVEPVVI K VEPVVI | | |
| Sbjct | 62 | DSE*LKSKIQDAEHK LCSIDEDFEN | | - | | | |
| Query | 1587 | TRTPKISPENSFLDTNYTNKECEONN TRTPKISPENSFL+ YT KECEONN | | | | | |
| Sbjct | 122 | TRTPKISPENSFLEATYT-KECEQNN | | | | | |

GA16943, partial [Drosophila pseudoobscura]

Sequence ID: gb|ADJ12832.1| Length: 190 Number of Matches: 1

▶ See 4 more title(s) Range 1: 3 to 150

| Score | E | xpect Method | Identities | Positives | Gaps | Frame | |
|---|------|--|------------|------------------------------|-----------------------|---------|--|
| 227 bits(578) 6e-65() Compositional matrix adjust. 122/150(81%) 130/150(86%) 2/150(1%) -2 | | | | | | | |
| Features: | | | | | | | |
| Query | 1947 | QQSASKSMNINGTLVNgsgsgsgssS OO A+KSMNINGT +G+GSGS S | | GKSAPIKIQSNG GKSAPIKIQSNG | | QI 1768 | |
| Sbjct | 3 | QQQATKSMNINGTDATENGNGSGSGS | | | | , z. – | |
| Query | 1767 | DSEILKSKIQDAEHKTLCSIDEDFEN DSE+LKSKIQDAEHK LCSIDEDFEN | | | QKTVEPVVI K VEPVVI | | |
| Sbjct | 62 | DSEMLKSKIQDAEHKKLCSIDEDFEN | | | | | |
| Query | 1587 | TRTPKISPENSFLDTNYTNKECEONN TRTPKISPENSFL+ YT KECEONN | | | | | |
| Sbjct | 122 | TRTPKISPENSFLEATYT-KECEQNN | | | | | |

PREDICTED: KH domain-containing protein C56G2.1 [Cimex lectularius] Sequence ID: ref|XP_014252448.1| Length: 639 Number of Matches: 1

▶ See 3 more title(s) kange 1: 286 to 626

| Score | Ex | kpect Method | Identities | Positives | Gaps | Frame |
|-----------|----------|---|----------------------|---------------------------|------------------------|---------|
| 239 bits | (609) 3e | e-64() Compositional matrix adjust. | 134/346(39%) | 203/346(58%) | 23/346(6%) | -2 |
| Features: | | | | | | |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSV DS + V ASPS+S S | | PRSEATRVK + +R | | -т 1285 |
| Sbjct | 286 | DSANHSPSEVMLASPSISNFSDAHSI | | | GSSLAGDLAT | LS 345 |
| Query | 1284 | TYEFLFPISLIGHLYGRKRAFINQII YEF+ P ++G L GR AF+++I- | | | | |
| Sbjct | 346 | LYEFVLPQVIVGRLIGRHGAFLHEI | | | | |
| Query | 1104 | AMIRQRLPAKRYPNFTMQRIHFALP(A IRO+ P +R+P T++++ F | QTIVPLSTESLY PL E | NLQLKLIEGIN + L+L+EG+N | | |
| Sbjct | 406 | AKIROKFPLRRFPQLTLEKVSFVTLI | | | | |
| Query | 924 | HIFIQhplhpshpslplLQKQLYDS H F+Q P HP++ SL L + + | | | DVWYRVQIVD WYR QI+D | |
| Sbjct | 463 | HFFLQQPSHPTYGSLSALNQIMNQV | | | | |
| Query | 744 | PEDEERCVIKFLDFGGYMNVGFNTLI E+ ++FLD+GGY+ + + LI | | | | |
| Sbjct | 523 | -EENSTSTVRFLDYGGYLLLASSNLI | | | | |

Query 567 EILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELV 430 + LT G +LQAQ+ Y P ++L+ S G V+ +N+ELV Sbjct 582 LFVQSLTLGQILQAQIYDYAEDCTPLVYLYTSNG-QEVVLVNEELV 626

PREDICTED: KH domain-containing protein C56G2.1-like [Halyomorpha halys]

Sequence ID: ref|XP_014271999.1| Length: 652 Number of Matches: 1

▶ See 6 more title(s) Range 1: 278 to 616

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------|------------------------|----------------------|-------|
| 237 bits | (605) 1e | e-63() Compositional matrix adjust. | 136/347(39%) | 202/347(58%) | 27/347(7%) | -2 |
| Features | s: | | | | | |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSV DS + + ASPS+S S | | | | |
| Sbjct | 278 | DS + + ASPS+S S DSANHSPSEIMLASPSISNFSDAHSI | | VAISPSRTPAG | SSL +A GSSLAGDQAP | |
| Query | 1290 | KTTYEFLFPISLIGHLYGRKRAFING YEF+ P ++G L GR F+N- | | | | |
| Sbjct | 338 | YEFVLPQVIVGRLIGRHGVFLNI | | | | |
| Query | 1110 | ALAMIRQRLPAKRYPNFTMQRIHFAI ALA IRO+ P +R+P T++++ F | LPQTIVPLSTES + PL E | | INNDVVVSAV | |
| Sbjct | 395 | ALAKIRQKFPLRRFPQLTLEKVSFV(| | | | |
| Query | 930 | GSHIFIQhplhpshpslplLQKQLYI +H F+Q P HPS+ SL L + | DSYSTMEAPLLE | SLELSAVCVIP + AVC P | | |
| Sbjct | 452 | AAHFFLQQPCHPSYSSLTALNTIMA(| | | | |
| Query | 750 | TDPEDEERCVIKFLDFGGYMNVGFN: + ED C +K+LD+GGY + | | | | |
| Sbjct | 512 | VE-EDGLHCTVKYLDYGGYSRIPATI | | | | |
| Query | 570 | AEILNKLTKGIVLQAQVAGYNSHNLI ++ LT G +L AQV Y | | | 430 | |
| Sbjct | 571 | RLFVHSLTCGQILHAQVYDYALDGSI | | | 616 | |

GA16943, partial [Drosophila pseudoobscura]

Sequence ID: gb|ADJ12839.1| Length: 190 Number of Matches: 1

▶ See 1 more title(s) Range 1: 3 to 152

| Score | E | Expect Method | Identities | Positives | Gaps | Frame |
|----------|------------|--|--------------|--------------|-----------|----------------|
| 221 bits | (564) 4 | e-63() Compositional matrix adjust. | 122/152(80%) | 130/152(85%) | 4/152(2%) | -2 |
| Features | S : | | | | | |
| Query | 1947 | QQSASKSMNINGTLVNgsgsgsgssS QQ A+KSMNINGT +G+GSGS S | | | | 100 1774 00 |
| Sbjct | 3 | QQQATKSMNINGTDATENGNGSGSGS | | | | |
| Query | 1773 | QIDSEILKSKIQDAEHKTLCSIDEDE QIDSE+LKSKIQDAEHK LCSIDEDE | | | | |
| Sbjct | 62 | QIDSEMLKSKIQDAEHKKLCSIDEDE | | | | |
| Query | 1593 | KATRTPKISPENSFLDTNYTNKECEÇ KATRTPKISPENSFL+ YT KECEÇ | | 3 | | |
| Sbjct | 122 | KATRTPKISPENSFLEATYT-KECEÇ | | | | |

GA16943, partial [Drosophila pseudoobscura]

Sequence ID: gb|ADJ12840.1| Length: 192 Number of Matches: 1

| Score | E | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|------------|---------|------------------------------|--------------|--------------|-----------|----------|
| 221 bits | (564) 4 | le-63() | Compositional matrix adjust. | 122/152(80%) | 130/152(85%) | 4/152(2%) | -2 |
| Features | S : | | | | | | |
| Query | 1947 | QQSA | ASKSMNINGTLVNgsgsgsgssS | DEKDSPTTMI | YGKSAPIKIQS | NGRTSNGKH | IQQ 1774 |

| Sbjct | 3 | QQ A+KSMNINGT +G+GSGS S DEKDSP TMLYGKSAPIKIQSNGRT G QQ QQQATKSMNINGTDATENGNGSGSGSGSDEKDSPNTMLYGKSAPIKIQSNGRTPPGV-QQ | 61 |
|-------|------|--|------|
| Query | 1773 | QIDSEILKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRVSFYNRKATQKTVEPVVI | 1594 |
| Sbjct | 62 | QIDSE+LKSKIQDAEHK LCSIDEDFENLSSPRDLPDSV+TRV F+NRK K VEPVVI QIDSEMLKSKIQDAEHKKLCSIDEDFENLSSPRDLPDSVSTRVLFHNRKTNSKVVEPVVI | 121 |
| Query | 1593 | KATRTPKISPENSFLDTNYTNKECEQNNNCEP 1498 KATRTPKISPENSFL+ YT KECEQNNNC+P | |
| Sbjct | 122 | KATRTPKISPENSFLEATYT-KECEQNNNCQP 152 | |

KH domain-containing protein [Operophtera brumata]

Sequence ID: gb|KOB79527.1| Length: 572 Number of Matches: 1

Range 1: 9 to 566

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|---------------------------|------------------------|-----------------------------|---------|
| 227 bits | (578) 1e | e-60() Compositional matrix adjust. | 194/624(31%) | 303/624(48%) | 109/624(17%) | -2 |
| Feature | s: | | | | | |
| Query | 2151 | KMVSGRPLLYLSLPGVAFILGVFW | | | | EP 1999 |
| Sbjct | 9 | KM R LL S+P +A +LG+FW KMAPSRQLLMWSVPSIAVLLGIFW | | | FE + A+N + EELAEALNTHA- | 65 |
| Query | 1998 | TVQARKANGVLQNGKLPQQSASKSI +ARKA+ + + + QSA | | gsgsgssSDEK- S +DE+ | | AP 1822 |
| Sbjct | 66 | EARKASPLGRADRSIIQSAPID | | | | K- 120 |
| Query | 1821 | IKIQSNGRTSNGKHQQQIDSE: + + R S G +Q + S+ | ILKSKIQDAEHI I+ S I | | DEDFENLS D++ +L+ | |
| Sbjct | 121 | -SVVNENRMSAGFDKÕHLVVSSSK | | | | |
| Query | 1677 | RDLPD-SVNTRVSFYNRKATQKTV | | | | |
| Sbjct | 180 | D +NT + + +T+ V ECTNDIDINTEKTASQQASTKSEV | М | TSEVNRI | NEANPSVĒAĒĒL | NV 224 |
| Query | 1506 | CEPKEEPSKKEAdqeeleqdqeQTY +EPS ++ T | | | SLSICS S S+C S | VQ 1345 |
| Sbjct | 225 | NNDIDEPSDSNDSDNRFST | | | | EG 279 |
| Query | 1344 | SGDSGKGSSLPRSEZ S DSGKG S +P | ATRVKTTYEFLE A R+ ++FL | | RKRAFINQIKAK + +F+ QIK+K | |
| Sbjct | 280 | SSDSGKGCSEAASPPPATIVPSES | | | | |
| Query | 1194 | ASVSVGKNPYSGKVRICTIEGTESTA+V V ++P S K +IC +EGT+ST | | | | |
| Sbjct | 337 | ATVYVRRHPDSVKQKICAVEGTQS | | | | |
| Query | 1014 | LSTESLYNLQLKLIEGINNDVVVS L E L+L+E +NND +++ | | | | |
| Sbjct | 397 | LVPEFLQLVESVNNDTIMT | | | | |
| Query | 834 | APLLPSLELSAVCVIPINDVWYRVO P LP | QIVDTDPEDEEF | RCVIKFLDFGGY | MNVGFNTLRQI | RT 655 |
| Sbjct | 452 | VPSLPR | PVISTSSES-DI | rsvvkLvDFGG? | ZLTVDNDQLKÕI | RS 492 |
| Query | 654 | DFMNVPFQSTECILSNIEPIGG'DFM++PFQ+TE +L+ ++P | TWSIEAAEILNE WS EA I+ | KLTKGIVLQAQV | /AGYNSHNLPEI /AGY+ LP | FL 481 |
| Sbjct | 493 | DFMSLPFQATEALLAFVKPANNEA | | | | 549 |
| Query | 480 | FASLGPNNVIFINKELVGRKLAKW VIF+N+ELV R LA+W | 409 | | | |
| Sbjct | 550 | QVIFLNRELVDRGLAEW | 566 | | | |

hypothetical protein D910_06197 [Dendroctonus ponderosae]

Sequence ID: gb|ERL88815.1| Length: 479 Number of Matches: 1

Range 1: 108 to 462

| Score | E | rpect Method | Identities | Positives | Gaps | Frame |
|-----------|----------|--|--------------------------|--------------|--------------------------|-------|
| 217 bits(| (552) 5e | e-58() Compositional matrix adjust. | 137/359(38%) | 199/359(55%) | 26/359(7%) | -2 |
| Features | s: | | | | | |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSVDS + ASPS+S S | | LPRSEAT | RVKT +KT | |
| Sbjct | 108 | DSANHSPCEAMLASPSMSSISDNHS | | | | · · - |
| Query | 1278 | EFLFPISLIGHLYGRKRAFINQIKAN | KTLASVSVGKNE A V V K+ | | CTIEGTESEI C +EGT EI | |
| Sbjct | 168 | EFLIPQQFVGKLIGRNGSFVKTIKE | | | | |
| Query | 1110 | ALAMIRQRLPAKRYPNFTMQRIHFAI AL MIR+R P ++Y T+++I A | LPQTIVPLSTES V L + | ~ | INNDVVVSAV +NND V+S + | |

| Sbjct | 228 | ALKMIRERFPLRKYSEITLEQIELAPSVATVSLIPDHLYLKLVEGVNNDTVLSCMVA | 284 |
|-------|-----|--|-----|
| Query | 930 | GSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLP-SLELSAVCVIPINDVWYRVQIV H+F+O P HPS+P+L +L + + YS+ +PLLP + + VC D W+R ++ | 754 |
| Sbjct | 285 | H+F+Q P $HPS+P+L$ $+L$ $+$ $+$ $YS+$ $+$ $PLLP$ $+$ $+$ VC D $W+R$ $++$ $PDHLFMQQPTHPSYPALSMLTRSMDSCYSSTHSPLLPYPIPENTVCAAFSVDSWHRAIVL$ | 344 |
| Query | 753 | DTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWS | 580 |
| Sbjct | 345 | TD ++ + +KFLDFGGY V ++LRQIR DFM +PFQ+ EC LSNI+ G W STD-DETKTSYVKFLDFGGYAYVENDSLRQIRHDFMLLPFQAAECFLSNIKSKSENGCWP | 403 |
| Query | 579 | IEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVE | 403 |
| Sbjct | 404 | EA ++ T+G ++ Q+A Y +P + F L V+F+N++LV A W+E EEAYSLVAASTRGRIIYTQIADYTPDGIPLVLCFIVLPDRGVVFLNRKLVDEGFADWIE | 462 |

hypothetical protein YQE_07610, partial [Dendroctonus ponderosae]

