# BLAST ®

# Basic Local Alignment Search Tool

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Blast report description

**Nucleotide Sequence (2753 letters)**

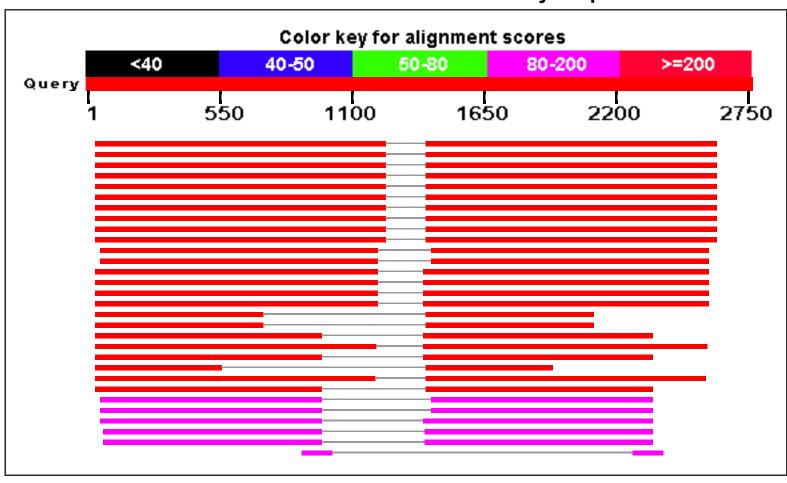| | | | |
|---|---|---|---|
| **RID** | B8BKDMC6014 (Expires on 02-06 12:09 pm) | | |
| **Query ID** | lcl|Query_32783 | **Database Name** | nr |
| **Description** | None | **Description** | All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects |
| **Molecule type** | nucleic acid | | |
| **Query Length** | 2753 | | |
| | | **Program** | BLASTX 2.3.1+ |

# ⊟ Graphic Summary

No putative conserved domains have been detected

### Distribution of 60 Blast Hits on the Query Sequence

## Descriptions

Sequences producing significant alignments:

| Description | Max score | Total score | Query cover | E value | Ident | Accession |
|---|---|---|---|---|---|---|
| LD21920p [Drosophila melanogaster] | 549 | 1098 | 87% | 4e-172 | 100% | ACD81851.1 |
| LP03212p [Drosophila melanogaster] | 558 | 1116 | 87% | 2e-169 | 100% | ACH95308.1 |
| GD11590 [Drosophila simulans] | 535 | 1070 | 87% | 2e-168 | 98% | XP_002082475.1 |
| domino, isoform A [Drosophila melanogaster] | 556 | 1113 | 87% | 5e-168 | 100% | NP_524833.2 |
| domino, isoform D [Drosophila melanogaster] | 556 | 1113 | 87% | 6e-168 | 100% | NP_726065.1 |
| domino, isoform G [Drosophila melanogaster] | 556 | 1112 | 87% | 9e-168 | 100% | NP_001286676.1 |
| helicase DOMINO A [Drosophila melanogaster] | 555 | 1110 | 87% | 1e-167 | 99% | AAF82185.1 |
| domino, isoform A [Drosophila yakuba] | 522 | 1044 | 87% | 4e-156 | 97% | XP_002091544.2 |
| domino, isoform B [Drosophila yakuba] | 522 | 1044 | 87% | 4e-156 | 97% | XP_015051886.1 |
| uncharacterized protein Dere_GG22110, isoform A [Drosophila erecta] | 521 | 1042 | 87% | 9e-156 | 97% | XP_001975047.1 |
| uncharacterized protein Dana_GF12812, isoform B [Drosophila ananassae] | 436 | 873 | 83% | 9e-127 | 88% | XP_014763429.1 |
| uncharacterized protein Dana_GF12812, isoform A [Drosophila ananassae] | 436 | 873 | 83% | 9e-127 | 88% | XP_001959323.1 |
| uncharacterized protein Dpse_GA24314, isoform B [Drosophila pseudoobscura pseudoobscura] | 427 | 849 | 85% | 9e-124 | 83% | XP_002138575.2 |
| uncharacterized protein Dpse_GA24314, isoform D [Drosophila pseudoobscura pseudoobscura] | 427 | 848 | 85% | 1e-123 | 83% | XP_015040038.1 |
| uncharacterized protein Dpse_GA24314, isoform E [Drosophila pseudoobscura pseudoobscura] | 426 | 846 | 85% | 3e-123 | 83% | XP_004444248.2 |
| GL16841 [Drosophila persimilis] | 422 | 839 | 85% | 9e-123 | 84% | XP_002018288.1 |
| GH12111p [Drosophila melanogaster] | 382 | 764 | 50% | 7e-117 | 100% | AAM48336.1 |
| uncharacterized protein Dsimw501_GD11590 [Drosophila simulans] | 382 | 764 | 50% | 8e-117 | 99% | KMY95527.1 |
| uncharacterized protein Dmoj_GI19071 [Drosophila mojavensis] | 320 | 634 | 68% | 2e-87 | 67% | XP_002005439.2 |
| uncharacterized protein Dwil_GK20897 [Drosophila willistoni] | 318 | 631 | 84% | 5e-87 | 68% | XP_002061395.2 |
| LOW QUALITY PROTEIN: uncharacterized protein Dvir_GJ20044 [Drosophila virilis] | 301 | 597 | 68% | 3e-81 | 65% | XP_002050736.2 |
| similar to Drosophila melanogaster domino [Drosophila yakuba] | 271 | 542 | 37% | 9e-81 | 97% | AAR09977.1 |
| dom [Drosophila busckii] | 276 | 553 | 83% | 5e-73 | 62% | ALC41615.1 |
| GH20710 [Drosophila grimshawi] | 267 | 535 | 67% | 4e-70 | 62% | XP_001986118.1 |
| PREDICTED: helicase domino isoform X2 [Ceratitis capitata] | 117 | 234 | 66% | 6e-23 | 49% | XP_004522560.1 |
| PREDICTED: helicase domino isoform X1 [Ceratitis capitata] | 117 | 234 | 66% | 7e-23 | 49% | XP_004522557.1 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| Helicase domino [Lucilia cuprina] | 114 | 223 | 67% | 2e-22 | 47% | | KNC26706.1 |
| PREDICTED: helicase domino [Musca domestica] | 111 | 220 | 67% | 3e-21 | 47% | | XP_011294691.1 |
| PREDICTED: helicase domino [Stomoxys calcitrans] | 103 | 207 | 67% | 6e-19 | 44% | | XP_013100224.1 |
| GM15831 [Drosophila sechellia] | 86.3 | 172 | 9% | 2e-13 | 86% | | XP_002039753.1 |

# ⊟ Alignments

LD21920p [Drosophila melanogaster]

Sequence ID: **gb|ACD81851.1|**  Length: 1350  Number of Matches: 2
Range 1: 575 to 974

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 549 bits(1414) | 4e-172() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  2606  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  2427
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  575   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  634

Query  2426  tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2247
             TAGQLQQLAQQSAVASGGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  635   TAGQLQQLAQQSAVASGGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  694

Query  2246  PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  2067
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  695   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  754

Query  2066  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  1887
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  755   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  814

Query  1886  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  1707
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  815   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  874

Query  1706  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  1527
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  875   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  934

Query  1526  RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF  1407
             RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct  935   RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF  974
```

Range 2: 575 to 974

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 549 bits(1414) | 4e-172() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  1241  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  1062
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  575   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  634

Query  1061  tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  882
             TAGQLQQLAQQSAVASGGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  635   TAGQLQQLAQQSAVASGGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  694

Query  881   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  702
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  695   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  754

Query  701   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  522
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  755   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  814

Query  521   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  342
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  815   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  874

Query  341   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  162
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  875   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  934

Query  161   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF  42
```

```
                              RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct    935         RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF        974
```

LP03212p [Drosophila melanogaster]

Sequence ID: **gb|ACH95308.1|** Length: 2642  Number of Matches: 2
Range 1: 1882 to 2281

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 558 bits(1437) | 2e-169() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query   2606   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   2427
               GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct   1882   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL   1941

Query   2426   tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   2247
               TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   1942   TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   2001

Query   2246   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   2067
               PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct   2002   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST   2061

Query   2066   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   1887
               AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct   2062   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   2121

Query   1886   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG   1707
               SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct   2122   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG   2181

Query   1706   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   1527
               TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct   2182   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2241

Query   1526   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF   1407
               RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   2242   RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF   2281
```

Range 2: 1882 to 2281

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 558 bits(1437) | 2e-169() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query   1241   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   1062
               GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct   1882   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL   1941

Query   1061   tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   882
               TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   1942   TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   2001

Query   881    PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   702
               PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct   2002   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST   2061

Query   701    AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   522
               AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct   2062   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   2121

Query   521    SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG   342
               SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct   2122   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG   2181

Query   341    TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   162
               TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct   2182   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2241

Query   161    RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF   42
               RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   2242   RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF   2281
```

GD11590 [Drosophila simulans]

Sequence ID: **ref|XP_002082475.1|** Length: 1178  Number of Matches: 2

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

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 535 bits(1377) | 2e-168() | Compositional matrix adjust. | 391/400(98%) | 392/400(98%) | 0/400(0%) | -1 |

Features:

```
Query  2606  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  2427
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  403   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  462

Query  2426  tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2247
             TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  463   TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  522

Query  2246  PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  2067
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNT MLRGQRIVST
Sbjct  523   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTAMLRGQRIVST  582

Query  2066  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  1887
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQ+TQ VTTKGIPV
Sbjct  583   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQSTQFVTTKGIPV  642

Query  1886  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  1707
             SAL QGGKTTVIPVTQQSGGAHIQL RQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  643   SALLQGGKTTVIPVTQQSGGAHIQLCRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  702

Query  1706  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  1527
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQART FIKQMAAGKQQLQ
Sbjct  703   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTHFIKQMAAGKQQLQ  762

Query  1526  RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF     1407
             RQVVSADGTTTT  AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  763   RQVVSADGTTTTKGAGDMLLVKRHNILAAQKAQQASGALF     802
```

Range 2: 403 to 802

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 535 bits(1377) | 2e-168() | Compositional matrix adjust. | 391/400(98%) | 392/400(98%) | 0/400(0%) | -1 |

Features:

```
Query  1241  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  1062
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  403   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  462

Query  1061  tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  882
             TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  463   TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  522

Query  881   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  702
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNT MLRGQRIVST
Sbjct  523   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTAMLRGQRIVST  582

Query  701   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  522
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQ+TQ VTTKGIPV
Sbjct  583   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQSTQFVTTKGIPV  642

Query  521   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  342
             SAL QGGKTTVIPVTQQSGGAHIQL RQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  643   SALLQGGKTTVIPVTQQSGGAHIQLCRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  702

Query  341   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  162
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQART FIKQMAAGKQQLQ
Sbjct  703   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTHFIKQMAAGKQQLQ  762

Query  161   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF     42
             RQVVSADGTTTT  AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  763   RQVVSADGTTTTKGAGDMLLVKRHNILAAQKAQQASGALF     802
```

domino, isoform A [Drosophila melanogaster]

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

▸ **See 2 more title(s)**

Range 1: 2423 to 2822

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 556 bits(1433) | 5e-168() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  2606  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  2427
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  2423  GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  2482
```

```
Query  2426  taggqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2247
             TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2483  TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2542

Query  2246  PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  2067
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  2543  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  2602

Query  2066  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  1887
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2603  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2662

Query  1886  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  1707
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  2663  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  2722

Query  1706  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  1527
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2723  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2782

Query  1526  RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF     1407
             RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2783  RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF     2822
```

Range 2: 2423 to 2822

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 556 bits(1433) | 5e-168() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  1241  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  1062
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  2423  GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  2482

Query  1061  taggqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  882
             TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2483  TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2542

Query  881   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  702
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  2543  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  2602

Query  701   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  522
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2603  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2662

Query  521   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  342
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  2663  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  2722

Query  341   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  162
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2723  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2782

Query  161   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF     42
             RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2783  RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF     2822
```

domino, isoform D [Drosophila melanogaster]

Sequence ID: **ref|NP_726065.1|**  Length: 3183  Number of Matches: 2

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

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 556 bits(1433) | 6e-168() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  2606  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  2427
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  2423  GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  2482

Query  2426  taggqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2247
             TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2483  TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2542

Query  2246  PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  2067
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  2543  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  2602

Query  2066  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  1887
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2603  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2662
```

```
Query  1886  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  1707
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  2663  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  2722

Query  1706  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  1527
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2723  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2782

