BLAST®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BH2HZF014

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Blast report description

Nucleotide Sequence (1393 letters)

RID <u>B8BH2HZF014</u> (Expires on 02-06 12:07 pm)

Query ID lcl|Query_51521

Description None

Molecule type nucleic acid

Query Length 1393

Database Name nr

Description All non-redundant GenBank CDS

translations + PDB + SwissProt + PIR + PRF

excluding environmental samples from

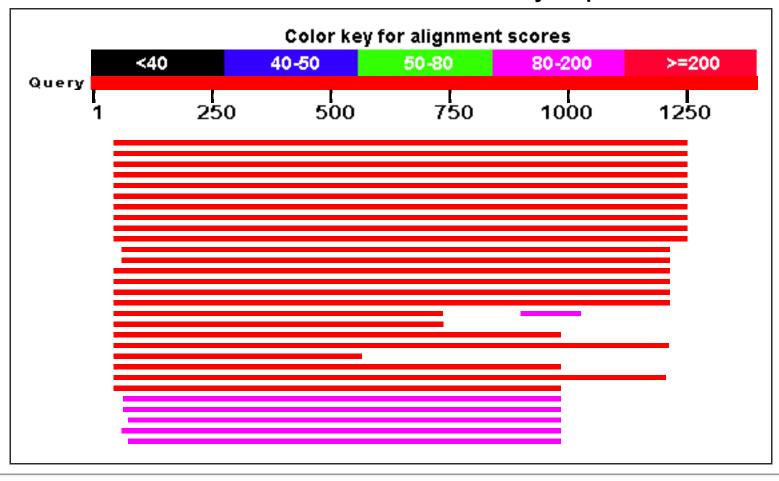
WGS projects

Program BLASTX 2.3.1+

□ Graphic Summary

No putative conserved domains have been detected

Distribution of 30 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 |
|------------------------------------------------------------------------------------------|-----------|-------------|----------------|------------|-------|----------------|
| LD21920p [Drosophila melanogaster] | 548 | 548 | 86% | 3e-178 | 100% | ACD81851.1 |
| LP03212p [Drosophila melanogaster] | 557 | 557 | 86% | 1e-175 | 100% | ACH95308.1 |
| domino, isoform A [Drosophila melanogaster] | 556 | 556 | 86% | 1e-174 | 100% | NP_524833.2 |
| GD11590 [Drosophila simulans] | 534 | 534 | 86% | 2e-174 | 98% | XP_002082475.1 |
| domino, isoform D [Drosophila melanogaster] | 556 | 556 | 86% | 2e-174 | 100% | NP_726065.1 |
| domino, isoform G [Drosophila melanogaster] | 555 | 555 | 86% | 3e-174 | 100% | NP_001286676.1 |
| helicase DOMINO A [Drosophila melanogaster] | 555 | 555 | 86% | 4e-174 | 99% | AAF82185.1 |
| domino, isoform B [Drosophila yakuba] | 521 | 521 | 86% | 3e-162 | 97% | XP_015051886.1 |
| uncharacterized protein Dere_GG22110, isoform A [Drosophila erecta] | 521 | 521 | 86% | 4e-162 | 97% | XP_001975047.1 |
| domino, isoform A [Drosophila yakuba] | 521 | 521 | 86% | 4e-162 | 97% | XP_002091544.2 |
| uncharacterized protein Dana_GF12812, isoform A [Drosophila ananassae] | 436 | 436 | 82% | 2e-132 | 88% | XP_001959323.1 |
| uncharacterized protein Dana_GF12812, isoform B [Drosophila ananassae] | 435 | 435 | 82% | 3e-132 | 88% | XP_014763429.1 |
| uncharacterized protein Dpse_GA24314, isoform B [Drosophila pseudoobscura pseudoobscura] | 421 | 421 | 83% | 4e-127 | 83% | XP_002138575.2 |
| uncharacterized protein Dpse_GA24314, isoform E [Drosophila pseudoobscura pseudoobscura] | 420 | 420 | 83% | 7e-127 | 83% | XP_004444248.2 |
| uncharacterized protein Dpse_GA24314, isoform D [Drosophila pseudoobscura pseudoobscura] | 419 | 419 | 83% | 9e-127 | 83% | XP_015040038.1 |
| GL16841 [Drosophila persimilis] | 416 | 416 | 83% | 4e-126 | 84% | XP_002018288.1 |
| uncharacterized protein Dsimw501_GD11590 [Drosophila simulans] | 382 | 382 | 49% | 2e-122 | 99% | KMY95527.1 |
| GH12111p [Drosophila melanogaster] | 382 | 382 | 49% | 2e-122 | 100% | AAM48336.1 |
| uncharacterized protein Dmoj_GI19071 [Drosophila mojavensis] | 314 | 314 | 67% | 4e-90 | 68% | XP_002005439.2 |
| uncharacterized protein Dwil_GK20897 [Drosophila willistoni] | 312 | 312 | 83% | 1e-89 | 68% | XP_002061395.2 |
| similar to Drosophila melanogaster domino [Drosophila yakuba] | 270 | 270 | 37% | 1e-84 | 97% | AAR09977.1 |
| LOW QUALITY PROTEIN: uncharacterized protein Dvir_GJ20044 [Drosophila virilis] | 296 | 296 | 67% | 6e-84 | 65% | XP_002050736.2 |
| dom [Drosophila busckii] | 276 | 276 | 82% | 3e-77 | 62% | ALC41615.1 |
| GH20710 [Drosophila grimshawi] | 267 | 267 | 67% | 3e-74 | 62% | XP_001986118.1 |
| PREDICTED: helicase domino isoform X1 [Ceratitis capitata] | 118 | 118 | 65% | 2e-24 | 49% | XP_004522557.1 |
| PREDICTED: helicase domino isoform | | | | | | |

| X2 [Ceratitis capitata] | 118 | 118 | 65% | 2e-24 | 49% | XP_004522560.1 |
|--------------------------------------------------|------|------|-----|-------|-----|----------------|
| PREDICTED: helicase domino [Musca domestica] | 110 | 110 | 64% | 5e-22 | 48% | XP_011294691.1 |
| Helicase domino [Lucilia cuprina] | 109 | 109 | 65% | 6e-22 | 47% | KNC26706.1 |
| PREDICTED: helicase domino [Stomoxys calcitrans] | 104 | 104 | 64% | 4e-20 | 45% | XP_013100224.1 |
| GM15831 [Drosophila sechellia] | 86.3 | 86.3 | 9% | 3e-14 | 86% | XP_002039753.1 |

■ <u>Alignments</u>

LD21920p [Drosophila melanogaster]

Sequence ID: gb|ACD81851.1| Length: 1350 Number of Matches: 1

Range 1: 575 to 974

| Score | E | Expect | Method | | | Identitie | s | Positives | 3 | Gaps | Fra | me |
|----------|----------|----------|----------------------|----------|--------------|-----------|---------|-----------|----------|----------|--------------|------|
| 548 bits | (1411) 3 | Be-178() | Composit | ional ma | trix adjust. | 400/400 | (100%) | 400/400(| 100%) | 0/400(0% | 6) -1 | |
| Features | s: | | | | | | | | | | | |
| Query | 1246 | | qqlqiqhL | | | | | | | | | 1067 |
| Sbjct | 575 | | QQLQIQHL QQLQIQHL | | | | | | | | | 634 |
| Query | 1066 | tagq | lqqlaqqs | avasgg | qssvsvvl | tTPVQTI | LPSVVQE | POIGSGA | QIVSI | SSQTLPV | NSS | 887 |
| Sbjct | 635 | | LQQLAQQS LQQLAQQS | | | | | | | | | 694 |
| Query | 886 | | SIVOTOSL | | | | | | | | | 707 |
| Sbjct | 695 | | SIVQTQSL SIVQTQSL | | | | | | | | | 754 |
| Query | 706 | | TLQQRTTA | | | | | | | | | 527 |
| Sbjct | 755 | | TLQQRTTA TLQQRTTA | | | | | | | | | 814 |
| Query | 526 | | QGGKTTVI | | | | | | | | | 347 |
| Sbjct | 815 | | QGGKTTVI QGGKTTVI | | | | | | | | | 874 |
| Query | 346 | | ASNMATHV | | | | | | | | | 167 |
| Sbjct | 875 | | ASNMATHV ASNMATHV | | | | | | | | | 934 |
| Query | 166 | | Sadgtttt | | | | | | | | | |
| Sbjct | 935 | | SADGTTTT SADGTTTT | | | | | | | | | |

