BLAST®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BKDMC6014

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Blast report description

Nucleotide Sequence (2753 letters)

RID <u>B8BKDMC6014</u> (Expires on 02-06 12:09 pm)

Query ID |c||Query_32783 | Description | None

Molecule type nucleic acid

Query Length 2753

Database Name nr

Description All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

excluding environmental samples from

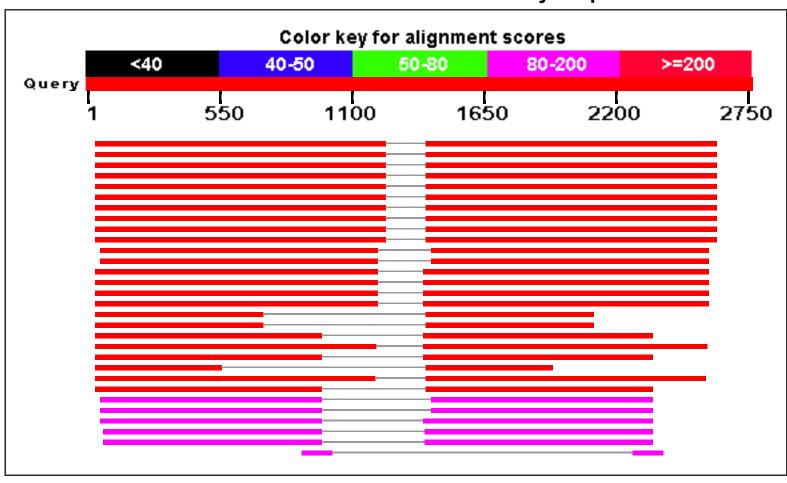
WGS projects

Program BLASTX 2.3.1+

□ Graphic Summary

No putative conserved domains have been detected

Distribution of 60 Blast Hits on the Query Sequence



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_Gl19071 [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

□ <u>Alignments</u>

LD21920p [Drosophila melanogaster]

Sequence ID: gb|ACD81851.1| Length: 1350 Number of Matches: 2

Range 1: 575 to 974

Score	I	Expect Method	Identities	Positives	Gaps	Frame
549 bits	(1414) 4	4e-172() Compositional matrix adjust	. 400/400(100%) 400/400(100%) 0/400(0%)	-1
Feature	s:					
Query	2606	GGqlqqlqiqhLTSSNVSPGQQTAII				
Sbjct	575	GGQLQQLQIQHLTSSNVSPGQQTAII GGQLQQLQIQHLTSSNVSPGQQTAII				
Query	2426	tagqlqqlaqqsavasggqssvsvvl				
Sbjct	635	TAĞQLQQLAQQSAVASĞĞQSSVSVVI TAGQLQQLAQQSAVASGGQSSVSVVI				
Query	2246	POLGSIVOTOSLPOvvsvstlptvgt				
Sbjct	695	PQLGSIVQTQSLPQVVSVSTLPTVGT PQLGSIVQTQSLPQVVSVSTLPTVGT				
Query	2066	AAGNTLQQRTTAGGQSIVSMPNLGQQ				
Sbjct	755	AAGNTLQQRTTAGGQSIVSMPNLGQQ AAGNTLQQRTTAGGQSIVSMPNLGQQ				
Query	1886	SALQQGGKTTVIPVTQQSGGAHIQLY				
Sbjct	815	SALQQGGKTTVIPVTQQSGGAHIQLY SALQQGGKTTVIPVTQQSGGAHIQLY				
Query	1706	TIIQASNMATHVTSQKVAVSGMPGTS TIIOASNMATHVTSOKVAVSGMPGTS				
Sbjct	875	TIIQASNMATHVTSQKVAVSGMPGTS	~	~ ~ ~	~ ~~	~
Query	1526	RQVVSadgtttttaagDMLLVKRHNI				
Sbjct	935	RQVVSADGTTTTTAAGDMLLVKRHNI RQVVSADGTTTTTAAGDMLLVKRHNI				

Range 2: 575 to 974

Score	Е	Expect	Method	Identities	Positives	Gaps	Frame
549 bits((1414) 4	e-172()	Compositional matrix adj	ust. 400/400(100%) 400/400(100%	%) 0/400(0%) -	.1
Features	s:						
Query	1241		qqlqiqhLTSSNVSPGQQT				
Sbjct	575		QQLQIQHLTSSNVSPGQQT QQLQIQHLTSSNVSPGQQT				
Query	1061		Lqqlaqqsavasggqssvs				
Sbjct	635		LQQLAQQSAVASGGQSSVS LQQLAQQSAVASGGQSSVS				
Query	881		SIVQTQSLPQvvsvstlpt SIVQTQSLPQVVSVSTLPT				
Sbjct	695		SIVÕTÕSLPÕVVSVSTLPT				
Query	701		TLQQRTTAGGQSIVSMPNL TLQQRTTAGGQSIVSMPNL				
Sbjct	755		TLQQRTTAGGQSIVSMPNL TLQQRTTAGGQSIVSMPNL		~	~	
Query	521		QGGKTTVIPVTQQSGGAHI QGGKTTVIPVTQQSGGAHI				
Sbjct	815		QGGKTTVIPVTQQSGGAHI QGGKTTVIPVTQQSGGAHI				
Query	341		ASNMATHVTSQKVAVSGMP ASNMATHVTSOKVAVSGMP				
Sbjct	875	~	ASNMATHVTSQKVAVSGMP ASNMATHVTSQKVAVSGMP	~	~ ~ ~	~ ~~	~
Query	161	RQVVS	SadgtttttaagDMLLVKR	HNILAAQKAQQASGA	ALF 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	E	Expect	Method		ld	entities	Pos	itives	Gaps	Fra	me
558 bits	(1437) 2	e-169()) Compositio	nal matrix ad	just. 40	0/400(10	00%) 400	/400(100%	%) 0/400(0	%) -1	
Features	s:										
Query	2606			SSNVSPGQQT							2427
Sbjct	1882			SSNVSPGQQT SSNVSPGQQT							1941
Query	2426	tagq.	lqqlaqqsay	asggqssvs	vvltT	PVOTLPS	SVVQPQI	GSGAQIV	SISSOTLP	VNSS	2247
Sbjct	1942			VASĞĞŌSSVS VASGGŌSSVS							2001
Query	2246			Ovvsvstlpt							2067
Sbjct	2002			QVVSVSTLPT QVVSVSTLPT							2061
Query	2066			GOSIVSMPNL GOSIVSMPNL							1887
Sbjct	2062			GÖSIVSMPNL							2121
Query	1886			/TQQSGGAHI /TQQSGGAHI							1707
Sbjct	2122			/TQQSGGAHI /TQQSGGAHI							2181
Query	1706			SOKVAVSGMP SOKVAVSGMP							1527
Sbjct	2182			SQKVAVSGMP SQKVAVSGMP							2241
Query	1526			aagDMLLVKR				1407			
Sbjct	2242			AAGDMLLVKR AAGDMLLVKR				2281			

Range 2: 1882 to 2281

Score	E	Expect	Method			Identities	s P	ositives	(Gaps	Fra	me
558 bits	(1437) 2	e-169()) Compositio	nal matrix ac	djust. 4	400/400(100%) 4	00/400(1	00%) ()/400(0%	_o) -1	
Features	s:											
Query	1241		qqlqiqhLTS									1062
Sbjct	1882		QQLQIQHLTS QQLQIQHLTS									1941
Query	1061		lqqlaqqsav									882
Sbjct	1942		LÕÕLAÕÕSA\ LÕÕLAÕÕSA\									2001
Query	881		SIVOTOSLPO									702
Sbjct	2002		SIVQTQSLPÇ SIVQTQSLPÇ									2061
Query	701		TLQQRTTAGO									522
Sbjct	2062		TLQQRTTAGO TLQQRTTAGO									2121
Query	521		QGGKTTVIP\									342
Sbjct	2122		QGGKTTVIP\ QGGKTTVIP\									2181
Query	341		ASNMATHVTS									162
Sbjct	2182		ASNMATHVTS ASNMATHVTS									2241
Query	161		Sadgttttta									
Sbjct	2242		SADGTTTTT <i>I</i> SADGTTTTT <i>I</i>									

GD11590 [Drosophila simulans]

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

Score		Expect	Method	Identities	Positives	Gaps I	Frame
535 bits	(1377)	2e-168()	Compositional matrix adjust.	391/400(98%)	392/400(98%)	0/400(0%) -	1
Features	s:						
Query	2606		qlqiqhLTSSNVSPGQQTAILI OLOIOHLTSSNVSPGOOTAILI				
Sbjct	403		QLQIQHLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL				
Query	2426	tagql	qqlaqqsavasggqssvsvvlt	TPVQTLPSVVQ	POIGSGAOIVS	ISSOTLPVNS	SS 2247
Sbjct	463		QQLAQQSA ASĞĞQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT				
Query	2246		IVQTQSLPQvvsvstlptvgtv				
Sbjct	523		IVQTQSLPQVVSVSTLPTVGTV IVQTQSLPQVVSVSTLPTVGTV				
Query	2066		LOORTTAGGOSIVSMPNLGOGA				
Sbjct	583		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQGA				
Query	1886		GGKTTVIPVTQQSGGAHIQLYR				
Sbjct	643		GGKTTVIPVTQQSGGAHIQL R GGKTTVIPVTQQSGGAHIQLCR				
Query	1706		SNMATHVTSQKVAVSGMPGTST				
Sbjct	703		SNMATHVTSQKVAVSGMPGTST SNMATHVTSQKVAVSGMPGTST				
Query	1526	~	adgtttttaagDMLLVKRHNII				
Sbjct	763		ADGTTTT AGDMLLVKRHNII ADGTTTTKGAGDMLLVKRHNII				