Query  1526  RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      1407
             RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2783  RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF      2822
```

Range 2: 2423 to 2822

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|-------|--------|--------|------------|-----------|------|-------|
| 556 bits(1433) | 6e-168() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  1241  GGqlqqlqiqhLTSSNVSPGQQTAILLHPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  1062
             GGQLQQLQIQHLTSSNVSPGQQTAILLHPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  2423  GGQLQQLQIQHLTSSNVSPGQQTAILLHPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  2482

Query  1061  tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  882
             TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2483  TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2542

Query  881   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  702
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  2543  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  2602

Query  701   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  522
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2603  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2662

Query  521   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  342
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  2663  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  2722

Query  341   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  162
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2723  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2782

Query  161   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      42
             RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2783  RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF      2822
```

domino, isoform G [Drosophila melanogaster]

Sequence ID: **ref|NP_001286676.1|** Length: 3233  Number of Matches: 2

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

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|-------|--------|--------|------------|-----------|------|-------|
| 556 bits(1432) | 9e-168() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query  2606  GGqlqqlqiqhLTSSNVSPGQQTAILLHPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  2427
             GGQLQQLQIQHLTSSNVSPGQQTAILLHPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct  2458  GGQLQQLQIQHLTSSNVSPGQQTAILLHPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL  2517

Query  2426  tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2247
             TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2518  TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2577

Query  2246  PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  2067
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct  2578  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST  2637

Query  2066  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  1887
             AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2638  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2697

Query  1886  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  1707
             SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct  2698  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG  2757

Query  1706  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  1527
             TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2758  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2817

Query  1526  RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      1407
             RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
```

```
Sbjct   2818    RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF      2857
```

Range 2: 2458 to 2857

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 556 bits(1432) | 9e-168() | Compositional matrix adjust. | 400/400(100%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query   1241    GGglqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl    1062
                GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct   2458    GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL    2517

Query   1061    tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS    882
                TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   2518    TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS    2577

Query   881     PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST    702
                PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct   2578    PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST    2637

Query   701     AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV    522
                AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct   2638    AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV    2697

Query   521     SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG    342
                SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct   2698    SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG    2757

Query   341     TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ    162
                TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct   2758    TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ    2817

Query   161     RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      42
                RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   2818    RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF      2857
```

helicase DOMINO A [Drosophila melanogaster]

Sequence ID: **gb|AAF82185.1|** Length: 3201 Number of Matches: 2

Range 1: 2426 to 2825

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 555 bits(1430) | 1e-167() | Compositional matrix adjust. | 399/400(99%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query   2606    GGglqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl    2427
                GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct   2426    GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL    2485

Query   2426    tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS    2247
                TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQ+LPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   2486    TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQSLPSVVQPQIGSGAQIVSISSQTLPVNSS    2545

Query   2246    PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST    2067
                PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct   2546    PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST    2605

Query   2066    AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV    1887
                AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct   2606    AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV    2665

Query   1886    SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG    1707
                SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct   2666    SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG    2725

Query   1706    TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ    1527
                TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct   2726    TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ    2785

Query   1526    RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      1407
                RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   2786    RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF      2825
```

Range 2: 2426 to 2825

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 555 bits(1430) | 1e-167() | Compositional matrix adjust. | 399/400(99%) | 400/400(100%) | 0/400(0%) | -1 |

Features:

```
Query   1241   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   1062
               GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL
Sbjct   2426   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL   2485

Query   1061   tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   882
               TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQ+LPSVVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   2486   TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQSLPSVVQPQIGSGAQIVSISSQTLPVNSS   2545

Query   881    PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   702
               PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST
Sbjct   2546   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST   2605

Query   701    AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   522
               AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct   2606   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   2665

Query   521    SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG   342
               SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG
Sbjct   2666   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG   2725

Query   341    TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   162
               TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct   2726   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2785

Query   161    RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF   42
               RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   2786   RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF   2825
```

domino, isoform A [Drosophila yakuba]

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

▸ **See 1 more title(s)**

Range 1: 2421 to 2820

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 522 bits(1344) | 4e-156() | Compositional matrix adjust. | 387/400(97%) | 391/400(97%) | 0/400(0%) | -1 |

Features:

```
Query   2606   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   2427
               GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVG SSSL
Sbjct   2421   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGASSSL   2480

Query   2426   tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   2247
               TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQ+LP+VVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   2481   TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQSLPAVVQPQIGSGAQIVSISSQTLPVNSS   2540

Query   2246   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   2067
               PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQ QQQHQTTAVTTLNT MLRGQRIVST
Sbjct   2541   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQQQQQHQTTAVTTLNTAMLRGQRIVST   2600

Query   2066   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   1887
               AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct   2601   AAGNTLQQRTTAGGQSIVSMPNLGQGVSPAQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   2660

Query   1886   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG   1707
               SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TGATANLVQAGG
Sbjct   2661   SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGATANLVQAGG   2720

Query   1706   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   1527
               TIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct   2721   TIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2780

Query   1526   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF   1407
               RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct   2781   RQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF   2820
```

Range 2: 2421 to 2820

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 522 bits(1344) | 4e-156() | Compositional matrix adjust. | 387/400(97%) | 391/400(97%) | 0/400(0%) | -1 |

Features:

```
Query   1241   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   1062
               GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVG SSSL
Sbjct   2421   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGASSSL   2480

Query   1061   tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   882
               TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQ+LP+VVQPQIGSGAQIVSISSQTLPVNSS
Sbjct   2481   TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQSLPAVVQPQIGSGAQIVSISSQTLPVNSS   2540

Query   881    PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   702
               PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQ QQQHQTTAVTTLNT MLRGQRIVST
Sbjct   2541   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQQQQQHQTTAVTTLNTAMLRGQRIVST   2600
```

```
Query  701   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  522
             AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2601  AAGNTLQQRTTAGGQSIVSMPNLGQGVSPAQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2660

Query  521   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  342
             SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TGATANLVQAGG
Sbjct  2661  SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGATANLVQAGG  2720

Query  341   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  162
             TIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2721  TIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2780

Query  161   RQVVSadgttttttaagDMLLVKRHNILAAQKAQQASGALF   42
             RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2781  RQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF   2820
```

domino, isoform B [Drosophila yakuba]

Sequence ID: **ref|XP_015051886.1|**  Length: 3195  Number of Matches: 2

▸ **See 1 more title(s)**

Range 1: 2421 to 2820

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 522 bits(1344) | 4e-156() | Compositional matrix adjust. | 387/400(97%) | 391/400(97%) | 0/400(0%) | -1 |

Features:

```
Query  2606  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  2427
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVG SSSL
Sbjct  2421  GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGASSSL  2480

Query  2426  tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  2247
             TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQ+LP+VVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2481  TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQSLPAVVQPQIGSGAQIVSISSQTLPVNSS  2540

Query  2246  PQLGSIVQTQSLPQvvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  2067
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQ QQQHQTTAVTTLNT MLRGQRIVST
Sbjct  2541  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQQQQQHQTTAVTTLNTAMLRGQRIVST  2600

Query  2066  AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  1887
             AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2601  AAGNTLQQRTTAGGQSIVSMPNLGQGVSPAQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2660

Query  1886  SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  1707
             SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TGATANLVQAGG
Sbjct  2661  SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGATANLVQAGG  2720

Query  1706  TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  1527
             TIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2721  TIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  2780

Query  1526  RQVVSadgttttttaagDMLLVKRHNILAAQKAQQASGALF   1407
             RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2781  RQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF   2820
```

Range 2: 2421 to 2820

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 522 bits(1344) | 4e-156() | Compositional matrix adjust. | 387/400(97%) | 391/400(97%) | 0/400(0%) | -1 |

Features:

```
Query  1241  GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl  1062
             GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVG SSSL
Sbjct  2421  GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGASSSL  2480

Query  1061  tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS  882
             TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQ+LP+VVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2481  TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQSLPAVVQPQIGSGAQIVSISSQTLPVNSS  2540

Query  881   PQLGSIVQTQSLPQvvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST  702
             PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQ QQQHQTTAVTTLNT MLRGQRIVST
Sbjct  2541  PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQQQQQHQTTAVTTLNTAMLRGQRIVST  2600

Query  701   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  522
             AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2601  AAGNTLQQRTTAGGQSIVSMPNLGQGVSPAQFQTQLRLAAVPTSPATQTTQLVTTKGIPV  2660

Query  521   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG  342
             SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TGATANLVQAGG
Sbjct  2661  SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGATANLVQAGG  2720

Query  341   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ  162
             TIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
```

```
Sbjct  2721   TIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2780

Query  161    RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      42
              RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2781   RQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF   2820
```

uncharacterized protein Dere_GG22110, isoform A [Drosophila erecta]

Sequence ID: **ref|XP_001975047.1|** Length: 3193  Number of Matches: 2

▸ **See 1 more title(s)**

Range 1: 2420 to 2819

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|-------|--------|--------|-----------|-----------|------|-------|
| 521 bits(1341) | 9e-156() | Compositional matrix adjust. | 387/400(97%) | 390/400(97%) | 0/400(0%) | -1 |

Features:

```
Query  2606   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   2427
              GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVG SSSL
Sbjct  2420   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGASSSL   2479

Query  2426   tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   2247
              TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQTLP+VVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2480   TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQTLPAVVQPQIGSGAQIVSISSQTLPVNSS   2539

Query  2246   PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   2067
              PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQ QQQHQTTAVTTLNT MLRGQRIVST
Sbjct  2540   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQQQQQHQTTAVTTLNTAMLRGQRIVST   2599

Query  2066   AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   1887
              AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2600   AAGNTLQQRTTAGGQSIVSMPNLGQGVSPAQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   2659

Query  1886   SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG   1707
              SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TG TANLVQAGG
Sbjct  2660   SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGPTANLVQAGG   2719

Query  1706   TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   1527
              TIIQAS+M THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2720   TIIQASSMGTHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2779

Query  1526   RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      1407
              RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2780   RQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF   2819
```

Range 2: 2420 to 2819

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|-------|--------|--------|-----------|-----------|------|-------|
| 521 bits(1341) | 9e-156() | Compositional matrix adjust. | 387/400(97%) | 390/400(97%) | 0/400(0%) | -1 |

Features:

```
Query  1241   GGqlqqlqiqhLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssl   1062
              GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVG SSSL
Sbjct  2420   GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGASSSL   2479

Query  1061   tagqlqqlaqqsavasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS   882
              TAGQLQQLAQQSA ASGGQSSVSVVLTTPVQTLP+VVQPQIGSGAQIVSISSQTLPVNSS
Sbjct  2480   TAGQLQQLAQQSAAASGGQSSVSVVLTTPVQTLPAVVQPQIGSGAQIVSISSQTLPVNSS   2539

Query  881    PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST   702
              PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQ QQQHQTTAVTTLNT MLRGQRIVST
Sbjct  2540   PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQQQQQHQTTAVTTLNTAMLRGQRIVST   2599

Query  701    AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   522
              AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV
Sbjct  2600   AAGNTLQQRTTAGGQSIVSMPNLGQGVSPAQFQTQLRLAAVPTSPATQTTQLVTTKGIPV   2659

Query  521    SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG   342
              SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TG TANLVQAGG
Sbjct  2660   SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGPTANLVQAGG   2719

Query  341    TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   162
              TIIQAS+M THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ
Sbjct  2720   TIIQASSMGTHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ   2779

Query  161    RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF      42
              RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  2780   RQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF   2819
```

uncharacterized protein Dana_GF12812, isoform B [Drosophila ananassae]

Sequence ID: **ref|XP_014763429.1|** Length: 3184 Number of Matches: 2

Range 1: 2425 to 2805

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 436 bits(1122) | 9e-127() | Compositional matrix adjust. | 337/385(88%) | 350/385(90%) | 7/385(1%) | -1 |

Features:

```
Query  2570  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  2391
             T + VSPGQQTAILLHQPQQQLRTHPGQ GQ+ TQQLVKTIVGTSSSLTAGQLQQLAQQS
Sbjct  2425  TGATVSPGQQTAILLHQPQQQLRTHPGQAGQTTTQQLVKTIVGTSSSLTAGQLQQLAQQS  2484

Query  2390  avasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  2214
             A  SGGQSSVSVVLTTPVQ+LP+VVQPQ GSGAQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2485  AANSGGQSSVSVVLTTPVQSLPAVVQPQTGSGAQIVSISSQTTLPVNSSPQLGSIVQTQT  2544