LP03212p [Drosophila melanogaster]

Expect Method

Sequence ID: gb|ACH95308.1| Length: 2642 Number of Matches: 1

Range 1: 1882 to 2281

Score

| | | · | | | | | | | | | |
|----------|-----------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------|------|--|--|--|--|--|--|--|--|
| 557 bits | 557 bits(1436) 1e-175() Compositional matrix adjust. 400/400(100%) 400/400(100%) 0/400(0%) -1 | | | | | | | | | | |
| Features | 3 : | | | | | | | | | | |
| Query | 1246 | GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl | 1067 | | | | | | | | |
| Sbjct | 1882 | GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL | 1941 | | | | | | | | |
| Query | 1066 | tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS | 887 | | | | | | | | |
| Sbjct | 1942 | TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS | 2001 | | | | | | | | |
| Query | 886 | PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST | 707 | | | | | | | | |
| Sbjct | 2002 | PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST | 2061 | | | | | | | | |
| Query | 706 | AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV | 527 | | | | | | | | |
| Sbjct | 2062 | AAGNTLQQRTTAGGQSIVSMPNLGQGASFSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV | 2121 | | | | | | | | |
| Query | 526 | SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG | 347 | | | | | | | | |
| Sbjct | 2122 | SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG | 2181 | | | | | | | | |

Identities

Positives

Gaps

Frame

| Query Sbict | 346 2182 | TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMH TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMH TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMH | GÕARTÕFIKÕMAAGKÕÕLÕ | 167 2241 |
|----------------|-------------|-------------------------------------------------------------------------------------------------------------------------------------|---------------------|-------------|
| Query | | RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF | 47 | |
| Sbjct | 2242 | RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF | 2281 | |

domino, isoform A [Drosophila melanogaster]

Sequence ID: ref|NP_524833.2| Length: 3198 Number of Matches: 1

▶ See 2 more title(s) Range 1: 2423 to 2822

| Score | | Expect | Method | | Identities | Positives | Gaps | Frame |
|----------|--------|----------|--------------------------------|----------------|--------------|-----------------|-------------|--------------|
| 556 bits | (1434) | 1e-174() |) Compositional r | natrix adjust. | 400/400(100% | b) 400/400(100% | %) 0/400(0% | %) -1 |
| Features | s: | | | | | | | |
| Query | 1246 | | qqlqiqhLTSSN | | | | | |
| Sbjct | 2423 | | QQLQIQHLTSSN QQLQIQHLTSSN | | | | | |
| Query | 1066 | | lqqlaqqsavas | | | | | |
| Sbjct | 2483 | | LÕÕLAÕÕSAVAS(LÕÕLAÕÕSAVAS(| | | | | |
| Query | 886 | POLGS | SIVQTQSLPQvvs SIVQTQSLPQVVs | svstlptvgt | vlttTANQPQQ | QHQttavttlnt | TMLRGORI | IVST 707 |
| Sbjct | 2543 | | SIVQTQSLPQVVS SIVQTQSLPQVVS | | | | | |
| Query | 706 | | TLOORTTAGGOS | | | | | |
| Sbjct | 2603 | | TLQQRTTAGGQS: TLQQRTTAGGQS: | | | | | |
| Query | 526 | | QGGKTTVIPVTQ(QGGKTTVIPVTQ(| | | | | |
| Sbjct | 2663 | | QGGKTTVIPVIQ(QGGKTTVIPVTQ(| | | | | |
| Query | 346 | | ASNMATHVTSOKV ASNMATHVTSOKV | | | | | |
| Sbjct | 2723 | ~ | ASNMATHVTSQK ASNMATHVTSQK | | ~ | ~ ~ ~ | ~ - | |
| Query | 166 | | SadgtttttaagI | | | | | |
| Sbjct | 2783 | | SADGTTTTTAAGI SADGTTTTTAAGI | | | | | |

GD11590 [Drosophila simulans]

Sequence ID: ref|XP_002082475.1| Length: 1178 Number of Matches: 1

▶ See 1 more title(s) Range 1: 403 to 802

| Score | | Expect | Method | | Identities | Positives | Gaps | Frame |
|-----------|-------|----------|------------------------------|----------------|--------------|--------------|-----------|-------|
| 534 bits(| 1375) | 2e-174() | Compositional | matrix adjust. | 391/400(98%) | 392/400(98%) | 0/400(0%) | -1 |
| Features | : | | | | | | | |
| Query | 1246 | | qlqiqhLTSSNV | | | | | |
| Sbjct | 403 | | QLQIQHLTSSNV QLQIQHLTSSNV | | | | | |
| Query | 1066 | | qqlaqqsavasç QQLAQQSA ASG | | | | | |
| Sbjct | 463 | | QQLAQQSA ASG QQLAQQSAAASG | | | | | |
| Query | 886 | | IVOTOSLPOVVS | | | | | |
| Sbjct | 523 | | IVQTQSLPQVVS IVQTQSLPQVVS | | | | | |
| Query | 706 | | LQQRTTAGGQSI LQQRTTAGGQSI | | | | | |
| Sbjct | 583 | | LQQRTTAGGQS1 LQQRTTAGGQS1 | ~ | ~ ~ ~ | ~ | ~ | |
| Query | 526 | | GGKTTVIPVTQQ | | | | | |
| Sbjct | 643 | | GGKTTVIPVTQÇ GGKTTVIPVTQÇ | | | | | |
| Query | 346 | | SNMATHVTSOKV | | | | | |
| Sbjct | 703 | | SNMATHVTSQKV SNMATHVTSQKV | | | | | |

Query 166 RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 47 RQVVSADGTTTT AGDMLLVKRHNILAAQKAQQASGALF Sbjct 763 RQVVSADGTTTTKGAGDMLLVKRHNILAAQKAQQASGALF 802

domino, isoform D [Drosophila melanogaster]

Sequence ID: ref|NP_726065.1| Length: 3183 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2423 to 2822

| Score | | Expect | Method | | Identities | Positives | Gaps | Frame |
|----------|------------|----------|------------------------------|----------------|--------------|----------------|-------------|---------|
| 556 bits | (1433) 2 | 2e-174() | Compositional | matrix adjust. | 400/400(100% |) 400/400(100% | b) 0/400(0% | o) -1 |
| Features | S : | | | | | | | |
| Query | 1246 | | qqlqiqhLTSSN | | | | | |
| Sbjct | 2423 | | QQLQIQHLTSSN QQLQIQHLTSSN | | | | | |
| Query | 1066 | tagq | lqqlaqqsavas | gggssvsvvl | tTPVQTLPSVV(| OPOIGSGAQIVS | SISSOTLPV | NSS 887 |
| Sbjct | 2483 | | LÕÕLAÕÕSAVAS LÕÕLAÕÕSAVAS | | | | | |
| Query | 886 | | SIVQTQSLPQvv SIVQTQSLPQVV | | | | | |
| Sbjct | 2543 | | SIVOTOSLPOVV SIVOTOSLPOVV | | | | | |
| Query | 706 | | TLQQRTTAGGQS TLQQRTTAGGQS | | | | | |
| Sbjct | 2603 | | TLQQRTTAGGQS TLQQRTTAGGQS | | | | | |
| Query | 526 | | QGGKTTVIPVTQ | | | | | |
| Sbjct | 2663 | | QGGKTTVIPVTQ QGGKTTVIPVTQ | | | | | |
| Query | 346 | | ASNMATHVTSOK | | | | | |
| Sbjct | 2723 | | ASNMATHVTSOK ASNMATHVTSOK | | | | | |
| Query | 166 | | Sadgtttttaag | | | | | |
| Sbjct | 2783 | | SADGTTTTTAAG SADGTTTTTAAG | | | | | |

domino, isoform G [Drosophila melanogaster]