Range 2: 403 to 802

Score		Expect	Method		Identities	Positives	Gaps	Frame
535 bits	(1377)	2e-168()	Compositiona	al matrix adjust.	391/400(98%)	392/400(98%)	0/400(0%)	-1
Features	S:							
Query	1241			NVSPGQQTAILI				
Sbjct	403			NVSPGQQTAILI NVSPGQQTAILI				
Query	1061	tagql	qqlaqqsava	sggqssvsvvlt	TPVQTLPSVVQ	POIGSGAOIVS	ISSOTLPVN	ISS 882
Sbjct	463			SĞĞQSSVSVVLT SGGQSSVSVVLT				
Query	881			vsvstlptvgtv				
Sbjct	523			VSVSTLPTVGTV VSVSTLPTVGTV				
Query	701			SIVSMPNLGOGA SIVSMPNLGOGA				
Sbjct	583			SIVSMPNLGQGA SIVSMPNLGQGA				
Query	521			QQSGGAHIQLYR OOSGGAHIOL R				
Sbjct	643	~		QQSGGAHIQL R QQSGGAHIQLCR	~ ~	~	~	
Query	341			KVAVSGMPGTST				
Sbjct	703			KVAVSGMPGTST KVAVSGMPGTST				
Query	161			gDMLLVKRHNII				
Sbjct	763			GDMLLVKRHNII GDMLLVKRHNII				

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	E	Expect	Method	Identities	Positives	Gaps	Frame	
556 bits(1	1433) 5	e-168()	Compositional matrix adjust.	400/400(100%)	400/400(100%)	0/400(0%)	-1	
Features:								
Query	2606		qqlqiqhLTSSNVSPGQQTAIL QQLQIQHLTSSNVSPGQQTAIL					7
Sbjct	2423		QQLQIQHLTSSNVSFGQQTAIL					2

Query 2	2426	tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS	2247
Sbjct 2	2483	TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS	2542
Query 2	2246	PQLGSIVQTQSLPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVST	2067
Sbjct 2	2543	PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST	2602
Query 2	2066	AAGNTLOORTTAGGOSIVSMPNLGOGASPSOFOTOLRLAAVPTSPATOTTOLVTTKGIPV	1887
Sbjct 2	2603	AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV	2662
Query 1	1886	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG	1707
Sbjct 2	2663	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG	2722
Query 1	1706	TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	1527
Sbjct 2	2723	TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	2782
Query 1	1526	ROVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 1407	
Sbjct 2	2783	RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF 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	S :						
Query	1241		qqlqiqhLTSSNVSPGQQTAIL QQLQIQHLTSSNVSPGQQTAIL				
Sbjct	2423		QQLQIQHLTSSNVSPGQQTAIL QQLQIQHLTSSNVSPGQQTAIL				
Query	1061		lqqlaqqsavasggqssvsvvl LQQLAQQSAVASGGQSSVSVVL				
Sbjct	2483		LQQLAQQSAVASGGQSSVSVVL LQQLAQQSAVASGGQSSVSVVL				
Query	881		SIVQTQSLPQvvsvstlptvgt SIVQTQSLPQVVSVSTLPTVGT				
Sbjct	2543		SIVQTQSLPQVVSVSTLPTVGT				
Query	701		TLQQRTTAGGQSIVSMPNLGQG TLQQRTTAGGQSIVSMPNLGQG				
Sbjct	2603		TLQQRTTAGGQSIVSMPNLGQG TLQQRTTAGGQSIVSMPNLGQG				
Query	521		QGGKTTVIPVTQQSGGAHIQLY QGGKTTVIPVTQQSGGAHIQLY				
Sbjct	2663		ÕGGKTTVIPVTÕÕSGGAHIÕLY				
Query	341		ASNMATHVTSQKVAVSGMPGTS ASNMATHVTSQKVAVSGMPGTS				
Sbjct	2723		ASNMATHVTSQKVAVSGMPGTS				
Query	161	~	SadgtttttaagDMLLVKRHNI	~ ~~			
Sbjct	2783		SADGTTTTTAAGDMLLVKRHNI SADGTTTTTAAGDMLLVKRHNI				

domino, isoform D [Drosophila melanogaster]

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

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

Score		Expect Method	Identities	Positives	Gaps	Frame
556 bits	(1433) 6	Se-168() Compositional matrix adjust	i. 400/400(100%) 400/400(100%) 0/400(0%) -1
Feature	s:					
Query	2606	GGqlqqlqiqhLTSSNVSPGQQTAI				
Sbjct	2423	GGQLQQLQIQHLTSSNVSPGQQTAI: GGQLQQLQIQHLTSSNVSPGQQTAI:				
Query	2426	tagqlqqlaqqsavasggqssvsvv TAGQLQQLAQQSAVASGGQSSVSVV				
Sbjct	2483	TAGQLQQLAQQSAVASGGQSSVSVV				
Query	2246	PQLGSIVQTQSLPQvvsvstlptvg PQLGSIVQTQSLPQVVSVSTLPTVG				
Sbjct	2543	PQLGSIVQTQSLPQVVSVSTLPTVG				
Query	2066	AAGNTLQQRTTAGGQSIVSMPNLGQ AAGNTLQQRTTAGGQSIVSMPNLGQ				
Sbjct	2603	AAGNTLQQRTTAGGQSIVSMPNLGQ				

Query	1886	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG	1707
Sbjct	2663	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG	2722
Query	1706	TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	1527
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 ı	matrix adjust.	400/400(100%)) 400/400(100%) 0/400(0%)	-1
Features	S :							
Query	1241	GGql	qqlqiqhLTSSN QQLQIQHLTSSN	VSPGQQTAIL	LHQPQQQLRTHE	PGQGGQSNTQQL	VKTIVGtss	sl 1062
Sbjct	2423		QQLQIQHLTSSN QQLQIQHLTSSN					
Query	1061		lqqlaqqsavas					
Sbjct	2483		LÕÕLAÕÕSAVAS(LÕÕLAÕÕSAVAS(
Query	881		SIVOTOSLPOVV					
Sbjct	2543		SIVQTQSLPQVV: SIVQTQSLPQVV:					
Query	701		TLOORTTAGGOS					
Sbjct	2603		TLQQRTTAGGQS: TLQQRTTAGGQS:					
Query	521		QGGKTTVIPVTQ					
Sbjct	2663		QGGKTTVIPVTQ QGGKTTVIPVTQ					
Query	341		ASNMATHVTSOK					
Sbjct	2723		ASNMATHVTSQK' ASNMATHVTSQK'					
Query	161		Sadgtttttaagl					
Sbjct	2783		SADĞTTTTTAAĞI SADGTTTTTAAGI					

domino, isoform G [Drosophila melanogaster]

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

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

Score	E	Expect	Method		Identities	Pos	itives	Gaps	Fran	ne
556 bits	(1432) 9	e-168()	Compositional ma	trix adjust.	400/400(10	0%) 400	/400(100%	%) 0/400(0%	%) -1	
Features	S :									
Query	2606		qqlqiqhLTSSNVS							2427
Sbjct	2458		QQLQIQHLTSSNVS QQLQIQHLTSSNVS							2517
Query	2426		lqqlaqqsavasgg LQQLAQQSAVASGG							2247
Sbjct	2518		LQQLAQQSAVASGG LQQLAQQSAVASGG							2577
Query	2246	POLGS	SIVQTQSLPQvvsv SIVQTQSLPQVVSV	stlptvgt	vlttTANQF	OQQHQt	tavttlnt	tTMLRGQRI	IVST	2067
Sbjct	2578		SIVQTQSLFQVVSV							2637
Query	2066		TLQQRTTAGGQSIV TLOORTTAGGOSIV							1887
Sbjct	2638		TLÕÕRTTAGGÖSIV TLÕÕRTTAGGÕSIV							2697
Query	1886		QGGKTTVIPVTQQS QGGKTTVIPVTQQS							1707
Sbjct	2698		ŽGGKTTVIPVTQOS ŽGGKTTVIPVTQQS							2757
Query	1706	TIIO	ASNMATHVTSOKVA ASNMATHVTSÕKVA	VSGMPGTS	TTVQAGNVV	ZSVOMHO	GOARTOF:	IKOMAAGK(OOLO	1527
Sbjct	2758		ASNMATHVTSÕKVA ASNMATHVTSÕKVA							2817
Query	1526		SadgtttttaagDM SADGTTTTTAAGDM				1407			

Range 2: 2458 to 2857

Score	E	Expect	Method			Identiti	es	Positiv	es	Gaps	Fra	me
556 bits	(1432) 9	e-168()) Composition	onal mati	rix adjust.	400/400	0(100%)	400/40	0(100%) 0/400(0°	%) -1	
Features	s:											
Query	1241		qqlqiqhLl									1062
Sbjct	2458		QQLQIQHL'I QLQIQHL'I									2517
Query	1061	tagq.	lqqlaqqsa	vasggq	ssvsvvl	tTPVQT	LPSVVQ	POIGS	AQIVS	ISSQTLP	VNSS	882
Sbjct	2518		LQQLAQQS <i>I</i> LQQLAQQS <i>I</i>									2577
Query	881		SIVOTOSLE									702
Sbjct	2578		SIVQTQSLE SIVQTQSLE									2637
Query	701		TLQQRTTAC									522
Sbjct	2638		TLQQRTTAC TLQQRTTAC									2697
Query	521		QGGKTTVII									342
Sbjct	2698		QGGKTTVII QGGKTTVII									2757
Query	341		ASNMATHVI									162
Sbjct	2758		ASNMATHVI ASNMATHVI									2817
Query	161		Sadgttttt						2			
Sbjct	2818		SADGTTTTT SADGTTTTT						357			