Sequence ID: gb|ENN75881.1| Length: 355 Number of Matches: 1

Range 1: 10 to 338

| Score | Е | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|------------------------------------|--------------|-------------------------|---------|
| 208 bits | (530) 36 | e-56() Compositional matrix adjust. | 129/333(39%) | 187/333(56%) | 22/333(6%) | -2 |
| Feature | s: | | | | | |
| Query | 1347 | QSGDSGKGSSLPRSEAT +S DSGKG S P S T | | | | |
| Sbjct | 10 | RSNDSGKGGSDVATPPSARTPQLAS | | | | |
| Query | 1200 | TLASVSVGKNPYSGKVRICTI A V V K+ ++C + | EGTESEIDAAL <i>I</i> EGT EI+ AL | | | AL 1033 |
| Sbjct | 70 | CHAYVYVQKHSEVVISKNLCQVCIV | | | | |
| Query | 1032 | PQTIVPLSTESLYNLQLKLIEGINN V L + LY LKL+EG+NN | DVVVSAVLSGSI D V+S +++ I | HIFIQhplhpsh | npslplLQKQL | YD 853 |
| Sbjct | 130 | SVATVSLIPDHLYLKLVEGVNN | | | | |
| Query | 852 | SYSTMEAPLLP-SLELSAVCVIPIN YS+ +PLLP + + VC | DVWYRVQIVDTI D W+R ++ TI | | | FN 676 |
| Sbjct | 187 | CYSSTHSPLLPYPIPENTVCAAFSV | | | | |
| Query | 675 | TLRQIRTDFMNVPFQSTECILSNIE +LRQIR DFM +PFQ+ EC LSNI+ | | | IVLQAQVAGYN ++ O+A Y | SH 502 |
| Sbjct | 246 | SLRQIRHDFMLLPFQAAECFLSNIK | | | | PD 305 |
| Query | 501 | NLPEIFLFASLGPNNVIFINKELVG +P + F L V+F+N++LV | RKLAKWVE 4(|)3 | | |
| Sbjct | 306 | GIPLVLCFIVLPDRGVVFLNRKLVD | | 38 | | |

PREDICTED: uncharacterized protein LOC106471261 [Limulus polyphemus]

Sequence ID: **ref|XP_013787306.1|** Length: 1386 Number of Matches: 1 Range 1: 1066 to 1383

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|---------------------------|--------------------------|------------------------|---------|
| 221 bits | (563) 46 | e-56() Compositional matrix adjust. | 126/326(39%) | 195/326(59%) | 20/326(6%) | -2 |
| Features | s: | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATR | | | | AS 1189 |
| Sbjct | 1066 | S DS KG+ +S +A STDSSKGAGDIQSGIEPSQALQAES | V T YEF P VITVYEFELPQD | | +N IK ++ HVNYIKHRSN | TK 1125 |
| Query | 1188 | VSVGKNPYSGKVRICTIEGTESEID +S+ ++P++ +++C +EGTE++I | | KRYPNFTMQRI YP T+ ++ | | |
| Sbjct | 1126 | ISIKRHPFNPHLKLCAVEGTETDIK | | | | |
| Query | 1011 | STESLYNLQLKLIEGINNDVVVSAV + LQL L EGI++DV++S++ | | | | |
| Sbjct | 1186 | TLQLHLPEGISSDVILSSM | | | | |
| Query | 831 | PLLPS-LELSAVCVIPINDVWYRVQ PLLP +E +C P+ WYR O | IVDTDPEDEERC +V ED E C | | | |
| Sbjct | 1240 | PLLPQPVEAGVICAAPMMGGWYRAQ | | | | |
| Query | 654 | DFMNVPFQSTECILSNIEPIGGT DFM +PFQ++EC L+N++P | | TKGIVLQAQVA HG VL+A V | | |
| Sbjct | 1299 | DFMILPFQASECYLANVKPKNDEAV | | | | |
| Query | 480 | FASLGPNNVIFINKELVGRKLAKWV + G + +FIN+ELV R A+W+ | | | | |
| Sbjct | 1359 | YRVQGV-STLFINRELVKRGAAEWI | | | | |
| | | | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like [Limulus polyphemus]

Sequence ID: ref|XP_013775508.1| Length: 475 Number of Matches: 1

Range 1: 153 to 473

| Score | Е | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|--------------|------------------------------|--------------|---------|
| 208 bits | (530) 36 | e-55() Compositional matrix adjust. | 117/328(36%) | 187/328(57%) | 17/328(5%) - | -2 |
| Features | s: | | | | | |
| Query | 1353 | SVQSGDSGKGSSLPRSEA'S S DSGKG S LP + | | | | L 1195 |
| Sbjct | 153 | S S DSGKG S LP + SEHSSDSGKGGSDIQPSSELPNPKG | | P L G L GR+ PQELCGRLIGRQ | | SN 212 |
| Query | 1194 | ASVSVGKNPYSGKVRICTIEGTESE ASV + ++P+S ++C +EGT E | | PAKRYPNFTMQ P R+ + T+ | | 7P 1015 |
| Sbjct | 213 | ASVLIKRHPFSKDFKLCGVEGTSEE: | | | | _ |
| Query | 1014 | LSTESLYNLQLKLIEGINNDVVVSAY + + LQL L EG++ DV++S+ | | | | |
| Sbjct | 272 | IPHTLQLHLPEGVSCDVILSS | | | | |
| Query | 834 | APLLP-SLELSAVCVIPINDVWYRVO P LP +E +C P+ D W+R O | | RCVIKFLDFGGY C +KF+D+GGY | | |
| Sbjct | 328 | TPTLPYPVEAGVICAAPVMDGWFRA | | | | |
| Query | 657 | TDFMNVPFQSTECILSNIEPIGG' | | KLTKGIVLQAQV -+ +G +LQA + | | |
| Sbjct | 387 | SDFMTLPFQAAEFYLASVKPVDEEL | | | | |
| Query | 483 | LFASLGPNNVIFINKELVGRKLAKW L+ G +V+FIN+ELV + LA W | | | | |
| Sbjct | 447 | LYRVQGV-SVVFINRELVNQGLASW: | | | | |

PREDICTED: uncharacterized protein LOC106806733 isoform X2 [Priapulus caudatus]

Sequence ID: ref|XP_014664261.1| Length: 795 Number of Matches: 1

Range 1: 472 to 791

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|----------------------------|------------------------------|----------------------|---------|
| 208 bits | (529) 46 | e-53() Compositional matrix adjust. | 124/327(38%) | 196/327(59%) | 19/327(5%) | -2 |
| Feature | s: | | | | | |
| Query | 1347 | QSGDSGKGSS-LPRSEATRVKT | TYEFLFPISLIG YEF P L+G | | | |
| Sbjct | 472 | +S DSGKG+S + +S E + ESNDSGKGASDIMQSHIDEPLHDFS | | | | |
| Query | 1179 | GKNPYSGKVRICTIEGTESEIDAAL. ++PY ++C +EGT EI AL. | | | L-PQTIVPLS + P +P | TE 1003 |
| Sbjct | 532 | KRHPYFDTYKLCAVEGTPEEIKLAL | | | | 587 |
| Query | 1002 | SLYNLQLKLIEGINNDVVVSAVLSG N+QL E I DV+VS+++S | SHIFIQhplhps | shpslplLQKQL ++P+L LL + + | YDSYSTMEA- | -P 829 |
| Sbjct | 588 | ENMQLPFPEEIPVDVIVSSLVSA | | | | |
| Query | 828 | LLPS-LELSAVCVIPINDVWYRV | QIVDTDPEDEEF Q+V T E +E | RCVIKFLDFGGY ++F D+GGY | | |
| Sbjct | 646 | QLPRPIEVGVICAVPVAGMDGWYRA | | | | |
| Query | 657 | TDFMNVPFQSTECILSNIEPIGGT- +DFM++PFQ+TEC L+NI P+ T | | KLTKGIVLQAQV +LT+G V+QAQ+ | AGYNSHNLPE G +P | |
| Sbjct | 705 | SDFMSLPFQATECYLANISPLDETE | | | | |
| Query | 483 | LFASLGPNNVIFINKELVGRKLAKW L++ + F+N+ELV R + +W | | | | |
| Sbjct | 765 | LYSPVSAVEAAFVNRELVNRGVVQW | _ | | | |

PREDICTED: uncharacterized protein LOC106806733 isoform X1 [Priapulus caudatus]

Sequence ID: ref|XP_014664258.1| Length: 796 Number of Matches: 1

▶ See 2 more title(s) kange 1: 472 to 792

Features:

| Score | Expect Method | Identities | Positives | Gaps | Frame |
|---------------|------------------------------------|-----------------|--------------|------------|-------|
| 205 bits(521) | 4e-52() Compositional matrix adjus | t. 123/327(38%) | 196/327(59%) | 18/327(5%) | -2 |

| Query | 1347 | QSGDSGKGSS-LPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSV +S DSGKG+S + +S E + YEF P L+G L G+ + ++ KT A+V + | 1180 |
|-------|------|--|------|
| Sbjct | 472 | ESNDSGKGASDIMQSHIDEPLHDFSLYEFEMPQQLVGKLIGKLGRNVKSLRDKTGANVYI | 531 |
| Query | 1179 | GKNPYSGKVRICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFAL-PQTIVPLSTE ++PY ++C +EGT EI ALA+I +R P ++P T+ +++ + P +P + + | 1003 |
| Sbjct | 532 | KRHPYFDTYKLCAVEGTPEEIKLALAVISKRFPPAKFPEMTLVQVNAPVDPSVFMPENMQ | 591 |
| Query | 1002 | SLYNLQLKLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAP QL E I DV+VS+++S +F+Q P HP++P+L LL + + Y T A P | 829 |
| Sbjct | 592 | QLPFPEEIPVDVIVSSLVSACQVFLQQPTHPTYPTLRLLDESMQLCYHTENAVIP | 646 |
| Query | 828 | LLPS-LELSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIR LP +E+ +C +P+ D WYR Q+V T E +E ++F D+GGY + ++LRQIR | 658 |
| Sbjct | 647 | QLPRPIEVGVICAVPVAGMDGWYRAQVVQTQDETDE-VDVRFCDYGGYCRMAASSLRQIR | 705 |
| Query | 657 | TDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIF +DFM++PFQ+TEC L+NI P+ T +SIEAA L +LT+G V+QAQ+ G +P + | 484 |
| Sbjct | 706 | SDFMSLPFQATECYLANISPLDETEGFSIEAAAELEELTQGRVIQAQIVGRAEDGVPYVH | 765 |
| Query | 483 | LFASLGPNNVIFINKELVGRKLAKWVE 403 L++ + F+N+ELV R + +W E | |
| Sbjct | 766 | L++ + F+N+ELV R + +W E LYSPVSAVEAAFVNRELVNRGVVQWTE 792 | |

hypothetical protein DAPPUDRAFT_322467 [Daphnia pulex]

Sequence ID: gb|EFX76340.1| Length: 456 Number of Matches: 1

Range 1: 119 to 450

| Score | E | rpect Method | Identities | Positives | Gaps | Frame | | | | | |
|-----------|----------|--|----------------------------|---------------|----------------------------|--------|--|--|--|--|--|
| 192 bits | (487) 2e | e-49() Compositional matrix adjust. | 126/339(37%) | 183/339(53%) | 53/339(15%) | -2 | | | | | |
| Features: | | | | | | | | | | | |
| Query | 1281 | YEFLFPISLIGHLYGRKRAFINQIK | | | | | | | | | |
| Sbjct | 119 | YEF P +L+G L G+ AF+NQIK YEFEIPQALVGLLIGKYGAFVNQIK | | | +EGT++EIDAA VEGTKTEIDAA | | | | | | |
| Query | 1101 | MIRQRLPAKRYPNFTMQRIHFALPQ +IR + P KRYP+ TM +I+ A P+ | TIVPLSTES | LYNLOLKLIEG | INNDVVVSAVL | SG 928 | | | | | |
| Sbjct | 177 | LIRDKFPIKRYPHITMAQINVA-PE | | | | | | | | | |
| Query | 927 | SHIFIQhplhpshpslplLQKQLYD +HIF+Q HP++PSL L + | | | | | | | | | |
| Sbjct | 233 | NHIFLQQITHPTYPSLARLDHCMAQ | | | | • | | | | | |
| Query | 753 | | | DEERCV E R | | | | | | | |
| Sbjct | 293 | VYPTASLASVDANVEKREVTGEVIS | | | | ~ - | | | | | |
| Query | 693 | MNVGFNTLRQIRTDFMNVPFQSTEC V + LRQIR DFM++PFQ+ EC | CILSNIEPIGGT | WSIEAAEIL | NKLTKGIVLQA LT+ +LO | | | | | | |
| Sbjct | 353 | SRVPVSCLRQIRADFMSLPFQAIEC | | | | | | | | | |
| Query | 519 | AGYNSHNLPEIFLFASLGPNNVIFI Y+ LP ++L+ + I | | | | | | | | | |
| Sbjct | 413 | MAYSLEGLPLVYLY-QMETTEEALI | N++LV R +A+ NRQLVNRGVAQ | | | | | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X2 [Lingula anatina]

Sequence ID: ref|XP_013383304.1| Length: 625 Number of Matches: 1

Range 1: 321 to 614

| Score | Е | Expect Method | Identities | Positives | Gaps | Frame | | | | | |
|-----------|---------|--|--------------------------------|--------------|------------------------|-------|--|--|--|--|--|
| 193 bits | (491) 7 | e-49() Compositional matrix adjust. | 109/298(37%) | 178/298(59%) | 9/298(3%) | -2 | | | | | |
| Features: | | | | | | | | | | | |
| Query | 1281 | YEFLFPISLIGHLYGRKRAFINQIKA | | | | | | | | | |
| Sbjct | 321 | YEF FP L G L G+ + I IK YEFEFPSELCGRLIGKHGSTITAIKT | | | | | | | | | |
| Query | 1101 | MIRQRLPAKRYPNFTMQRIHFALPQT +IR++ P ++PN ++++ + + | | | VVVSAVLSOV+VS++++ | | | | | | |
| Sbjct | 381 | LIRRKFPKNQFPNVDLRQLSTHVQE | | | | | | | | | |
| Query | 921 | IFIQhplhpshpslplLQKQLYDSYS IF+Q P HP++PSL L + + Y | | | DVWYRVQIV D WYR O+V | | | | | | |
| Sbjct | 438 | IFVQQPTHPTYPSLERLNQFMIMCYQ | | | | | | | | | |
| Query | 747 | DPEDEERCVIKFLDFGGYMNVGFNTI E +E C IK++D+GGY + I | LRQIRTDFMNVPI L+QIR+DFM +PI | | | | | | | | |
| Sbjct | 498 | QDETDE-CDIKYVDYGGYARIQACAI | | | | | | | | | |
| Query | 573 | AAEILNKLTKGIVLQAQVAGYNSHNI | LPEIFLFASLGPI | NNV-IFINKELV | GRKLAKWVI | E 403 | | | | | |