Sequence ID: ref|NP_001286676.1| Length: 3233 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2458 to 2857

| Score | E | Expect | Method | Identities | Positives | Gaps | Frame |
|-----------|------------|---------|------------------------------------------|----------------------|----------------|----------------|--------|
| 555 bits(| 1431) 3 | e-174() | Compositional matrix a | adjust. 400/400(100% |) 400/400(100% | %) 0/400(0%) - | -1 |
| Features | : : | | | | | | |
| Query | 1246 | | qqlqiqhLTSSNVSPGQQ | | | | |
| Sbjct | 2458 | | QÕLÕIÕHLTSSNVSPGQ(QQLÕIÕHLTSSNVSPGQ(| | | | |
| Query | 1066 | tagql | Lqqlaqqsavasggqss | vsvvltTPVQTLPSVV | OPOIGSGAOIVS | SISSOTLPVNS | SS 887 |
| Sbjct | 2518 | | LÕÕLAÕÕSAVASÕÕÕSS\ LQQLAÕQSAVASGGQSS\ | | | | |
| Query | 886 | | SIVOTOSLPOVVSVStl | | | | |
| Sbjct | 2578 | | SIVQTQSLPQVVSVSTLI SIVQTQSLPQVVSVSTLI | | | | |
| Query | 706 | | rloorttaggosivsmpm rloorttaggosivsmpm | | | | |
| Sbjct | 2638 | | TLQQRTTAGGQSIVSMP1 TLQQRTTAGGQSIVSMP1 | | | | |
| Query | 526 | | QGGKTTVIPVTQQSGGAF QGGKTTVIPVTQQSGGAF | | | | |
| Sbjct | 2698 | | QGGKTTVIPVTQQSGGAF QGGKTTVIPVTQQSGGAF | | | | |
| Query | 346 | | ASNMATHVTSQKVAVSGN ASNMATHVTSQKVAVSGN | | | | |
| Sbjct | 2758 | | ASNMATHVTSQKVAVSGN ASNMATHVTSQKVAVSGN | | | | |
| Query | 166 | | SadgtttttaagDMLLV | | | | |
| Sbjct | 2818 | | SADGTTTTTAAGDMLLVI SADGTTTTTAAGDMLLVI | | | | |

helicase DOMINO A [Drosophila melanogaster]

Sequence ID: **gb|AAF82185.1|** Length: 3201 Number of Matches: 1 Range 1: 2426 to 2825

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|----------|----------|---------------------------------------------------|--------------|---------------|-----------|-------|
| 555 bits | (1430) 4 | 4e-174() | Compositional matrix adjust. | 399/400(99%) | 400/400(100%) | 0/400(0%) | -1 |
| Features | s: | | | | | | |
| Query | 1246 | | qqlqiqhLTSSNVSPGQQTAILI QLQIQHLTSSNVSPGQQTAILI | | | | |
| Sbjct | 2426 | | QLQIQHLTSSNVSPGQQTAILI QLQIQHLTSSNVSPGQQTAILI | | | | |
| Query | 1066 | | .qqlaqqsavasggqssvsvvlt QQLAQQSAVASGGQSSVSVVLT | | | | |
| Sbjct | 2486 | | QQLAQQSAVASGGQSSVSVVL1 | | | | |
| Query | 886 | | SIVQTQSLPQvvsvstlptvgtv | | | | |
| Sbjct | 2546 | | IVQTQSLPQVVSVSTLPTVGT\ IVQTQSLPQVVSVSTLPTVGT\ | | | | |
| Query | 706 | | LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQGA | | | | |
| Sbjct | 2606 | | LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQGA | | | | |
| Query | 526 | | GGKTTVIPVTQQSGGAHIQLYF GGKTTVIPVTQQSGGAHIQLYF | | | | |
| Sbjct | 2666 | | GGKTTVIPVTQQSGGAHIQLYF | | | | |
| Query | 346 | ~ | SNMATHVTSQKVAVSGMPGTST | ~ | ~ ~ ~ | ~ ~~ | ~ |
| Sbjct | 2726 | | SNMATHVTSQKVAVSGMPGTS1 SNMATHVTSQKVAVSGMPGTS1 | | | | |
| Query | 166 | | SadgtttttaagDMLLVKRHNII | | | | |
| Sbjct | 2786 | | ADGTTTTTAAGDMLLVKRHNII ADGTTTTTAAGDMLLVKRHNII | | | | |
| | | | | | | | |

domino, isoform B [Drosophila yakuba]

Sequence ID: ref|XP_015051886.1| Length: 3195 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2421 to 2820

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|------------|------|----------|--------------------------------------------------|--------------|--------------|-----------------------|--------|
| 521 bits(1 | 341) | 3e-162() | Compositional matrix adjust. | 387/400(97%) | 391/400(97%) | 0/400(0%) | -1 |
| Features: | | | | | | | |
| Query | 1246 | | qlqiqhLTSSNVSPGQQTAILL | | | | |
| Sbjct : | 2421 | | ÓLÓIÓHLTSSNVSPGQQTAILL ÓLÓIÓHLTSSNVSPGQQTAILL | | | | |
| Query | 1066 | tagql | qqlaqqsavasggqssvsvvlt OOLAOOSA ASGGOSSVSVVLT | TPVQTLPSVVQI | POIGSGAQIVSI | ISSOTLPVN | SS 887 |
| Sbjct : | 2481 | | QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT | | | | |
| Query | 886 | POLGS | IVQTQSLPQvvsvstlptvgtv IVQTQSLPQVVSVSTLPTVGTV | lttTANQPQQQI | HQttavttlnt | rmlrgoriv Mirgoriv | ST 707 |
| Sbjct : | 2541 | | IVQTQSLPQVVSVSTLPTVGTV IVQTQSLPQVVSVSTLPTVGTV | | | | |
| Query | 706 | | LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQG | | | | |
| Sbjct | 2601 | | LQQRTTAGGQSIVSMPNLGQGV | | | | |
| Query | 526 | | GGKTTVIPVTQQSGGAHIQLYR GGKTTVIP TQQSGGAHIQLYR | | | | |
| Sbjct | 2661 | | GGKTTVIP TOOSGGAHIODIK GGKTTVIPGTÕÕSGGAHIÕLYR | | | | |
| Query | 346 | | SNMATHVTSQKVAVSGMPGTST SNM THVTSQKVAVSGMPGTS+ | | | | |
| Sbjct : | 2721 | | SNMGTHVTSQKVAVSGMPGTSS | | | | |
| Query | 166 | | adgtttttaagDMLLVKRHNIL ADGTTTTT AGDMLLVKRHNIL | | | | |
| Sbjct | 2781 | | ADGTTTTTGAGDMLLVKRHNIL | | | | |

Sequence ID: ref|XP_001975047.1| Length: 3193 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2420 to 2819

| Score | | Expect | Method | Identities | Positives | Gaps F | rame |
|----------|------------|----------|----------------------------------------------------|--------------|--------------|-------------|------|
| 521 bits | (1341) | 4e-162() | Compositional matrix adjust. | 387/400(97%) | 390/400(97%) | 0/400(0%) - | 1 |
| Features | S : | | | | | | |
| Query | 1246 | | qqqiqhLTSSNVSPGQQTAILI QLQIQHLTSSNVSPGQQTAILI | | | | |
| Sbjct | 2420 | | QLQIQHLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL | | | | |
| Query | 1066 | | .qqlaqqsavasggqssvsvvlt QQLAQQSA ASGGQSSVSVVLT | | | | |
| Sbjct | 2480 | | QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT | | | | |
| Query | 886 | | IVQTQSLPQvvsvstlptvgtv | | | | |
| Sbjct | 2540 | | IVQTQSLPQVVSVSTLPTVGTV IVQTQSLPQVVSVSTLPTVGTV | | | | |
| Query | 706 | | LOORTTAGGOSIVSMPNLGOGA | | | | |
| Sbjct | 2600 | | 'LÖÖRTTAGGÖSIVSMPNLGÖG 'LQORTTAGGOSIVSMPNLGOGV | | | | |
| Query | 526 | | GGKTTVIPVTQQSGGAHIQLYR | | | | |
| Sbjct | 2660 | | GGKTTVIP TQQSGGAHIQLYR GGKTTVIPGTQQSGGAHIQLYR | | | | |
| Query | 346 | | SNMATHVTSQKVAVSGMPGTST | | | | |
| Sbjct | 2720 | | .S+M THVTSQKVAVSGMPGTST .SSMGTHVTSQKVAVSGMPGTST | | | | |
| Query | 166 | | adgtttttaagDMLLVKRHNII | | | | |
| Sbjct | 2780 | | ADĞTTTTT AĞDMLLVKRHNII ADGTTTTTGAGDMLLVKRHNII | | | | |
| | | | | | | | |

domino, isoform A [Drosophila yakuba]

Sequence ID: ref|XP_002091544.2| Length: 3180 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2421 to 2820