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	S:						
Query	2606		ıqlqiqhLTSSNVSPGQQTAILI QLQIQHLTSSNVSPGQQTAILI				
Sbjct	2426		QLQIQHLTSSNVSFGQQTAILI QLQIQHLTSSNVSPGQQTAILI				
Query	2426		.qqlaqqsavasggqssvsvvlt .QQLAQQSAVASGGQSSVSVVL				
Sbjct	2486		JOQLAQQSAVASGGQSSVSVVL JQQLAQQSAVASGGQSSVSVVL				
Query	2246		SIVQTQSLPQvvsvstlptvgtv				
Sbjct	2546		SIVQTQSLPQVVSVSTLPTVGTV SIVQTQSLPQVVSVSTLPTVGTV				
Query	2066		LOORTTAGGOSIVSMPNLGOGA				
Sbjct	2606		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQGA				
Query	1886)GGKTTVIPVTQQSGGAHIQLYI)GGKTTVIPVTQQSGGAHIQLYI				
Sbjct	2666		GGKTTVIPVTQQSGGAHIQLYI QGGKTTVIPVTQQSGGAHIQLYI				
Query	1706		ASNMATHVTSQKVAVSGMPGTS				
Sbjct	2726		ASNMATHVTSQKVAVSGMPGTS ASNMATHVTSQKVAVSGMPGTS				
Query	1526		SadgtttttaagDMLLVKRHNII				
Sbjct	2786		SADGTTTTTAAGDMLLVKRHNII SADGTTTTTAAGDMLLVKRHNII				

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
Sbjct	2426	GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL GGQLQQLQIQHLTSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGTSSSL	2485
Query	1061	tagqlqqlaqqsavasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQTLPVNSS	882
Sbjct	2486	TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQ+LPSVVQPQIGSGAQIVSISSQTLPVNSS TAGQLQQLAQQSAVASGGQSSVSVVLTTPVQSLPSVVQPQIGSGAQIVSISSQTLPVNSS	2545
Query	881	POLGSIVOTOSLPOvvsvstlptvgtvlttTANOPQQQHQttavttlntTMLRGQRIVST	702
Sbjct	2546	PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST PQLGSIVQTQSLPQVVSVSTLPTVGTVLTTTANQPQQQHQTTAVTTLNTTMLRGQRIVST	2605
Query	701	AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV	522
Sbjct	2606	AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV	2665
Query	521	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG	342
Sbjct	2666	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATGATANLVQAGG	2725
Query	341	TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	162
Sbjct	2726	TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	2785
Query	161	RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 42	
Sbjct	2786	RQVVSADGTTTTTAAGDMLLVKRHNILAAQKAQQASGALF 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	S :						
Query	2606		qlqiqhLTSSNVSPGQQTAILI				
Sbjct	2421		QLQIQHLTSSNVSPGQQTAILI QLQIQHLTSSNVSPGQQTAILI				
Query	2426	tagql	qqlaqqsavasggqssvsvvlt QQLAQQSA ASGGQSSVSVVLT	TPVQTLPSVVQ	POIGSGAQIVS:	ISSOTLPVN	SS 2247
Sbjct	2481		QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT				
Query	2246		IVQTQSLPQvvsvstlptvgtv IVOTOSLPOVVSVSTLPTVGTV				
Sbjct	2541		IVQTQSLPQVVSVSTLPTVGTV				
Query	2066		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQG				
Sbjct	2601		LQQRTTAGGQSIVSMPNLGQG LQQRTTAGGQSIVSMPNLGQGV				
Query	1886		GGKTTVIPVTQQSGGAHIQLYR GGKTTVIP TQQSGGAHIQLYR				
Sbjct	2661		GGKTTVIP 1005GGAH10L1K GGKTTVIPGTQQSGGAH1QLYR				
Query	1706		SNMATHVTSQKVAVSGMPGTST SNM THVTSQKVAVSGMPGTS+				
Sbjct	2721		SNM THVISQKVAVSGMPGIST SNMGTHVTSQKVAVSGMPGTSS				
Query	1526	ROVVS	adgtttttaagDMLLVKRHNII ADGTTTTT AGDMLLVKRHNII	AAQKAQQASGA	LF 1407		
Sbjct	2781		ADGTTTTT AGDMLLVKRHNIL ADGTTTTTGAGDMLLVKRHNIL				

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	s:						
Query	1241		qlqiqhLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL				
Sbjct	2421		QLQIQHLTSSNVSPGQQTAILL				
Query	1061		qqlaqqsavasggqssvsvvlt QQLAQQSA ASGGQSSVSVVLT				
Sbjct	2481		QQLAQQSAAASGGQSSVSVVLT				
Query	881		IVQTQSLPQvvsvstlptvgtv IVQTQSLPQVVSVSTLPTVGTV				
Sbjct	2541		IVQTQSLPQVVSVSTLPTVGTV				

Query	701	AAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPV AAGNTLQQRTTAGGQSIVSMPNLGQG SP+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV	522
Sbjct	2601	AAGNTLQQRTTAGGQSIVSMPNLGQG SF+QFQTQLRLAAVPTSPATQTTQLVTTKGIPV	2660
Query	521	SALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGG SALQQGGKTTVIP TQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAG TGATANLVQAGG	342
Sbjct	2661	SALQQGGKTTVIPGTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGGTGATANLVQAGG	2720
Query	341	TIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ TIIQASNM THVTSQKVAVSGMPGTS+TVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	162
Sbjct	2721	TIIQASNMGTHVTSQKVAVSGMPGTSSTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQ	2780
Query	161	RQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 42 RQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF	
Sbjct	2781	RQVVSADGITTT AGDMLLVKRHNILAAQKAQQASGALF 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	s:						
Query	2606		qlqiqhLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL				
Sbjct	2421		QLQIQHLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL				
Query	2426	tagql	qqlaqqsavasggqssvsvvlt QQLAQQSA ASGGQSSVSVVLT	TPVQTLPSVVQ	POIGSGAQIVSI	ISSOTLPVN	SS 2247
Sbjct	2481		QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT				
Query	2246		IVQTQSLPQvvsvstlptvgtv IVQTQSLPQVVSVSTLPTVGTV				
Sbjct	2541		IVQTQSLPQVVSVSTLPTVGTV				
Query	2066		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQG				
Sbjct	2601		LQQRTTAGGQSIVSMPNLGQGV				
Query	1886		GGKTTVIPVTQQSGGAHIQLYR GGKTTVIP TQQSGGAHIQLYR				
Sbjct	2661		GGKTTVIF TOOSGGAHIOLIK GGKTTVIPGTQQSGGAHIQLYR				
Query	1706		SNMATHVTSQKVAVSGMPGTST SNM THVTSOKVAVSGMPGTS+				
Sbjct	2721		SNMGTHVTSQKVAVSGMPGTSS				
Query	1526		adgtttttaagDMLLVKRHNIL ADGTTTTT AGDMLLVKRHNIL				
Sbjct	2781		ADGTTTTTGAGDMLLVKRHNIL				

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		qlqiqhLTSSNVSPGQQTAILL				
Sbjct	2421		QLQIQHLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL				
Query	1061	tagql	qqlaqqsavasggqssvsvvlt QQLAQQSA ASGGQSSVSVVLT	TPVQTLPSVVQI	POIGSGAOIVSI	SSOTLPVNS	SS 882
Sbjct	2481		QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT				
Query	881		IVQTQSLPQvvsvstlptvgtv IVQTQSLPQVVSVSTLPTVGTV				
Sbjct	2541		IVQTQSLPQVVSVSTLPTVGTV				
Query	701		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQG				
Sbjct	2601		LÖÖRTTAGGÖSIVSMPNLGÖGV				
Query	521		GGKTTVIPVTQQSGGAHIQLYR GGKTTVIP TQQSGGAHIQLYR				
Sbjct	2661	~~	GGKTTVIF TOOSGGAHIOLIK GGKTTVIPGTQQSGGAHIQLYR	~	~	~	
Query	341		SNMATHVTSQKVAVSGMPGTST SNM THVTSQKVAVSGMPGTS+				

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 260		[qlqiqhLTSSNVSPGQQTAILL				
Sbjct 242		QLQIQHLTSSNVSPGQQTAILL QLQIQHLTSSNVSPGQQTAILL				
Query 242	tagql	.qqlaqqsavasggqssvsvvlt QQLAQQSA ASGGQSSVSVVLT	TPVQTLPSVVQ	POIGSGAOIVS	ISSOTLPVN	ISS 2247
Sbjct 248		QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT				
Query 224		SIVQTQSLPQvvsvstlptvgtv SIVQTQSLPQVVSVSTLPTVGTV	lttTANQPQQQ	HQttavttlnt	TMLRGORIV	ST 2067
Sbjct 254		SIVQTQSLPQVVSVSTLPTVGTV				
Query 206		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQG				
Sbjct 260		LOOKTTAGGOSTVSMFNLGOG LOORTTAGGOSTVSMPNLGOGV				
Query 188		GGKTTVIPVTQQSGGAHIQLYR GGKTTVIP TÖÖSGGAHIÖLYR				
Sbjct 266		GGKTTVIP 100SGGAH10LIK GGKTTVIPGTQQSGGAH1QLYR				
Query 170		SNMATHVTSQKVAVSGMPGTST S+M THVTSQKVAVSGMPGTST				
Sbjct 272		SSMGTHVTSQKVAVSGMPGTST				
Query 152		adgtttttaagDMLLVKRHNIL ADGTTTTT AGDMLLVKRHNIL				
Sbjct 278		SADGTTTTTGAGDMLLVKRHNIL				

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		[qlqiqhLTSSNVSPGQQTAILL				
Sbjct 2420		ĮQLQIQHLTSSNVSPGQQTAILL ĮQLQIQHLTSSNVSPGQQTAILL				
Query 1061		.qqlaqqsavasggqssvsvvlt OOLAOOSA ASGGOSSVSVVLT				
Sbjct 2480		QQLAQQSA ASGGQSSVSVVLT QQLAQQSAAASGGQSSVSVVLT				
Query 881	POLGS	IVQTQSLPQvvsvstlptvgtv IVQTQSLPQVVSVSTLPTVGTV	lttTANQPQQQ	HQttavttlnt	MLRGORIV	ST 702
Sbjct 2540		IVÕTÕSLPÕVVSVSTLPTVGTV				
Query 701		LQQRTTAGGQSIVSMPNLGQGA LQQRTTAGGQSIVSMPNLGQG				
Sbjct 2600		LQQRTTAGGQSIVSMPNLGQGV				
Query 521		GGKTTVIPVTQQSGGAHIQLYR GGKTTVIP TQQSGGAHIQLYR				
Sbjct 2660		GGKTTVIPGTQQSGGAHIQLYR				
Query 341		SNMATHVTSQKVAVSGMPGTST S+M THVTSQKVAVSGMPGTST				
Sbjct 2720		SSMGTHVTSQKVAVSGMPGTST				
Query 161		adgtttttaagDMLLVKRHNIL ADGTTTTT AGDMLLVKRHNIL				
Sbjct 2780		ADGTTTTTGAGDMLLVKRHNIL				