PREDICTED: LOW QUALITY PROTEIN: KH domain-containing protein C56G2.1 [Apis florea]

Sequence ID: ref|XP_012339869.1| Length: 585 Number of Matches: 1

Range 1: 183 to 570

| Score | Е | xpect Method | Identities | Positives | Gaps F | rame |
|----------|----------|---|------------------------------|---------------------------|----------------------|--------|
| 192 bits | (488) 86 | e-49() Compositional matrix adjust. | 136/399(34%) | 214/399(53%) | 22/399(5%) - | 2 |
| Feature | s: | | | | | |
| Query | 1575 | KISPENSFLDTNYTNKECEQN | | | | V 1414 |
| Sbjct | 183 | K+S EN ++ Y TN+E + N KLSSENKSIECQYKRIDTNEENDIN | N C P +EPS NECNYLPSKEPS | | + T E SKTPTQALSER | D 239 |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSVQSG +N + V S + S S | DSGKGSSLP-RS | SEATRVKTTYEF ++ + TYEF | | |
| Sbjct | 240 | SANHSPVSGVLEGSVTDEARSEGST | | | | |
| Query | 1236 | RKRAFINQIKAKTLASVSVGKNPYS R +F+ I+ K + V ++P | | ESEIDAALAMIR I+ AL MIR | | |
| Sbjct | 300 | RHGSFLQNIRHKAEVHIVVKRHPVW | | | | |
| Query | 1056 | MQRIHFALPQTIVPLSTESLYN +++I LP I +P TE | LQLKLIEGINNI +QL L+EG+NNI | OVVVSAVLSGSH | IFIQhplhpsh | p 886 |
| Sbjct | 360 | LEQILPLKIPEEIPWVTEL | | | | |
| Query | 885 | slpllQKQLYDSYSTMEAPLLP-SL SL +L + + Y T E+P P L | | | PEDEERCVIKF | |
| Sbjct | 414 | SLRILDENMTQLYETTESPPAPDEL | | | | |
| Query | 708 | DFGGYMNVGFNTLRQIRTDFMNVPF D GGY +R+IR+D++++PF | | | | |
| Sbjct | 473 | DHGGYWVFSNTEMRKIRSDYLSLPF | | | | |
| Query | 528 | AQVAGYNSHNLPEIFLFASLGPNNV AQ+ GY + N + L+ ++ + V | | LAK 412 A+ | | |
| Sbjct | 533 | AQT G1 + N + LT + T V AQIVGYINTNT-YVNLYLNIHKHGV | | | | |

PREDICTED: KH domain-containing protein C56G2.1-like isoform X1 [Apis mellifera]

Sequence ID: ref|XP_006564454.1| Length: 586 Number of Matches: 1

▶ See 4 more title(s) Range 1: 184 to 580

| Score | Ex | spect Method | Identities | Positives | Gaps | Frame |
|----------|------------|---|------------------------------|--------------------------|--------------------------|---------|
| 192 bits | (488) 1e | -48() Compositional matrix adjust. | 137/408(34%) | 218/408(53%) | 22/408(5%) | -2 |
| Features | 3 : | | | | | |
| Query | 1575 | KISPENSFLDTNYTNKECEQNI K+S EN ++ Y TN+E + NI | NNCEPKEEPS N C P +EPS | KKEAdqeeleq | dqeQTVLKEE' + T E | VV 1414 |
| Sbjct | 184 | KLSSENKSIECQYKRIDTNEENDIN | | | | RD 240 |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSVQSGI +N + V S + S S I | | EATRVKTTYEF: + + TYEF | | |
| Sbjct | 241 | SANHSPVSGVLEGSVTDEARSEGST | | | | |
| Query | 1236 | RKRAFINQIKAKTLASVSVGKNPYSOR +F+ I+ K + V ++P | GKVRICTIEGTE +IC IEG+ | | QRLPAKRYPN Q+ P K+YP+ | |
| Sbjct | 301 | RHGSFLQNIRHKAEVHIVVKRHPVW | | | | |
| Query | 1056 | MQRIHFALPQTIVPLSTESLYNI +++I LP I +P TE | LQLKLIEGINND +QL L+EG+NND | | | |
| Sbjct | 361 | LEQILPLKIPEEIPWITEL | | | | |
| Query | 885 | slplLQKQLYDSYSTMEAPLLP-SLI SL +L + + Y T E+P P L | | VWYRVQIVDTD: W RV I D | | |
| Sbjct | 415 | SLRILDENMTQLYETTESPPAPDELS | | | | |
| Query | 708 | DFGGYMNVGFNTLRQIRTDFMNVPFO D GGY +R+IR+D++++PFO | | | ILNKLTKGIV ++ + GIV | ~ |
| Sbjct | 474 | D GGY +R+IR+D++++PFO DHGGYWVFSNTEMRKIRSDYLSLPFO | | | | ~ |
| Query | 528 | AQVAGYNSHNLPEIFLFASLGPNNV AO+ GY + N + L+ ++ + V | | | 385 | |
| Sbjct | 534 | AQIVGYINTNT-YVNLYLNIHKHGV | | | 580 | |
| | | | | | | |

PREDICTED: KH domain-containing protein C56G2.1-like isoform X1 [Apis dorsata]

Sequence ID: ref|XP_006623065.1| Length: 585 Number of Matches: 1

▶ See 2 more title(s) Range 1: 183 to 570

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------------|---------------------------|---------------------------|---------|
| 192 bits | (487) 16 | e-48() Compositional matrix adjust. | 136/399(34%) | 214/399(53%) | 22/399(5%) - | -2 |
| Features | s: | | | | | |
| Query | 1575 | KISPENSFLDTNYTNKECEQN K+S EN ++ Y TN+E + N | NNCEPKEEPS | SKKEAdqeeleg | dqeQTVLKEE\ + T E | /V 1414 |
| Sbjct | 183 | KLSSENKSIECQYKRIDTNEENDIN | | | | RD 239 |
| Query | 1413 | DSNGNQKRNVDAASPSLSICSVQSG +N + V S + S S | | SEATRVKTTYEF ++ + TYEF | | |
| Sbjct | 240 | SANHSPVSGVLEGSVTDEARSEGST | | | | |
| Query | 1236 | RKRAFINQIKAKTLASVSVGKNPYS R +F+ I+ K + V ++P | GKVRICTIEGTE +IC IEG+ | | QRLPAKRYPNE O+ P K+YP+ | |
| Sbjct | 300 | R +F+ I+ K + V ++P RHGSFLQNIRHKAEVHIVVKRHPVW | | | | |
| Query | 1056 | MQRIHFALPQTIVPLSTESLYN +++I LP I +P TE | LQLKLIEGINNI +QL L+EG+NNI | | | |
| Sbjct | 360 | LEQILPLKIPEEIPWVTEL | | | | |
| Query | 885 | slpllQKQLYDSYSTMEAPLLPS-L SL +L + + Y T E+P P L | | | PEDEERCVIKE | |
| Sbjct | 414 | SLRILDENMTQLYETTESPPAPDEL | | | | |
| Query | 708 | DFGGYMNVGFNTLRQIRTDFMNVPF D GGY +R+IR+D++++PF | | | | ~ |
| Sbjct | 473 | DHGGYWIFSNTEMRKIRSDYLSLPF | | | | |
| Query | 528 | AQVAGYNSHNLPEIFLFASLGPNNV AQ+ GY + N + L+ ++ + V | | | | |
| Sbjct | 533 | AQT GI T N T LT TT V AQIVGYINTNT-YVNLYLNIHKHGV | | | | |
| | | | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X3 [Crassostrea gigas]

Sequence ID: ref|XP_011449476.1| Length: 742 Number of Matches: 1

Range 1: 414 to 740

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|-------------------------|--------------|-------------------------|-----------------|
| 194 bits | (493) 16 | e-48() Compositional matrix adjust. | 123/340(36%) | 200/340(58%) | 25/340(7%) | -2 |
| Features | s: | | | | | |
| Query | 1383 | DAASPSLSICSVQSGDSGKGSSLPR | | | | F <u>I</u> 1219 |
| Sbjct | 414 | D+ S S DSG+G S+ DSNSSGCDNASEASNDSGRGPSM | +E + T+ TELSTPNTSPNF | | G L GR+ CGRLIGRQGK | NI 471 |
| Query | 1218 | NQIKAKTLASVSVGKNPYSGKVRIC N IK K+ A++++ NP++ + ++C | | | RYPNFTMQRI | |
| Sbjct | 472 | NFIKEKSGANITLSANPFTPEFQLO | | | · · · • | |
| Query | 1038 | ALPQTIVPLSTESLYN-LQLKLIEG +P PS + + +QL L EG | | | | |
| Sbjct | 526 | -IPSGDNPQSAVLVPDIMQLSLPEG | | | | |
| Query | 861 | LYDSYSTMEAPLLPSLELSAV + Y M+ L+P L E+ + | CVIPINDVWYRVC P+ + WYR | | RCVIKFLDFG C IK++D+G | |
| Sbjct | 585 | MIACYMQDGLVPQLPRPLEVGVI | | | | |
| Query | 693 | MNVGFNTLRQIRTDFMNVPFQSTEC V + LRQIR+DFM +PFQ+ EC | | | | |
| Sbjct | 642 | SRVQGSLLRQIRSDFMTLPFQACEC | | | | |
| Query | 519 | AGYNSHNLPEIFLFASLGPNNVIFI G + +P + ++ G V + | | | | |
| Sbjct | 702 | VGRSEEGIPYVHIYQING-EKVTLV | | | | |

PREDICTED: KH domain-containing protein C56G2.1 [Nasonia vitripennis] Sequence ID: **ref|XP_001601576.1|** Length: 578 Number of Matches: 1

▶ See 3 more title(s) Range 1: 255 to 571

Score Expect Method Identities Positives Gaps Frame

| 191 bits | (486) 26 | e-48() Compositional matrix adjust. 117/322(36%) 187/322(58%) 7/322(2%) -2 | |
|----------|------------|---|------|
| Features | S : | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPY S DSGKG S+ TTYEF+ P+ L+G L GR F+ QI++ + ++V ++P | 1165 |
| Sbjct | 255 | STDSGKGSIKCHLKDTHITTYEFVIPVKLVGKLIGRGGKFLQQIRSTSGVYIAVRRHPT | 314 |
| Query | 1164 | SGKVRICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNL- | 988 |
| Sbjct | 315 | +++C IEG I +AL +IRQ+ P K YP+ T+++ + +VP + L DRDLKLCCIEGLPDGIASALELIRQQFPEKNYPHLTLEQFEYPPLVPEEVSWVPELM | 371 |
| Query | 987 | QLKLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLP-SLE | 811 |
| Sbjct | 372 | QL LIEG+NNDV+VS ++ +H+FIQ P HP+ PSL +L +++ Y T E+P +P L QLSLIEGVNNDVIVSHIIKPNHLFIQLPTHPTFPSLRILDEKMTQLYETNESPPVPDQLN | 431 |
| Query | 810 | LSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQ + V + W RV T + DP+ E+ + + +D GGY +R+TR+D++ +PFO | 631 |
| Sbjct | 432 | + V $+$ W RV I $+$ DP $+$ E $+$ $+$ $+$ $+$ D GGY $+$ R $+$ IR $+$ D $+$ + $+$ PFQ KGMIVVAKWYNKWVRVFIENPDPKGEQ $-$ TLARLVDHGGYWTFSNADMRKIRSDYLTLPFQ | 490 |
| Query | 630 | STECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVI | 451 |
| Sbjct | 491 | + E L+NI+P WS EA ++ ++ GIV QAQ+ GY + I L+ ++ + VI AIEVFLANIQPKEEEWSQEAYTVVAQICTGIVGQAQIVGYADCST-FINLYYNIHKHGVI | 549 |
| Query | 450 | FINKELVGRKLAKWVEMSD*QP 385 | |
| Sbjct | 550 | I EL+ R LA+ + + + P SIADELIARGLAEPMSLEEVAP 571 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X2 [Crassostrea gigas]

Sequence ID: **ref|XP_011449475.1**| Length: 749 Number of Matches: 1 Range 1: 414 to 747

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|-----------------------------|--------------|--------------------------|--------------|
| 193 bits | (491) 26 | e-48() Compositional matrix adjust. | 124/345(36%) | 202/345(58%) | 28/345(8%) | -2 |
| Features | s: | | | | | |
| Query | 1383 | DAASPSLSICSVQSGDSGKGSSLPR D+ S S DSG+G S+ | | | | |
| Sbjct | 414 | D+ S S DSG+G S+ DSNSSGCDNASEASNDSGRGPSM | | | G L GR+ CGRLIGRQGF | I KNI 471 |
| Query | 1218 | NQIKAKTLASVSVGKNPYSGKVRIC N IK K+ A++++ NP++ + ++C | | | | HF 1039 |
| Sbjct | 472 | NFIKEKSGANITLSANPFTPEFQLC | | | | |
| Query | 1038 | ALPQTIVPLSTESLYNL-QL PO+ +VP + + + OL | KLIEGINNDVVV L EG++ DVVV | /SAVLSGSHIFI | Ohplhpshps | slp 877 |
| Sbjct | 527 | PSGDNPÕSAVLVPDIMQVMPGISÕL | | | | |
| Query | 876 | <pre>llokolydsystmeapllpsl L + + Y M+ L+P L</pre> | | | PEDEERCVIK E +E C IK | |
| Sbjct | 587 | RLNQFMIACYMQDGLVPQLPRPL | | | | - |
| Query | 708 | DFGGYMNVGFNTLRQIRTDFMNVPF D+GG+ V + LRQIR+DFM +PF | | | AEILNKLTKO A +L +LT+O | |
| Sbjct | 644 | DYGGFSRVQGSLLRQIRSDFMTLPF | | | | |
| Query | 534 | LQAQVAGYNSHNLPEIFLFASLGPN LQAQV G + +P + ++ G | | | 00 | |
| Sbjct | 704 | LQAQVVGRSEEGIPYVHIYQING-E | | | 47 | |

PREDICTED: KH domain-containing protein C56G2.1 [Athalia rosae] Sequence ID: ref|XP_012251572.1| Length: 535 Number of Matches: 1