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|-----------|--------|----------|-------------------------------------------------|--------------|--------------|-------------|-------|
| 521 bits(| (1341) | 4e-162() | Compositional matrix adjust | 387/400(97%) | 391/400(97%) | 0/400(0%) - | 1 |
| Features | S: | | | | | | |
| Query | 1246 | | qlqiqhLTSSNVSPGQQTAIL | | | | |
| Sbjct | 2421 | | ÕLÕIÕHLTSSNVSPGQQTAIL QLQIQHLTSSNVSPGQQTAIL | | | | |
| Query | 1066 | | qqlaqqsavasggqssvsvvl QQLAQQSA ASGGQSSVSVVL | | | | |
| Sbjct | 2481 | | QQLAQQSAAASGGQSSVSVVL | | | | |
| Query | 886 | | IVQTQSLPQvvsvstlptvgt IVQTQSLPQVVSVSTLPTVGT | | | | |
| Sbjct | 2541 | | IVQTQSLPQVVSVSTLPTVGT | | | | |
| Query | 706 | | LQQRTTAGGQSIVSMPNLGQG. LQQRTTAGGQSIVSMPNLGQG | | | | |
| Sbjct | 2601 | | LÕÕRTTAGGÕSIVSMPNLGÕG | | | | |
| Query | 526 | | GGKTTVIPVTQQSGGAHIQLY GGKTTVIP TQQSGGAHIQLY | | | | |
| Sbjct | 2661 | | GGKTTVIPGTQQSGGAHIQLY: | | | | |
| Query | 346 | | SNMATHVTSQKVAVSGMPGTS SNM THVTSQKVAVSGMPGTS | | | | |
| Sbjct | 2721 | | SNMGTHVTSQKVAVSGMPGTS | | | | |
| Query | 166 | | adgtttttaagDMLLVKRHNI ADGTTTTT AGDMLLVKRHNI | | | | |
| Sbjct | 2781 | | ADGTTTTTGAGDMLLVKRHNI | | | | |

uncharacterized protein Dana_GF12812, isoform A [Drosophila ananassae] Sequence ID: **ref|XP_001959323.1**| Length: 3199 Number of Matches: 1

See 1 more title(s)

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|--------|----------|--------------------------------------------------|----------------------------|--------------|------------------------|-------|
| 436 bits | (1120) | 2e-132() | Compositional matrix adjust. | 337/385(88%) | 350/385(90%) | 7/385(1%) | -1 |
| Features | s: | | | | | | |
| Query | 1210 | | SPGQQTAILLHQPQQQLRTHPG SPGQQTAILLHQPQQQLRTHPG | | | | |
| Sbjct | 2425 | | SPGQQTAILLHQPQQQLRTHPG | | | | |
| Query | 1030 | | gqssvsvvltTPVQTLPSVVQP GQSSVSVVLTTPVQ+LP+VVQP | | | | |
| Sbjct | 2485 | | GQSSVSVVLTTPVQSLPAVVQP | | | | |
| Query | 853 | LPQVV | svstlptvgtvlttTANQPQQQ SVSTLPTVG+VLTTTA QQ | HQttavttlnt' OTT VTTLNT | | | |
| Sbjct | 2545 | | SVSTLPTVGSVLTTTASQQ | | | | |
| Query | 673 | | IVSMPNLGQGASPSQFQTQLRL IVSMPNLGQG + QFQ QLRL | | | | |
| Sbjct | 2602 | | IVSMPNLGQGVN-QQFQAQLRL | | | | |
| Query | 493 | IPVTQ | QSGGAHIQLYRQRSLKVLQTTT Q GGAHIQLYRQRSLKVLQTTT | 'QAVPsgsagate 'OA G+A T | | GGTIIQASN GGTIIÕASN | |
| Sbjct | 2661 | | Q GGAHIQLYRQRSLKVLQTTT | | ~ | ~ | |
| Query | 319 | | QKVAVSGMPGTSTTVQAGNVVS OKVAVSG+PG+STTVOAGNVVS | | | | |
| Sbjct | 2721 | | QKVAVSGIPGSSTTVQAGNVVS | | | | |
| Query | 139 | | agDMLLVKRHNILAAQKAQQ AGDMLLVKRHNILAAQKAQQ | 65 | | | |
| Sbjct | 2781 | | AGDMLLVKRHNILAAQKAQQ | 2805 | | | |
| | | | | | | | |

uncharacterized protein Dana_GF12812, isoform B [Drosophila ananassae] Sequence ID: **ref|XP_014763429.1|** Length: 3184 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2425 to 2805

| Score | E | Expect | Method | | lde | entities | Positive | s | Gaps | Frai | me |
|----------|----------|----------|--------------------------|--------------------------|---------|------------------------|----------|-------|--------------------|--------------|------|
| 435 bits | (1119) 3 | Be-132() | Composition | nal matrix adju | ust. 33 | 7/385(88%) | 350/385 | (90%) | 7/385(19 | %) -1 | |
| Features | s: | | | | | | | | | | |
| Query | 1210 | | | LHQPQQQLRT | | | | | | | 1031 |
| Sbjct | 2425 | | | LHQPQQQLRT LHQPQQQLRT | | | | | | | 2484 |
| Query | 1030 | | | tTPVQTLPSV | | | | | | | 854 |
| Sbjct | 2485 | | | TTPVÕSLPAV | | | | | | | 2544 |
| Query | 853 | | vsvstlptvg VSVSTLPTVG | tvlttTANQP | | ttavttlnt IT VTTLNT | | | | | 674 |
| Sbjct | 2545 | | | SVLTTTA | | | | | | | 2601 |
| Query | 673 | | | GASPSQFQTQ G + QFQ Q | | | | | | | 494 |
| Sbjct | 2602 | | | GVN-QÕFÕAÕ | | | | | | | 2660 |
| Query | 493 | | | YRQRSLKVLÇ YRORSLKVLÇ | | | | | GGTIIQA GGTIIOA | | 320 |
| Sbjct | 2661 | | | YRÕRSLKVLÕ | | | | | | | 2720 |
| Query | 319 | | | GTSTTVQAGN G+STTVQAGN | | | | | | | 140 |
| Sbjct | 2721 | | | GSSTTVQAGN | | | | | | | 2780 |
| Query | 139 | | | HNILAAQKAQ HNILAAQKAQ | | | | | | | |
| Sbjct | 2781 | | | HNILAAÕKAÕ | | 05 | | | | | |

uncharacterized protein Dpse_GA24314, isoform B [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref[XP_002138575.2**] Length: 3270 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2505 to 2890

| ocoic Expect method identities i ositives oups i fame | Score | Expect | Method | Identities | Positives | Gaps | Frame |
|-------------------------------------------------------|-------|--------|--------|------------|-----------|------|-------|
|-------------------------------------------------------|-------|--------|--------|------------|-----------|------|-------|

421 bits(1081) 4e-127() Compositional matrix adjust. 324/390(83%) 343/390(87%) 6/390(1%) -1

Features:

| Query | 1210 | TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs | 1031 |
|-------|------|------------------------------------------------------------------------------------------------------------------------------|------|
| Sbjct | 2505 | TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS | 2564 |
| Query | 1030 | avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+ | 854 |
| Sbjct | 2565 | AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT | 2624 |
| Query | 853 | LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT LPQVVSVSTLPTV + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT | 677 |
| Sbjct | 2625 | LPQVVSVSTLPTVGSVLTTTASQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT | 2684 |
| Query | 676 | TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT | 497 |
| Sbjct | 2685 | NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT | 2743 |
| Query | 496 | VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT VIP TQQ GGAHIQLYRQRSLKVLQT V G+AG ATANLVQ GTIIQA NM T | 317 |
| Sbjct | 2744 | VIPGTÕÕPGGAHIÕLYRÕRSLKVLÕTOPATV-GGTAGGGVATANLVÕTAGTIIÕAGNMPT | 2802 |
| Query | 316 | HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt HVTSQKVAVSGMPG VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T | 137 |
| Sbjct | 2803 | HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST | 2860 |
| Query | 136 | tttaagDMLLVKRHNILAAQKAQQASGALF 47 T+ AAGDMLLVKRHNILA QKAQQA+GALF | |
| Sbjct | 2861 | TSAAAGDMLLVKRHNILATQKAQQATGALF 2890 | |

uncharacterized protein Dpse_GA24314, isoform E [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_004444248.2|** Length: 3290 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2540 to 2925