▶ **See 1 more title(s)** 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		SPGQQTAILLHQPQQQ SPGQQTAILLHQPQQQ					
Sbjct	2425		SPGQQTATLLHQPQQQ SPGQQTATLLHQPQQQ					
Query	2390		gqssvsvvltTPVQTI GOSSVSVVLTTPVO+I					
Sbjct	2485		GÕSSVSVVLTTPVÕSI					
Query	2213		rsvstlptvgtvlttTA SVSTLPTVG+VLTTTA		HQttavttlnt QTT VTTLNT			
Sbjct	2545		SVSTLPTVGSVLTTT <i>F</i>					
Query	2033		IVSMPNLGQGASPSQE IVSMPNLGQG + QE					
Sbjct	2602		IVSHPNLGQG					
Query	1853		QSGGAHIQLYRQRSLK O GGAHIOLYRORSLK				GGTIIQASN GGTIIOASN	
Sbjct	2661		QPGGAHIQLYRQRSLK					
Query	1679		QKVAVSGMPGTSTTVÇ OKVAVSG+PG+STTVÇ					
Sbjct	2721		ŎĸvAvSG+FG+S11vÇ ŎĸvAvSGIPGSSTTVÇ					
Query	1499		agDMLLVKRHNILAAÇ AGDMLLVKRHNILAAÇ		1425			
Sbjct	2781		AGDMLLVKRHNILAAÇ		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	S:						
Query	1205		SPGQQTAILLHQPQQQLRTHPQ				
Sbjct	2425		'SPGQQTAILLHQPQQQLRTHPG 'SPGQQTAILLHQPQQQLRTHPG				
Query	1025		ggssvsvvltTPVQTLPSVVQF GQSSVSVVLTTPVQ+LP+VVQF				
Sbjct	2485		GQSSVSVVLTTPVQ+LP+VVQF GQSSVSVVLTTPVQSLPAVVQF				
Query	848	~	rsvstlptvgtvlttTANQPQQQ SVSTLPTVG+VLTTTA QQ	HQttavttlnt OTT VTTLNT			
Sbjct	2545		SVSTLPTVGSVLTTTASQQ				
Query	668		IVSMPNLGQGASPSQFQTQLRI IVSMPNLGQG + QFQ QLRI	AAVPTSPATQT AAVP+SPATQT			
Sbjct	2602		IVSMPNLGQGVN-QQFQAQLRI				
Query	488	IPVTQ	QSGGAHIQLYRQRSLKVLQTTT O GGAHIOLYRORSLKVLOTTT	QAVPsgsagat OA G+A T		GGTIIQASN GGTIIOASN	
Sbjct	2661	~	QPGGAHIQLYRQRSLKVLQTTT	~	~	~	
Query	314		QKVAVSGMPGTSTTVQAGNVVS QKVAVSG+PG+STTVQAGNVVS				
Sbjct	2721		OKVAVSGIPGSSTTVQAGNVVS QKVAVSGIPGSSTTVQAGNVVS				
Query	134		agDMLLVKRHNILAAQKAQQ AGDMLLVKRHNILAAQKAQQ	60			
Sbjct	2781		AGDMLLVKRHNILAAQKAQQ AGDMLLVKRHNILAAQKAQQ	2805			

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

• See 1 more title(s) 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

Feature	S:		
Query	2570	TSSNVSPGQQTAILLHQPQQQLRTHPGQGGQSNTQQLVKTIVGtsssltagqlqqlaqqs T + VSPGQQTAILLHQPQQQLRTHPGQ GQ+ TQQLVKTIVGTSSSLTAGQLQQLAQQS	2391
Sbjct	2425	TGATVSPGQQTAILLHQPQQQLRTHPGQ GQ+ IQQLVKTIVGTSSSLTAGQLQQLAQQS	2484
Query	2390	avasggqssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS A SGGQSSVSVVLTTPVQ+LP+VVQPQ GSGAQIVSISSQT LPVNSSPQLGSIVQTQ+	2214
Sbjct	2485	AANSGGQSSVSVVLTTPVQSLPAVVQPQTGSGAQIVSISSQTTLPVNSSPQLGSIVQTQT	2544
Query	2213	LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT LPQVVSVSTLPTVG+VLTTTA QQ QTT VTTLNT MLRGQRIVS AAGNTLQQRTT	2034
Sbjct	2545	LPÕVVSVSTLPTVGSVLTTTASÕÕQQÕTTGVTTLNTAMLRGÕRIVSAAAGNTLÕÕRTT	2601
Query	2033	AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV AGGQSIVSMPNLGQG + QFQ QLRLAAVP+SPATQTTQLVTTKGIPVSALQQGGKTTV	1854
Sbjct	2602	AGGQSIVSMPNLGQGVN-QQFQAQLRLAAVPSSPATQTTQLVTTKGIPVSALQQGGKTTV	2660
Query	1853	IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMA IP TQQ GGAHIQLYRQRSLKVLQTTTQA G+A T A +LVQAGGTIIQASNM	1680
Sbjct	2661	IPGTŐŐPGGAHIŐLYRŐRSLKVLŐTTTŐAAAGGAAAGTAGGATTSLVŐAGGTIIÓASNMP	2720
Query	1679	THVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgt THVTSQKVAVSG+PG+STTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQVV+ADGT	1500
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) 9	9e-127()	Compositional ma	atrix adjust.	337/385(88%)	350/385(90%)	7/385(1%)	-1
Features	s:							
Query	1205	TSSNV	SPGQQTAILLHQP SPGQQTAILLHQP	QQQLRTHPG	QGGQSNTQQLVI	KTIVGtssslta	agglqqlag	gs 1026
Sbjct	2425		SPGQQTAILLHQP					
Query	1025		gqssvsvvltTPV GQSSVSVVLTTPV					
Sbjct	2485		GÕSSVSVVLTTPV GÕSSVSVVLTTPV					
Query	848		svstlptvgtvlt SVSTLPTVG+VLT		HQttavttlnt			
Sbjct	2545		SVSTLPTVGSVLT					
Query	668		IVSMPNLGQGASP IVSMPNLGQG +					
Sbjct	2602		IVSMPNLGQGVN-					
Query	488	IPVTQ	QSGGAHIQLYRQR O GGAHIOLYROR	SLKVLQTTT SLKVLOTTT	QAVPsgsagato QA G+A T		GGTIIQASN GGTIIÕASN	
Sbjct	2661		QPGGAHIQLYRQR					
Query	314		QKVAVSGMPGTST QKVAVSG+PG+ST					
Sbjct	2721		QKVAVSGIPGSST					
Query	134		agDMLLVKRHNIL AGDMLLVKRHNIL		60			
Sbjct	2781		AGDMLLVKRHNIL		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
Feature	s:						
Query	2570		SPGQQTAILLHQPQQQLRTHPG				
Sbjct	2505		SPGQQTAILLHQPQQQ+RTHPG SPGQQTAILLHQPQQQMRTHPG				
Query	2390	avasg	gqssvsvvltTPVQTLPSVVQP GQSSVSVVLTTPVQ+LP+VVQ	QIGSGAQIVSI	SSQT-LPVNSSI	POLGSIVOT	QS 2214
Sbjct	2565	AAANP	GQSSVSVVLTTPVQ+LP+VVQ GQSSVSVVLTTPVQSLPAVVQT	QSGSAAQIVSI	SSQTTLPVNSSI	PÕLGSIVÕT PÕLGSIVÕT	QT 2624
Query	2213	LPQvv	svstlptv-gtvlttTANQPQQ	QHQttavttln	tTMLRGQRIVS7	raagntlqq	RT 2037

Sbjct	2625	$ \begin{array}{llllllllllllllllllllllllllllllllllll$	2684
Query	2036	TAGGOSIVSMPNLGOGASPSOFOTOLRLAAVPTSPATOTTOLVTTKGIPVSALQOGGKTT	1857
Sbjct	2685	A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTT NAAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTT	2743
Query	1856	VIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMAT	1677
Sbjct	2744	VIP TQQ GGAHIQLYRQRSLKVLQT V G+AG ATANLVQ GTIIQA NM T VIPGTQQPGGAHIQLYRQRSLKVLQTQPATV-GGTAGGGVATANLVQTAGTIIQAGNMPT	2802
Query	1676	HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt HVTSOKVAVSGMPG VOA NVVSSVOMHGOARTOFIKOMA+ KO LOROV+SADG+T	1497
Sbjct	2803	HVTSQKVAVSGMPG VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T HVTSQKVAVSGMPGAG-VVQAANVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST	2860
Query	1496	tttaagDMLLVKRHNILAAQKAQQASGALFTTTTG 1392 T+ AAGDMLLVKRHNILA QKAQQA+GALFTTTT	
Sbict	2861	TSAAAGDMLLVKRHNILATOKAOOATGALFTTTTA 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	S :						
Query	1205		SPGQQTAILLHQPQQQLRTHPG SPGQQTAILLHQPQQQ+RTHPG				
Sbjct	2505		SPGQQTAILLHQPQQQQ+RTHPG SPGQQTAILLHQPQQQMRTHPG				
Query	1025		rgqssvsvvltTPVQTLPSVVQP GQSSVSVVLTTPVQ+LP+VVQ				
Sbjct	2565		GQSSVSVVLTTPVQ+LP+VVQ GQSSVSVVLTTPVQSLPAVVQT				
Query	848		rsvstlptv-gtvlttTANQPQQ SVSTLPTV + TT + O OO		tTMLRGQRIVST T MLRGQRIVS		
Sbjct	2625		SVSTLPTV + 11 + Q QQ SVSTLPTVGSVLTTTASQQQQQ				
Query	671		SIVSMPNLGQGASPSQFQTQLR SIVS+PNLGQG SP+QFQTQLR				
Sbjct	2685		SIVSVPNLGQG SF OFOTOLK SIVSVPNLGQGVSPAQFQTQLR				
Query	491		QQSGGAHIQLYRQRSLKVLQTT QQ GGAHIQLYRQRSLKVLQT	TQAVPsgsaga V G+AG		GTIIQASNM GTIIOA NM	
Sbjct	2744		OO GGANIQLIKOKSLKVLQTQ QQPGGAHIQLYRQRSLKVLQTQ				
Query	311		KVAVSGMPGTSTTVQAGNVVSS		IKQMAAGKQQL(IKQMA+ KQ L(
Sbjct	2803		KVAVSGMPGAG-VVQAANVVSS				
Query	131		.gDMLLVKRHNILAAQKAQQASG .GDMLLVKRHNILA QKAQQA+G				
Sbjct	2861		GDMLLVKRHNILATQKAQQATG				