▶ **See 1 more title(s)** kange 1: 239 to 534

| Score | E | expect Method | Identities | Positives | Gaps | Frame |
|----------|---------|---|---------------------|-----------------------------|-----------|---------|
| 190 bits | (482) 3 | e-48() Compositional matrix adjust. | 110/301(37%) | 183/301(60%) | 7/301(2%) | -2 |
| Feature | s: | | | | | |
| Query | 1290 | KTTYEFLFPISLIGHLYGRKRAFINQ +T YEF+ P SLIG L GR F++ | | GKNPYSGKVRIC ++P + K+++C | | DA 1111 |
| Sbjct | 239 | QTVYEFVLPQSLIGRLIGRHGVFLHS | | _ | _ | HT 298 |
| Query | 1110 | ALAMIRQRLPAKRYPNFTMQRIHFAL AL MIRO+ P +YP+ T++++ F | PQTIVPLSTESI P E | | | |
| Sbjct | 299 | ALEMIRQKFPENKYPSVTLEQVTFLQ | | ~ | | |
| Query | 930 | GSHIFIQhplhpshpslplLQKQLYD | SYST-MEAPLLI | P-SLELSAVCVI | PINDVWYRV | 7QI 757 |

| Sbjct | 356 | + H + F + P + PS + PSL + L + + Y + T + AP + P + LE + V + D W + RV + I + P + P + P + P + P + P + P + P + P | 415 |
|-------|-----|--|-----|
| Query | 756 | VDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSI DP+ E+ +++ +D GG+ + +R+IR D++ +PFQ+ E L+NI+P GTW | 577 |
| Sbjct | 416 | QKPDPQG-EKNLVRLIDHGGFWYFKNSEMRKIRYDYLTLPFQAIEVFLANIQPKNGTWVP | 474 |
| Query | 576 | EAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEMS | 397 |
| Sbjct | 475 | EA ++ ++T+GIV+QAQ+ Y + + L+ ++ + VI + ELV R A+ V++ EAYSLVCQITQGIVVQAQIHSYVDRDT-HVNLYLNIQKHGVISLADELVARGYAERVQLE | 533 |
| Query | 396 | D 394 | |
| Sbjct | 534 | + E 534 | |

PREDICTED: KH domain-containing protein C56G2.1 [Bombus terrestris] Sequence ID: **ref|XP_012169146.1**| Length: 583 Number of Matches: 1

▶ See 2 more title(s) Range 1: 184 to 573

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|-----------------------------|------------------------------|-------------------------|---------|
| 188 bits | (477) 26 | e-47() Compositional matrix adjust. | 129/399(32%) | 213/399(53%) | 14/399(3%) | -2 |
| Features | s: | | | | | |
| Query | 1575 | KISPENSFLDTNYTNKECEQNNNCE K++PEN + N+E + NN C | | | | |
| Sbjct | 184 | KLAPENKSTEVVNQNEENDTNNECN | | • | | |
| Query | 1401 | NQKRNVDAASPSLSICSVQSGDSGK + V S + S S DSGK | | RVKTTYEFLFPI + YEF P | SLIGHLYGRK +L+G L GR | RA 1225 |
| Sbjct | 241 | SPVSGVLEGSVTDEARSEGSTDSGK | | | | GC 300 |
| Query | 1224 | FINQIKAKTLASVSVGKNPYSGKVR F+ I+ KT ++ ++P S + | | DAALAMIRQRLP - AL MIRQ+ P | | |
| Sbjct | 301 | FLQNIRHKTEVNIVLKRHPISRDQK | | | | _ |
| Query | 1044 | HFALPQTIVPLSTESLYNL-QLKLI | EGINNDVVVSAV EG+NNDVV+ + | | | |
| Sbjct | 361 | SPLIAPEHGPWIAELRQLSLV | | | | |
| Query | 867 | KQLYDSYSTMEAPLLP-SLELSAVC +++ Y+T E+P P L + | | | CVIKFLDFGG +++ +D GG | |
| Sbjct | 417 | ERMTQLYNTTESPPAPDELTSGMIL | | | | |
| Query | 690 | NVGFNTLRQIRTDFMNVPFQSTECI + +R+IR+D++ +PFO+ E | | | | |
| Sbjct | 476 | VFSSSEMRKIRSDYLLLPFQAIEVF | | | | |
| Query | 510 | NSHNLPEIFLFASLGPNNVIFINKE + N I L+ ++ + VI + E | LVGRKLAKWVEN L+ R A+ + + | | | |
| Sbjct | 536 | INTNT-YISLYLNIQKHGVISLADE | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X1 [Crassostrea gigas] Sequence ID: **ref|XP_011449473.1**| Length: 751 Number of Matches: 1

▶ See 1 more title(s) Range 1: 414 to 749

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------|---------------------------|---|----------|
| 190 bits | (483) 36 | e-47() Compositional matrix adjust. | 125/347(36%) | 202/347(58%) | 30/347(8%) | -2 |
| Features | s: | | | | | |
| Query | 1383 | DAASPSLSICSVQSGDSGKGSSLPR | | | | AFI 1219 |
| Sbjct | 414 | D+ S S DSG+G S+ DSNSSGCDNASEASNDSGRGPSM | · - · - · | | G L GR+ CGRLIGRQGK | NI 471 |
| Query | 1218 | NQIKAKTLASVSVGKNPYSGKVRIC N IK K+ A++++ NP++ + ++C | | | | HF 1039 |
| Sbjct | 472 | NFIKEKSGANITLSANPFTPEFQLC | | | · · · - · · · · · · · · · · · · · · · · | |
| Query | 1038 | ALPQTIVPLSTESLYNL- PQ+ +VP + S+ L | | | FIQhplhpsh FIQ P HPS | |
| Sbjct | 527 | PSGDNPQSAVLVPDIMQIPSIVVLG | | | | |
| Query | 882 | lplLQKQLYDSYSTMEAPLLPSL L L + + Y M+ L+P L | | NDVWYRVQIVD - + WYR QI | TDPEDEERCV E +E C | |
| Sbjct | 587 | LERLNQFMIACYMQDGLVPQLPR | | | | |
| Query | 714 | FLDFGGYMNVGFNTLRQIRTDFMNV | PFQSTECILSNI | EPIGGTWSI | EAAEILNKLT | TKG 541 |

| Sbjct | 644 | ++D+GG+ V + LRQIR+DFM +PFQ+ EC ++NI P+ +S EAA +L +LT+G YVDYGGFSRVQGSLLRQIRSDFMTLPFQACECYMANITPLQDEEYFSSEAANVLEELTQG | 703 |
|-------|-----|--|-----|
| Query | 540 | IVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAKWVEM 400 +LOAOV G + +P + +++ G V +N+E+V R + +W+E+ | |
| Sbjct | 704 | QMLQAQVVGRSEEGIPYVHIYQING-EKVTLVNREMVNRGVTRWIEV 749 | |

K Homology domain containing protein, partial [Oryctes borbonicus] Sequence ID: **gb|KRT85600.1|** Length: 533 Number of Matches: 1 Range 1: 7 to 533

| Score | Ex | spect Method | Identities | Positives | Gaps F | rame |
|-----------|------------|--|--------------------|----------------------------|--------------------------|-------------|
| 187 bits(| (474) 3e | -47() Compositional matrix adjust. | 171/562(30%) | 265/562(47%) | 88/562(15%) -2 | 2 |
| Features | S : | | | | | |
| Query | 2136 | RPLLYLSLPGVAFILGVFWFRRRY- R LL +LP +A IL FWF+++ | KNCLDKPDD: K+ + | | ~ | ъ 1966 |
| Sbjct | 7 | R LL +LP +A IL FWF+++ RQLLVWTLPTIALILSYFWFKKKRI | | | | D 66 |
| Query | 1965 | QNGKLPQQSASKSMN-INGTLVNgs P +S S+S++ ++ ++ | gsgsgssSDEK | | APIKIQSNGRTS PI I | N 1789 |
| Sbjct | 67 | AGNSSPNRSFSRSLSGVDTAPIDII | | | | - 107 |
| Query | 1788 | GKHQQQIDSEILKSKIQDAE + +D EI +KS + | HKTLCSIDED- | | SPRDLPDSVN SP P++ | - 1654 |
| Sbjct | 108 | DEDLDLEIQKIKSMKSAAAEPF | | | | 'S 164 |
| Query | 1653 | -TRVSFYNRKATQKTVEPVVIKATR T SF + T K P VIK T | | DTNYTNKECEQ | NNNCEPKEEPSK E K E +K | |
| Sbjct | 165 | VTPESFISTPITPKYKSPKVIKCT- | | | | |
| Query | 1476 | EAdqeeleqdqeQTVLKEEVVDS EA + T ++E V+S | | | ASPSLSICSVQ- ASPSLS S | - 1345 |
| Sbjct | 219 | EALDTTDGPKKLPTPNSIEERNVES | | | | S 278 |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTT S DSGKG S + +R | | YEFLFPISLIG YEF P +L+G | ~ | |
| Sbjct | 279 | EGSNDSGKGGSDVATPPSRTPADDG | | | | |
| Query | 1209 | KAKTLASVSVGKNPYSGKVRICTIE K K+ + + K+P + K++IC IE | | MIRQRLPAKRY MIR++ P KRY | | L 1033 |
| Sbjct | 339 | KEKSRTRIMIKKHPSNSKMKICAIE | | | | A 398 |
| Query | 1032 | PQTIVPLSTESLYNLQLKLIEGINN P ++ P L LKLIEGINN | IDVVVSAVLSGS | | | D 853 |
| Sbjct | 399 | PVSLTPDQLHLKLIEGINN | | | | V 452 |
| Query | 852 | SYSTMEAPLLPS-LELSAVCVIPINGSY++ E+PLLP + + +C | | | | 'N 676 + |
| Sbjct | 453 | SYNSAESPLLPKPIVENTICAAQSE | | | | |
| Query | 675 | TLRQIRTDFMNVPFQSTECILS 6 LRQIR DF+ +PFQ+ EC+L+ | 10 | | | |
| Sbjct | 512 | | 33 | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X1 [Lingula anatina]

Sequence ID: ref|XP_013383303.1| Length: 640 Number of Matches: 1

Range 1: 321 to 629

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------------|---------------------------|------------|--------|
| 187 bits | (475) 86 | e-47() Compositional matrix adjust. | 109/313(35%) | 178/313(56%) | 24/313(7%) | -2 |
| Feature | s: | | | | | |
| Query | 1281 | YEFLFPISLIGHLYGRKRAFINQIK YEF FP L G L G+ + I IK | | | | |
| Sbjct | 321 | YEFEFPSELCGRLIGKHGSTITAIK | | | - | |
| Query | 1101 | MIRQRLPAKRYPNFTMQRIHFALPQ +IR++ P ++PN ++++ + + | | NLQLKLIEGINN +OL L EG+ | | |
| Sbjct | 381 | LIRRKFPKNQFPNVDLRQLSTHVQE | | | | |
| Query | 921 | IFIQhplhpshpslplLQKQLYDSY IF+Q P HP++PSL L + + Y | | | | DT 748 |
| Sbjct | 438 | IFVQQPTHPTYPSLERLNQFMIMCY | | | | SV 497 |
| Query | 747 | DPEDEERCVIKFLDFGGYMNVGFNT E +E C IK++D+GGY + | LRQIRTDFMNVE L+OIR+DFM +E | | | |
| Sbjct | 498 | QDETDE-CDIKYVDYGGYARIQACA | | | | |
| Query | 573 | AAEILNKLTKGIVLQAQVAGYNSHN A+ +L ++++G +LQ Q + | LPEIFLFASLGE +P + L+ | PNNV + | IF | |

Sbjct 557 ASAVLEEVSQGRMLQLQTLSAAADGIPYVQLYTQGAQGTLFTAQNGEPVWPPQSEPILIN 616

Query 441 KELVGRKLAKWVE 403
++LV R + +WVE
Sbjct 617 RDLVDRGVVRWVE 629

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X2 [Aplysia californica]

Sequence ID: ref|XP_005093022.2| Length: 860 Number of Matches: 1

Range 1: 512 to 847

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|-------------------------------------|------------------------|-------------------------|---------|
| 188 bits | (477) 46 | e-46() Compositional matrix adjust. | 122/343(36%) | 189/343(55%) | 22/343(6%) | -2 |
| Feature | s: | | | | | |
| Query | 1383 | DAASPSLS-ICSVQSGDSGKGS | | | | AF 1222 |
| Sbjct | 512 | D+ + S+S +C S S DSG+G DSPTKSISPVCDNNSEGSNDSGRGY | | | L G G++ CLCGRFIGKQG | KN 571 |
| Query | 1221 | INQIKAKTLASVSVGKNPYSGKVRI IN +K KT A+VS+ NP++ + +T | CTIEGTESEID <i>F</i> C + GT++E+D | | KRYPNFTMQR P TM | IH 1042 |
| Sbjct | 572 | INYLKQKTGANVSLTYNPFTPEYQI | | | | 627 |
| Query | 1041 | FALPQTIVPLSTESLYNLQLK +P + P ++E +OL | LIEGINNDVVVS L EG++ +V VS | | hplhpshpsl P H S SL | |
| Sbjct | 628 | VPVNLTPAASEHPVLVPDVMQLS | | | | |
| Query | 873 | LQKQLYDSYST-MEAPLLPS-LELS | | RVQIVDTDPED R I + E | EERCVIKFLD E C +KF+D | |
| Sbjct | 686 | LNYFLNTAYGQDPNIPPVPTPVECG | | | | • |
| Query | 699 | GYMNVGFNTLRQIRTDFMNVPFQST GY + + L+QIRTDFM++PFQ+ | | | LNKLTKGIVL L ++T+ +L | ~ |
| Sbjct | 745 | GYAQMPVSCLKQIRTDFMSLPFQAV | | | | |
| Query | 525 | QVAGYNSHNLPEIFLFASLGPNNV- QV +P + L+ NN | IFINKELVGRKI + IN+ LV ++I | |) | |
| Sbjct | 805 | QVVARTETGIPHVHLYQIDAENNSP | | | , | |

PREDICTED: KH domain-containing protein akap-1 [Diachasma alloeum] Sequence ID: **ref|XP_015113342.1|** Length: 541 Number of Matches: 1