| Score | | Expect | Method | | Identities | Positives | Gaps | Frame |
|----------|------------|----------|--------------|------------------------------|--------------------------------|--------------|------------------------|--------|
| 420 bits | (1079) 7 | 7e-127() | Compositiona | ıl matrix adjust. | 324/390(83%) | 343/390(87%) | 6/390(1%) | -1 |
| Features | S : | | | | | | | |
| Query | 1210 | | | | GOGGOSNTOOLV GOG OS TOOLV | | | |
| Sbjct | 2540 | | | | GOG OS TOOLV. GOGOOSATÕÕLV. | | | |
| Query | 1030 | avasg | gqssvsvvlt | TPVQTLPSVVQF | POIGSGAQIVSI O GS AQIVSI | SSOT-LPVNSS | POLGSIVOT | QS 854 |
| Sbjct | 2600 | | | | QSGSAAQIVSI | | | |
| Query | 853 | | svstlptv-g | | QQHQttavttln QQ QTTAVTTLN | | | |
| Sbjct | 2660 | | | | QQQTTAVTTLN | | | |
| Query | 676 | | | | RLAAVPTSPATQ RLAAVPTSPATQ | | | |
| Sbjct | 2720 | | | | RLAAVPTSPATÕ | | | |
| Query | 496 | | | | TQAVPsgsaga V G+AG | | GTIIQASNM GTIIÕA NM | |
| Sbjct | 2779 | | | | PATV-GGTAGG | | | |
| Query | 316 | | | | SVQMHGQARTQF SVQMHGQARTQF | | | |
| Sbjct | 2838 | | | | SVÕMHGÕARTÕF | | | |
| Query | 136 | | | ILAAQKAQQASG ILA QKAQQA+G | | | | |
| Sbjct | 2896 | | | ILATOKAQQATG | | | | |

uncharacterized protein Dpse_GA24314, isoform D [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref[XP_015040038.1]** Length: 3305 Number of Matches: 1

• See 3 more title(s) Range 1: 2540 to 2925

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|----------------|----------|------------------------------|--------------|--------------|-----------|--------|
| 419 bits(1078) | 9e-127() | Compositional matrix adjust. | 324/390(83%) | 343/390(87%) | 6/390(1%) | -1 |

419 bits(1078) 9e-127() Compositional matrix adjust. 324/390(83%) 343/390(87%) 6/390(1%) -1

Features:

| Query | 1210 | TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs | 1031 |
|-------|------|------------------------------------------------------------------------------------------------------------------------------|------|
| Sbjct | 2540 | TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS | 2599 |
| Query | 1030 | avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS | 854 |
| Sbjct | 2600 | A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+ AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT | 2659 |
| Query | 853 | LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT LPQVVSVSTLPTV + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT | 677 |
| Sbjct | 2660 | LPQVVSVSTLPTVGSVLTTTASQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT | 2719 |
| Query | 676 | TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT | 497 |
| Sbjct | 2720 | NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT | 2778 |
| Query | 496 | VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT | 317 |
| Sbjct | 2779 | VIP TQQ GGAHIQLYRQRSLKVLQT V G+AG ATANLVQ GTIIQA NM T VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGGVATANLVQTAGTIIQAGNMPT | 2837 |
| Query | 316 | HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt | 137 |
| Sbjct | 2838 | HVTSQKVAVSGMPG VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST | 2895 |
| Query | 136 | tttaagDMLLVKRHNILAAQKAQQASGALF 47 | |
| Sbjct | 2896 | T+ AAGDMLLVKRHNILA QKAQQA+GALF TSAAAGDMLLVKRHNILATQKAQQATGALF 2925 | |

GL16841 [Drosophila persimilis]

Sequence ID: ref|XP_002018288.1| Length: 2139 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1374 to 1757

| Score | | Expect | Method | | Identities | Positives | Gaps | Frame |
|-----------|------------|----------|------------------------------|----------------|------------------------------|----------------------------|------------------------|---------|
| 416 bits(| (1068) | 4e-126() | Compositional | matrix adjust. | 328/390(84%) | 347/390(88%) | 8/390(2%) | -1 |
| Features | 3 : | | | | | | | |
| Query | 1210 | | | | GOGGOSNTOOLV | | | |
| Sbjct | 1374 | | | | QG QS TQQLV /QGQQSATQQLV | | | |
| Query | 1030 | | | | POIGSGAQIVSI O GS AQIVSI | | | |
| Sbjct | 1434 | | | | TQSGSAAQIVSI | | | |
| Query | 853 | | | | QHQttavttlnt Q QTTAVTTLNT | | | |
| Sbjct | 1494 | | | | QQTTAVTTLNT QQQTTAVTTLNT | | | |
| Query | 673 | | | | LAAVPTSPATQT LAAVPTSPATQ | | | |
| Sbjct | 1553 | AAGQS | IVSVPNLGQG (| SPAQFQTQLRI | LAAVPTSPATQ- | TQLVTTKGIFV TQLVTTKGIPV | TALQQGGKI | TV 1611 |
| Query | 493 | | QSGGAHIQLYR Q GGAHIQLYR | | TQAVP-sgsaga TO P G+AG | | GTIIQASNM GTIIQA NM | |
| Sbjct | 1612 | | | | TÕPAPVGGTAGG | | | |
| Query | 316 | | KVAVSGMPGTS' KVAVSGMPG | | SVQMHGQARTQF SVQMHGQARTQF | | | |
| Sbjct | 1670 | | | | SVOMHGÓARTÓF SVÕMHGÕARTÕF | | | |
| Query | 136 | | gDMLLVKRHNII GDMLLVKRHNII | | | | | |
| Sbjct | 1728 | | GDMLLVKRHNII GDMLLVKRHNII | | | | | |

uncharacterized protein Dsimw501_GD11590 [Drosophila simulans] Sequence ID: **gb|KMY95527.1|** Length: 591 Number of Matches: 1 Range 1: 1 to 230

| Score | | Expect I | Method | Identities | Positives | Gaps | Frame |
|----------|-------|------------|--------------------------------------------------|--------------|--------------|-----------|-------|
| 382 bits | (981) | 2e-122() (| Compositional matrix adjust. | 229/230(99%) | 229/230(99%) | 0/230(0%) | -1 |
| Features | s: | | | | | | |
| Query | 736 | | IVSTAAGNTLQQRTTAGGQSIV IVSTAAGNTLQQRTTAGGQSIV | | | | |
| Sbjct | 1 | | IVSTAAGNTLQQRTTAGGQSIV IVSTAAGNTLQQRTTAGGQSIV | | | | |
| Query | 556 | | GIPVSALQQGGKTTVIPVTQQS GIPVSALQQGGKTTVIPVTQQS | | | | |

| Sbjct | 61 | QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG | 120 |
|-------|-----|------------------------------------------------------------------------------------------------------------------------------|-----|
| Query | 376 | atANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK | 197 |
| Sbjct | 121 | ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK | 180 |
| Query | 196 | QMAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 47 QMAAGKQQLQRQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF | |
| Sbict | 181 | OMAAGKOOLOROVVSADGTTTTTGAGDMLLVKRHNILAAOKAOOASGALF 230 | |

GH12111p [Drosophila melanogaster]

Sequence ID: **gb|AAM48336.1|** Length: 591 Number of Matches: 1 Range 1: 1 to 230

| Score | | Expect | Method | Identities | Positives | Gaps | Frame |
|----------|---------|----------|----------------------------------------------------|---------------|---------------|-----------|-------|
| 382 bits | (980) 2 | 2e-122() | Compositional matrix adjust. | 230/230(100%) | 230/230(100%) | 0/230(0%) | -1 |
| Features | s: | | | | | | |
| Query | 736 | | ORIVSTAAGNTLQQRTTAGGQS ORIVSTAAGNTLQQRTTAGGQS | | | | |
| Sbjct | 1 | | RIVSTAAGNTLQQRTTAGGQS. RIVSTAAGNTLQQRTTAGGQS. | | | | |
| Query | 556 | | KGIPVSALQQGGKTTVIPVTQQ KGIPVSALQQGGKTTVIPVTQQ | | | | |
| Sbjct | 61 | | KGIPVSALQQGGKTTVIPVTQÇ | | | | |
| Query | 376 | | .VQAGGTIIQASNMATHVTSQKV .VQAGGTIIQASNMATHVTSQKV | | ~ | ~ ~ | |
| Sbjct | 121 | | JVQAGGTIIQASNMATHVTSQKV | | | | |
| Query | 196 | | KQQLQRQVVSadgtttttaagI KQQLQRQVVSADGTTTTTAAGI | | | 47 | |
| Sbjct | 181 | | KQQLQRQVVSADGTTTTTAAGI | | | 230 | |

uncharacterized protein Dmoj_GI19071 [Drosophila mojavensis]