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)** Kange 1: 2540 to 2930

Score		Expect	Method		Identities	Positives	Gaps	Frame
427 bits(1098)	1e-123()	Compositiona	al matrix adjust.	328/395(83%)) 347/395(87%)	6/395(1%)	-1
Features):							
Query	2570			HQPQQQLRTHPQ				
Sbjct	2540			HQPQQQ+RTHPO HQPQQQMRTHPO				
Query	2390	avasg	ggssvsvvlt	TPVQTLPSVVQI TPVQ+LP+VVQ	OIGSGAQIVSI	SSQT-LPVNSS	POLGSIVOT	QS 2214
Sbjct	2600			TPVQ+LP+VVQ TPVQSLPAVVQT				
Query	2213		svstlptv-g SVSTLPTV	tvlttTANQPQQ	OHOttavttln	ntTMLRGQRIVS NT MLRGQRIVS	TAAGNTLQQ	RT 2037
Sbjct	2660			VLTTTASQÕQÕÕ				
Query	2036			GASPSQFQTQLF G SP+QFQTQLF				
Sbjct	2720			GVSPAÕFÕTÕLF				
Query	1856			YRQRSLKVLQTT YRQRSLKVLQT			GTIIQASNM GTIIOA NM	
Sbjct	2779			YRÕRSLKVLÕTÇ				

Query	1676	HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt HVTSQKVAVSGMPG VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T	1497
Sbjct	2838		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	s:						
Query	1205		SPGQQTAILLHQPQQQLRTHPQ				
Sbjct	2540		SPGQQTAILLHQPQQQ+RTHPO SPGQQTAILLHQPQQQMRTHPO				
Query	1025		gqssvsvvltTPVQTLPSVVQF GQSSVSVVLTTPVQ+LP+VVQ				
Sbjct	2600		GQSSVSVVLTTPVQ+LP+VVQ GQSSVSVVLTTPVQSLPAVVQ1				
Query	848	LPQVV	rsvstlptv-gtvlttTANQPQQ SVSTLPTV + TT + Q QQ	QHQttavttln	tTMLRGORIVS	TAAGNTLQQ	RT 672
Sbjct	2660	LPQVV	SVSTLPTVGSVLTTTASQQQQQQ	QQQTTAVTTLN QQQQTTAVTTLN	TAMLRGQRIVS	ASTGNTLÕÕ	RT 2719
Query	671		SIVSMPNLGQGASPSQFQTQLF SIVS+PNLGQG SP+QFQTQLF				
Sbjct	2720		SIVSVPNLGQGVSPAQFQTQLF				
Query	491		QQSGGAHIQLYRQRSLKVLQTT QQ GGAHIQLYRQRSLKVLQT	TQAVPsgsaga V G+AG		GTIIQASNM GTIIÕA NM	
Sbjct	2779		OQ GGAHIQLYRQRSLKVLQTÇ OQPGGAHIQLYRQRSLKVLQTÇ				
Query	311		KVAVSGMPGTSTTVQAGNVVSS KVAVSGMPG VQA NVVSS				
Sbjct	2838		KVAVSGMPGAG-VVQAANVVSS				
Query	131		.gDMLLVKRHNILAAQKAQQASG .GDMLLVKRHNILA QKAQQA+G				
Sbjct	2896		GDMLLVKRHNILATQKAQQATG				

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)** kange 1: 2540 to 2930

Score		Expect	Method		Identities	Positives	Gaps	Frame
426 bits	(1095) 3	3e-123()	Composition	nal matrix adjust.	328/395(83%)	347/395(87%)	6/395(1%) -	-1
Features	S :							
Query	2570			LHOPOOOLRTHPO				
Sbjct	2540			LHQPQQQ+RTHPO LHQPQQQMRTHPO				
Query	2390	avasg	gqssvsvvlt	tTPVQTLPSVVQI ITPVQ+LP+VVQ	POIGSGAQIVSI	SSQT-LPVNSS	POLGSIVOTO	OS 2214
Sbjct	2600			TTPVQSLPAVVQ1				
Query	2213		svstlptv-c	gtvlttTANQPQQ	QQHQttavttlr	ntTMLRGQRIVS NT MLRGQRIVS	TAAGNTLQQI	RT 2037
Sbjct	2660			SVLTTTASQÕQÕÕ	QQQTTAVTTLN QQQQTTAVTTLN	TAMLRGÕRIVS	ASTGNTLÕÕI	RT 2719
Query	2036			QGASPSQFQTQLF QG SP+QFQTQLF				
Sbjct	2720			ŽGVSPAQFQTQLF				
Query	1856	VIPVT	QQSGGAHIQI	LYRQRSLKVLQTT LYRQRSLKVLQT	TTQAVPsgsaga	ntgatANLVQAG ATANLVO	GTIIQASNMA GTIIOA NM	AT 1677
Sbjct	2779			LYRQRSLKVLQTÇ				
Query	1676			rsttvoagnvvss				
Sbjct	2838		KVAVSGMPG KVAVSGMPG		SVQMHGQARTQFIKQMA+ KQ LQRQV+SA SVQMHGQARTQFIKQMAS-KQSLQRQVISA			
Query	1496			NILAAQKAQQASO		.392		
Sbjct	2896			NILA QKAQQA+0 NILATQKAQQATO		930		

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	S :						
Query	1205	TSSNV	SPGQQTAILLHQPQQQLRTHPG	GOGGOSNTOOLV	KTIVGtssslt	agglqqlaq	qs 1026
Sbjct	2540		SPGQQTAILLHQPQQQ+RTHPG SPGQQTAILLHQPQQQMRTHPG				
Query	1025		rgqssvsvvltTPVQTLPSVVQF GQSSVSVVLTTPVQ+LP+VVQ				
Sbjct	2600		GQSSVSVVLTTPVQ+LP+VVQ GQSSVSVVLTTPVQSLPAVVQT				
Query	848		rsvstlptv-gtvlttTANQPQQ SVSTLPTV + TT + O OO	QOHQttavttln QO QTTAVTTLN	tTMLRGQRIVS	TAAGNTLQQ	RT 672
Sbjct	2660		SVSTLPTVGSVLTTTASQQQQQQ	Į Į Į Į Į Į Į Į Į Į Į Į Į Į Į Į Į Į Į	TAMLRGÕRIVS	ASTGNTLÕÕ	RT 2719
Query	671		SIVSMPNLGQGASPSQFQTQLF SIVS+PNLGQG SP+OFQTQLF				
Sbjct	2720		SIVSVPNLGQG SI OFQTQLR				
Query	491		QQSGGAHIQLYRQRSLKVLQTT QQ GGAHIQLYRQRSLKVLQT	TQAVPsgsaga V G+AG		GTIIQASNM GTIIÕA NM	
Sbjct	2779		OQ GGANIQLIKQKSLKVLQI QQPGGAHIQLYRQRSLKVLQTQ				
Query	311		KVAVSGMPGTSTTVQAGNVVSS	SVOMHGOARTOF SVOMHGOARTOF			
Sbjct	2838		KVAVSGMPGAG-VVQAANVVSS				
Query	131		.gDMLLVKRHNILAAQKAQQASG .GDMLLVKRHNILA QKAQQA+G				
Sbjct	2896		GDMLLVKRHNILATQKAQQATG				

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) 9	9e-123()	Compositional matrix	adjust.	332/395(84%) 351/395(88%	o) 8/395(2%)	-1
Features	s:							
Query	2570		SPGQQTAILLHQPQQQ					
Sbjct	1374		SPGQQTAILLHQPQQQ SPGQQTAILLHQPQQQ					
Query	2390		gqssvsvvltTPVQTL GQSSVSVVLTTPVQ+L					
Sbjct	1434	AAANP	GQSSVSVVLTTPVQSL GQSSVSVVLTTPVQSL	PAVVQT	Q GS AQIVSI QSGSAAQIVSI	ISSQTTLPVNS:	SPOLGSIVOI SPOLGSIVOI	TQT 1493
Query	2213	LPOVV	svstlptvgtvlttTA SVSTLPTVG+VLTTTA	NOPOOO	HQttavttlnt	TMLRGORIVS	TAAGNTLQQF	RTT 2034
Sbjct	1494		SVSTLPTVGSVLTTTA					
Query	2033		IVSMPNLGQGASPSQF IVS+PNLGQG SP+QF					
Sbjct	1553		IVSTFNLGOG SFTOF IVSVPNLGQGVSPAQF					
Query	1853		QSGGAHIQLYRQRSLK Q GGAHIQLYRQRSLK				GGTIIQASNM GTIIÕA NM	
Sbjct	1612		Q GGAHIQLINGKSLK QPGGAHIQLYRQRSLK					
Query	1676		KVAVSGMPGTSTTVQA KVAVSGMPG VQA			FIKOMAAGKOO FIKOMA+ KO		
Sbjct	1670		KVAVSGMPGAG-VVÕA					
Query	1496		gDMLLVKRHNILAAQK GDMLLVKRHNILA QK		_	1392		
Sbjct	1728		GDMLLVKRHNILATÕK			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	s:						
Query	1205		SPGQQTAILLHQPQQQLRTHPG SPGQQTAILLHQPQQQ+RTHP				
Sbjct	1374		SPGQQTAILLHQPQQQTRTHPV SPGQQTAILLHQPQQQMRTHPV				