Query  2213  LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT  2034
             LPQVVSVSTLPTVG+VLTTTA    QQ QTT VTTLNT MLRGQRIVS AAGNTLQQRTT
Sbjct  2545  LPQVVSVSTLPTVGSVLTTTA---SQQQQTTGVTTLNTAMLRGQRIVSAAAGNTLQQRTT  2601

Query  2033  AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV  1854
             AGGQSIVSMPNLGQG +  QFQ QLRLAAVP+SPATQTTQLVTTKGIPVSALQQGGKTTV
Sbjct  2602  AGGQSIVSMPNLGQGVN-QQFQAQLRLAAVPSSPATQTTQLVTTKGIPVSALQQGGKTTV  2660

Query  1853  IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatA--NLVQAGGTIIQASNMA  1680
             IP TQQ GGAHIQLYRQRSLKVLQTTTQA    G+A  T   A  +LVQAGGTIIQASNM
Sbjct  2661  IPGTQQPGGAHIQLYRQRSLKVLQTTTQAAAGGAAAGTAGGATTSLVQAGGTIIQASNMP  2720

Query  1679  THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt  1500
             THVTSQKVAVSG+PG+STTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQVV+ADGT
Sbjct  2721  THVTSQKVAVSGIPGSSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVVAADGT  2780

Query  1499  ttttaagDMLLVKRHNILAAQKAQQ  1425
             TTTT AGDMLLVKRHNILAAQKAQQ
Sbjct  2781  TTTTGAGDMLLVKRHNILAAQKAQQ  2805
```

Range 2: 2425 to 2805

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 436 bits(1122) | 9e-127() | Compositional matrix adjust. | 337/385(88%) | 350/385(90%) | 7/385(1%) | -1 |

Features:

```
Query  1205  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  1026
             T + VSPGQQTAILLHQPQQQLRTHPGQ GQ+ TQQLVKTIVGTSSSLTAGQLQQLAQQS
Sbjct  2425  TGATVSPGQQTAILLHQPQQQLRTHPGQAGQTTTQQLVKTIVGTSSSLTAGQLQQLAQQS  2484

Query  1025  avasgggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  849
             A  SGGQSSVSVVLTTPVQ+LP+VVQPQ GSGAQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2485  AANSGGQSSVSVVLTTPVQSLPAVVQPQTGSGAQIVSISSQTTLPVNSSPQLGSIVQTQT  2544

Query  848   LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT  669
             LPQVVSVSTLPTVG+VLTTTA    QQ QTT VTTLNT MLRGQRIVS AAGNTLQQRTT
Sbjct  2545  LPQVVSVSTLPTVGSVLTTTA---SQQQQTTGVTTLNTAMLRGQRIVSAAAGNTLQQRTT  2601

Query  668   AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV  489
             AGGQSIVSMPNLGQG +  QFQ QLRLAAVP+SPATQTTQLVTTKGIPVSALQQGGKTTV
Sbjct  2602  AGGQSIVSMPNLGQGVN-QQFQAQLRLAAVPSSPATQTTQLVTTKGIPVSALQQGGKTTV  2660

Query  488   IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatA--NLVQAGGTIIQASNMA  315
             IP TQQ GGAHIQLYRQRSLKVLQTTTQA    G+A  T   A  +LVQAGGTIIQASNM
Sbjct  2661  IPGTQQPGGAHIQLYRQRSLKVLQTTTQAAAGGAAAGTAGGATTSLVQAGGTIIQASNMP  2720

Query  314   THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt  135
             THVTSQKVAVSG+PG+STTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQVV+ADGT
Sbjct  2721  THVTSQKVAVSGIPGSSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVVAADGT  2780

Query  134   ttttaagDMLLVKRHNILAAQKAQQ  60
             TTTT AGDMLLVKRHNILAAQKAQQ
Sbjct  2781  TTTTGAGDMLLVKRHNILAAQKAQQ  2805
```

uncharacterized protein Dana_GF12812, isoform A [Drosophila ananassae]
Sequence ID: **ref|XP_001959323.1|** Length: 3199 Number of Matches: 2

Range 1: 2425 to 2805

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 436 bits(1122) | 9e-127() | Compositional matrix adjust. | 337/385(88%) | 350/385(90%) | 7/385(1%) | -1 |

Features:

```
Query  2570  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  2391
             T + VSPGQQTAILLHQPQQQLRTHPGQ GQ+ TQQLVKTIVGTSSSLTAGQLQQLAQQS
Sbjct  2425  TGATVSPGQQTAILLHQPQQQLRTHPGQAGQTTTQQLVKTIVGTSSSLTAGQLQQLAQQS  2484

Query  2390  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  2214
             A   SGGQSSVSVVLTTPVQ+LP+VVQPQ GSGAQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2485  AANSGGQSSVSVVLTTPVQSLPAVVQPQTGSGAQIVSISSQTTLPVNSSPQLGSIVQTQT  2544

Query  2213  LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT  2034
             LPQVVSVSTLPTVG+VLTTTA   QQ QTT VTTLNT MLRGQRIVS AAGNTLQQRTT
Sbjct  2545  LPQVVSVSTLPTVGSVLTTTA---SQQQQTTGVTTLNTAMLRGQRIVSAAAGNTLQQRTT  2601

Query  2033  AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV  1854
             AGGQSIVSMPNLGQG +  QFQ QLRLAAVP+SPATQTTQLVTTKGIPVSALQQGGKTTV
Sbjct  2602  AGGQSIVSMPNLGQGVN-QQFQAQLRLAAVPSSPATQTTQLVTTKGIPVSALQQGGKTTV  2660

Query  1853  IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatA--NLVQAGGTIIQASNMA  1680
             IP TQQ GGAHIQLYRQRSLKVLQTTTQA   G+A  T   A  +LVQAGGTIIQASNM
Sbjct  2661  IPGTQQPGGAHIQLYRQRSLKVLQTTTQAAAGGAAAGTAGGATTSLVQAGGTIIQASNMP  2720

Query  1679  THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt  1500
             THVTSQKVAVSG+PG+STTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQVV+ADGT
Sbjct  2721  THVTSQKVAVSGIPGSSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVVAADGT  2780

Query  1499  ttttaagDMLLVKRHNILAAQKAQQ  1425
             TTTT AGDMLLVKRHNILAAQKAQQ
Sbjct  2781  TTTTGAGDMLLVKRHNILAAQKAQQ  2805
```

Range 2: 2425 to 2805

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 436 bits(1122) | 9e-127() | Compositional matrix adjust. | 337/385(88%) | 350/385(90%) | 7/385(1%) | -1 |

Features:

```
Query  1205  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  1026
             T + VSPGQQTAILLHQPQQQLRTHPGQ GQ+ TQQLVKTIVGTSSSLTAGQLQQLAQQS
Sbjct  2425  TGATVSPGQQTAILLHQPQQQLRTHPGQAGQTTTQQLVKTIVGTSSSLTAGQLQQLAQQS  2484

Query  1025  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  849
             A   SGGQSSVSVVLTTPVQ+LP+VVQPQ GSGAQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2485  AANSGGQSSVSVVLTTPVQSLPAVVQPQTGSGAQIVSISSQTTLPVNSSPQLGSIVQTQT  2544

Query  848   LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT  669
             LPQVVSVSTLPTVG+VLTTTA   QQ QTT VTTLNT MLRGQRIVS AAGNTLQQRTT
Sbjct  2545  LPQVVSVSTLPTVGSVLTTTA---SQQQQTTGVTTLNTAMLRGQRIVSAAAGNTLQQRTT  2601

Query  668   AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV  489
             AGGQSIVSMPNLGQG +  QFQ QLRLAAVP+SPATQTTQLVTTKGIPVSALQQGGKTTV
Sbjct  2602  AGGQSIVSMPNLGQGVN-QQFQAQLRLAAVPSSPATQTTQLVTTKGIPVSALQQGGKTTV  2660

Query  488   IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatA--NLVQAGGTIIQASNMA  315
             IP TQQ GGAHIQLYRQRSLKVLQTTTQA   G+A  T   A  +LVQAGGTIIQASNM
Sbjct  2661  IPGTQQPGGAHIQLYRQRSLKVLQTTTQAAAGGAAAGTAGGATTSLVQAGGTIIQASNMP  2720

Query  314   THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt  135
             THVTSQKVAVSG+PG+STTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQVV+ADGT
Sbjct  2721  THVTSQKVAVSGIPGSSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVVAADGT  2780

Query  134   ttttaagDMLLVKRHNILAAQKAQQ  60
             TTTT AGDMLLVKRHNILAAQKAQQ
Sbjct  2781  TTTTGAGDMLLVKRHNILAAQKAQQ  2805
```

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

▶ **See 1 more title(s)**
Range 1: 2505 to 2895

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 427 bits(1099) | 9e-124() | Compositional matrix adjust. | 328/395(83%) | 347/395(87%) | 6/395(1%) | -1 |

Features:

```
Query  2570  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  2391
             TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS
Sbjct  2505  TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS  2564

Query  2390  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  2214
             A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2565  AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT  2624

Query  2213  LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT  2037
```

```
         LPQVVSVSTLPTV    + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  2625  LPQVVSVSTLPTVGSVLTTTASQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT  2684

Query  2036  TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT  1857
              A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT
Sbjct  2685  NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT  2743

Query  1856  VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT  1677
              VIP TQQ GGAHIQLYRQRSLKVLQT   V  G+AG   ATANLVQ  GTIIQA NM T
Sbjct  2744  VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGGVATANLVQTAGTIIQAGNMPT  2802

Query  1676  HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt  1497
              HVTSQKVAVSGMPG    VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  2803  HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST  2860

Query  1496  tttaagDMLLVKRHNILAAQKAQQASGALFTTTTG   1392
              T+ AAGDMLLVKRHNILA QKAQQA+GALFTTTT
Sbjct  2861  TSAAAGDMLLVKRHNILATQKAQQATGALFTTTTA   2895
```

Range 2: 2505 to 2890

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 421 bits(1082) | 2e-121() | Compositional matrix adjust. | 324/390(83%) | 343/390(87%) | 6/390(1%) | -1 |

Features:

```
Query  1205  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagglqqlaqqs  1026
              TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS
Sbjct  2505  TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS  2564

Query  1025  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  849
              A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2565  AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT  2624

Query  848   LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT  672
              LPQVVSVSTLPTV   + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  2625  LPQVVSVSTLPTVGSVLTTTASQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT  2684

Query  671   TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT  492
              A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT
Sbjct  2685  NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT  2743

Query  491   VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT  312
              VIP TQQ GGAHIQLYRQRSLKVLQT   V  G+AG   ATANLVQ  GTIIQA NM T
Sbjct  2744  VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGGVATANLVQTAGTIIQAGNMPT  2802

Query  311   HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt  132
              HVTSQKVAVSGMPG    VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  2803  HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST  2860

Query  131   tttaagDMLLVKRHNILAAQKAQQASGALF   42
              T+ AAGDMLLVKRHNILA QKAQQA+GALF
Sbjct  2861  TSAAAGDMLLVKRHNILATQKAQQATGALF   2890
```

uncharacterized protein Dpse_GA24314, isoform D [Drosophila pseudoobscura pseudoobscura]
Sequence ID: **ref|XP_015040038.1|** Length: 3305 Number of Matches: 2

▸ **See 3 more title(s)**
Range 1: 2540 to 2930

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 427 bits(1098) | 1e-123() | Compositional matrix adjust. | 328/395(83%) | 347/395(87%) | 6/395(1%) | -1 |

Features:

```
Query  2570  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagglqqlaqqs  2391
              TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS
Sbjct  2540  TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS  2599

Query  2390  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  2214
              A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2600  AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT  2659

Query  2213  LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT  2037
              LPQVVSVSTLPTV   + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  2660  LPQVVSVSTLPTVGSVLTTTASQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT  2719

Query  2036  TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT  1857
              A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT
Sbjct  2720  NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT  2778

Query  1856  VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT  1677
              VIP TQQ GGAHIQLYRQRSLKVLQT   V  G+AG   ATANLVQ  GTIIQA NM T
Sbjct  2779  VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGGVATANLVQTAGTIIQAGNMPT  2837
```

```
Query  1676   HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt   1497
              HVTSQKVAVSGMPG   VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  2838   HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST   2895

Query  1496   tttaagDMLLVKRHNILAAQKAQQASGALFTTTTG   1392
              T+ AAGDMLLVKRHNILA QKAQQA+GALFTTTT
Sbjct  2896   TSAAAGDMLLVKRHNILATQKAQQATGALFTTTTA   2930
```

Range 2: 2540 to 2925

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 420 bits(1080) | 3e-121() | Compositional matrix adjust. | 324/390(83%) | 343/390(87%) | 6/390(1%) | -1 |

Features:

```
Query  1205   TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs   1026
              TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS
Sbjct  2540   TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS   2599

Query  1025   avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS   849
              A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2600   AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT   2659

Query  848    LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT   672
              LPQVVSVSTLPTV  + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  2660   LPQVVSVSTLPTVGSVLTTTASQQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT   2719

Query  671    TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT   492
               A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT
Sbjct  2720   NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT   2778

Query  491    VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT   312
              VIP TQQ GGAHIQLYRQRSLKVLQT    V  G+AG    ATANLVQ  GTIIQA NM T
Sbjct  2779   VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGVATANLVQTAGTIIQAGNMPT   2837

Query  311    HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt   132
              HVTSQKVAVSGMPG   VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  2838   HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST   2895

Query  131    tttaagDMLLVKRHNILAAQKAQQASGALF   42
              T+ AAGDMLLVKRHNILA QKAQQA+GALF
Sbjct  2896   TSAAAGDMLLVKRHNILATQKAQQATGALF   2925
```

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

▸ **See 1 more title(s)**
Range 1: 2540 to 2930

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 426 bits(1095) | 3e-123() | Compositional matrix adjust. | 328/395(83%) | 347/395(87%) | 6/395(1%) | -1 |

Features:

```
Query  2570   TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs   2391
              TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS
Sbjct  2540   TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS   2599

Query  2390   avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS   2214
              A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2600   AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT   2659

Query  2213   LPQvvsvstlptv-gtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT   2037
              LPQVVSVSTLPTV  + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  2660   LPQVVSVSTLPTVGSVLTTTASQQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT   2719

Query  2036   TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT   1857
               A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT
Sbjct  2720   NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT   2778

Query  1856   VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT   1677
              VIP TQQ GGAHIQLYRQRSLKVLQT    V  G+AG    ATANLVQ  GTIIQA NM T
Sbjct  2779   VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGVATANLVQTAGTIIQAGNMPT   2837

Query  1676   HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt   1497
              HVTSQKVAVSGMPG   VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  2838   HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST   2895

Query  1496   tttaagDMLLVKRHNILAAQKAQQASGALFTTTTG   1392
              T+ AAGDMLLVKRHNILA QKAQQA+GALFTTTT
Sbjct  2896   TSAAAGDMLLVKRHNILATQKAQQATGALFTTTTA   2930
```

Range 2: 2540 to 2925

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 419 bits(1078) | 6e-121() | Compositional matrix adjust. | 324/390(83%) | 343/390(87%) | 6/390(1%) | -1 |

Features:

```
Query  1205  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  1026
             TS+NVSPGQQTAILLHQPQQQ+RTHPGQG QS TQQLVKTIVGTSS+LTAGQLQQLAQQS
Sbjct  2540  TSANVSPGQQTAILLHQPQQQMRTHPGQGQQSATQQLVKTIVGTSSNLTAGQLQQLAQQS  2599

Query  1025  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  849
             A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  2600  AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT  2659

Query  848   LPQvvsvstlptv-gtvltttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRT  672
             LPQVVSVSTLPTV   + TT + Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  2660  LPQVVSVSTLPTVGSVLTTTASQQQQQQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRT  2719

Query  671   TAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTT  492
              A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT
Sbjct  2720  NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT  2778

Query  491   VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT  312
             VIP TQQ GGAHIQLYRQRSLKVLQT     V  G+AG   ATANLVQ  GTIIQA NM T
Sbjct  2779  VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGGVATANLVQTAGTIIQAGNMPT  2837

Query  311   HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt  132
             HVTSQKVAVSGMPG    VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  2838  HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST  2895

Query  131   tttaagDMLLVKRHNILAAQKAQQASGALF      42
             T+ AAGDMLLVKRHNILA QKAQQA+GALF
Sbjct  2896  TSAAAGDMLLVKRHNILATQKAQQATGALF      2925
```

GL16841 [Drosophila persimilis]

Sequence ID: **ref|XP_002018288.1|** Length: 2139 Number of Matches: 2

▶ **See 1 more title(s)**

Range 1: 1374 to 1762

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 422 bits(1086) | 9e-123() | Compositional matrix adjust. | 332/395(84%) | 351/395(88%) | 8/395(2%) | -1 |

Features:

```
Query  2570  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  2391
             TS+NVSPGQQTAILLHQPQQQ+RTHP QG QS TQQLVKTIVGTSS+LTAGQLQQLA QS
Sbjct  1374  TSANVSPGQQTAILLHQPQQQMRTHPVQGQQSATQQLVKTIVGTSSNLTAGQLQQLAHQS  1433

Query  2390  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  2214
             A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  1434  AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT  1493

Query  2213  LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT  2034
             LPQVVSVSTLPTVG+VLTTTA+Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  1494  LPQVVSVSTLPTVGSVLTTTASQ-QQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRTN  1552

Query  2033  AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV  1854
             A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTTV
Sbjct  1553  AAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTTV  1611

Query  1853  IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVP-sgsagatgatANLVQAGGTIIQASNMAT  1677
             IP TQQ GGAHIQLYRQRSLKVLQ   TQ P  G+AG   ATANLVQ  GTIIQA NM T
Sbjct  1612  IPGTQQPGGAHIQLYRQRSLKVLQ--TQPAPVGGTAGGGVATANLVQTAGTIIQAGNMPT  1669

Query  1676  HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt  1497
             HVTSQKVAVSGMPG    VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  1670  HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST  1727

Query  1496  tttaagDMLLVKRHNILAAQKAQQASGALFTTTTG    1392
             T+ AAGDMLLVKRHNILA QKAQQA+GALFTTTT
Sbjct  1728  TSAAAGDMLLVKRHNILATQKAQQATGALFTTTTA    1762
```

Range 2: 1374 to 1757

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 416 bits(1069) | 2e-120() | Compositional matrix adjust. | 328/390(84%) | 347/390(88%) | 8/390(2%) | -1 |

Features:

```
Query  1205  TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs  1026
             TS+NVSPGQQTAILLHQPQQQ+RTHP QG QS TQQLVKTIVGTSS+LTAGQLQQLA QS
Sbjct  1374  TSANVSPGQQTAILLHQPQQQMRTHPVQGQQSATQQLVKTIVGTSSNLTAGQLQQLAHQS  1433
```

```
Query  1025  avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS  849
             A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+
Sbjct  1434  AAANPGQSSVSVVLTTPVQSLPAVVQTQGSSAAQIVSISSQTTLPVNSSPQLGSIVQTQT  1493

Query   848  LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT  669
             LPQVVSVSTLPTVG+VLTTTA+Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT
Sbjct  1494  LPQVVSVSTLPTVGSVLTTTASQ-QQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRTN  1552

Query   668  AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV  489
             A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTTV
Sbjct  1553  AAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTTV  1611

Query   488  IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVP-sgsagatgatANLVQAGGTIIQASNMAT  312
             IP TQQ GGAHIQLYRQRSLKVLQ   TQ  P  G+AG   ATANLVQ  GTIIQA NM T
Sbjct  1612  IPGTQQPGGAHIQLYRQRSLKVLQ--TQPAPVGGTAGGGVATANLVQTAGTIIQAGNMPT  1669

Query   311  HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt  132
             HVTSQKVAVSGMPG   VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T
Sbjct  1670  HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST  1727

Query   131  tttaagDMLLVKRHNILAAQKAQQASGALF   42
             T+ AAGDMLLVKRHNILA QKAQQA+GALF
Sbjct  1728  TSAAAGDMLLVKRHNILATQKAQQATGALF   1757
```

GH12111p [Drosophila melanogaster]

Sequence ID: **gb|AAM48336.1|**  Length: 591  Number of Matches: 2
Range 1: 1 to 230

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 382 bits(980) | 7e-117() | Compositional matrix adjust. | 230/230(100%) | 230/230(100%) | 0/230(0%) | -1 |

Features:

```
Query  2096  MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT  1917
             MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT
Sbjct     1  MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT    60

Query  1916  QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatg  1737
             QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG
Sbjct    61  QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG   120

Query  1736  atANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK  1557
             ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK
Sbjct   121  ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK   180

Query  1556  QMAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF  1407
             QMAAGKQQLQRQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   181  QMAAGKQQLQRQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF   230
```

Range 2: 1 to 230

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 382 bits(980) | 7e-117() | Compositional matrix adjust. | 230/230(100%) | 230/230(100%) | 0/230(0%) | -1 |

Features:

```
Query   731  MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT   552
             MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT
Sbjct     1  MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT    60

Query   551  QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatg   372
             QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG
Sbjct    61  QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG   120

Query   371  atANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK   192
             ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK
Sbjct   121  ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK   180

Query   191  QMAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF   42
             QMAAGKQQLQRQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF
Sbjct   181  QMAAGKQQLQRQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF   230
```

uncharacterized protein Dsimw501_GD11590 [Drosophila simulans]

Sequence ID: **gb|KMY95527.1|**  Length: 591  Number of Matches: 2
Range 1: 1 to 230

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 382 bits(980) | 8e-117() | Compositional matrix adjust. | 229/230(99%) | 229/230(99%) | 0/230(0%) | -1 |

Features:

```
Query  2096  MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT  1917
             MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT
Sbjct  1     MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT  60

Query  1916  QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatg  1737
             QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG
Sbjct  61    QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG  120

Query  1736  atANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK  1557
             ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK
Sbjct  121   ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK  180

Query  1556  QMAAGKQQLQRQVVSadgttttaagDMLLVKRHNILAAQKAQQASGALF  1407
             QMAAGKQQLQRQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  181   QMAAGKQQLQRQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF  230
```

Range 2: 1 to 230

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 382 bits(980) | 8e-117() | Compositional matrix adjust. | 229/230(99%) | 229/230(99%) | 0/230(0%) | -1 |

Features:

```
Query  731   MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT  552
             MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT
Sbjct  1     MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT  60

Query  551   QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatg  372
             QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG
Sbjct  61    QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG  120

Query  371   atANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK  192
             ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK
Sbjct  121   ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK  180

Query  191   QMAAGKQQLQRQVVSadgttttaagDMLLVKRHNILAAQKAQQASGALF  42
             QMAAGKQQLQRQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  181   QMAAGKQQLQRQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF  230
```

uncharacterized protein Dmoj_GI19071 [Drosophila mojavensis]
Sequence ID: **ref|XP_002005439.2|** Length: 3285 Number of Matches: 2

▸ **See 1 more title(s)**
Range 1: 2539 to 2858

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 320 bits(820) | 2e-87() | Compositional matrix adjust. | 224/334(67%) | 246/334(73%) | 32/334(9%) | -1 |

Features:

```
Query  2342  PVQTLPSVVQPQIGSGAQIVSISSQ-TLPVNSSPQLGSIVQTQSLPQvvsvstlptvgtv  2166
             PVQ+LP +     GS AQIVSISSQ TLPVN++PQ+GSIVQTQ+LPQVVSV  L T  T
Sbjct  2539  PVQSLP-IATHNNGSTAQIVSISSQSTLPVNTAPQVGSIVQTQTLPQVVSVGPLTTTATG  2597

Query  2165  lttTANQPQQQHQttavttlntTMLRGQRIVSTAAG--NTLQ-----QRTTAGGQSIVSM  2007
                      T    TMLRGQRIVS A G  NTLQ     QRTTAGGQSIVSM
Sbjct  2598  QQQQQ---------QQQATGVTMLRGQRIVSAAGGGGNTLQDVVLQQRTTAGGQSIVSM  2648

Query  2006  PNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGG  1827
             P+LGQG +P+QFQTQLRLAAV  SPATQTTQLVTTKGIPVSALQQGGK TV+P TQQ
Sbjct  2649  PSLGQGVTPAQFQTQLRLAAVSGSPATQTTQLVTTKGIPVSALQQGGK-TVLPGTQQQ-A  2706

Query  1826  AHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAG-----GTIIQASNM---ATHV  1671
             AHIQLYRQR+LKVLQ  +Q  P +        + AG    GTIIQASN+   +THV
Sbjct  2707  AHIQLYRQRNLKVLQ-ASQGAPGTATAGGLNPTVVQTAGGALATGTIIQASNLMQTSTHV  2765

Query  1670  TSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtttt  1491
             TSQKVAVSGMPG +TTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQV++ DG+  +
Sbjct  2766  TSQKVAVSGMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVLTTDGSGAS  2824