Sequence ID: ref|XP_002005439.2| Length: 3285 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2539 to 2854

| Score | E | xpect Method | Identities | Positives | Gaps I | Frame |
|----------|----------|-------------------------------------------------------|-----------------------------|--------------|----------------------------|---------|
| 314 bits | (804) 46 | e-90() Compositional matrix adjust. | 223/330(68%) | 245/330(74%) | 32/330(9%) - | 1 |
| Feature | s: | | | | | |
| Query | 982 | PVQTLPSVVQPQIGSGAQIVSISSQ- | | | | |
| Sbjct | 2539 | PVQ+LP + GS AQIVSISSQ PVQSLP-IATHNNGSTAQIVSISSQ | | | | - |
| Query | 805 | lttTANQPQQQHQttavttlntTML | RGORIVSTAAG- RGORIVS A G | | RTTAGGOSIVS RTTAGGOSIVS | |
| Sbjct | 2597 | QQ Q T TML1 GQQQQQQQQATGTVTML1 | | | | |
| Query | 646 | PNLGQGASPSQFQTQLRLAAVPTSP P+LGQG +P+QFQTQLRLAAV SP | | | | G 467 |
| Sbjct | 2649 | PSLGQG +F+QFQFQTQLRLAAV SFA | | | | -A 2706 |
| Query | 466 | AHIQLYRQRSLKVLQTTTQAVPsgsaAHIQLYRQR+LKVLQ +Q P + | | | QASNMATH OASN+ +TH | |
| Sbjct | 2707 | AHIQLYRQRNLKVLQ +Q P + AHIQLYRQRNLKVLQ-ASQGAPGTA | | _ | ~ | |
| Query | 310 | TSQKVAVSGMPGTSTTVQAGNVVSSYTSQKVAVSGMPG +TTVQAGNVVSSY | | | | t 131 |
| Sbjct | 2766 | TSQKVAVSGMPG-ATTVQAGNVVSS | | | | S 2824 |
| Query | 130 | taagDMLLVKRHNILAAQKAQQA A DMLLVKRHNILAAOKAOOA | | | | |
| Sbjct | 2825 | VAPGTSDMLLVKRHNILAAQKAQQA' | | | | |
| | | | | | | |

uncharacterized protein Dwil_GK20897 [Drosophila willistoni]

Sequence ID: ref|XP_002061395.2| Length: 3248 Number of Matches: 1

See 1 more title(s) Range 1: 2477 to 2867

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|-------------------------------------------------------|------------------------------|-----------------------------|----------------------------|--------------|
| 312 bits | (800) 1e | e-89() Compositional matrix adjust. | 277/407(68%) | 295/407(72%) | 36/407(8%) | -1 |
| Features | s: | | | | | |
| Query | 1207 | SSNVSPGQQTAILLHQPQQQLRTHP | | | | sa 1028 |
| Sbjct | 2477 | ++NVS GQQTAILLHQ Q + TANVSTGQQTAILLHQTTPQQQQQM | | /KTIVGTSSSL /KTIVGTSSSLM | | GG 2536 |
| Query | 1027 | vasggqssvsvvltTPVQTLPSVVQ | | | | |
| Sbjct | 2537 | A+ Ğ +SVSVVLTTPVQTLP+VVQ NATTGPTSVSVVLTTPVQTLPAVVQ | | | | |
| Query | 850 | PQvvsvstlptvgtvlttTANQPQQePOVVSV ++ T | | TMLRGQRIVST | | |
| Sbjct | 2597 | PQVVSV ++ T PQVVSVGSVLTTTASQQQQT | TAVTTLN TAVTTLN <i>E</i> | | GNT+QQRT' GPGNTVQQRT' | |
| Query | 670 | GGQSIVSMPNLGQGASPSQFQTQLR GQSIVSMP+LGQ P QFQT +R | | | PVSALQQGGK' PVSALQQGGK' | |
| Sbjct | 2648 | TGQSIVSMPSLGQNVGP-QFQTHVR | | | | |
| Query | 496 | VIPVTQQS-GGAHIQLYRQRSLKVL | | | NL NL | |
| Sbjct | 2706 | VIPGTQQQPGGAHIQLYRQRSLKVL | | | | V VV 2763 |
| Query | 358 | QAGGTIIQASNMATHVTSQKVAVSG O GTIIO SNM THVTSOKVAVSG | | | | |
| Sbjct | 2764 | Q GTIIQ SNM THVTSQKVAVSG QTAGTIIQTSNMPTHVTSQKVAVSG | | | | |
| Query | 178 | QQLQRQVVSadgtttttaagDM | | | 47 | |
| Sbjct | 2823 | Q LQRQVVS T TTT GDM: QGLQRQVVSADGTTTTATTTTGGDM: | LLVKRHNIL AÇ LLVKRHNIL-AÇ | | 2867 | |

similar to Drosophila melanogaster domino, partial [Drosophila yakuba]

Sequence ID: gb|AAR09977.1| Length: 185 Number of Matches: 1

Range 1: 1 to 173

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|-------|-----------------------------------------------------------|--------------|--------------|-----------|-------|
| 270 bits | (691) | 1e-84() Compositional matrix adjust. | 168/173(97%) | 169/173(97%) | 0/173(0%) | -1 |
| Features | S: | | | | | |
| Query | 565 | QTTQLVTTKGIPVSALQQGGKTTVIPV QTTQLVTTKGIPVSALQQGGKTTVIP | | | | |
| Sbjct | 1 | QTTQLVTTKGIPVSALQQGGKTTVIPG | | | | |
| Query | 385 | atgatANLVQAGGTIIQASNMATHVTS TGATANLVOAGGTIIOASNM THVTS | | | | |
| Sbjct | 61 | GTGATANLVQAGGTIIQASNMGTHVTS | | | | |
| Query | 205 | FIKQMAAGKQQLQRQVVSadgttttta FIKQMAAGKQQLQRQVVSADGTTTTT | | | | |
| Sbjct | 121 | FIKOMAAGKOOLOKOVVSADGIIIII FIKOMAAGKOOLOROVVSADGTTTTTG | | | | |

LOW QUALITY PROTEIN: uncharacterized protein Dvir_GJ20044 [Drosophila virilis] Sequence ID: **ref|XP_002050736.2|** Length: 3172 Number of Matches: 1

See 1 more title(s)

Score

Range 1: 2490 to 2813

Expect Method

| | | · | |
|----------|---------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| 296 bits | (757) 6 | e-84() Compositional matrix adjust. 217/332(65%) 236/332(71%) 28/332(8%) -1 | |
| Feature | s: | | |
| Query | 982 | PVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQSLPQvvsvstlptvg PVQ+LP + GS AQIVSISSQT LPVN++PQLGSIVQTQ+LPQVVSV L T | 812 |
| Sbjct | 2490 | PVQSLPIATHSNVNAGSTAQIVSISSQTTLPVNTAPQLGSIVQTQTLPQVVSVGPLTTTA | 2549 |
| Query | 811 | tvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTAGGQSIV | 653 |
| Sbjct | 2550 | T Q Q T TMLRGQRIVST A GNTLQ QRTTAGGQSIV $TGQQQQQQQQQQQQTATGTVTMLRGQRIVSTGAAGGNTLQDVVLQQRTTAGGQSIV$ | 2604 |
| Query | 652 | SMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQS | 473 |
| Sbjct | 2605 | SMP LGQ + QFQTQLRLAAV SPATQTTQLVTTKGIPVSALQQ GK V+ TQQ SMPGLGQSVTQGQFQTQLRLAAVSASPATQTTQLVTTKGIPVSALQQSGK-AVLSGTQQQ | 2663 |
| Query | 472 | GGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT | 317 |
| Sbjct | 2664 | ${ m AHIQLYRQR+LKVLQ}$ ${ m A}$ ${ m G}$ ${ m A+}$ ${ m +}$ ${ m AG}$ ${ m GTIIQASN+}$ ${ m +T}$ ${ m -AAHIQLYRQRNLKVLQAPQGAQGGGGVTASLNQTVVQTAGGALATGTIIQASNLMQTST}$ | 2722 |
| | | | |

Identities

Gaps

Frame

Positives

| Query | 316 | HVTSOKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt- | 140 |
|-------|------|-----------------------------------------------------------------------------------------------------------------------------|------|
| Sbjct | 2723 | HVTSQKVAV+ MPG +TTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQV++ DG+ HVTSQKVAVTCMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVLATDGSG | 2781 |
| Query | 139 | -ttttaagDMLLVKRHNILAAQKAQQASGALF 47 | |
| Sbjct | 2782 | + DMLLVKRHNILAAQKAQQA+G LF GSGAPGTSDMLLVKRHNILAAQKAQQATGPLF 2813 | |

dom [Drosophila busckii]