Query	1025	avasgggssvsvvltTPVQTLPSVVQPQIGSGAQIVSISSQT-LPVNSSPQLGSIVQTQS	849
Sbjct	1434	A A+ GQSSVSVVLTTPVQ+LP+VVQ Q GS AQIVSISSQT LPVNSSPQLGSIVQTQ+ AAANPGQSSVSVVLTTPVQSLPAVVQTQSGSAAQIVSISSQTTLPVNSSPQLGSIVQTQT	1493
Query	848	LPQvvsvstlptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTT	669
Sbjct	1494	LPQVVSVSTLPTVG+VLTTTA+Q QQQ QTTAVTTLNT MLRGQRIVS + GNTLQQRT LPQVVSVSTLPTVGSVLTTTASQ-QQQQQTTAVTTLNTAMLRGQRIVSASTGNTLQQRTN	1552
Query	668	AGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTV A GQSIVS+PNLGQG SP+QFQTQLRLAAVPTSPATQ TQLVTTKGIPV+ALQQGGKTTV	489
Sbjct	1553	AAGQSIVSVPNLGQGVSPAQFQTQLRLAAVPTSPATQ-TQLVTTKGIPVTALQQGGKTTV	1611
Query	488	IPVTQQSGGAHIQLYRQRSLKVLQTTTQAVP-sgsagatgatANLVQAGGTIIQASNMAT IP TQQ GGAHIQLYRQRSLKVLQ TQ P G+AG ATANLVQ GTIIQA NM T	312
Sbjct	1612	IPGTQQPGGAHIQLYRQRSLKVLQTQPAPVGGTAGGGVATANLVQTAGTIIQAGNMPT	1669
Query	311	HVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtt HVTSQKVAVSGMPG VQA NVVSSVQMHGQARTQFIKQMA+ KQ LQRQV+SADG+T	132
Sbjct	1670	HVTSQKVAVSGMPG VQA NVVSSVQMHGQARTQFIKQMAS-KQSLQRQVISADGST	1727
Query	131	tttaagDMLLVKRHNILAAQKAQQASGALF 42 T+ AAGDMLLVKRHNILA QKAQQA+GALF	
Sbict	1728	TSAAAGDMLLVKRHNILATOKAOOATGALF 1757	

GH12111p [Drosophila melanogaster]

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

Score	E	rpect Method	Identities	Positives	Gaps	Frame
382 bits	(980) 7e	e-117() Compositional matrix adjust.	230/230(100%)	230/230(100%)	0/230(0%)	-1
Features	S:					
Query	2096	MLRGQRIVSTAAGNTLQQRTTAGGQ MLRGQRIVSTAAGNTLQQRTTAGGQ				
Sbjct	1	MLRGQRIVSTAAGNTLQQRTTAGGQ				
Query	1916	QLVTTKGIPVSALQQGGKTTVIPVT QLVTTKGIPVSALQQGGKTTVIPVT				
Sbjct	61	QLVTTKGIPVSALQQGGKTTVIPVT				
Query	1736	atANLVQAGGTIIQASNMATHVTSQ ATANLVQAGGTIIQASNMATHVTSQ		~	~ ~	
Sbjct	121	ATANLVÕAGGTITÕASNMATHVTSÕ				
Query	1556	QMAAGKQQLQRQVVSadgtttttaa QMAAGKQQLQRQVVSADGTTTTTAA				
Sbjct	181	QMAAGKQQLQRQVVSADGTTTTTAA				

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	s:						
Query	731		QRIVSTAAGNTLQQRTTAGGQS				
Sbjct	1		QRIVSTAAGNTLQQRTTAGGQS QRIVSTAAGNTLQQRTTAGGQS				
Query	551		TKGIPVSALQQGGKTTVIPVTQ TKGIPVSALQQGGKTTVIPVTQ				
Sbjct	61		TKGIPVSALQQGGKTTVIPVTQ				
Query	371		LVQAGGTIIQASNMATHVTSQK LVQAGGTIIQASNMATHVTSQK				
Sbjct	121		LVQAGGTIIQASNMATHVTSQK				
Query	191		GKQQLQRQVVSadgtttttaag GKQQLQRQVVSADGTTTTTAAG			42	
Sbjct	181		SKQQLQRQVVSADGTTTTTAAG			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	S :		
Query	2096	MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT	1917
Sbjct	1	MLRGQRIVSTAAGNTLQQRTTAGGQSIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTT	60
Query	1916	QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatg	1737
Sbjct	61	QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG QLVTTKGIPVSALQQGGKTTVIPVTQQSGGAHIQLYRQRSLKVLQTTTQAVPSGSAGATG	120
Query	1736	atANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK	1557
Sbjct	121	ATANLVQAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIK	180
Query	1556	QMAAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 1407	
Sbjct	181	QMAAGKQQLQRQVVSADGTTTTT AGDMLLVKRHNILAAQKAQQASGALF QMAAGKQQLQRQVVSADGTTTTTGAGDMLLVKRHNILAAQKAQQASGALF 230	

Range 2: 1 to 230

Score		Expect	Method	Identities	Positives	Gaps Fr	ame
382 bits	(980)	8e-117()	Compositional matrix adjust.	229/230(99%)	229/230(99%)	0/230(0%) -1	
Features	S :						
Query	731		RIVSTAAGNTLQQRTTAGGQSI RIVSTAAGNTLQQRTTAGGQSI				552
Sbjct	1		RIVSTAAGNTLÕÕRTTAGGÕSI RIVSTAAGNTLÕÕRTTAGGÕSI				60
Query	551		KGIPVSALQQGGKTTVIPVTQQ KGIPVSALQQGGKTTVIPVTQQ				372
Sbjct	61	~	KGIPVSALQQGGKTTVIPVTQQ	~ ~ ~	~ ~		120
Query	371		VQAGGTIIQASNMATHVTSQKV VQAGGTIIQASNMATHVTSQKV				192
Sbjct	121		VÕAGGTIIÕASNMATHVTSÕKV				180
Query	191		KQQLQRQVVSadgtttttaagD KQQLQRQVVSADGTTTTT AGD			42	
Sbjct	181		KQQLQRQVVSADGTTTTTGAGD			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	E	kpect Method	Identities	Positives	Gaps	Frame
320 bits((820) 2e	e-87() Compositional matrix adjust.	224/334(67%)	246/334(73%)	32/334(9%)	-1
Features	3:					
Query	2342	PVQTLPSVVQPQIGSGAQIVSISSQ-				
Sbjct	2539	PVQ+LP + GS AQIVSISSQ PVQSLP-IATHNNGSTAQIVSISSQS				T TG 2597
Query	2165	lttTANQPQQQHQttavttlntTMLH				
Sbjct	2598	QQQQQQQQATGTVTMLI	RGQRIVS A G RGQRIVSAAGGG		RTTAGGQSIV RTTAGGQSIV	
Query	2006	PNLGQGASPSQFQTQLRLAAVPTSPA P+LGQG +P+QFQTQLRLAAV SPA	ATOTTOLVTTKO	GIPVSALQQGGK	TTVIPVTQQS	GG 1827
Sbjct	2649	PSLGQGVTPAQFQTQLRLAAVSGSPA				-A 2706
Query	1826	AHIQLYRQRSLKVLQTTTQAVPsgsa AHIOLYROR+LKVLO +O P +				HV 1671
Sbjct	2707	AHIQLYRQRNLKVLQ +Q P + AHIQLYRQRNLKVLQ-ASQGAPGTA				
Query	1670	TSQKVAVSGMPGTSTTVQAGNVVSSV TSQKVAVSGMPG +TTVQAGNVVSSV				tt 1491 +
Sbjct	2766	TSQKVAVSGMPG-ATTVQAGNVVSSV				
Query	1490	taagDMLLVKRHNILAAQKAQQAS A DMLLVKRHNILAAQKAQQA-		.395		
Sbjct	2825	VAPGTSDMLLVKRHNILAAQKAQQA		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 97	PVQTLPSVVQPQIGSGAQIVSISSQ-TLPVNSSPQLGSIVQTQSLPQvvsvstlptvgtv 80 PVQ+LP + GS AQIVSISSQ TLPVN++PQ+GSIVQTQ+LPQVVSV L T T)1
Sbjct 253		597
Query 800	lttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTAGGQSIVSM 64 T TMLRGORIVS A G NTLO ORTTAGGOSIVSM	12
Sbjct 259		548
Query 64	PNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVTQQSGG 46 P+LGQG +P+QFQTQLRLAAV SPATQTTQLVTTKGIPVSALQQGGK TV+P TQQ	52
Sbjct 26		706
Query 46	AHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASNMATHV 30 AHIQLYRQR+LKVLQ +Q P + + AG GTIIQASN+ +THV)6
Sbjct 270		765
Query 30!	TSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVVSadgtttt 12	26
Sbjct 27	TSQKVAVSGMPG +TTVQAGNVVSSVQMHGQARTQFIKQMAAGKQ LQRQV++ DG+ + TSQKVAVSGMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAAGKQGLQRQVLTTDGSGAS 28	324
Query 12	taagDMLLVKRHNILAAQKAQQASGALF 42	
Sbjct 282	A DMLLVKRHNILAAQKAQQA+G LF 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	E	xpect Method	Identities	Positives	Gaps	Frame
318 bits	(816) 56	e-87() Compositional matrix adjust.	281/411(68%)	299/411(72%)	36/411(8%)	-1
Features	S:					
Query	2567	SSNVSPGQQTAILLHQPQQQLRTHPO				ısa 2388
Sbjct	2477	++NVS GQQTAILLHQ Q + TANVSTGQQTAILLHQTTPQQQQQMI	G + TQQLV RTGQTTTTQQLV			AGG 2536
Query	2387	vasggqssvsvvltTPVQTLPSVVQI A+ G +SVSVVLTTPVQTLP+VVQ				
Sbjct	2537	NATTGPTSVSVVLTTPVQTLPAVVQ				
Query	2210	PQvvsvstlptvgtvlttTANQPQQQ POVVSV ++ T	QHQttavttlnt TAVTTLN	TMLRGQRIVST MLRGQRIVS	AAGNTLQQRT GNT+OORT	
Sbjct	2597	PQVVSVGSVLTTTASQQQQT				
Query	2030	GGQSIVSMPNLGQGASPSQFQTQLRI GQSIVSMP+LGQ P QFQT +RI		TTQLVTTKGI- TTOLVTTKGI		
Sbjct	2648	TGQSIVSMPSLGQNVGP-QFQTHVR				
Query	1856	VIPVTQQS-GGAHIQLYRQRSLKVLQ VIP TOO GGAHIOLYRORSLKVLQ	QTTTQAVPsgsa OTT A P G A		NL NL	V 1719 V
Sbjct	2706	VIPGTQQQPGGAHIQLYRQRSLKVL				-
Query	1718	QAGGTIIQASNMATHVTSQKVAVSGI Q GTIIQ SNM THVTSQKVAVSGI				
Sbjct	2764	QTAGTIIQTSNMPTHVTSQKVAVSGI				
Query	1538	QQLQRQVVSadgtttttaagDMI Q LQRQVVS T TTT GDMI	LLVKRHNILAAQ LLVKRHNIL AQ			
Sbjct	2823	QGLQRQVVS 1 111 GDM QGLQRQVVSADGTTTTATTTTGGDM				