Query  1490  ta--agDMLLVKRHNILAAQKAQQASGALFTTTT  1395
              A    DMLLVKRHNILAAQKAQQA+G LFTTTT
Sbjct  2825  VAPGTSDMLLVKRHNILAAQKAQQATGPLFTTTT  2858
```

Range 2: 2539 to 2854

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 313 bits(803) | 3e-85() | Compositional matrix adjust. | 220/330(67%) | 242/330(73%) | 32/330(9%) | -1 |

Features:

```
Query  977   PVQTLPSVVQPQIGSGAQIVSISSQ-TLPVNSSPQLGSIVQTQSLPQvvsvstlptvgtv  801
             PVQ+LP +     GS AQIVSISSQ TLPVN++PQ+GSIVQTQ+LPQVVSV  L T  T
Sbjct  2539  PVQSLP-IATHNNGSTAQIVSISSQSTLPVNTAPQVGSIVQTQTLPQVVSVGPLTTTATG  2597

Query  800   lttTANQPQQQHQttavttlntTMLRGQRIVSTAAG--NTLQ-----QRTTAGGQSIVSM  642
                T     TMLRGQRIVS A G  NTLQ      QRTTAGGQSIVSM
Sbjct  2598  QQQQQ---------QQQATGTVTMLRGQRIVSAAGGGGNTLQDVVLQQRTTAGGQSIVSM  2648

Query  641   PNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGG  462
             P+LGQG +P+QFQTQLRLAAV  SPATQTTQLVTTKGIPVSALQQGGK TV+P TQQ
Sbjct  2649  PSLGQGVTPAQFQTQLRLAAVSGSPATQTTQLVTTKGIPVSALQQGGK-TVLPGTQQQ-A  2706

Query  461   AHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAG-----GTIIQASNM---ATHV  306
             AHIQLYRQR+LKVLQ  +Q  P  +      +  AG      GTIIQASN+   +THV
Sbjct  2707  AHIQLYRQRNLKVLQ-ASQGAPGTATAGGLNPTVVQTAGGALATGTIIQASNLMQTSTHV  2765

Query  305   TSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtttt  126
             TSQKVAVSGMPG +TTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQV++ DG+  +
Sbjct  2766  TSQKVAVSGMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVLTTDGSGAS  2824

Query  125   ta--agDMLLVKRHNILAAQKAQQASGALF    42
              A    DMLLVKRHNILAAQKAQQA+G LF
Sbjct  2825  VAPGTSDMLLVKRHNILAAQKAQQATGPLF  2854
```


uncharacterized protein Dwil_GK20897 [Drosophila willistoni]

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

▸ **See 1 more title(s)**

Range 1: 2477 to 2871

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 318 bits(816) | 5e-87() | Compositional matrix adjust. | 281/411(68%) | 299/411(72%) | 36/411(8%) | -1 |

Features:

```
Query  2567  SSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqsa  2388
             ++NVS GQQTAILLHQ  Q +   G  + TQQLVKTIVGTSSSL AGQLQQLA
Sbjct  2477  TANVSTGQQTAILLHQTTPQQQQQMRTGQTTTTQQLVKTIVGTSSSLMAGQLQQLAAAGG  2536

Query  2387  vasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQSL  2211
              A+ G +SVSVVLTTPVQTLP+VVQ Q  SGAQIVSISSQT LPV+S+PQLGSIVQTQ+L
Sbjct  2537  NATTGPTSVSVVLTTPVQTLPAVVQTQNQSGAQIVSISSQTSLPVSSAPQLGSIVQTQTL  2596

Query  2210  PQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTA  2031
             PQVVSV ++ T            TAVTTLN  MLRGQRIVS   GNT+QQRTT
Sbjct  2597  PQVVSVGSVLTTTASQQQQT---------TAVTTLNAAMLRGQRIVSAGPGNTVQQRTTG  2647

Query  2030  GGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQ--TTQLVTTKGIPVSALQQGGKTT  1857
              GQSIVSMP+LGQ   P QFQT +RLAAVP + A   TTQLVTTKGIPVSALQQGGKT
Sbjct  2648  TGQSIVSMPSLGQNVGP-QFQTHVRLAAVPAAQAGNQTTQLVTTKGIPVSALQQGGKT-  2705

Query  1856  VIPVTQQS-GGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatA--------NL-----V  1719
             VIP TQQ  GGAHIQLYRQRSLKVLQTT  A P G A AT         NL     V
Sbjct  2706  VIPGTQQQPGGAHIQLYRQRSLKVLQTT--AAPQGGATATAGGVAGGAGNSGNLTNPTVV  2763

Query  1718  QAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGK  1539
             Q  GTIIQ SNM THVTSQKVAVSGMPG +TTVQAGNVVSSVQMH QARTQ IKQMAA K
Sbjct  2764  QTAGTIIQTSNMPTHVTSQKVAVSGMPG-ATTVQAGNVVSSVQMHQQARTQLIKQMAANK  2822

Query  1538  QQLQRQVVS---adgtttttaagDMLLVKRHNILAAQKAQQASGALFTTTT    1395
             Q LQRQVVS     T TTT  GDMLLVKRHNIL AQK QQ + ALFTTTT
Sbjct  2823  QGLQRQVVSADGTTTTATTTTGGDMLLVKRHNIL-AQKGQQGT-ALFTTTT    2871
```


Range 2: 2477 to 2867

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 312 bits(799) | 8e-85() | Compositional matrix adjust. | 277/407(68%) | 295/407(72%) | 36/407(8%) | -1 |

Features:

```
Query  1202  SSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqsa  1023
             ++NVS GQQTAILLHQ  Q +   G  + TQQLVKTIVGTSSSL AGQLQQLA
Sbjct  2477  TANVSTGQQTAILLHQTTPQQQQQMRTGQTTTTQQLVKTIVGTSSSLMAGQLQQLAAAGG  2536

Query  1022  vasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQSL  846
              A+ G +SVSVVLTTPVQTLP+VVQ Q  SGAQIVSISSQT LPV+S+PQLGSIVQTQ+L
Sbjct  2537  NATTGPTSVSVVLTTPVQTLPAVVQTQNQSGAQIVSISSQTSLPVSSAPQLGSIVQTQTL  2596

Query  845   PQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTA  666
             PQVVSV ++ T            TAVTTLN  MLRGQRIVS   GNT+QQRTT
Sbjct  2597  PQVVSVGSVLTTTASQQQQT---------TAVTTLNAAMLRGQRIVSAGPGNTVQQRTTG  2647

Query  665   GGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQ--TTQLVTTKGIPVSALQQGGKTT  492
```

```
                 GQSIVSMP+LGQ    P QFQT +RLAAVP + A    TTQLVTTKGIPVSALQQGGKT
Sbjct  2648   TGQSIVSMPSLGQNVGP-QFQTHVRLAAVPAAQAGNQTTTQLVTTKGIPVSALQQGGKT-  2705

Query   491   VIPVTQQS-GGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatA--------NL-----V  354
                 VIP TQQ  GGAHIQLYRQRSLKVLQTT  A P G A AT          NL     V
Sbjct  2706   VIPGTQQQPGGAHIQLYRQRSLKVLQTT--AAPQGGATATAGGVAGGAGNSGNLTNPTVV  2763

Query   353   QAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGK  174
                 Q  GTIIQ SNM THVTSQKVAVSGMPG +TTVQAGNVVSSVQMH QARTQ IKQMAA K
Sbjct  2764   QTAGTIIQTSNMPTHVTSQKVAVSGMPG-ATTVQAGNVVSSVQMHQQARTQLIKQMAANK  2822

Query   173   QQLQRQVVS---adgtttttaagDMLLVKRHNILAAQKAQQASGALF    42
                 Q LQRQVVS     T TTT  GDMLLVKRHNIL AQK QQ + ALF
Sbjct  2823   QGLQRQVVSADGTTTTTATTTTGGDMLLVKRHNIL-AQKGQQGT-ALF    2867
```

LOW QUALITY PROTEIN: uncharacterized protein Dvir_GJ20044 [Drosophila virilis]

Sequence ID: **ref|XP_002050736.2|**  Length: 3172  Number of Matches: 2

▸ **See 1 more title(s)**

Range 1: 2490 to 2817

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 301 bits(771) | 3e-81() | Compositional matrix adjust. | 220/336(65%) | 240/336(71%) | 28/336(8%) | -1 |

Features:

```
Query  2342   PVQTLPSVVQPQI--GSGAQIVSISSQT-LPVNSSPQLGSIVQTQSLPQvvsvstlptvg  2172
                 PVQ+LP    +  GS AQIVSISSQT LPVN++PQLGSIVQTQ+LPQVVSV  L T
Sbjct  2490   PVQSLPIATHSNVNAGSTAQIVSISSQTTLPVNTAPQLGSIVQTQTLPQVVSVGPLTTTA  2549

Query  2171   tvlttTANQPQQQHQttavttlntTMLRGQRIVSTAA--GNTLQ-----QRTTAGGQSIV  2013
                 T      Q     Q     T   TMLRGQRIVST A  GNTLQ     QRTTAGGQSIV
Sbjct  2550   TGQQQQQQQ-----QQQQTATGTVTMLRGQRIVSTGAAGGNTLQDVVLQQRTTAGGQSIV  2604

Query  2012   SMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQS  1833
                 SMP LGQ  +   QFQTQLRLAAV  SPATQTTQLVTTKGIPVSALQQ GK  V+  TQQ
Sbjct  2605   SMPGLGQSVTQGQFQTQLRLAAVSASPATQTTQLVTTKGIPVSALQQSGK-AVLSGTQQQ  2663

Query  1832   GGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAG-----GTIIQASNM---AT  1677
                  AHIQLYRQR+LKVLQ    A  G    A+      + AG    GTIIQASN+   +T
Sbjct  2664   -AAHIQLYRQRNLKVLQAPQGAQGGGGVTASLNQTVVQTAGGALATGTIIQASNLMQTST  2722

Query  1676   HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt-  1500
                 HVTSQKVAV+ MPG +TTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQV++ DG+
Sbjct  2723   HVTSQKVAVTCMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVLATDGSG  2781

Query  1499   -ttttaagDMLLVKRHNILAAQKAQQASGALFTTTT    1395
                  +      DMLLVKRHNILAAQKAQQA+G LFTTT+
Sbjct  2782   GSGAPGTSDMLLVKRHNILAAQKAQQATGPLFTTTS    2817
```

Range 2: 2490 to 2813

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 296 bits(757) | 2e-79() | Compositional matrix adjust. | 217/332(65%) | 236/332(71%) | 28/332(8%) | -1 |

Features:

```
Query   977   PVQTLPSVVQPQI--GSGAQIVSISSQT-LPVNSSPQLGSIVQTQSLPQvvsvstlptvg  807
                 PVQ+LP    +  GS AQIVSISSQT LPVN++PQLGSIVQTQ+LPQVVSV  L T
Sbjct  2490   PVQSLPIATHSNVNAGSTAQIVSISSQTTLPVNTAPQLGSIVQTQTLPQVVSVGPLTTTA  2549

Query   806   tvlttTANQPQQQHQttavttlntTMLRGQRIVSTAA--GNTLQ-----QRTTAGGQSIV  648
                 T      Q     Q     T   TMLRGQRIVST A  GNTLQ     QRTTAGGQSIV
Sbjct  2550   TGQQQQQQQ-----QQQQTATGTVTMLRGQRIVSTGAAGGNTLQDVVLQQRTTAGGQSIV  2604

Query   647   SMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQS  468
                 SMP LGQ  +   QFQTQLRLAAV  SPATQTTQLVTTKGIPVSALQQ GK  V+  TQQ
Sbjct  2605   SMPGLGQSVTQGQFQTQLRLAAVSASPATQTTQLVTTKGIPVSALQQSGK-AVLSGTQQQ  2663

Query   467   GGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAG-----GTIIQASNM---AT  312
                  AHIQLYRQR+LKVLQ    A  G    A+      + AG    GTIIQASN+   +T
Sbjct  2664   -AAHIQLYRQRNLKVLQAPQGAQGGGGVTASLNQTVVQTAGGALATGTIIQASNLMQTST  2722

Query   311   HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt-  135
                 HVTSQKVAV+ MPG +TTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQV++ DG+
Sbjct  2723   HVTSQKVAVTCMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVLATDGSG  2781

Query   134   -ttttaagDMLLVKRHNILAAQKAQQASGALF    42
                  +      DMLLVKRHNILAAQKAQQA+G LF
Sbjct  2782   GSGAPGTSDMLLVKRHNILAAQKAQQATGPLF    2813
```

similar to Drosophila melanogaster domino, partial [Drosophila yakuba]

Sequence ID: **gb|AAR09977.1|**  Length: 185  Number of Matches: 2

Range 1: 1 to 173

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 271 bits(692) | 9e-81() | Compositional matrix adjust. | 168/173(97%) | 169/173(97%) | 0/173(0%) | -1 |

Features:

```
Query  1925  QTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsag  1746
             QTTQLVTTKGIPVSALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG
Sbjct  1     QTTQLVTTKGIPVSALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG  60

Query  1745  atgatANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQ  1566
              TGATANLVQAGGTIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQ
Sbjct  61    GTGATANLVQAGGTIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQ  120

Query  1565  FIKQMAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF     1407
             FIKQMAAGKQQLQRQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  121   FIKQMAAGKQQLQRQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF     173
```

Range 2: 1 to 173

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 271 bits(692) | 9e-81() | Compositional matrix adjust. | 168/173(97%) | 169/173(97%) | 0/173(0%) | -1 |

Features:

```
Query  560   QTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsag  381
             QTTQLVTTKGIPVSALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG
Sbjct  1     QTTQLVTTKGIPVSALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG  60

Query  380   atgatANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQ  201
              TGATANLVQAGGTIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQ
Sbjct  61    GTGATANLVQAGGTIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQ  120

Query  200   FIKQMAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF     42
             FIKQMAAGKQQLQRQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF
Sbjct  121   FIKQMAAGKQQLQRQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF     173
```

dom [Drosophila busckii]

Sequence ID: **gb|ALC41615.1|**  Length: 3526  Number of Matches: 2

Range 1: 2764 to 3182

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 276 bits(706) | 5e-73() | Compositional matrix adjust. | 267/432(62%) | 296/432(68%) | 60/432(13%) | -1 |

Features:

```
Query  2561  NVSPGQQTAILLHQPQQQ----------LRTHPGQGGQSNT-QQLVKTIVGtsssltagq  2415
             +V+P QQTAILL Q  QQ          LRT        QSNT QQLVKTIVGT+++LTAGQ
Sbjct  2764  HVTPTQQTAILLQQQPQQQQQQQQQQQQQLRT------QSNTTQQLVKTIVGTTANLTAGQ  2817

Query  2414  lqqlaqqsav--------asggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-L  2262
             LQQLA  S            +SGGQSSVSVVLTTPVQTLP    Q GS AQIV+IS+QT L
Sbjct  2818  LQQLAAASNAGGSVQLQQSSGGQSSVSVVLTTPVQTLPLATHSQGGSTAQIVAISTQTTL  2877

Query  2261  PVNSSPQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQ  2082
             PVN++PQLGSIVQTQ+LPQVVSV  L    T +      QQHQ   V TLNT +LRG
Sbjct  2878  PVNTAPQLGSIVQTQTLPQVVSVGPLTQTTTSVQQQQ----QQHQGNTVATLNTAILRGP  2933

Query  2081  R-----IVSTAAGNT-------LQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPT  1938
             R     + + +AG T       LQQR  AGGQSIV+MP LGQ  S +QFQTQLRLAAV
Sbjct  2934  RSVQAIVAAASAGGTPLHTDVVLQQRGNAGGQSIVTMPALGQNVSAAQFQTQLRLAAVSA  2993

Query  1937  SPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPs  1758
             + + QTTQLVTTKGIPVSALQQ GK TV+P TQQ  GAHIQLYRQR+LKVLQ T  A
Sbjct  2994  ANSNQTTQLVTTKGIPVSALQQSGK-TVLPGTQQP-GAHIQLYRQRNLKVLQATQAAAAG  3051

Query  1757  gsagatgatANL----VQ------AGGTIIQASNMA---THVTSQKVAVSGMPGTSTTVQ  1617
             G+A A G T NL    VQ      A GTIIQ SN+    THV+SQKVAVSGM G +TTVQ
Sbjct  3052  GAATAGGGTGNLSSTVVQTTGGTLAPGTIIQTSNLMQAQTHVSSQKVAVSGMAG-ATTVQ  3110

Query  1616  AGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVV--SadgtttttaagDMLLVKRHNILA  1443
             AGNVVSSVQMHGQ RTQFIKQM AGKQ LQRQV+    A G+         MLLVKRHNILA
Sbjct  3111  AGNVVSSVQMHGQPRTQFIKQMTAGKQTLQRQVLATEAGGSGGAGTTDGMLLVKRHNILA  3170

Query  1442  AQKAQQASGALF     1407
             AQKAQQA+G LF
Sbjct  3171  AQKAQQATGPLF     3182
```

Range 2: 2764 to 3182

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 276 bits(706) | 5e-73() | Compositional matrix adjust. | 267/432(62%) | 296/432(68%) | 60/432(13%) | -1 |

Features:

```
Query  1196  NVSPGQQTAILLHQPQQQ----------LRTHPGQGGQSNT-QQLVKTIVGtsssltagq  1050
             +V+P QQTAILL Q  QQ          LRT       QSNT QQLVKTIVGT+++LTAGQ
Sbjct  2764  HVTPTQQTAILLQQQPQQQQQQQQQQQQLRT------QSNTTQQLVKTIVGTTANLTAGQ  2817

Query  1049  lqqlaqqsav--------asgqqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-L  897
             LQQLA  S          +SGGQSSVSVVLTTPVQTLP    Q GS AQIV+IS+QT L
Sbjct  2818  LQQLAAASNAGGSVQLQQSSGGQSSVSVVLTTPVQTLPLATHSQGGSTAQIVAISTQTTL  2877

Query  896   PVNSSPQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQ  717
             PVN++PQLGSIVQTQ+LPQVVSV  L   T +     QQHQ   V TLNT +LRG
Sbjct  2878  PVNTAPQLGSIVQTQTLPQVVSVGPLTQTTTSVQQQQ----QQHQGNTVATLNTAILRGP  2933

Query  716   R-----IVSTAAGNT-------LQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPT  573
             R     + + +AG T       LQQR  AGGQSIV+MP LGQ  S +QFQTQLRLAAV
Sbjct  2934  RSVQAIVAAASAGGTPLHTDVVLQQRGNAGGQSIVTMPALGQNVSAAQFQTQLRLAAVSA  2993

Query  572   SPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPs  393
             + + QTTQLVTTKGIPVSALQQ GK TV+P TQQ  GAHIQLYRQR+LKVLQ  T  A
Sbjct  2994  ANSNQTTQLVTTKGIPVSALQQSGK-TVLPGTQQP-GAHIQLYRQRNLKVLQATQAAAAG  3051

Query  392   gsagatgatANL----VQ------AGGTIIQASNMA---THVTSQKVAVSGMPGTSTTVQ  252
             G+A A G T NL    VQ       A GTIIQ SN+    THV+SQKVAVSGM G +TTVQ
Sbjct  3052  GAATAGGGTGNLSSTVVQTTGGTLAPGTIIQTSNLMQAQTHVSSQKVAVSGMAG-ATTVQ  3110

Query  251   AGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVV--SadgtttttaagDMLLVKRHNILA  78
             AGNVVSSVQMHGQ RTQFIKQM AGKQ LQRQV+    A G+         MLLVKRHNILA
Sbjct  3111  AGNVVSSVQMHGQPRTQFIKQMTAGKQTLQRQVLATEAGGSGGAGTTDGMLLVKRHNILA  3170

Query  77    AQKAQQASGALF    42
             AQKAQQA+G LF
Sbjct  3171  AQKAQQATGPLF    3182
```

GH20710 [Drosophila grimshawi]

Sequence ID: **ref|XP_001986118.1|** Length: 3285 Number of Matches: 2

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

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 267 bits(683) | 4e-70() | Compositional matrix adjust. | 209/336(62%) | 231/336(68%) | 39/336(11%) | -1 |

Features:

```
Query  2342  PVQTLPSVVQPQIG--SGAQIVSISSQ-TLPVNSSPQLGSIVQTQSLPQvvsvstlptvg  2172
             PVQ+LP     +   S AQIVSISSQ TLPVN+ PQLGSIVQTQ+LPQVVSV   L T
Sbjct  2571  PVQSLPIATHSNVNANSTAQIVSISSQSTLPVNTPPQLGSIVQTQTLPQVVSVGPLTTTT  2630

Query  2171  tvlttTANQPQQQHQttavttlntTMLRGQRIVSTAA----GNT------LQQRTTAGGQ  2022
             +          T    TMLRGQR+VS AA    GNT       LQQRTTA GQ
Sbjct  2631  SGGQQQQ--------QQQTATGVTMLRGQRLVSAAAASAAGNTTLHDVVLQQRTTAIGQ  2682

Query  2021  SIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVT  1842
              IVS   LGQ  + + FQ QLRL+AV  SPATQTTQLVTTKGIPV+ALQQ GKT V+P T
Sbjct  2683  PIVS---LGQSVANAHFQAQLRLSAVSGSPATQTTQLVTTKGIPVTALQQTGKT-VLPGT  2738

Query  1841  QQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatAN--LVQ------AGGTIIQASN  1686
             QQ       HIQLYRQR+LKVLQ  Q   G  G   A N +VQ       A GTIIQASN
Sbjct  2739  QQQT-PHIQLYRQRNLKVLQAP-QVAQGGVVGGGTANLNPTVVQTAGGALATGTIIQASN  2796

Query  1685  MA---THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVV  1515
             +      THVTSQKVAVSGMPG +TTVQAGNVVSSVQMHGQARTQFIKQMA GKQ +QRQ++
Sbjct  2797  LMQTPTHVTSQKVAVSGMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAVGKQGVQRQMI  2855

Query  1514  SadgtttttaagDMLLVKRHNILAAQKAQQASGALF    1407
             + DG+   + A GDMLLVKRHNILAAQKAQQA+G LF
Sbjct  2856  TTDGSGGSGATGDMLLVKRHNILAAQKAQQATGPLF    2891
```

Range 2: 2571 to 2891

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 267 bits(683) | 4e-70() | Compositional matrix adjust. | 209/336(62%) | 231/336(68%) | 39/336(11%) | -1 |

Features:

```
Query  977   PVQTLPSVVQPQIG--SGAQIVSISSQ-TLPVNSSPQLGSIVQTQSLPQvvsvstlptvg  807
             PVQ+LP     +   S AQIVSISSQ TLPVN+ PQLGSIVQTQ+LPQVVSV  L T
Sbjct  2571  PVQSLPIATHSNVNANSTAQIVSISSQSTLPVNTPPQLGSIVQTQTLPQVVSVGPLTTTT  2630

Query  806   tvlttTANQPQQQHQttavttlntTMLRGQRIVSTAA----GNT------LQQRTTAGGQ  657
             +         T  TMLRGQR+VS AA    GNT      LQQRTTA GQ
Sbjct  2631  SGGQQQQ--------QQQTATGTVTMLRGQRLVSAAAASAAGNTTLHDVVLQQRTTAIGQ  2682

Query  656   SIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVT  477
              IVS   LGQ + + FQ QLRL+AV  SPATQTTQLVTTKGIPV+ALQQ GKT V+P T
Sbjct  2683  PIVS---LGQSVANAHFQAQLRLSAVSGSPATQTTQLVTTKGIPVTALQQTGKT-VLPGT  2738

Query  476   QQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatAN--LVQ------AGGTIIQASN  321
             QQ    HIQLYRQR+LKVLQ   Q   G  G   A N  +VQ      A GTIIQASN
Sbjct  2739  QQQT-PHIQLYRQRNLKVLQAP-QVAQGGVVGGGTANLNPTVVQTAGGALATGTIIQASN  2796

Query  320   MA---THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVV  150
             +      THVTSQKVAVSGMPG +TTVQAGNVVSSVQMHGQARTQFIKQMA GKQ +QRQ++
Sbjct  2797  LMQTPTHVTSQKVAVSGMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAVGKQGVQRQMI  2855

Query  149   SadgtttttaagDMLLVKRHNILAAQKAQQASGALF   42
             + DG+  + A GDMLLVKRHNILAAQKAQQA+G LF
Sbjct  2856  TTDGSGGSGATGDMLLVKRHNILAAQKAQQATGPLF   2891
```

PREDICTED: helicase domino isoform X2 [Ceratitis capitata]

Sequence ID: **ref|XP_004522560.1|** Length: 3368 Number of Matches: 2

Range 1: 2674 to 2979

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 117 bits(292) | 6e-23() | Compositional matrix adjust. | 164/336(49%) | 194/336(57%) | 61/336(18%) | -1 |

Features:

```
Query  2342  PVQTLPSVVQP--QIG--SGAQIVSISSQTLPVNSSPQLGS-IVQT---QSLPQvvsvst  2187
             PVQTLPS VQ   Q G  S AQIVSIS QT+ + + Q GS IVQT   Q+LPQVVSVS
Sbjct  2674  PVQTLPSSVQSAQQHGQSSTAQIVSISPQTIVSSGASQNGSSIVQTIPSQTLPQVVSVSQ  2733

Query  2186  lptvgtvlttTAN-QPQQQHQttavttlntTMLRGQRIVSTAAGN----TLQQRTTAGGQ  2022
             L TVGTVLTT+AN QP      +   VTTLN + LR QRIV+  AG     LQQR+
Sbjct  2734  LATVGTVLTTSANLQP-----SATVTTLNPSALRAQRIVAATAGTLQDVVLQQRSGNPSP  2788

Query  2021  SIVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPV  1845
             +IVSM NLG   + +QFQ TQLRLA++P     T+Q VT   +PVS LQQGGK      +
Sbjct  2789  TIVSMSNLGPSVAAAQFQATQLRLASMPG-----TSQQVTK--VPVSTLQQGGK-----L  2836

Query  1844  TQQSGGA---HIQLYRQR-SLKVLQTTT-QAVPsgsagatgatANLVQAGGTIIQASNMA  1680
             T  GG    HIQLYRQR  LKVLQT+T Q          LV A GTIIQ S +
Sbjct  2837  TANVGGNQPPHIQLYRQRQQLKVLQTSTGQGGGGQTLVQTASGQTALVNAAGTIIQGSLVQ  2896

Query  1679  T-------HVTSQKVAVSGMPGTSTTVQA--GNV---VSSVQMHGQARTQFIKQMAAGKQ  1536
             T      +   QKVAV+ +  +S  V A  G V   V++VQ+  Q RTQFIKQ+  GKQ
Sbjct  2897  TAGGQATMQMQGQKVAVATV-SSSNMVAAPSGGVATSVATVQVAHQGRTQFIKQV-GGKQ  2954

Query  1535  QLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQ   1428
             + RQ+          DM+LVKR  I A QKAQ
Sbjct  2955  TIARQM-----------GDDMVLVKRQVIGAHQKAQ   2979
```

Range 2: 2674 to 2979

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 117 bits(292) | 6e-23() | Compositional matrix adjust. | 164/336(49%) | 194/336(57%) | 61/336(18%) | -1 |

Features:

```
Query  977   PVQTLPSVVQP--QIG--SGAQIVSISSQTLPVNSSPQLGS-IVQT---QSLPQvvsvst  822
             PVQTLPS VQ   Q G  S AQIVSIS QT+ + + Q GS IVQT   Q+LPQVVSVS
Sbjct  2674  PVQTLPSSVQSAQQHGQSSTAQIVSISPQTIVSSGASQNGSSIVQTIPSQTLPQVVSVSQ  2733

Query  821   lptvgtvlttTAN-QPQQQHQttavttlntTMLRGQRIVSTAAGN----TLQQRTTAGGQ  657
             L TVGTVLTT+AN QP      +   VTTLN + LR QRIV+  AG     LQQR+
Sbjct  2734  LATVGTVLTTSANLQP-----SATVTTLNPSALRAQRIVAATAGTLQDVVLQQRSGNPSP  2788

Query  656   SIVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPV  480
             +IVSM NLG   + +QFQ TQLRLA++P     T+Q VT   +PVS LQQGGK      +
Sbjct  2789  TIVSMSNLGPSVAAAQFQATQLRLASMPG-----TSQQVTK--VPVSTLQQGGK-----L  2836

Query  479   TQQSGGA---HIQLYRQR-SLKVLQTTT-QAVPsgsagatgatANLVQAGGTIIQASNMA  315
             T  GG    HIQLYRQR  LKVLQT+T Q          LV A GTIIQ S +
Sbjct  2837  TANVGGNQPPHIQLYRQRQQLKVLQTSTGQGGGGQTLVQTASGQTALVNAAGTIIQGSLVQ  2896

Query  314   T-------HVTSQKVAVSGMPGTSTTVQA--GNV---VSSVQMHGQARTQFIKQMAAGKQ  171
             T      +   QKVAV+ +  +S  V A  G V   V++VQ+  Q RTQFIKQ+  GKQ
Sbjct  2897  TAGGQATMQMQGQKVAVATV-SSSNMVAAPSGGVATSVATVQVAHQGRTQFIKQV-GGKQ  2954

Query  170   QLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQ   63
```

PREDICTED: helicase domino isoform X1 [Ceratitis capitata]

Sequence ID: **ref|XP_004522557.1|** Length: 3372 Number of Matches: 2

▸ **See 1 more title(s)**

Range 1: 2674 to 2979

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 117 bits(292) | 7e-23() | Compositional matrix adjust. | 164/336(49%) | 194/336(57%) | 61/336(18%) | -1 |

Features:

```
Query  2342   PVQTLPSVVQP--QIG--SGAQIVSISSQTLPVNSSPQLGS-IVQT---QSLPQvvsvst  2187
              PVQTLPS VQ   Q G  S AQIVSIS QT+  + + Q GS IVQT   Q+LPQVVSVS
Sbjct  2674   PVQTLPSSVQSAQQHGQSSTAQIVSISPQTIVSSGASQNGSSIVQTIPSQTLPQVVSVSQ  2733

Query  2186   lptvgtvlttTAN-QPQQQHQttavttlntTMLRGQRIVSTAAGN----TLQQRTTAGGQ  2022
              L TVGTVLTT+AN QP       +  VTTLN + LR QRIV+  AG     LQQR+
Sbjct  2734   LATVGTVLTTSANLQP-----SATVTTLNPSALRAQRIVAATAGTLQDVVLQQRSGNPSP  2788

Query  2021   SIVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPV  1845
              +IVSM NLG   + +QFQ TQLRLA++P       T+Q VT   +PVS LQQGGK    +
Sbjct  2789   TIVSMSNLGPSVAAAQFQATQLRLASMPG-----TSQQVTK--VPVSTLQQGGK-----L  2836

Query  1844   TQQSGGA---HIQLYRQR-SLKVLQTTT-QAVPsgsagatgatANLVQAGGTIIQASNMA  1680
              T   GG    HIQLYRQR  LKVLQT+T Q           LV A GTIIQ S +
Sbjct  2837   TANVGGNQPPHIQLYRQRQQLKVLQTSTGQGGGGQTLVQTASGQTALVNAAGTIIQGSLVQ  2896

Query  1679   T-------HVTSQKVAVSGMPGTSTTVQA--GNV---VSSVQMHGQARTQFIKQMAAGKQ  1536
              T        +   QKVAV+ +  +S  V A  G V   V++VQ+  Q RTQFIKQ+  GKQ
Sbjct  2897   TAGGQATMQMQGQKVAVATV-SSSNMVAAPSGGVATSVATVQVAHQGRTQFIKQV-GGKQ  2954

Query  1535   QLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQ    1428
               + RQ+                DM+LVKR   I A QKAQ
Sbjct  2955   TIARQM-----------GDDMVLVKRQVIGAHQKAQ    2979
```

Range 2: 2674 to 2979

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 117 bits(292) | 7e-23() | Compositional matrix adjust. | 164/336(49%) | 194/336(57%) | 61/336(18%) | -1 |

Features:

```
Query  977    PVQTLPSVVQP--QIG--SGAQIVSISSQTLPVNSSPQLGS-IVQT---QSLPQvvsvst  822
              PVQTLPS VQ   Q G  S AQIVSIS QT+  + + Q GS IVQT   Q+LPQVVSVS
Sbjct  2674   PVQTLPSSVQSAQQHGQSSTAQIVSISPQTIVSSGASQNGSSIVQTIPSQTLPQVVSVSQ  2733

Query  821    lptvgtvlttTAN-QPQQQHQttavttlntTMLRGQRIVSTAAGN----TLQQRTTAGGQ  657
              L TVGTVLTT+AN QP       +  VTTLN + LR QRIV+  AG     LQQR+
Sbjct  2734   LATVGTVLTTSANLQP-----SATVTTLNPSALRAQRIVAATAGTLQDVVLQQRSGNPSP  2788

Query  656    SIVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPV  480
              +IVSM NLG   + +QFQ TQLRLA++P       T+Q VT   +PVS LQQGGK    +
Sbjct  2789   TIVSMSNLGPSVAAAQFQATQLRLASMPG-----TSQQVTK--VPVSTLQQGGK-----L  2836

Query  479    TQQSGGA---HIQLYRQR-SLKVLQTTT-QAVPsgsagatgatANLVQAGGTIIQASNMA  315
              T   GG    HIQLYRQR  LKVLQT+T Q           LV A GTIIQ S +
Sbjct  2837   TANVGGNQPPHIQLYRQRQQLKVLQTSTGQGGGGQTLVQTASGQTALVNAAGTIIQGSLVQ  2896

Query  314    T-------HVTSQKVAVSGMPGTSTTVQA--GNV---VSSVQMHGQARTQFIKQMAAGKQ  171
              T        +   QKVAV+ +  +S  V A  G V   V++VQ+  Q RTQFIKQ+  GKQ
Sbjct  2897   TAGGQATMQMQGQKVAVATV-SSSNMVAAPSGGVATSVATVQVAHQGRTQFIKQV-GGKQ  2954

Query  170    QLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQ    63
               + RQ+                DM+LVKR   I A QKAQ
Sbjct  2955   TIARQM-----------GDDMVLVKRQVIGAHQKAQ    2979
```

Helicase domino [Lucilia cuprina]

Sequence ID: **gb|KNC26706.1|** Length: 1269 Number of Matches: 2
Range 1: 522 to 862

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 114 bits(286) | 2e-22() | Compositional matrix adjust. | 167/359(47%) | 194/359(54%) | 60/359(16%) | -1 |

Features:

```
Query  2342  PVQTLPSVVQPQ--------IGSGAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvst  2187
             PVQT+ S V  Q          S AQIVS+S Q   V+SSPQ+GSIVQTQSLPQVVSVS
Sbjct  522   PVQTISSTVTNQQQHHSNQVSSSTAQIVSLSPQQTIVSSSPQVGSIVQTQSLPQVVSVSQ  581

Query  2186  lptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQ----QRTTAGGQS  2019
             L TVGTVLTT++    Q  T  VTTLNT+ LR QRIV+ ++G TLQ   Q+ +AG  S
Sbjct  582   LATVGTVLTTSSG---MQQPTATVTTLNTSALRAQRIVAASSGTTLQDVVLQQRSAGNPS  638

Query  2018  --IVSMPNLGQGASPSFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIP  1848
               IVSM +LG   + +Q Q TQ +LA++P+    TQ V TKGI VS+LQQG K
Sbjct  639   PTIVSMSSLGTNVAQAQLQATQFQLASMPSG-----TQQVVTKGIRVSSLQQGQKIAAAA  693

Query  1847  VTQQSGGA----HIQLYRQR-SLKVLQ--TTTQAVPsgsagatgatANLVQAGGTIIQAS  1689
             +       HIQLYRQR  LKVLQ    Q             LV A GTIIQ S
Sbjct  694   QAGNNQQGQPHTHIQLYRQRQQLKVLQAGAPGQQGQQTVVQTASGQTALVNAQGTIIQGS  753

Query  1688  NMATH--------VTSQKVAVSGMPGTSTTVQAGNVVSSV-------QMHGQARTQFIKQ  1554
              M T          V  QKVAV+    TT A VV++V          Q   Q R QFIKQ
Sbjct  754   LMQTGSGPTTVQVVQGQKVAVATSNVAVTTPSATGVVTTVAASQVHQQQAQQTRAQFIKQ  813

Query  1553  MAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAA--QKAQQA---SGALFTTTTG  1392
             +AAGKQ + RQV            DMLLVKR  I AA   QKA Q      G +FTTTT
Sbjct  814   VAAGKQTITRQV----------GESDMLLVKRQMISAATQQKAAQVLQQGGQIFTTTTA  862
```

## Range 2: 522 to 848

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 108 bits(271) | 2e-20() | Compositional matrix adjust. | 161/345(47%) | 187/345(54%) | 57/345(16%) | -1 |

Features:

```
Query  977  PVQTLPSVVQPQ--------IGSGAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvst  822
            PVQT+ S V  Q          S AQIVS+S Q   V+SSPQ+GSIVQTQSLPQVVSVS
Sbjct  522  PVQTISSTVTNQQQHHSNQVSSSTAQIVSLSPQQTIVSSSPQVGSIVQTQSLPQVVSVSQ  581