Sequence ID: **gb|ALC41615.1|** Length: 3526 Number of Matches: 1 Range 1: 2764 to 3182

| Score | Ex | kpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|------------------------------------------------------|-------------------------------|---------------------------|----------------------------|---------|
| 276 bits | (706) 3e | e-77() Compositional matrix adjus | t. 267/432(62%) | 296/432(68%) | 60/432(13%) | -1 |
| Features | s: | | | | | |
| Query | 1201 | NVSPGQQTAILLHQPQQQ | LRTHPGQG | GOSNT-QOLVK | TIVGtssslta | gq 1055 |
| Sbjct | 2764 | +V+P QQTAILL Q QQ HVTPTQQTAILLQQQPQQQQQQQ | | QSNT QQLVK -QSNTTQQLVK | | |
| Query | 1054 | lqqlaqqsavasggqs LQQLA S +SGGQS | SSVSVVLTTPVQT | LPSVVQPQIGS | GAQIVSISSQT | -L 902 |
| Sbjct | 2818 | LQQLAAASNAGGSVQLQQSSGGQS | | | | |
| Query | 901 | PVNSSPQLGSIVQTQSLPQvvsvs PVN++PQLGSIVQTQ+LPQVVSV | | ANQPQQQHQtt OOHO | avttlntTMLR V TLNT +LR | |
| Sbjct | 2878 | PVNTAPQLGSIVQTQTLPQVVSV | | | | |
| Query | 721 | RIVSTAAGNTLQ R + + + +AG T LQ | QQRTTAGGQSIVS QQR AGGQSIV+ | | QFQTQLRLAAV QFQTQLRLAAV | |
| Sbjct | 2934 | RSVQAIVAAASAGGTPLHTDVVLÇ | | | | |
| Query | 577 | SPATQTTQLVTTKGIPVSALQQGC + + OTTOLVTTKGIPVSALOO (| | | | Ps 398 |
| Sbjct | 2994 | ANSNOTTOLVITKGIPVSALOO | | | | AG 3051 |
| Query | 397 | gsagatgatANLVQG+A A G T NL VO | -AGGTIIQASNMA A GTIIQ SN+ | | AVSGMPGTSTT AVSGM G +TT | |
| Sbjct | 3052 | GAATAGGGTGNLSSTVVQTTGGTI | | | | |
| Query | 256 | AGNVVSSVQMHGQARTQFIKQMAAAGNVVSSVQMHGQ RTQFIKQM A | | Sadgtttttaa A G+ | gDMLLVKRHNI MLLVKRHNI | |
| Sbjct | 3111 | AGNVVSSVQMHGQPRTQFIKQMTA | | | | |
| Query | 82 | AQKAQQASGALF 47 | | | | |
| Sbjct | 3171 | AQKAQQA+G LF AQKAQQATGPLF 3182 | | | | |

GH20710 [Drosophila grimshawi]

Sequence ID: ref|XP_001986118.1| Length: 3285 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2571 to 2891

| Score | Ex | rpect Method | Identities | Positives | Gaps | Frame |
|----------|------------|-------------------------------------------------------|----------------------------|-----------------|---------------------|-------|
| 267 bits | (683) 3e | e-74() Compositional matrix adjust. | 209/336(62%) | 231/336(68%) | 39/336(11%) | -1 |
| Features | S : | | | | | |
| Query | 982 | PVQTLPSVVQPQIGSGAQIVSIS | | | | |
| Sbjct | 2571 | PVQ+LP + S AQIVSIS PVQSLPIATHSNVNANSTAQIVSIS | SQ TLPVN+ POSQSTLPVNTPPO | | | |
| Query | 811 | tvlttTANQPQQQHQttavttlntT | MLRGQRIVSTA MLRGQR+VS A | | LQQRTTAG LOORTTA | |
| Sbjct | 2631 | SGGQQQQQQQTATGTVT | | | | |
| Query | 661 | SIVSMPNLGQGASPSQFQTQLRLAA IVS LGQ + + FQ QLRL+A | | | | |
| Sbjct | 2683 | PIVSLGÕSVANAHFÕAÕLRLSA | | | | |
| Query | 481 | QQSGGAHIQLYRQRSLKVLQTTTQA QQ HIQLYRQR+LKVLQ Q | VPsgsagatga | tANLVQ N +VQ | | |
| Sbjct | 2739 | QQ HIQLIKOK LKVLQ Q QQQT-PHIQLYRQRNLKVLQAP-QV | | | | |
| Query | 325 | MATHVTSQKVAVSGMPGTSTTV + THVTSQKVAVSGMPG +TTV | | | | |
| Sbjct | 2797 | LMQTPTHVTSQKVAVSGMPG-ATTV | | | | |
| Query | 154 | SadgtttttaagDMLLVKRHNILAA + DG+ + A GDMLLVKRHNILAA | | 47 | | |

PREDICTED: helicase domino isoform X1 [Ceratitis capitata]

Sequence ID: ref|XP_004522557.1| Length: 3372 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2674 to 2979

| Score | Ex | spect Method | Identities | Positives | Gaps | Frame |
|-----------|----------|------------------------------------------------------|---------------------------|--------------|--------------------------|---------|
| 118 bits(| (295) 2e | -24() Compositional matrix adjust. | 164/336(49%) | 194/336(57%) | 61/336(18%) | -1 |
| Features | S: | | | | | |
| Query | 982 | PVQTLPSVVQPQIGSGAQIVS | | | | |
| Sbjct | 2674 | PVQTLPS VQ Q G S AQIVS PVQTLPSSVQSAQQHGQSSTAQIVS | | | | |
| Query | 826 | lptvgtvlttTAN-QPQQQHQttav L TVGTVLTT+AN QP + V | | | TLQQRTTAG LOOR+ | GQ 662 |
| Sbjct | 2734 | LATVGTVLTTSANLQPSATV | | | | SP 2788 |
| Query | 661 | SIVSMPNLGQGASPSQFQ-TQLRLA +IVSM NLG + +QFQ TQLRLA | | | ALQQGGKTTVI LÕÕGGK | PV 485 |
| Sbjct | 2789 | TIVSMSNLGPSVAAAÕFÕATÕLRLA | | | | |
| Query | 484 | TQQSGGAHIQLYRQR-SLKVLQ T GG HIQLYRQR LKVLQ | | | QAGGTIIQASN A GTIIO S | |
| Sbjct | 2837 | TANVGGNQPPHIQLYRQRQQLKVLQ | | | | |
| Query | 319 | THVTSQKVAVSGMPGTST T + QKVAV+ + +S | | | | KQ 176 |
| Sbjct | 2897 | TAGGQATMQMQGQKVAVATV-SSSN | | | | |
| Query | 175 | QLQRQVVSadgtttttaagDMLLVK + RO+ DM+LVK | RHNILAAQKAQ R I A OKAO | 68 | | |
| Sbjct | 2955 | + RÖ+ DM+LVK TIARÕMGDDMVLVK | RQVIGAHÕKAÕ | 2979 | | |

PREDICTED: helicase domino isoform X2 [Ceratitis capitata]

Sequence ID: **ref|XP_004522560.1|** Length: 3368 Number of Matches: 1 Range 1: 2674 to 2979

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|----------|------------------------------------------------------|-----------------------------|----------------------|-----------------------------|---------|
| 118 bits | (295) 2e | e-24() Compositional matrix adjust. | 164/336(49%) | 194/336(57%) | 61/336(18%) - | -1 |
| Feature | s: | | | | | |
| Query | 982 | PVOTLPSVVOPQIGSGAQIVS | | | | |
| Sbjct | 2674 | PVQTLPS VQ Q G S AQIVS PVQTLPSSVQSAQQHGQSSTAQIVS | SIS QT+ + + SISPQTIVSSGA | | | |
| Query | 826 | lptvgtvlttTAN-QPQQQHQttav | ttlntTMLRGQ | RIVSTAAGN RIV+ AG | TLQQRTTAGO LOOR+ | GQ 662 |
| Sbjct | 2734 | L TVGTVLTT+AN QP + \ LATVGTVLTTSANLQPSAT\ | TTLN + LR Q TTLNPSALRAQ | RIVAATAGTLQ | | SP 2788 |
| Query | 661 | SIVSMPNLGQGASPSQFQ-TQLRLA +IVSM NLG + +QFQ TQLRLA | | | ALQQGGKTTVII LQQGGK | PV 485 |
| Sbjct | 2789 | TIVSMSNLGPSVAAAQFQATQLRLA | | | | |
| Query | 484 | TQQSGGAHIQLYRQR-SLKVLQ T GG HIQLYRQR LKVLQ | | | QAGGTIIQASNN A GTIIO S + | |
| Sbjct | 2837 | TANVGGNQPPHIQLYRQRQQLKVLQ | | | | |
| Query | 319 | THVTSQKVAVSGMPGTST T + QKVAV+ + +S | | | | |
| Sbjct | 2897 | TAGGQATMQMQGQKVAVATV-SSSN | | | | |
| Query | 175 | QLQRQVVSadgtttttaagDMLLVF + RQ+ DM+LVF | | | | |
| Sbjct | 2955 | + RQ+ DM+LVF TIARQMGDDMVLVF | KR I A QKAQ KRQVIGAHQKAQ | 2979 | | |
| | | | | | | |