Range 2: 2477 to 2867

Score	E	xpect Method	Identities	Positives	Gaps	Frame
312 bits	(799) 86	e-85() Compositional matrix adjust.	277/407(68%)	295/407(72%)	36/407(8%)	-1
Features	s:					
Query	1202	SSNVSPGQQTAILLHQPQQQLRTHP ++NVS GQQTAILLHQ Q +				ısa 1023
Sbjct	2477	TANVSTGQQTAILLHQTTPQQQQQM				AGG 2536
Query	1022	vasggqssvsvvltTPVQTLPSVVQ				
Sbjct	2537	A+ Ğ +SVSVVLTTPVQTLP+VVQ NATTGPTSVSVVLTTPVQTLPAVVQ		ISSQT LPV+S+ ISSQTSLPVSSA		
Query	845	PQvvsvstlptvgtvlttTANQPQQ POVVSV ++ T			AAGNTLQQRT GNT+OORT	
Sbjct	2597	PQVVSV ++ T PQVVSVGSVLTTTASQQQQT	TAVTTLN TAVTTLNA	MLRGQRIVS AAMLRGQRIVSA		
Query	665	GGQSIVSMPNLGQGASPSQFQTQLR	LAAVPTSPATQ-	TTQLVTTKGI	PVSALQQGGK	TT 492

Sbjct	2648	GQSIVSMP+LGQ P QFQT +RLAAVP + A TTQLVTTKGIPVSALQQGGKT TGQSIVSMPSLGQNVGP-QFQTHVRLAAVPAAQAGNQTTTQLVTTKGIPVSALQQGGKT-	2705
Query	491	VIPVTQQS-GGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLV VIP TQQ GGAHIQLYRQRSLKVLQTT A P G A AT NL V	354
Sbjct	2706	VIPGTQQQPGGAHIQLYRQRSLKVLQTTAAPQGGATATAGGVAGGAGNSGNLTNPTVV	2763
Query	353	QAGGTIIQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGK Q GTIIQ SNM THVTSQKVAVSGMPG +TTVQAGNVVSSVQMH QARTQ IKQMAA K	174
Sbjct	2764	QTAGTIIQTSNMPTHVTSQKVAVSGMPG-ATTVQAGNVVSSVQMHQQARTQLIKQMAANK	2822
Query	173	QQLQRQVVSadgtttttaagDMLLVKRHNILAAQKAQQASGALF 42	
Sbjct	2823	Q LQRQVVS T TTT GDMLLVKRHNIL AQK QQ + ALF QGLQRQVVSADGTTTTATTTTGGDMLLVKRHNIL-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	E	kpect Method	Identities	Positives	Gaps	Frame
301 bits	(771) 3e	e-81() Compositional matrix adjust.	220/336(65%)	240/336(71%)	28/336(8%)	-1
Features	S :					
Query	2342	PVQTLPSVVQPQIGSGAQIVSIS				_
Sbjct	2490	PVQ+LP + GS AQIVSIS PVQSLPIATHSNVNAGSTAQIVSIS	SQT LPVN++PÇ SQTTLPVNTAPÇ			
Query	2171	tvlttTANQPQQQHQttavttlntT	MLRGQRIVSTAA MLRGQRIVST A		-QRTTAGGQS QRTTAGGQS	
Sbjct	2550	$egin{array}{cccccccccccccccccccccccccccccccccccc$				
Query	2012	SMPNLGQGASPSQFQTQLRLAAVPT SMP LGQ + QFQTQLRLAAV	SPATOTTOLVTT SPATOTTOLVTT			=
Sbjct	2605	SMPGLGQSVTQGQFQTQLRLAAVSA				~
Query	1832	GGAHIQLYRQRSLKVLQTTTQAVPS AHIOLYROR+LKVLO A				AT 1677 +T
Sbjct	2664	-AAHIQLYRQRNLKVLQAPQGAQGG				· -
Query	1676	HVTSQKVAVSGMPGTSTTVQAGNVV HVTSQKVAV+ MPG +TTVQAGNVV				
Sbjct	2723	HVTSQKVAVTCMPG-ATTVQAGNVV				
Query	1499	-ttttaagDMLLVKRHNILAAQKAQ + DMLLVKRHNILAAQKAQ		1395		
Sbjct	2782	GSGAPGTSDMLLVKRHNILAAQKAQ		2817		

Range 2: 2490 to 2813

Score	E	rpect Method	Identities	Positives	Gaps	Frame
296 bits	(757) 2e	e-79() Compositional matrix adjust.	217/332(65%)	236/332(71%)	28/332(8%)	-1
Features	eatures:					
Query	977	PVQTLPSVVQPQIGSGAQIVSIS				
Sbjct	2490	PVQ+LP + GS AQIVSIS PVQSLPIATHSNVNAGSTAQIVSIS	SQT LPVN++PQ SQTTLPVNTAPQ			
Query	806	tvlttTANQPQQQHQttavttlntT	MLRGQRIVSTAA MLRGQRIVST A		-QRTTAGGQS ORTTAGGOS	
Sbjct	2550	T Q Q T				
Query	647	SMPNLGQGASPSQFQTQLRLAAVPT SMP LGQ + QFQTQLRLAAV	SPATQTTQLVTT SPATQTTQLVTT			-
Sbjct	2605	SMPGLGQSVTQGQFQTQLRLAAVSA				
Query	467	GGAHIQLYRQRSLKVLQTTTQAVPS AHIOLYROR+LKVLO A				AT 312 +T
Sbjct	2664	-AAHIQLYRQRNLKVLQAPQGAQGG			2	· -
Query	311	HVTSQKVAVSGMPGTSTTVQAGNVV HVTSQKVAV+ MPG +TTVQAGNVV				
Sbjct	2723	HVTSQKVAVTCMPG-ATTVQAGNVV				
Query	134	-ttttaagDMLLVKRHNILAAQKAQ + DMLLVKRHNILAAQKAQ				
Sbjct	2782	GSGAPGTSDMLLVKRHNILAAQKAQ		.3		

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	E	xpect Method	Identities	Positives	Gaps	Frame
271 bits(692) 9e	e-81() Compositional matrix adjust.	168/173(97%)	169/173(97%)	0/173(0%)	-1
Features						
Query	1925	QTTQLVTTKGIPVSALQQGGKTTVIPV QTTQLVTTKGIPVSALQQGGKTTVIP				
Sbjct	1	QTTQLVTTKGIPVSALQQGGKTTVIP				
Query	1745	atgatANLVQAGGTIIQASNMATHVTS				
Sbjct	61	GTGATANLVQAGGTIIQASNMGTHVTS				
Query	1565	FIKQMAAGKQQLQRQVVSadgttttta FIKQMAAGKQQLQRQVVSADGTTTTT				7
Sbjct	121	FIKQMAAGKQQLQRQVVSADGTTTTT(3

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	S :					
Query	560	QTTQLVTTKGIPVSALQQGGKTTVIPV QTTQLVTTKGIPVSALQQGGKTTVIP				
Sbjct	1	QTTQLVTTKGIPVSALQQGGKTTVIP				
Query	380	atgatANLVQAGGTIIQASNMATHVTS TGATANLVQAGGTIIQASNM THVTS				
Sbjct	61	GTGATANLVQAGGTIIQASNMGTHVTS				
Query	200	FIKQMAAGKQQLQRQVVSadgttttta FIKQMAAGKQQLQRQVVSADGTTTTT				
Sbjct	121	FIKOMAAGKOOLOROVVSADGTTTTTC				

dom [Drosophila busckii]

Sequence ID: **gb|ALC41615.1|** Length: 3526 Number of Matches: 2 Range 1: 2764 to 3182