▶ See 1 more title(s) Range 1: 218 to 534

| Score | E | xpect Method | Identities | Positives | Gaps Fra | ame |
|------------|---------|---|-----------------------------|--------------------------|----------------------------|------|
| 183 bits(4 | 465) 5e | e-46() Compositional matrix adjust. | 112/322(35%) | 184/322(57%) | 7/322(2%) -2 | |
| Features: | : | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTT-YEFL S DSGKG S+ R TT YEF | FPISLIGHLYGI P +L+G + G- | | | 1168 |
| Sbjct | 218 | STDSGKGGSINGQLTKRKSTTIYEFA | | | | 277 |
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIRQ + +++C IEG I+ AL +IRO | RLPAKRYPNFTI R P K+YP T- | | VPLSTESLYNL +P TE + | 988 |
| Sbjct | 278 | TTKHLKLCVIEGLPENINTALDLIRQ | | | | 334 |
| Query | 987 | QLKLIEGINNDVVVSAVLSGSHIFIQ OL L++G+NNDV+V +L +FIO | hplhpshpslp: P HP++PSL 1 | LLQKQLYDSYST LL + Y+T | MEAPLLPS-LE +E+P +P L | 811 |
| Sbjct | 335 | QLHLVDGVNNDVMVCHILQPDRLFIQ | | | | 394 |
| Query | 810 | LSAVCVIPINDVWYRVQIVDTDPEDE + V + W R + + DP E | | | IRTDFMNVPFQ IR+D++ +PFO | |
| Sbjct | 395 | QGMIVVAKWYEKWVRALVEEADPAGE | | | | |
| Query | 630 | STECILSNIEPIGGTWSIEAAEILNK + E L+NI+P G W EA +++ + | | | | 451 |
| Sbjct | 454 | AIEVSLANIKPKNGEWQQEAYDVVAQ | | | | 512 |
| Query | 450 | FINKELVGRKLAKWVEMSD*QP 38 + EL+ R LA+ V + P | 5 | | | |
| Sbjct | 513 | SVAHELIARGLAESVSFEEMLP 53 | 4 | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like isoform X1 [Aplysia californica]

Sequence ID: ref|XP_012934994.1| Length: 886 Number of Matches: 1

Range 1: 538 to 873

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------------|--------------|------------------------|---------|
| 187 bits | (476) 56 | e-46() Compositional matrix adjust. | 122/343(36%) | 189/343(55%) | 22/343(6%) | -2 |
| Feature | s: | | | | | |
| Query | 1383 | DAASPSLS-ICSVQSGDSGKGS | | | LIGHLYGRKR | AF 1222 |
| Sbjct | 538 | D+ + S+S +C S S DSG+G DSPTKSISPVCDNNSEGSNDSGRGY | | | | KN 597 |
| Query | 1221 | INQIKAKTLASVSVGKNPYSGKVRI IN +K KT A+VS+ NP++ + +I | | | | IH 1042 |
| Sbjct | 598 | IN TK KI ATVST NPTT T TI INYLKQKTGANVSLTYNPFTPEYQI | | | | 653 |
| Query | 1041 | FALPQTIVPLSTESLYNLQLK +P + P ++E +OL | LIEGINNDVVVS L EG++ +V VS | | hplhpshpsl P H S SL | - |
| Sbjct | 654 | VPVNLTPAASEHPVLVPDVMQLS | | | | |
| Query | 873 | LQKQLYDSYST-MEAPLLPS-LELS | | /RVQIVDTDPED | EERCVIKFLD | |
| Sbjct | 712 | LNYFLNTAYGQDPNIPPVPTPVECG | _ | | | _ |
| Query | 699 | GYMNVGFNTLRQIRTDFMNVPFQST GY + + L+QIRTDFM++PFQ+ | | | LNKLTKGIVL | |
| Sbjct | 771 | GYAQMPVSCLKQIRTDFMSLPFQAV | | | | ~ |
| Query | 525 | QVAGYNSHNLPEIFLFASLGPNNV- QV +P + L+ NN | IFINKELVGRKI + IN+ LV ++I | | | |
| Sbjct | 831 | QVVARTETGIPHVHLYQIDAENNSP | | | | |

PREDICTED: KH domain-containing protein C56G2.1 [Bombus impatiens] Sequence ID: **ref|XP_003485511.1**| Length: 586 Number of Matches: 1

▶ See 2 more title(s) Range 1: 263 to 576

| Score | E | expect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------------|--------------|------------------------|----------------|
| 184 bits | (467) 66 | e-46() Compositional matrix adjust. | 112/320(35%) | 183/320(57%) | 9/320(2%) | -2 |
| Features | S: | | | | | |
| Query | 1344 | SGDSGKGSSLP-RSEATRVKTTYEFI | | | | |
| Sbjct | 263 | S DSGKG S+ ++ T + YEF STDSGKGGSIKGHTKDTVMPMIYEFS | P SL+G L GI SIPQSLVGRLIGI | | | |
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIR(S ++C IEG+ I+ AL MIR(| | | VPLSTESLY VP | NL 988 |
| Sbjct | 323 | ISRDQKLCAIEGSTEGINVALEMIR | | | | |
| Query | 987 | -QLKLIEGINNDVVVSAVLSGSHIFI QL L+EG+NNDVV+ ++ + +F- | Ohplhpshpsl | ollQKQLYDSYS | | S-L 814 L |
| Sbjct | 379 | RQLSLVEGVNNDVVICHIVKPNRLFV | | | | _ |
| Query | 813 | ELSAVCVIPINDVWYRVQIVDTDPEI + V + W RV + DP | DEERCVIKFLDFO | | QIRTDFMNV +IR+D++ + | |
| Sbjct | 439 | TNGMILVAKWYNTWVRVYVEQPDPHO | | | | |
| Query | 633 | QSTECILSNIEPIGGTWSIEAAEILN Q+ E L+N++P G W+ EA + | NKLTKGIVLQAQV ++ GIV QAQ- | | | INV 454 - V |
| Sbjct | 498 | QAIEIFLANVQPKDGEWNQEAYNTVA | | | | - |
| Query | 453 | IFINKELVGRKLAKWVEMSD 394 I + EL+ R A+ + + + | | | | |
| Sbjct | 557 | ISLADELIARGFAESIPLEN 576 | | | | |

PREDICTED: KH domain-containing protein C56G2.1-like isoform X2 [Ceratosolen solmsi marchali] Sequence ID: **ref|XP_011499408.1**| Length: 570 Number of Matches: 1

▶ See 1 more title(s) Range 1: 248 to 560

| Score | E | Expect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|---------------------------|--------------|---------------------|---------|
| 183 bits | (465) 8 | Be-46() Compositional matrix adjust. | 112/318(35%) | 180/318(56%) | 6/318(1%) | -2 |
| Feature | s: | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYEFLE S DSGKG S+ +T YEFL | PISLIGHLYGR I L+G L GR | | LASVSVGKN + V ++ | |
| Sbjct | 248 | STDSGKGGSIKGHPKDNNRTIYEFLV | | | | - |
| Query | 1164 | SGKVRICTIEGTESEIDAALAMIRQF | RLPAKRYPNFTM | QRIHFALPQTIV | PLSTESLYN | ILQ 985 |

| Sbjct | 308 | +IC+I+GT I AL MIRQ P K P ++++I + +P +E +Q ERDYKICSIDGTPENIATALDMIRQLFPEKTTPFLSLEQIAYEILPEEIPWVSELMQ | 364 |
|-------|-----|--|-----|
| Query | 984 | LKLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPS-LEL L LIEG+NNDV+VS + +H+FIO P HP++PSL +L ++ + Y T+E+P +P L | 808 |
| Sbjct | 365 | LSLIEGVNNDVIVSHIYKPNHLFIQLPTHPTYPSLRILDDKMTELYETVESPPVPDELRK | 424 |
| Query | 807 | SAVCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQS + V + W RV I DP+ E+ +++ +D GGY + +R+IR+D++++PFO+ | 628 |
| Sbjct | 425 | GMIVVAKWYNKWVRVYIETPDPKGEQ-SLVRLVDHGGYWIFSNSNMRKIRSDYLSLPFQA | 483 |
| Query | 627 | TECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIF E L+N+ P WS EA ++ ++ IV ÕAÕ+ GY + I L+ ++ + VI | 448 |
| Sbjct | 484 | IEVFLANVRPKDEEWSQEAYNVVGQICSRIVGQAQIVGYVDCST-FINLYFNIHKHGVIS | 542 |
| Query | 447 | INKELVGRKLAKWVEMSD 394 I EL+ R +A+ + + + | |
| Sbjct | 543 | IADELIARGIAESISLDE 560 | |

PREDICTED: KH domain-containing protein C56G2.1 [Fopius arisanus] Sequence ID: **ref|XP_011312236.1**| Length: 536 Number of Matches: 1 Range 1: 213 to 532

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|------------------------------|--------------|--------------------------|--------|
| 182 bits | (463) 96 | e-46() Compositional matrix adjust. | 114/326(35%) | 187/326(57%) | 12/326(3%) | -2 |
| Features | 3: | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYES S DSGKG S+ + T+ K TTYES | | | | |
| Sbjct | 213 | STDSGKGGSI-NGQVTKRKCVTTYE | | | | |
| Query | 1170 | PYSGKVRICTIEGTESEIDAALAMI | RQRLPAKRYPNE R R P K++P | | TIVPLSTESL +P TE | YN 991 |
| Sbjct | 272 | PTTNHLKLCVIEGLPDNINRALDLI | | | | 328 |
| Query | 990 | LQLKLIEGINNDVVVSAVLSGSHIF | IQhplhpshpsl IQ P HP+HPSI | | STMEAPLLPS +T+E+P +P | -L 814 |
| Sbjct | 329 | MQLHLVDGVNNDVMVCHILQPDRLF | | | | QL 388 |
| Query | 813 | ELSAVCVIPINDVWYRVQIVDTDPE | DEERCVIKFLDE E+ V + +D | | RQIRTDFMNV R+IR+D++ + | |
| Sbjct | 389 | AQGMIVVAKWYDTWVRALVEEADPA | | | | |
| Query | 633 | QSTECILSNIEPIGGTWSIEAAEIL Q+ E L+NI+P G W EA +++ | | | IFLFASLGPN I L+ ++ + | |
| Sbjct | 448 | QAIEVSLANIKPKNGEWQPEAYDVV | | | | |
| Query | 453 | IFINKELVGRKLAKWVEMSD*QI I + EL+ R LA+ V EM Q | | | | |
| Sbjct | 507 | ISVAHELIARGLAEAVAFEEMIPEÕ | | | | |

PREDICTED: uncharacterized protein LOC106075240 [Biomphalaria glabrata]

Sequence ID: ref|XP_013091637.1| Length: 948 Number of Matches: 1

Range 1: 593 to 947

| Score | Ex | rpect Method | Identities | Positives | Gaps | Frame |
|-----------|----------|---|-----------------------------|------------------------------|----------------------|--------------|
| 187 bits(| (475) 1e | e-45() Compositional matrix adjust. | 131/359(36%) | 197/359(54%) | 22/359(6%) | -2 |
| Features | 3: | | | | | |
| Query | 1422 | EVVDSNGNQKRNVDAASPSLSIC++VD+N SP+ S +6 | CSVQSGDSG C S S DSG | | RVKTTYEFLF +T F F | 1267 |
| Sbjct | 593 | DIVDNNNLASNEHKPGSPTKSSSPM | | | | NM 652 |
| Query | 1266 | PISLIGHLYGRKRAFINQIKAKTLA P L G G++ IN +K+KT A | SVSVGKNPYSGK +VS+ NPY+ + | | | |
| Sbjct | 653 | PSELCGRFIGKQGKNINFLKSKTGA | | | | |
| Query | 1086 | LPAKRYPNFTMQRIHFALPQTIV P +P TM I+ +P IV | | | | HI 919 HI |
| Sbjct | 713 | FPLNEFPLLTMLPINVNPVVPAPIV | | -QL L EG++ + MQLSLPEGVSVE | | |
| Query | 918 | FIQhplhpshpslplLQKQLYDSYS F+Q P H S SL L L Y | -TMEAPLLPS-I P +P+ + | LELSAVCVIPIN | | |
| Sbjct | 771 | FVQQPTHRSFMSLEKLTYFLNTVYG | | | | + PE 830 |
| Query | 744 | PEDEERCVIKFLDFGGYMNVGFNTL | | | | |
| Sbjct | 831 | ED E V KF+D+GGY + ++L NEDGETQV-KFVDYGGYAVMPVSSL | | | | |
| Query | 570 | AEILNKLTKGIVLQAQVAGYNSHNL L+ +T+ +LQ QV + +; | PEIFLFASLGP- P I L+ + P | NNVIFINKEL N+ + IN+ L | | |

KH domain-containing protein C56G2.1 [Melipona quadrifasciata]

Sequence ID: gb|KOX67995.1| Length: 712 Number of Matches: 1

Range 1: 393 to 706

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|-------------------------|-------------------------|----------------------------|----------------|
| 184 bits | (466) 36 | e-45() Compositional matrix adjust. | 118/323(37%) | 186/323(57%) | 12/323(3%) | -2 |
| Features | 3: | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVK-TTYEFI S DSGKG S+ V YEF | | RKRAFINQIKA R +F+ I+ | | |
| Sbjct | 393 | S DSGKG S+ V YEF STDSGKGGSIKGHAKNNVMPMAYEFS | | | | · - |
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIRQ +IC IEG+ + I+ AL MIRO | | | TIVPLSTESLY | YN 991 |
| Sbjct | 453 | MWRDQKICAIEGSMNGINIALDMIRQ | | | | 508 |
| Query | 990 | LQLKLIEGINNDVVVSAVLSGSHIFI QL L+EG+NNDVVV ++ + F+ | | | | |
| Sbjct | 509 | KÕLSLVEGVNNDVVVCHIVKPNRFFV | | | | |
| Query | 813 | ELSAVCVIPINDVWYRVQIVDTDPED + V + W RV I DP | EERCVIKFLDF E +++ +D | | RQIRTDFMNV: ++IR+D++ +: | |
| Sbjct | 569 | SRGMILVAKWYNTWVRVYIEQPDPRO | | | | |
| Query | 633 | QSTECILSNIEPIGGTWSIEAAEILN Q+ E L+NIEP G W+ EA + | | | | |
| Sbjct | 625 | QAIEIFLANIEPKDGEWNQEAYNTVA | | | | |
| Query | 453 | IFINKELVGRKLAKWVEMSD*QP 3 I + EL+ R A+ V + + P | 885 | | | |
| Sbjct | 684 | | 06 | | | |

PREDICTED: KH domain-containing protein C56G2.1-like isoform X1 [Ceratosolen solmsi marchali]