PREDICTED: helicase domino [Musca domestica]

Sequence ID: ref|XP_011294691.1| Length: 2336 Number of Matches: 1

Range 1: 1601 to 1910

Expect Method Identities Positives Frame **Score** Gaps

110 bits(274) 5e-22() Compositional matrix adjust. 158/330(48%) 185/330(56%) 49/330(14%) -1

Features:

| Query | 982 | PVQTLPSVVQPQIGSGAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvstl | 824 |
|-------|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| Sbjct | 1601 | PVQT+ S VQ Q+ S AQIVS+S QT+ V+SS Q+GSIV TQSLPQVVSVS L PVQTISSNVQNQVAHHSQVSSSTAQIVSLSPQTI-VSSSAQVGSIVHTQSLPQVVSVSQL | 1659 |
| Query | 823 | ptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTAGGQS- | 659 |
| Sbjct | 1660 | $	ext{TVGTVLTT++} \qquad Q \qquad 	ext{T} \qquad 	ext{VTTLNT+} \qquad 	ext{LR} \qquad QRIV+ \ 	ext{++G} \qquad 	ext{TLQ} \qquad Q+ \ 	ext{TAG} \qquad S$ $	ext{ATVGTVLTTSSGMQQPTGTVTTLNTSALRAQRIVAASSGTTLQDVVLQQRTAGNPSP}$ | 1716 |
| Query | 658 | -IVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT | 497 |
| Sbjct | 1717 | $ \begin{array}{cccccccccccccccccccccccccccccccccccc$ | 1771 |
| Query | 496 | VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASN Q AHIQ YRQR LKVLQ T Q P+ A+G A LV A GTII | 326 |
| Sbjct | 1772 | Q AHIQ YRQR LKVLQ T Q P+ A+G A LV A GTII GGTTAQGQQSAHIQSYRQRQLKVLQATGPGQQGQPTVVQTASGQAA-LVNAQGTIIGTGP | 1830 |
| Query | 325 | MATHVT-SQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQM-AAGKQQL | 170 |
| Sbjct | 1831 | V QKV V+ TT A VV++V QMH Q R QFIKQ+ A+GKQ TTVQVVQGQKVTVATSNVAVTTPSATGVVTTVANQMHAQQVQQTRAQFIKQVSASGKQIF | 1890 |
| Query | 169 | QRQVVSadgtttttaagDMLLVKRHNILAA 80 | |
| Sbjct | 1891 | RQV DMLLVKR I AA TRQVGDSDMLLVKRQMISAA 1910 | |

Helicase domino [Lucilia cuprina]

Sequence ID: gb|KNC26706.1| Length: 1269 Number of Matches: 1

Range 1: 522 to 848

| Score | | Expect Method | Identities | Positives | Gaps | Frame |
|----------|-------|----------------------------------------------------|-------------------------|------------------------------|---------------------------|-------|
| 109 bits | (273) | Se-22() Compositional matrix adjust. | 161/345(47%) | 187/345(54%) | 57/345(16%) | -1 |
| Feature | s: | | | | | |
| Query | 982 | PVQTLPSVVQPQIGSGAQ | | | | t 827 |
| Sbjct | 522 | PVQT+ S V Q S AQ PVQTISSTVTNQQQHHSNQVSSSTAQ | | +SSPQ+GSIVQ' SSSPQVGSIVQ' | | Q 581 |
| Query | 826 | lptvgtvlttTANQPQQQHQttavtt L TVGTVLTT++ Q T VTT | lntTMLRGORI | VSTAAGNTLQ- | QRTTAGGQ O+ +AG | |
| Sbjct | 582 | LATVGTVLTTSSGMQQPTATVTT | | | | _ |
| Query | 658 | IVSMPNLGQGASPSQFQ-TQLRLA IVSM +LG + +Q Q TQ +LA | | | | P 488 |
| Sbjct | 639 | PTIVSMSSLGTNVAQAQLQATQFQLA | | | | A 693 |
| Query | 487 | VTQQSGGAHIQLYRQR-SLKVI + HIQLYRQR LKVI | | | LVQAGGTIIQA LV A GTIIO | |
| Sbjct | 694 | QAGNNQQGQPHTHIQLYRQRQQLKVI | | _ | | _ |
| Query | 328 | NMATHVTSQKVAVSGMPG M T V QKVAV+ | GTSTTVQAGNVV TT A VV | | | |
| Sbjct | 754 | LMQTGSGPTTVQVVQGQKVAVATSNV | | | | |
| Query | 193 | MAAGKQQLQRQVVSadgtttttaagI | MLLVKRHNILA | AQKAQQ 6 | 5 | |
| Sbjct | 814 | +AAGKQ + RQV | MLLVKRQMISA | ATQQKAAQ 8 | 48 | |

PREDICTED: helicase domino [Stomoxys calcitrans]

Sequence ID: **ref|XP_013100224.1|** Length: 3504 Number of Matches: 1 Range 1: 2758 to 3077

| Score | E | xpect Method | Identities | Positives | Gaps | Frame |
|----------|------------|-------------------------------------------------|---------------------------|----------------------------|-------------|--------------|
| 104 bits | (259) 4e | e-20() Compositional matrix adjust. | 155/343(45%) | 184/343(53%) | 65/343(18%) | -1 |
| Features | S : | | | | | |
| Query | 982 | PVQTLPSVVQPQIGSGA PVOT+ S P GS A | QIVSISSQTLP QIVS+S QT+ | | | |
| Sbjct | 2758 | PVQTISSTTLPNQGSHHSQVASSSA | | | | |
| Query | 826 | lptvgtvlttTANQPQQQHQttavt L TVGTVLTT++ O V | tlntTMLRGQR LNT+ LR OR | | | GOS 659 S |
| Sbjct | 2817 | LATVGTVLTTSSGMQQPATVA | ~ | ~ | ~ | |
| Query | 658 | IVSMPNLGQGASPSQFQ-TQLRI IVSM +LG + + O TO +I | | TQLVTTKGIPV TQ V TKGI V | | 7IP 488 I |
| Sbjct | 2873 | PTIVSMSSLGTNVAQAPIQGTQFQI | | | | _ |

| Query | 487 | VTQQSGGAHIQLYRQR-SLKVLQTTTQAVPsgsagatgatANLVQAGGTI SGG AHIQLYRQR LKVLQ + Q LV A GTI | 341 |
|-------|------|----------------------------------------------------------------------------------------|------|
| Sbjct | 2925 | AGNASGGTVQGQGQAAHIÕLYRÕRQQLKVLÕASGPGÕQGQQTVVQTASGQTALVNAQGTI | 2984 |
| Query | 340 | IQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQ IQ + M T | 206 |
| Sbjct | 2985 | IQGNIMQTSAGPTTVQVVQGQKVTVATSNVALTTPSTAGVVTTVANQMHPQQVQQQTRTQ | 3044 |
| Query | 205 | FIKQM-AAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAA 80 +IKQ+ A+GKQ + RQV DMLLVKR + AA | |
| Sbict | 3045 | YIKOVSASGKOTIAROVGDTDMLLVKROMLSAA 3077 | |

GM15831 [Drosophila sechellia]

Sequence ID: ref|XP_002039753.1| Length: 2550 Number of Matches: 1

▶ See 1 more title(s) Range 1: 2509 to 2550

| Score | | Expect M | lethod | Identities | Positives | Gaps | Frame |
|-----------|------------|------------|-----------------------------------------------|------------|------------|----------|-------|
| 86.3 bits | s(212) | 3e-14() Co | omposition-based stats. | 36/42(86%) | 36/42(85%) | 0/42(0%) | -3 |
| Features | 3 : | | | | | | |
| Query | 1022 | FWGPVQCE | DAAR 897 DAAR | | | | |
| Sbjct | 2509 | | EC NHSSTDTSVGGATPDRL ECSTNHSSTDTSVGGATPDRL | | | | |