Query  821  lptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQ----QRTTAGGQS  654
            L TVGTVLTT++    Q  T  VTTLNT+ LR QRIV+ ++G TLQ   Q+ +AG  S
Sbjct  582  LATVGTVLTTSSG---MQQPTATVTTLNTSALRAQRIVAASSGTTLQDVVLQQRSAGNPS  638

Query  653  --IVSMPNLGQGASPSFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIP  483
              IVSM +LG   + +Q Q TQ +LA++P+    TQ V TKGI VS+LQQG K
Sbjct  639  PTIVSMSSLGTNVAQAQLQATQFQLASMPSG-----TQQVVTKGIRVSSLQQGQKIAAAA  693

Query  482  VTQQSGGA----HIQLYRQR-SLKVLQ--TTTQAVPsgsagatgatANLVQAGGTIIQAS  324
            +       HIQLYRQR  LKVLQ    Q             LV A GTIIQ S
Sbjct  694  QAGNNQQGQPHTHIQLYRQRQQLKVLQAGAPGQQGQQTVVQTASGQTALVNAQGTIIQGS  753

Query  323  NMATH--------VTSQKVAVSGMPGTSTTVQAGNVVSSV-------QMHGQARTQFIKQ  189
             M T          V  QKVAV+    TT A VV++V          Q   Q R QFIKQ
Sbjct  754  LMQTGSGPTTVQVVQGQKVAVATSNVAVTTPSATGVVTTVAASQVHQQQAQQTRAQFIKQ  813

Query  188  MAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAA--QKAQQ  60
            +AAGKQ + RQV            DMLLVKR  I AA   QKA Q
Sbjct  814  VAAGKQTITRQV----------GESDMLLVKRQMISAATQQKAAQ  848
```

PREDICTED: helicase domino [Musca domestica]

Sequence ID: **ref|XP_011294691.1|**  Length: 2336  Number of Matches: 2

Range 1: 1601 to 1929

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 111 bits(277) | 3e-21() | Compositional matrix adjust. | 165/349(47%) | 194/349(55%) | 54/349(15%) | -1 |

Features:

```
Query  2342  PVQTLPSVVQPQIG-------SGAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvstl  2184
             PVQT+ S VQ Q+        S AQIVS+S QT+ V+SS Q+GSIV TQSLPQVVSVS L
Sbjct  1601  PVQTISSNVQNQVAHHSQVSSSTAQIVSLSPQTI-VSSSAQVGSIVHTQSLPQVVSVSQL  1659

Query  2183  ptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQ----QRTTAGGQS-  2019
              TVGTVLTT++    Q  T  VTTLNT+ LR QRIV+ ++G TLQ   Q+ TAG  S
Sbjct  1660  ATVGTVLTTSSG---MQQPTGTVTTLNTSALRAQRIVAASSGTTLQDVVLQQRTAGNPSP  1716

Query  2018  -IVSMPNLGQGASPSFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGK----TT  1857
              IVSM +LG     + Q Q +LA++P+    TQ V TKGI VS+LQQG K
Sbjct  1717  TIVSMSSLGSNVGQASLQAAFQLASMPSG-----TQQVVTKGIRVSSLQQGQKLAPGGA  1771

Query  1856  VIPVTQQSGGAHIQLYRQRSLKVLQTT---TQAVPsgsagatgatANLVQAGGTIIQASN  1686
                Q   AHIQ YRQR LKVLQ T    Q  P+      A+G  A LV A GTII
Sbjct  1772  GGTTAQGQQSAHIQSYRQRQLKVLQATGPGQQGQQPTVVQTASGQAA-LVNAQGTIIGTGP  1830

Query  1685  MATHVT-SQKVAVSGMPGTSTTVQAGNVVSSV--QMHG----QARTQFIKQM-AAGKQQL  1530
                V   QKV V+    TT A VV++V  QMH     Q R QFIKQ+ A+GKQ
Sbjct  1831  TTVQVVQGQKVTVATSNVAVTTPSATGVVTTVANQMHAQQVQQTRAQFIKQVSASGKQIF  1890

Query  1529  QRQVVSadgtttttaagDMLLVKRHNILAA--QKAQQA---SGALFTTT  1398
```

```
                    RQV               DMLLVKR  I AA   QK  Q      G ++TTT
Sbjct  1891  TRQV---------GDSDMLLVKRQMISAAGQQKTAQVIQQGGQIYTTT  1929
```

## Range 2: 1601 to 1910

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 109 bits(272) | 1e-20() | Compositional matrix adjust. | 158/330(48%) | 185/330(56%) | 49/330(14%) | -1 |

Features:

```
Query  977   PVQTLPSVVQPQIG-------SGAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvstl  819
             PVQT+ S VQ Q+        S AQIVS+S QT+ V+SS Q+GSIV TQSLPQVVSVS L
Sbjct  1601  PVQTISSNVQNQVAHHSQVSSSTAQIVSLSPQTI-VSSSAQVGSIVHTQSLPQVVSVSQL  1659

Query  818   ptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQ----QRTTAGGQS-  654
              TVGTVLTT++     Q  T   VTTLNT+ LR QRIV+ ++G TLQ     Q+ TAG  S
Sbjct  1660  ATVGTVLTTSSG---MQQPTGTVTTLNTSALRAQRIVAASSGTTLQDVVLQQRTAGNPSP  1716

Query  653   -IVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGK----TT  492
              IVSM +LG     + Q Q +LA++P+        TQ V TKGI VS+LQQG K
Sbjct  1717  TIVSMSSLGSNVGQASLQAAQFQLASMPSG-----TQQVVTKGIRVSSLQQGQKLAPGGA  1771

Query  491   VIPVTQQSGGAHIQLYRQRSLKVLQTT---TQAVPsgsagatgatANLVQAGGTIIQASN  321
                  Q   AHIQ YRQR LKVLQ T   Q  P+     A+G  A LV A GTII
Sbjct  1772  GGTTAQGQQSAHIQSYRQRQLKVLQATGPGQQGQPTVVQTASGQAA-LVNAQGTIIGTGP  1830

Query  320   MATHVT-SQKVAVSGMPGTSTTVQAGNVVSSV--QMHG----QARTQFIKQM-AAGKQQL  165
                  V   QKV V+     TT A  VV++V  QMH      Q R QFIKQ+ A+GKQ
Sbjct  1831  TTVQVVQGQKVTVATSNVAVTTPSATGVVTTVANQMHAQQVQQTRAQFIKQVSASGKQIF  1890

Query  164   QRQVVSadgtttttaagDMLLVKRHNILAA    75
              RQV              DMLLVKR  I AA
Sbjct  1891  TRQV---------GDSDMLLVKRQMISAA    1910
```

PREDICTED: helicase domino [Stomoxys calcitrans]

Sequence ID: **ref|XP_013100224.1|**  Length: 3504  Number of Matches: 2

## Range 1: 2758 to 3096

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 103 bits(258) | 6e-19() | Compositional matrix adjust. | 159/362(44%) | 193/362(53%) | 70/362(19%) | -1 |

Features:

```
Query  2342  PVQTLPSVVQPQIGS--------GAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvst  2187
             PVQT+ S    P GS        AQIVS+S QT+ V+SS Q+GSIVQTQSLPQVVSVS
Sbjct  2758  PVQTISSTTLPNQGSHHSQVASSSAQIVSLSPQTI-VSSSAQVGSIVQTQSLPQVVSVSQ  2816

Query  2186  lptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQ----QRTTAGGQS  2019
             L TVGTVLTT++     Q   V   LNT+ LR QRIV+ + G TLQ     Q+ +AG  S
Sbjct  2817  LATVGTVLTTSSG----MQQPATVAALNTSALRAQRIVAASGGTTLQDVVLQQRSAGNPS  2872

Query  2018  --IVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIP  1848
               IVSM +LG   ++  Q TQ +LA++P        TQ V TKGI VS+LQQGQK   I
Sbjct  2873  PTIVSMSSLGTNVAQAPIQGTQFQLASMPAG-----TQQVVTKGIRVSSLQQGQK---IA  2924

Query  1847  VTQQSGG--------AHIQLYRQR-SLKVLQTT--TQAVPsgsagatgatANLVQAGGTI  1701
               SGG        AHIQLYRQR LKVLQ +   Q            LV A GTI
Sbjct  2925  AGNASGGTVQGQGQAAHIQLYRQRQQLKVLQASGPGQQGQQTVVQTASGQTALVNAQGTI  2984

Query  1700  IQASNMATH--------VTSQKVAVSGMPGTSTTVQAGNVVSSV--QMH-----GQARTQ  1566
             IQ + M T         V QKV V+     TT    VV++V  QMH       Q RTQ
Sbjct  2985  IQGNIMQTSAGPTTVQVVQGQKVTVATSNVALTTPSTAGVVTTVANQMHPQQVQQQTRTQ  3044

Query  1565  FIKQM-AAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQA-----SGALFT  1404
             +IKQ+ A+GKQ + RQV              DMLLVKR  + AA + + A      G ++T
Sbjct  3045  YIKQVSASGKQTIARQV---------GDTDMLLVKRQMLSAATQPKAAQVIQQGGQIYT  3094

Query  1403  TT  1398
             T+
Sbjct  3095  TS  3096
```

## Range 2: 2758 to 3077

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 103 bits(257) | 9e-19() | Compositional matrix adjust. | 155/343(45%) | 184/343(53%) | 65/343(18%) | -1 |

Features:

```
Query  977   PVQTLPSVVQPQIGS--------GAQIVSISSQTLPVNSSPQLGSIVQTQSLPQvvsvst  822
             PVQT+ S    P GS        AQIVS+S QT+ V+SS Q+GSIVQTQSLPQVVSVS
Sbjct  2758  PVQTISSTTLPNQGSHHSQVASSSAQIVSLSPQTI-VSSSAQVGSIVQTQSLPQVVSVSQ  2816
```

```
Query   821   lptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQ----QRTTAGGQS   654
              L TVGTVLTT++        Q   V  LNT+ LR QRIV+ + G TLQ      Q+ +AG  S
Sbjct  2817   LATVGTVLTTSSG----MQQPATVAALNTSALRAQRIVAASGGTTLQDVVLQQRSAGNPS   2872

Query   653   --IVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIP   483
                IVSM +LG    + +  Q TQ +LA++P        TQ V TKGI VS+LQQG K    I
Sbjct  2873   PTIVSMSSLGTNVAQAPIQGTQFQLASMPAG-----TQQVVTKGIRVSSLQQGQK---IA   2924

Query   482   VTQQSGG--------AHIQLYRQR-SLKVLQTT--TQAVPsgsagatgatANLVQAGGTI   336
                  SGG         AHIQLYRQR  LKVLQ +   Q            LV A GTI
Sbjct  2925   AGNASGGTVQGQGQAAHIQLYRQRQQLKVLQASGPGQQGQQTVVQTASGQTALVNAQGTI   2984

Query   335   IQASNMATH--------VTSQKVAVSGMPGTSTTVQAGNVVSSV--QMH-----GQARTQ   201
              IQ + M T         V  QKV V+      TT       VV++V  QMH       Q RTQ
Sbjct  2985   IQGNIMQTSAGPTTVQVVQGQKVTVATSNVALTTPSTAGVVTTVANQMHPQQVQQQTRTQ   3044

Query   200   FIKQM-AAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAA   75
              +IKQ+ A+GKQ + RQV            DMLLVKR   + AA
Sbjct  3045   YIKQVSASGKQTIARQV----------GDTDMLLVKRQMLSAA   3077
```

GM15831 [Drosophila sechellia]

Sequence ID: **ref|XP_002039753.1|** Length: 2550  Number of Matches: 2

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

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 86.3 bits(212) | 2e-13() | Composition-based stats. | 36/42(86%) | 36/42(85%) | 0/42(0%) | -3 |

Features:

```
Query  2382   FWGPVQCECGPNHSSTDTSVGGATPDRLWCPDRFDLVTDAAR   2257
               W PVQCEC  NHSSTDTSVGGATPDRLWCPDR  LVTDAAR
Sbjct  2509   LWWPVQCECSTNHSSTDTSVGGATPDRLWCPDRVHLVTDAAR   2550
```

Range 2: 2509 to 2550

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---|---|---|---|---|---|---|
| 86.3 bits(212) | 2e-13() | Composition-based stats. | 36/42(86%) | 36/42(85%) | 0/42(0%) | -3 |

Features:

```
Query  1017   FWGPVQCECGPNHSSTDTSVGGATPDRLWCPDRFDLVTDAAR   892
               W PVQCEC  NHSSTDTSVGGATPDRLWCPDR  LVTDAAR
Sbjct  2509   LWWPVQCECSTNHSSTDTSVGGATPDRLWCPDRVHLVTDAAR   2550
```