Sequence ID: ref|XP_011499407.1| Length: 649 Number of Matches: 1

Range 1: 327 to 639

| Score | E | xpect Method | Identities | Positives | Gaps I | Frame | |
|-----------|---------|---|------------------------------|---------------------|--------------------------|--------------|--|
| 183 bits | (464) 3 | e-45() Compositional matrix adjust. | 112/318(35%) | 180/318(56%) | 6/318(1%) - | 2 | |
| Features: | | | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYEFLF | PISLIGHLYGRI I L+G L GR | RAFINQIKAKT F I+ | LASVSVGKNI + V ++I | | |
| Sbjct | 327 | S DSGKG S+ +T YEFL STDSGKGGSIKGHPKDNNRTIYEFLV | | | | | |
| Query | 1164 | SGKVRICTIEGTESEIDAALAMIROR +IC+I+GT I AL MIRO | LPAKRYPNFTM(PKP++- | | | LO 985 FÕ | |
| Sbjct | 387 | ERDYKICSIDGTPENIATALDMIRQL | | | | | |
| Query | 984 | LKLIEGINNDVVVSAVLSGSHIFIQh L LIEG+NNDV+VS + +H+FIO | plhpshpslplI P HP++PSL +I | | | EL 808 | |
| Sbjct | 444 | LSLIEGVNNDVIVSHIYKPNHLFIQL | | | | RK 503 | |
| Query | 807 | SAVCVIPINDVWYRVQIVDTDPEDEE + V + W RV I DP+ E+ | RCVIKFLDFGGY +++ +D GGY | | RTDFMNVPF(R+D++++PF(| | |
| Sbjct | 504 | GMIVVAKWYNKWVRVYIETPDPKGEQ | | | | | |
| Query | 627 | TECILSNIEPIGGTWSIEAAEILNKL E L+N+ P WS EA ++ ++ | | | FASLGPNNV] + ++ + V] | | |
| Sbjct | 563 | IEVFLANVRPKDEEWSQEAYNVVGQI | | | | | |
| Query | 447 | INKELVGRKLAKWVEMSD 394 I EL+ R +A+ + + + | | | | | |
| Sbjct | 622 | IADELIARGIAESISLDE 639 | | | | | |

A-kinase anchor protein 1, mitochondrial, partial [Stegodyphus mimosarum]

Sequence ID: gb|KFM63633.1| Length: 639 Number of Matches: 1

Range 1: 372 to 636

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---------------|---------|------------------------------|-------------|--------------|-----------|-------|
| 182 bits(462) | 5e-45() | Compositional matrix adjust. | 97/271(36%) | 163/271(60%) | 9/271(3%) | -2 |

Features:

| Query | 1281 | YEFLFPISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALA YEF P L G L G+ + IK ++ A+V + ++PY +++I ++G++S+++ AL | 1102 |
|-------|------|---|------|
| Sbjct | 372 | YEFELPQELCGRLIGKHGKHVKSIKERSNANVFIKRHPYDPQLKIVAVQGSQSDVNNALE | 431 |
| Query | 1101 | MIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNLQLKLIEGINNDVVVSAVLSGSH +IR++ P ++P T+ + + PL +LQL L +G + DV++S+++S H | 922 |
| Sbjct | 432 | IIRRKFPPSQFPTVTLVQTNLVNSHGL-PLPESLQLHLPDGASCDVILSSLVSAGH | 486 |
| Query | 921 | IFIQhplhpshpslplLQKQLYDSYSTMEAPLLPS-LELSAVCVIPINDVWYRVQIVDTD F+Q P HP++PSL L + + + YS ++ PLLP +E +C P+ WYR Q++ | 745 |
| Sbjct | 487 | FFLQQPTHPTYPSLSTLDQCMMNCYSQLDTPLLPHPVEAGVICAAPVLRGWYRAQVIFVF | 546 |
| Query | 744 | PEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEA E C IKF+D+GG+ V NTLRQIR+DFM +PFQ++EC L+N+ P+ + WS EA | 571 |
| Sbjct | 547 | DNGTE-CEIKFVDYGGFSQVPTNTLRQIRSDFMTLPFQASECYLANVSPVDSSEGWSAEA | 605 |
| Query | 570 | AEILNKLTKGIVLQAQVAGYNSHNLPEIFLF 478 +L +G +LQA + Y +P + L+ | |
| Sbjct | 606 | TATFEELAQGQILQAVLVEYAEDGIPCVHLY 636 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Megachile rotundata] Sequence ID: **ref|XP_012135254.1|** Length: 580 Number of Matches: 1

▶ See 4 more title(s) Range 1: 12 to 564

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|-----------------------------|-----------------------------|---------------------------|---------------|
| 180 bits | (457) 1e | e-44() Compositional matrix adjust. | 171/582(29%) | 280/582(48%) | 43/582(7%) | -2 |
| Features | s: | | | | | |
| Query | 2118 | SLPGVAFILGVFWFRRRYKNCLD | KPDDEDSS <i>F</i> D+ D + | | ~ | GK 1954 |
| Sbjct | 12 | + P A I+G+ W+RRR + D TFPAFALIIGLLWYRRRRVDRTDPG | | | K+N + PSKSNLNFYDS | SG 68 |
| Query | 1953 | LPQQSASKSMNINGTLVNgsgsgsg + O + S+N + L++ | SSSDEKDSPTTM S+ D P | ILYGKSAPIKIQ KS + | | QQ 1774 QQ |
| Sbjct | 69 | + Q + S+N + L++ I-QFDETSSLNSSNQLIDDIICSPR | | | | QQ 123 |
| Query | 1773 | QIDSEILKSKIQDAEHKTLCSI I++ K +IO + + + | | | YNRKATQKTVI K VI | |
| Sbjct | 124 | WYGYINTPASKMEIQLSSNPKIS | | | | |
| Query | 1602 | VVIKATRTPKISPENSFLDTNYTNK K+ EN +T NK | ECEQNNNCEPKE + + + + E | _ | leqdqeQTVLI L++ + | KE 1423 |
| Sbjct | 179 | EEEQKLPGENNTELDNK | | | | AL 230 |
| Query | 1422 | EVVDS-NGNQKRNVDAASPSLSICS DS N + V S + + S | VQSGDSGKGSSI S DSGKG S+ | JPRSEATRV - P+ A V | | |
| Sbjct | 231 | SERDSANHSPISGVLEGSVTDEVRS | | | | |
| Query | 1254 | IGHLYGRKRAFINQIKAKTLASVSV +G L G +F+ I+ K + + | | | ALAMIRORLPA AL MIRO+ P | |
| Sbjct | 289 | LGKLIGHHGSFLQSIRVKAEVYIVI | | | | |
| Query | 1074 | RYPNFTMQRI-HFALPQTIVPLSTE +YP T+++I LP+ I P TE | | GINNDVVVSAVL G+NNDVV+ ++ | | |
| Sbjct | 349 | KYPQVTLEQIVSSKLPEEI-PWVTE | | | | |
| Query | 897 | pshpslplLQKQLYDSYSTMEAPLL PS+P L +L + + Y T E+P + | | PINDVWYRVQI + W RV | | |
| Sbjct | 405 | PSYPYLRILDENMTQLYDTTESPPV | PDDLSRGMILV <i>A</i> | | | |
| Query | 720 | <pre>IKFLDFGGYMNVGFNTLRQIRTDFM ++ +D GGY + +++IR+D++</pre> | NVPFQSTECILS +PFO+ E L+ | | | KG 541 |
| Sbjct | 464 | VRLVDHGGYWFFSNSEMKKIRSDYL | | | | SR 523 |
| Query | 540 | IVLQAQVAGYNSHNLPEIFLFASLG IV QAQ+AGY + N + L+ ++ | PNNVIFINKELV + VI + EL+ | | | |
| Sbjct | 524 | IVGQAQIAGYINTNT-YVNLYFNIN | | | | |

KH domain-containing protein C56G2.1 [Habropoda laboriosa]

Sequence ID: gb|KOC60170.1| Length: 583 Number of Matches: 1

Range 1: 260 to 571

| Score | Expect Method | Identities | Positives | Gaps | Frame |
|---------------|---|--------------------------|--------------|-----------|---------------|
| 179 bits(454) | 2e-44() Compositional matrix adjust. | 111/318(35%) | 179/318(56%) | 9/318(2%) | -2 |
| Features: | | | | | |
| Query 134 | 4 SGDSGKGSSLP-RSEATRVKTTYEFL S DSGKG S+ ++ + YEF | FPISLIGHLYG P L+G L G | ~ | | XNP 1168 P |

| Sbjct | 260 | STDSGKGGSIKGHTKDSAGPVLYEFCIPQHLVGRLIGRHGNFLHSIRLKAEVHIVVKNYP | 319 |
|-------|------|--|-----|
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTESLYNL +IC IEG+ ++ AL MIRO+ P ++YPN T+++I + TE + | 988 |
| Sbjct | 320 | IMKDQKICAIEGSSEGVNIALDMIRQKFPEEKYPNVTLEQILSSKTSEENQWITELM | 376 |
| Query | 987 | QLKLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPS-LE QL L+EG+NNDVVV V+ + +F+Q P HP++PSL +L++ + Y T+E P +P L | 811 |
| Sbjct | 377 | QLSLVEGVNNDVVVCHVVKPNRVFVQLPTHPTYPSLRILERNMTQLYDTIETPPVPDELS | 436 |
| Query | 810 | LSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQ + V + W RV + DP E+ +++ +D GGY ++++IR+D++ +PFO | 631 |
| Sbjct | 437 | KGMILVAKWYNNWVRVCVEQPDPHGEQH-LVRLVDHGGYWQFSNAEMKKIRSDYLTLPFQ | 495 |
| Query | 630 | STECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGY-NSHNLPEIFLFASLGPNNV + E L+N++P G W+ EA ++ + GIV QAQ+ GY N+ + LF ++ + V | 454 |
| Sbjct | 496 | AIEIFLANVQPKNGEWTQEALNVVAHMCYGIVGQAQIEGYINTSTYVNLFLNIHNHGV | 553 |
| Query | 453 | IFINKELVGRKLAKWVEM 400 I + EL+ R LA+ V + | |
| Sbict | 554 | ISLADELIARGLAESVPL 571 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Strongylocentrotus purpuratus]

Sequence ID: ref|XP_001199246.2| Length: 671 Number of Matches: 1

▶ See 1 more title(s) Range 1: 290 to 647

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|--|-------------------------|--------------|--------------------------|-------------|
| 179 bits | (454) 6e | e-44() Compositional matrix adjust. | 128/373(34%) | 190/373(50%) | 41/373(10%) | -2 |
| Features | s: | | | | | |
| Query | 1434 | VLKEEVVDSNGNQKRNVDAASPSLS +L E+ SNG N ++ S | | | SEATRVKTT | 1282 |
| Sbjct | 290 | LLDEKAHSSNGTSLGNNESNSTGYL | OVSSEVNSEGSS | | | SA 349 |
| Query | 1281 | YEFLFPISLIGHLYGRKF Y+F FP L G L G+ | | | GKVRICTIEGT +IC +EG | ES 1123 |
| Sbjct | 350 | MKEGPVMYQFEFPSKLCGRLIGKSO | | | | RG 409 |
| Query | 1122 | EIDAALAMIRQRLPAKRYPNFT E+D ALA I+++ P+ R N | MQRIHFALPQT Q+ + + T | | | |
| Sbjct | 410 | EVDGALAYIKKKFPSVDLSRRANTÇ | | | | + SI 457 |
| Query | 951 | VVSAVLSGSHIFIQhplhpshpslp ++S+V+SG HIFIQ P+H ++ L | lLQKQLYDSYS + + Y | | LELSAVCVIPII +E +C P+ | |
| Sbjct | 458 | LISSVVSGGHIFIQQPVHQTYQGL | | | | _ |
| Query | 777 | VWYRVQIVDTDPEDEERCVIKFLDE WYR O+V+ E +E ++FLD+ | GGYMNVGFNTL GGY V L | | | |
| Sbjct | 518 | GWYRAQVVEVTHETDE-VDVRFLDY | | | | |
| Query | 597 | IGGTWSI-EAAEI-LNKLTKGI-VI + G E+ I + +L + I V+ | | | | |
| Sbjct | 577 | + G E+ I + +L + I V+ LPGDADFSESCRIFIEQLAQSIGVN | | | | |
| Query | 432 | VGRKLAKWVEMSD 394 V + L W E ++ | | | | |
| Sbjct | 635 | V T L W E TT VNQGLVSWYEGTE 647 | | | | |

PREDICTED: KH domain-containing protein C56G2.1 [Orussus abietinus] Sequence ID: **ref|XP_012282550.1|** Length: 566 Number of Matches: 1

▶ See 1 more title(s) Range 1: 243 to 555

| Score | E | Expect Method | Identities | Positives | Gaps | Frame |
|----------|------------|---|-----------------------------|---------------------------|---------------------|--------------|
| 175 bits | (443) 6 | e-43() Compositional matrix adjust. | 107/319(34%) | 182/319(57%) | 8/319(2%) | -2 |
| Features | S : | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYEFLE S DSGKG S+ YEFL | PISLIGHLYGRI | | LASVSVGKN ++SV + | NPY 1165 |
| Sbjct | 243 | SMDSGKGGSIKGHIKHPDPINYEFLV | | | | EMI 302 |
| Query | 1164 | SGKVRICTIEGTESEIDAALAMIROF +IC+I+G++ I AL +IR+ | | | | |
| Sbjct | 303 | VKNNKICSIKGSQEGIAIALELIREI | - | | | |
| Query | 987 | QLKLIEGINNDVVVSAVLSGSHIFIÇ L L+E +NNDV+V ++ + +F+Ç |)hplhpshpslp) P HP++P+L | llQKQLYDSYST +L + + Y+ | | -LE 811 L |

| Sbjct | 360 | -LSLVEAVNNDVLVCNIVRPNRLFVQLPTHPTYPALRMLDENMTLLYNNTDSPPVPDELV | 418 |
|-------|-----|---|-----|
| Query | 810 | LSAVCVIPINDVWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQ + + W RV I + DP E R +++F+D GGY + + +R +RTD++ +PFO | 631 |
| Sbjct | 419 | RGMIVAAKWYNQWVRVYIENPDPAGE-RHLVRFVDHGGYWTFSNSDMRSLRTDYLTLPFQ | 477 |
| Query | 630 | STECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVI + E LSN++P G W+ EA +++ ++ GIV QAQ+ GY + N+ + L+ ++ + VI | 451 |
| Sbjct | 478 | AIEVFLSNVKPRNGEWTQEAYDLVGHISSGIVGQAQIEGYVNGNV-YVSLYLNIQKHGVI | 536 |
| Query | 450 | FINKELVGRKLAKWVEMSD 394 | |
| Sbjct | 537 | + EL+ R LA + + D SVADELIARGLADPIALED 555 | |

Identities

Positives

Gaps

Frame

PREDICTED: KH domain-containing protein akap-1-like [Polistes canadensis] Sequence ID: **ref|XP_014605983.1|** Length: 581 Number of Matches: 1

Range 1: 8 to 564

Expect Method

Score

| 173 bits | (439) 36 | e-42() Compositional matrix adjust. 156/586(27%) 274/586(46%) 42/586(7%) -2 | |
|----------|----------|---|------|
| Feature | s: | | |
| Query | 2130 | LLYLSLPGVAFILGVFWFRRRYKNCLDKPDDEDSSAINDSSIEPTVQARKANGVLQNGKL ++ S P VA I+G+FW++R+ D D I+ S++ T+ KA+ +N L | 195 |
| Sbjct | 8 | IIKWSFPAVALIVGLFWYKRKSADRADPGGISTSNVLETIDKLKASSSRENVNL | 61 |
| Query | 1950 | PQQSASKSMNINGTLVNgsgsgsgssSDEKDSPTTMLYGKSAPIKIQSNGRT + + +++ + + S++K +TM+ + P+ + + + + + + + + + + + + + + + + | 1795 |
| Sbjct | 62 | SDSGINANDSYSSLHAQSIEEPINNCKEISEQKIGISTMMPLAALPVLVPVPSSLEEIHS | 121 |
| Query | 1794 | SNGKHQQQIDSEILKSKIQDAEHKTLCSIDEDFENLSSPRDLPDSVNTRVSFYNR-KATQ G + +E+L DA + + + D +S N + + N O | 1618 |
| Sbjct | 122 | G++E+L DA $+++D$ $+SN++N$ Q WYGNVENICHNEVLYENHPDASEFQMATGNVDTTTNYYNNVTNNSENMQNVYVNNIDIEQ | 181 |
| Query | 1617 | KTVEPVVIKATRTPKISPENSFLDT-NYTNKECEQNNNCEPKEEPSKKEAdqeeleqdqe + E ++ +P + +N T + N++ EO N P+EE + | 1441 |
| Sbjct | 182 | + E ++ +P + +N T + N++ EQ N P+EE + QNNEQLLSPSMDKQNEINHTSDINNEQTEQIQNYPPEEENKNQ | 224 |
| Query | 1440 | QTVLKEEVVDSNGNQKRNVDAASPSLSICSVQSGDSGKGSSLP-RSEATRVKTTYEFLFP | 1264 |
| Sbjct | 225 | T E +N + V S + S S DSGKG S+ + + ++ YEF -TQALSERDSANYSPVSGVLEGSVTDEARSEGSTDSGKGGSIEGQMKDDSMQYVYEFAIR | 283 |
| Query | 1263 | ISLIGHLYGRKRAFINQIKAKTLASVSVGKNPYSGKVRICTIEGTESEIDAALAMIRQRL | 1084 |
| Sbjct | 284 | L+G L GR +F++ I+ K+ + V + P S +IC I+G+ I AL +IR++ NDLVGKLIGRNGSFLHNIRTKSGVYIIVKRYPMSMNEKICAIQGSNKGISIALDIIRRKF | 343 |
| Query | 1083 | PAKRYPNFTMQRIHFALPQTIVPLSTESLYNL-QLKLIEGINNDVVVSAVLSGSHIFIQh | 907 |
| Sbjct | 344 | P K+YP+ T+Q+I | 400 |
| Query | 906 | plhpshpslplLQKQLYDSYSTMEAPLLPSLELSAVCVIPIND-VWYRVQIVDTDPEDEE | 730 |
| Sbjct | 401 | $ar{	t P}$ $ar{	t HPSHP}$ $ar{	t L}$ $ar{	t +}$ $ar{	t Y}$ $ar{	t +}$ $ar{	t P}$ $ar{	t +}$ $ar{	t +}$ $ar{	t P}$ $ar{	t +}$ $ar{	t P}$ $ar{	t HPSHPMLRKLDTDMAELYNSAIPPMPDKVTKGMILAAPVDDGKWARVYVVDPDSRGET}$ | 460 |
| Query | 729 | RCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEPIGGTWSIEAAEILNKL | 550 |
| Sbjct | 461 | ${ m V}$ + +D GGY +LRQIRTDF+ +PFQ+ E L+++ P G W ++ +L ++ NLV-RLVDHGGYRTYPNCSLRQIRTDFLTLPFQAVEVFLAHVRPKNGEWHPDSLNVLEQI | 519 |
| Query | 549 | TKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKLAK 412 | |
| Sbjct | 520 | G V AQ+ GY + + LF ++G + +I + EL+ R+ A+ VTGRVGLAQIVGYIDTQV-HVNLFFNIGKHGIISLADELIAREYAE 564 | |
| | | | |

PREDICTED: KH domain-containing protein C56G2.1 [Copidosoma floridanum] Sequence ID: **ref|XP_014214042.1|** Length: 627 Number of Matches: 1

▶ See 2 more title(s) Range 1: 314 to 609

| S | core | Expect | Method | Identities | Positives | Gaps | Frame | |
|----|------------|----------------|--|--------------|--------------|------------------------|-------|--|
| 17 | 73 bits(43 | 9) 4e-42() | Compositional matrix adjust. | 103/301(34%) | 173/301(57%) | 7/301(2%) | -2 | |
| Fe | eatures: | | | | | | | |
| Qu | ery 13 | 311 RSEA RS | ATRVKTTYEFLFPISLIGHLYGR +T YEFL P L+G L GR | | | SGKVRICTI ++CTT | | |
| Sb | ojct 31 | | EDNSRTFYEFLIPTKLVGKLIGR | | | | • | |
| Qu | ery 1 | 131 TESI | EIDAALAMIRQRLPAKRYPNFTM I AL +IR+ P K YP T+ | | | QLKLIEGIN OL L+EG+N | | |
| Sb | ojct 37 | 74 TPEI | NITVALDIIRRHFPEKTYPYLTL | | | ~ | | |

| Query | 954 | VVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPLLPS-LELSAVCVIPIND 7 V V +++ +H FIQ HP++PSL +L +++ Y+T+E+PL+P L + D | 778 |
|-------|-----|---|-----|
| Sbjct | 432 | | 491 |
| Query | 777 | VWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPFQSTECILSNIEP 5 W RV I + DP+ +E+ +++ +D GGY +R +R D++ +PFO+ E L+N++P | 598 |
| Sbjct | 492 | ~ | 550 |
| Query | 597 | IGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNVIFINKELVGRKL 4 G W+ EA +++++LT V ÖAÖ+ GY+ N I L+ ++ + + +EL R L | 418 |
| Sbjct | 551 | | 808 |
| Query | 417 | A 415 A | |
| Sbjct | 609 | Ā 609 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Trichogramma pretiosum]

Sequence ID: ref|XP_014232188.1| Length: 648 Number of Matches: 1

▶ See 1 more title(s) Range 1: 330 to 639

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|------------|--|--------------|--------------|-----------------------|----------|
| 173 bits | (439) 5e | e-42() Compositional matrix adjust. | 107/319(34%) | 173/319(54%) | 18/319(5%) | -2 |
| Features | S : | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRVKTTYEFL S DSG+G S+ ++ + K + F | | | | IPY 1165 |
| Sbjct | 330 | SNDSGRGGSIKENKKSLEKRVFIFQ | | | | NN 389 |
| Query | 1164 | SGKVRICTIEGTESEIDAALAMIRQ + R+C++ GT +I+ AL IR+ | | | HFALPQTIVE | |
| Sbjct | 390 | DTEYRMCSLCGTPQQIENALLKIRK | | | | |
| Query | 1008 | TESLYNLQLKLIEGINNDVVVSAVL TE L L+EGI NDVVV ++ | | | | |
| Sbjct | 450 | TELSLVEGITNDVVVCHIV | | | | |
| Query | 828 | LLP-SLELSAVCVIPINDVWYRVQI P LE + V V +N W RV + | | | VGFNTLRQIR + L+ +R | |
| Sbjct | 504 | AAPKELEPNMVLVAKVNGRWVRVIV | | | | • • — |
| Query | 651 | FMNVPFQSTECILSNIEPIGGTWSI F +P Q+ E L+N+ P G W | | | | |
| Sbjct | 562 | FAALPCQAIEVFLANVVPKNGEWKQ | | | | |
| Query | 471 | LGPNNVIFINKELVGRKLA 415 VI + ELV R LA | | | | |
| Sbjct | 621 | FNRQVVISLGDELVARGLA 639 | | | | |

PREDICTED: KH domain-containing protein C56G2.1 isoform X2 [Harpegnathos saltator]

Sequence ID: **ref|XP_011146583.1**| Length: 533 Number of Matches: 1 Range 1: 205 to 512

| Score | E | xpect Method | Identities | Positives | Gaps F | rame |
|----------|------------|---|-------------------------------|--------------|-------------------------|-------|
| 171 bits | (432) 16 | e-41() Compositional matrix adjust. | 109/312(35%) | 171/312(54%) | 5/312(1%) -2 | 2 |
| Features | 3 : | | | | | |
| Query | 1344 | SGDSGKGSSLPRSEATRV-KTTYEFI S DSGKG S+ T V +T Y F | FPISLIGHLYGF P L+G L GF | | | |
| Sbjct | 205 | STDSGKGGSINGYRKTNVEQTIYYFA | | | | |
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIRQ +IC+IEG I AL +IR- |)RLPAKRYPNFTN -+ P KR+P T+ | | | L 988 |
| Sbjct | 265 | GFTDQKICSIEGNAEGIKTALELIR | | | | S 322 |
| Query | 987 | QLKLIEGINNDVVVSAVLSGSHIFIQ Q+ L+EG+NND+VVS ++ + +FFQ | | | | L 808 |
| Sbjct | 323 | QMFLVEGVNNDIVVSHIVKPNWLFVQ | | | | R 382 |
| Query | 807 | SAVCVIPINDVWYRVQIVDTDPEDEE V D+W RV++ DP E+ | | | RTDFMNVPFQ R ++++PFO | |
| Sbjct | 383 | GMFYVANWFDIWVRVRMEKPDPSGER | | | | |
| Query | 627 | TECILSNIEPIGGTWSIEAAEILNKI E L++I+P G W EA ++ ++ | TKGIVLQAQVAC - G+V OAOV C | | FASLGPNNVI + ++ VI | |
| Sbjct | 442 | IEIFLAHIQPKNGVWLDEAYHVIAQI | | | | |
| Query | 447 | INKELVGRKLAK 412 + ELV R A+ | | | | |

PREDICTED: KH domain-containing protein C56G2.1 isoform X1 [Harpegnathos saltator]

Sequence ID: ref|XP_011146579.1| Length: 570 Number of Matches: 1

▶ See 3 more title(s) Range 1: 242 to 549

| Score | E | xpect Method | | Identities | Positives | Gaps F | rame |
|----------|---------|----------------------------------|---|-----------------------------|--------------|-------------------------|--------|
| 170 bits | (431) 3 | e-41() Composition | al matrix adjust. | 109/312(35%) | 171/312(54%) | 5/312(1%) -2 | 2 |
| Features | s: | | | | | | |
| Query | 1344 | SGDSGKGSSLPRSI | | | | | |
| Sbjct | 242 | S DSGKG S+ STDSGKGGSINGYF | | P L+G L GI IPQQLVGRLIGI | | | _ |
| Query | 1167 | YSGKVRICTIEGTE +IC+IEG | | RLPAKRYPNFTN + P KR+P T- | | | IL 988 |
| Sbjct | 302 | GFTDQKICSIEGNA | | | | • | is 359 |
| Query | 987 | QLKLIEGINNDVV\ Q+ L+EG+NND+V\ | | | | | L 808 |
| Sbjct | 360 | QMFLVEGVNNDIV\ | | | | | 'R 419 |
| Query | 807 | SAVCVIPINDVWYF | | | | RTDFMNVPFQ R ++++PFO | |
| Sbjct | 420 | GMFYVANWFDIWVE | • | | | | |
| Query | 627 | TECILSNIEPIGGT E L++I+P G | TWSIEAAEILNKI W EA ++ ++ | | | FASLGPNNVI + ++ VI | |
| Sbjct | 479 | IEIFLAHIQPKNG\ | | | | | |
| Query | 447 | INKELVGRKLAK + ELV R A+ | 412 | | | | |
| Sbjct | 538 | LADELVARGFAE | 549 | | | | |

A kinase anchor protein 1, mitochondrial [Crassostrea gigas]

Sequence ID: gb|EKC18066.1| Length: 744 Number of Matches: 1

Range 1: 414 to 740

| Score | Ex | rpect Method | Identities | Positives | Gaps | Frame |
|----------|------------|---|--------------|--------------|--------------------------|-------------|
| 172 bits | (435) 4e | -41() Compositional matrix adjust. | 120/346(35%) | 191/346(55%) | 45/346(13%) | -2 |
| Features | S : | | | | | |
| Query | 1383 | DAASPSLSICSVQSGDSGKGSSLPR | | | | |
| Sbjct | 414 | D+ S S DSG+G S+ DSNSSGCDNASEASNDSGRGPSM | | | + G L GR+ ICGRLIGRQGK | NI 471 |
| Query | 1218 | NQIKAKTLASVSVGKNPYSGKVRIC N IK K+ A++++ NP++ + ++C | | | | HF 1039 |
| Sbjct | 472 | NFIKEKSGANITLSANPFTPEFQLO | | | | • |
| Query | 1038 | ALPQTIVPLSTESLYNLQ PQ+ +VP + + + | | | | |
| Sbjct | 527 | PSGDNPQSAVLVPDIMQVMPGISQI | | | | |
| Query | 903 | lhpshpslplLQKQLYDSYSTMEAF HPS PSL L + + Y M+ | | | | ED 736 E |
| Sbjct | 587 | THPSFPSLERLNQFMIACYMQDG | | | | |
| Query | 735 | EERCVIKFLDFGGYMNVGFNTLRQI +E C IK++D+GG+ V + LRQI | | | GGTWSIEAA +S EAA | |
| Sbjct | 645 | DE-CDIKYVDYGGFSRVQGSLLRQI | | | | |
| Query | 561 | LNKLTKGIVLQAQVAGYNSHNLPEI L +LT+G +LQAQV G + +P + | | | 424 | |
| Sbjct | 704 | LEELTQGQMLQAQVVGRSEEGIPYV | | | 740 | |
| | | | | | | |

A-kinase anchor protein 1, mitochondrial-like [Scleropages formosus]

Sequence ID: gb|KPP61448.1| Length: 323 Number of Matches: 1

Range 1: 6 to 321

| Score | Expect Method | Identities | Positives | Gaps | Frame |
|-------|---------------|------------|-----------|------|-------|
|-------|---------------|------------|-----------|------|-------|

164 bits(415) 5e-41() Compositional matrix adjust. 102/326(31%) 179/326(54%) 16/326(4%) -2

Features:

| Query | 1362 | SICSVQSGDSGKGSSLPRSEATRVKTTYEFLFPISLIGHLYGRKRAFINQIKAKTLASVS | 1183 |
|-------|------|--|------|
| Sbjct | 6 | S C++ +GD S T +E P L+G L G++ +++ +K + A + SGCTLGAGDGSHASRQATHPQTSELIIWEIEVPKHLVGRLIGKQGRYVSFLKQSSGAKIY | 65 |
| Query | 1182 | VGKNPYSGKVRICTIEGTESEIDAALAMIRQRLPAKRYPNFTMQRIHFALPQTIVPLSTE + PY+ + +IC IEGT+ ++D ALA+I K++ + + + P +P++ | 1003 |
| Sbjct | 66 | ISTLPYTQEFQICHIEGTQQQVDKALALIGKKFKDLDLTNLYAPPPLPITLP | 117 |
| Query | 1002 | SL-YNLQLKLIEGINNDVVVSAVLSGSHIFIQhplhpshpslplLQKQLYDSYSTMEAPL SL L L G+ +V+V ++S H F+Q HP++ +L L +Q++ YS P | 826 |
| Sbjct | 118 | SLPMTSWLLLPNGVTVEVIVVNIVSAGHAFVQQHTHPTYHALRSLDQQMFLCYSQPGTPA | 177 |
| Query | 825 | LPS-LELSAVCVIPIND-VWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTD LPS +E+ +C P + W+R Q++ +D I+++D+GGY V +TLRQIR+D | 652 |
| Sbjct | 178 | LPSPVEVGVICAAPAGEGAWWRAQVISFY-KDSGEVEIRYVDYGGYDRVKIDTLRQIRSD | 236 |
| Query | 651 | FMNVPFQSTECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSH-NLPEIFL F+ +PFQ E +L N+ P+ G +S EA L ++T+G+ L AQV Y+S+ LP + L | 481 |
| Sbjct | 237 | FVTLPFQGAEVLLDNLAPLPGADRFSPEATAALEEMTRGVPLLAQVTNYDSNTGLPLVQL | 296 |
| Query | 480 | FASLGPNNVIFINKELVGRKLAKWVE 403 + +G + ++ +N+ L R WV+ | |
| Sbjct | 297 | WNMVG-DELVSVNRTLAERGFGTWVD 321 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Xiphophorus maculatus]

Sequence ID: ref|XP_014327381.1| Length: 825 Number of Matches: 1

Range 1: 504 to 823

| Score | E | xpect Method | Identities | Positives | Gaps F | rame |
|----------|----------|--|-----------------------------|------------------|---------------------------|------|
| 171 bits | (434) 16 | e-40() Compositional matrix adjust. | 108/341(32%) | 189/341(55%) | 26/341(7%) - | 2 |
| Features | s: | | | | | |
| Query | 1410 | SNGNQKRNVDAASPSLSICSVQSGD | | | | |
| Sbjct | 504 | S+ N +VD+ ++SIC Q + SDVNSMDSVDSGC-TMSICENQGNN | S + + STSS | | P L+G L G+ PKHLVGRLIGK | |
| Query | 1230 | RAFINQIKAKTLASVSVGKNPYSGK +++ +K + A + + PY+ | VRICTIEGTESE +IC IEG + + | | LPAKRYPNFTM K++ + + | |
| Sbjct | 555 | GRYVSFLKQNSGAKIYISTLPYTQD | | | = | |
| Query | 1050 | RIHFALPQTIVPLSTESLYNLQLKL + +A P T+ L S L L | | | | |
| Sbjct | 610 | NL-YAPPLTLPSLPITSWLLL | | | | |
| Query | 870 | QKQLYDSYSTMEAPLLPS-LELSAV +Q++ YS P LPS E+ + | | | | |
| Sbjct | 665 | DQQMFLCYSQPGTPALPSPAEMGVI | | | | _ |
| Query | 696 | YMNVGFNTLRQIRTDFMNVPFQSTE Y V +TLRQIR+DF+ +PFQS E | | | | |
| Sbjct | 724 | YDKVKLDTLRÕIRSDFVTLPFÕSAE | | | | |
| Query | 522 | VAGYNSH-NLPEIFLFASLGPNNVI V+ Y+ + LP + L+ +G + VI | | AKWVE 403 WV+ | | |
| Sbjct | 784 | VSNYDDNTGLPLVHLWNLVG-DEVI | | • • • • | | |

PREDICTED: KH domain-containing protein akap-1 [Polistes dominula] Sequence ID: **ref|XP_015175799.1**| Length: 588 Number of Matches: 1 Range 1: 263 to 577

| Score | Е | expect Method | Identities | Positives | Gaps | Frame |
|----------|---------|--|--------------|--------------------------|----------------------|----------------|
| 168 bits | (426) 1 | e-40() Compositional matrix adjust. | 108/320(34%) | 180/320(56%) | 11/320(3%) | -2 |
| Features | s: | | | | | |
| Query | 1344 | SGDSGKGSSLP-RSEATRVKTTYEFI S DSGKG S+ + + YEF- | | RKRAFINQIKA R +F+ I + | | |
| Sbjct | 263 | STDSGKGGSIEGQMKEDGTTYVYEF | | | | · - |
| Query | 1167 | YSGKVRICTIEGTESEIDAALAMIR(S RICTI+G+ + I AL +IR- | | | TIVPLSTESI ++P+ + | YN 991 |
| Sbjct | 323 | ISMNDRICTIQGSNNGICIALDIIR | | | · · · · · | 379 |
| Query | 990 | LQLKLIEGINNDVVVSAVLSGSHIFT OL LIE +NND V V+ + +F- | | | | |
| Sbjct | 380 | RQLTLIEEVNNDASVCYVMKPNRLFI | | | | + SIM 439 |

| Query | 810 | LSAVCVIPIND-VWYRVQIVDTDPEDEERCVIKFLDFGGYMNVGFNTLRQIRTDFMNVPF V PI+D W RV +VD DP + +++ +D GGY ++LR+IRTDF+++PF | 634 |
|-------|-----|---|-----|
| Sbjct | 440 | KGLVYAAPIDDGKWARVCVVDPDPYG-QTTLVRLVDHGGYRTYPNSSLRKIRTDFLSLPF | 498 |
| Query | 633 | QSTECILSNIEPIGGTWSIEAAEILNKLTKGIVLQAQVAGYNSHNLPEIFLFASLGPNNV O+ E L+N++P G W ++ ++ ++ G V AO+A Y + + LF ++ + | 454 |
| Sbjct | 499 | | 557 |
| Query | 453 | IFINKELVGRKLAKWVE 403 I + EL+ R A+ W E | |
| Sbjct | 558 | ISVADELIARGYAEPVSWEE 577 | |

PREDICTED: A-kinase anchor protein 1, mitochondrial [Sarcophilus harrisii] Sequence ID: **ref|XP_003768007.1|** Length: 888 Number of Matches: 1

See 1 more title(s) Range 1: 560 to 882

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|------------|---|--------------|--------------|-------------------------|---------|
| 171 bits | (433) 2e | e-40() Compositional matrix adjust. | 109/333(33%) | 185/333(55%) | 24/333(7%) | -2 |
| Features | S : | | | | | |
| Query | 1359 | ICSVQSGDSGKGSSLPR + S+ S DSG G S P | | | | |
| Sbjct | 560 | VNSMDSVDSGCGLRKTESHPSPQPG | | | | |
| Query | 1206 | AKTLASVSVGKNPYSGKVRICTIEG + A + + PY+ +IC IEG | | | ~ | LP 1030 |
| Sbjct | 620 | QTSGAKIYISTLPYTQNFQICHIEG | | | • • | |
| Query | 1029 | QTIVPLSTESLYNLQLKLIEGINND +P + + L L +G+ + | | | slplLQKQLY +L L +O+Y | |
| Sbjct | 675 | SLTLPSLPMTSWLMLPDGVTVE | | | ~ | |
| Query | 849 | YSTMEAPLLPS-LELSAVCVIP-IN YS P LP+ +E++ +C P ++ | | | LDFGGYMNVG +D+GGY V | FN 676 |
| Sbjct | 732 | YSQPGIPTLPTPVEVAVICAAPGVD | | | | TE 790 |
| Query | 675 | TLRQIRTDFMNVPFQSTECILSNIE LRQIR+DF+ +PFQ E +L N+ | | | VLQAQVAGYN L AOV YN | |
| Sbjct | 791 | ILRÕIRSDFVTLPFÕGAEVLLDNVA | | | | |
| Query | 501 | NLPEIFLFASLGPNNVIFINKELVG LP I L++ +G + + IN+ LV | _ |)3 | | |
| Sbjct | 851 | GLPLIQLWSMIG-DEAVSINRTLVE | | 32 | | |

PREDICTED: KH domain-containing protein C56G2.1 [Microplitis demolitor] Sequence ID: **ref|XP_008550029.1|** Length: 618 Number of Matches: 1

▶ See 1 more title(s) Range 1: 289 to 607

| Score | Ex | spect Method | Identities | Positives | Gaps | Frame |
|-----------|----------|---|---------------------------|--------------------------|-------------------------|---------|
| 168 bits(| (426) 2e | -40() Compositional matrix adjust. | 110/327(34%) | 181/327(55%) | 13/327(3%) | -2 |
| Features | s: | | | | | |
| Query | 1359 | ICSVQSGDSGKGSSL-PRSEATRVKTIS S DSGKG S+ + T K | | | | VS 1183 |
| Sbjct | 289 | IRSEGSTDSGKGGSINGKVSKTNDK | | | | |
| Query | 1182 | VGKNPYSGKVRICTIEGTESEIDAAI + +P +R+C IEG I AI | LAMIRQRLPAKR L +IRQ+ + | | AL-PQTIVPL P+ I+ + | ST 1006 |
| Sbjct | 349 | IDFHPTEENLRLCIIEGLSENITRA | | | | PE 408 |
| Query | 1005 | ESLYNLQLKLIEGINNDVVVSAVLSO +QL+LI+G+NNDV+V +L | | | LYDSYSTMEAT + YST+E+ | |
| Sbjct | 409 | LMQLQLIDGLNNDVLVCHILQI | | | | |
| Query | 825 | LPS-LELSAVCVIPINDVWYRVQIVI +P L + V P D W R + | OTDPEDEERCVI | KFLDFGGYMNV | GFNTLRQIRT | |
| Sbjct | 465 | VPDQLNRGMIVVAPWYDKWVRAFVEI | | | | |
| Query | 648 | MNVPFQSTECILSNIEPIGGTWSIEF + +PFQ+ E L+N++PI G WS EF | | VLQAQVAGYNS + QAQ+ GY | HNLPEIFLI E+F L | |
| Sbjct | 524 | LTLPFQTLEVNLANVKPIAGEWSQE | | | | |
| Query | 474 | SLGPNNVIFINKELVGRKLAKWVEMS +L VI + EL+ R A+ V | SD 394 | | | |
| Sbjct | 581 | TLPKYGVISLADELIARGYAESVSFI | EE 607 | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like [Salmo salar]

Sequence ID: ref|XP_014018688.1| Length: 902 Number of Matches: 1

Range 1: 569 to 900

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|---|-------------------------|--------------|---------------------------------------|--------------|
| 169 bits | (428) 96 | e-40() Compositional matrix adjust. | 110/349(32%) | 193/349(55%) | 26/349(7%) | -2 |
| Features | s: | | | | | |
| Query | 1422 | EVVDSNGNQKRNVDAASPSLSICSV | | | | |
| Sbjct | 569 | E S G+ ++D+ S C++ ETDQSGGSDVNSMDSVDSGCTM | + DSG + GARDSGSPAMAI | | E P L+G EIEVPKHLVG | |
| Query | 1242 | YGRKRAFINQIKAKTLASVSVGKNP | | | | |
| Sbjct | 622 | IGKQGRYVSFLKQSSGAKIYISTLP | | | | |
| Query | 1062 | FTMQRIHFALPQTIVPLSTESLYNL + + +A P +PL+ SL +L | QLKLIEGI L L G+ | NNDVVVSAVLS | GSHIFIQhpl | hp 895 HP |
| Sbjct | 677 | LDLTNL-YAPPSLPLTLPSLPSL | | | | |
| Query | 894 | shpslplLQKQLYDSYSTMEAPLLP; ++ +L L +Q++ YS E P LP; | | | | CV 721 |
| Sbjct | 734 | TYHALRSLDQQMFLCYSQPETPTLP | | | · · · · · · · · · · · · · · · · · · · | VE 792 |
| Query | 720 | IKFLDFGGYMNVGFNTLRQIRTDFM I+++D+GGY V +TLRQIR+DF+ | | | SIEAAEILNK S EA L + | |
| Sbjct | 793 | IRYVDYGGYDRVKIDTLRÕIRSDFV | | | | _ |
| Query | 546 | KGIVLQAQVAGY-NSHNLPEIFLFA +G+ L AQV Y N+ LP + ++ | | | | |
| Sbjct | 853 | RGVALLAQVTNYDNNTGLPLVQIWN | | | | |

PREDICTED: A-kinase anchor protein 1, mitochondrial-like [Nannospalax galili]

Sequence ID: ref|XP_008840942.1| Length: 363 Number of Matches: 1

Range 1: 34 to 357

| Score | Ex | rpect Method | Identities | Positives | Gaps | Frame |
|----------|------------|--|----------------------------|--------------------|--------------------------|--------------|
| 160 bits | (405) 3e | e-39() Compositional matrix adjust. | 108/348(31%) | 190/348(54%) | 36/348(10%) | -2 |
| Features | S : | | | | | |
| Query | 1410 | SNGNQKRNVDAASPSLSICSVQS S+GN +VD+ + S+ +VO+ | | SEATRVKTTYE: +E | | |
| Sbjct | 34 | SDGNSMDSVDSCGLTKPDSLQNVQA | AGSSPKKVDL | | | |
| Query | 1236 | RKRAFINQIKAKTLASVSVGKNPYS | | | RQRLPAKRYPN K++ | IFT 1057 |
| Sbjct | 85 | KQGRYVSFLKQTSGAKIYISTLPYT | | | | ELN 139 |
| Query | 1056 | MQRIHFALPQTIVPLSTES + I+ ALP +P+++ | SLYNLQLKLIEG L L +G | | | hp 895 HP |
| Sbjct | 140 | LTNIYAPPLPSLALPSLPMTS | | | | |
| Query | 894 | shpslplLQKQLYDSYSTMEAPLLE + +L L +Q+Y YS P LE | | | | RCV 721 |
| Sbjct | 192 | TFHALRSLDQQMYLCYSQPGIPTLE | | | | -VE 250 |
| Query | 720 | IKFLDFGGYMNVGFNTLRQIRTDFM I+++D+GGY V + LRQIR+DF+ | NVPFQSTECIL - +PFQ E +L | | WSIEAAEILNK +S EA +++ | |
| Sbjct | 251 | IRYVDYGGYKRVKVDVLRQIRSDFV | | | | · - |
| Query | 546 | KGIVLQAQVAGYNSHNLPEIFLFAS L AQV Y++ LP I L++ | | | | |
| Sbjct | 311 | GNTALLAQVTSYSATGLPLIQLWSV | | | | |