Score	Ex	spect Method	Identities	Positives	Gaps	Frame
276 bits((706) 5e	-73() Compositional matrix adjust.	267/432(62%)	296/432(68%)	60/432(13%)	-1
Features	S:					
Query	2561	NVSPGQQTAILLHQPQQQ	LRTHPGQG LRT	GOSNT-QQLVK' QSNT QQLVK'	TIVGtssslta	agq 2415
Sbjct	2764	HVTPTQQTAILLQQQPQQQQQQQQQQ				
Query	2414	lqqlaqqsavasggqss LOOLA S +SGGOSS	vsvvltTPVQT			
Sbjct	2818	LQQLAAASNAGGSVQLQQSSGGQSS	VSVVLTTPVÕT	LPLATHSQGGS'	TAQIVIISTQI TAQIVAISTQI	TTL 2877
Query	2261	PVNSSPQLGSIVQTQSLPQvvsvst PVN++POLGSIVOTO+LPOVVSV	lptvgtvlttT L T +	ANQPQQQHQtt	avttlntTMLF V TLNT +LF	RGQ 2082
Sbjct	2878	PVNTAPQLGSIVQTQTLPQVVSVGF				
Query	2081	RIVSTAAGNTLQC R + + +AG T LQC			QFQTQLRLAAV QFQTQLRLAAV	
Sbjct	2934	RSVQAIVAAASAGGTPLHTDVVLQQ				
Query	1937	SPATQTTQLVTTKGIPVSALQQGGK + + QTTQLVTTKGIPVSALQQ GK		GAHIQLYRQRS: GAHIOLYROR+:		7Ps 1758
Sbjct	2994	ANSNOTTOLVTTKGIPVSALQOGK				AAG 3051
Query	1757	gsagatgatANLVQA G+A A G T NL VQ A	AGGTIIQASNMA AGTIIQ SN+	THVTSQKV	AVSGMPGTSTT AVSGM G +TT	
Sbjct	3052	GAATAGGGTGNLSSTVVQTTGGTLA	PGTIIQTSNLM	QAQTHVSSQKV		
Query	1616	AGNVVSSVQMHGQARTQFIKQMAAG AGNVVSSVQMHGQ RTQFIKQM AG		Sadgtttttaa A G+	gDMLLVKRHNI MLLVKRHNI	
Sbjct	3111	AGNVVSSVQMHGQPRTQFIKQMTAG				
Query	1442	AQKAQQASGALF 1407 AQKAQQA+G LF				
Sbjct	3171	AQKAQQATGPLF 3182				

Score	E	rpect Method	Identities	Positives	Gaps	Frame
276 bits	(706) 5e	e-73() Compositional matrix adjust.	267/432(62%)	296/432(68%)	60/432(13%) -	1
Features	s:					
Query	1196	NVSPGQQTAILLHQPQQQ	LRTHPGQG LRT	GOSNT-QOLVK	TIVGtsssltag	gg 1050
Sbjct	2764	+V+P QQTAILL Q QQ HVTPTQQTAILLQQQPQQQQQQQQ			TIVGT+++LTAĞ TIVGTTANLTAG	
Query	1049	lqqlaqqsavasggqs: LQQLA S +SGGQS	svsvvltTPVQT SVSVVLTTPVQT	LPSVVQPQIGS	GAQIVSISSQT-	-L 897
Sbjct	2818	LQQLAAASNAGGSVQLQQSSGGQS				
Query	896	PVNSSPQLGSIVQTQSLPQvvsvs PVN++PQLGSIVQTQ+LPQVVSV		ANQPQQQHQtt OOHO	avttlntTMLRG V TLNT +LRG	
Sbjct	2878	PVNTAPQLGSIVQTQTLPQVVSVG				
Query	716	RLQQ R + + + + AG T LOQ	QRTTAGGQSIVS QR AGGQSIV+			PT 573
Sbjct	2934	RSVQAIVAAASAGGTPLHTDVVLQ				SA 2993
Query	572	SPATOTTOLVTTKGIPVSALQQGGI + + OTTOLVTTKGIPVSALQQ GI	KTTVIPVTQQSG	GAHIQLYRORS	LKVLQTTTQAVE LKVLO T A	Ps 393
Sbjct	2994	ANSNOTTOLVTTKGIPVSALOOSGI				AG 3051
Query	392	gsagatgatANLVQ G+A A G T NL VO	AGGTIIQASNMA A GTIIQ SN+		AVSGMPGTSTTV AVSGM G +TTV	
Sbjct	3052	GAATAGGGTGNLSSTVVÕTTGGTL				
Query	251	AGNVVSSVQMHGQARTQFIKQMAAGAGNVVSSVQMHGQ RTQFIKQM AG			gDMLLVKRHNII MLLVKRHNII	
Sbjct	3111	AGNVVSSVQMHGQPRTQFIKQMTA				
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) kange 1: 2571 to 2891

Score	E	xpect Method	Identities	Positives	Gaps	Frame
267 bits	(683) 46	e-70() Compositional matrix adjust.	209/336(62%) 231/336(68%)	39/336(11%)	-1
Feature	s:					
Query	2342	PVQTLPSVVQPQIGSGAQIVSIS				
Sbjct	2571	PVQ+LP + S AQIVSIS PVQSLPIATHSNVNANSTAQIVSIS		POLGSIVOTO+LI POLGSIVOTOTLI		
Query	2171	tvlttTANQPQQQHQttavttlntT				
Sbjct	2631	+ T T SGGQQQQQQQTATGTVT	MLRGQR+VS A MLRGQRLVSAA		LQQRTTA (VVLQQRTTAI)	
Query	2021	SIVSMPNLGQGASPSQFQTQLRLAA IVS LGQ + + FQ QLRL+A		LVTTKGIPVSAI LVTTKGIPV+AI		
Sbjct	2683	PIVSLGQSVANAHFQAQLRLSA				
Query	1841	QQSGGAHIQLYRQRSLKVLQTTTQA QQ HIQLYRQR+LKVLQ Q	AVPsgsagatga	ntANLVQ	AGGTIIQA A GTIIOA	
Sbjct	2739	QQQT-PHIQLYRQRNLKVLQAP-QV				
Query	1685	MATHVTSQKVAVSGMPGTSTTV + THVTSQKVAVSGMPG +TTV				
Sbjct	2797	LMQTPTHVTSQKVAVSGMPG-ATTV				
Query	1514	SadgtttttaagDMLLVKRHNILAA				
Sbjct	2856	+ DG+ + A GDMLLVKRHNILAA TTDGSGGSGATGDMLLVKRHNILAA				

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	PVQTLPSVVQPQIGSGAQIVSISSQ-TLPVNSSPQLGSIVQTQSLPQvvsvstlptvg PVQ+LP + S AQIVSISSQ TLPVN+ PQLGSIVQTQ+LPQVVSV L T	807
Sbjct	2571	PVQSLPIATHSNVNANSTAQIVSISSQSTLPVNTPPQLGSIVQTQTLPQVVSVGPLTTTT	2630
Query	806	tvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTAGGQ + T TMLRGQR+VS AA GNT LQQRTTA GQ	657
Sbjct	2631	+ T TMLRGQR+VS AA GNT LQQRTTA GQ SGGQQQQQQQTATGTVTMLRGQRLVSAAAASAAGNTTLHDVVLQQRTTAIGQ	2682
Query	656	SIVSMPNLGQGASPSQFQTQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIPVT IVS LGQ + + FQ QLRL+AV SPATQTTQLVTTKGIPV+ALQQ GKT V+P T	477
Sbjct	2683	PIVSLGQSVANAHFQAQLRLSAVSGSPATQTTQLVTTKGIPVTALQQGKT-VLPGT	2738
Query	476	QQSGGAHIQLYRQRSLKVLQTTTQAVPsgsagatgatANLVQAGGTIIQASN QQ HIQLYRQR+LKVLQ Q G G A N +VQ A GTIIQASN	321
Sbjct	2739	QQQT-PHIQLYRQRNLKVLQAP-QVAQGGVVGGGTANLNPTVVQTAGGALATGTIIQASN	2796
Query	320	MATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQFIKQMAAGKQQLQRQVV	150
Sbjct	2797	+ THVTSQKVAVSGMPG +TTVQAGNVVSSVQMHGQARTQFIKQMA GKQ +QRQ++ LMQTPTHVTSQKVAVSGMPG-ATTVQAGNVVSSVQMHGQARTQFIKQMAVGKQGVQRQMI	2855
Query	149	SadgtttttaagDMLLVKRHNILAAQKAQQASGALF 42	
Sbjct	2856	+ DG+ + A GDMLLVKRHNILAAQKAQQA+G LF 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	E	xpect Method	Identities	Positives	Gaps	Frame
117 bits	(292) 6e	e-23() Compositional matrix adjust.	164/336(49%)	194/336(57%)	61/336(18%)	-1
Features	s:					
Query	2342	PVQTLPSVVQPQIGSGAQIVS				
Sbjct	2674	PVQTLPS VQ Q G S AQIVS PVQTLPSSVQSAQQHGQSSTAQIVS				
Query	2186	lptvgtvlttTAN-QPQQQHQttav L TVGTVLTT+AN QP + V	ttlntTMLRGQ	RIVSTAAGN RIV+ AG	TLQQRTTAG LOOR+	GQ 2022
Sbjct	2734	LATVGTVLTTSANLQPSATV				SP 2788
Query	2021	SIVSMPNLGQGASPSQFQ-TQLRLA +IVSM NLG + +QFQ TQLRLA			ALQQGGKTTVI LQQGGK	PV 1845
Sbjct	2789	TIVSMSNLGPSVAAAQFQATQLRLA				
Query	1844	TQQSGGAHIQLYRQR-SLKVLQ T GG HIQLYRQR LKVLQ	OTTT-QAVPsgs		QAGGTIIQASN A GTIIO S	
Sbjct	2837	TANVGGNQPPHIQLYRQRQQLKVLQ				
Query	1679	THVTSQKVAVSGMPGTST T + QKVAV+ + +S				KQ 1536 KO
Sbjct	2897	TAGGQATMQMQGQKVAVATV-SSSN				
Query	1535	QLQRQVVSadgtttttaagDMLLVF + RQ+ DM+LVF	KRHNILAAQKAQ KR I A QKAQ			
Sbjct	2955	TIARQMGDDMVLV				

Range 2: 2674 to 2979

Score	E	kpect Method	Identities	Positives	Gaps	Frame
117 bits	(292) 6e	e-23() Compositional matrix adjust.	164/336(49%)	194/336(57%)	61/336(18%)	-1
Features	s:					
Query	977	PVOTLPSVVOPQIGSGAQIVS				
Sbjct	2674	PVQTLPS VQ Q G S AQIVS PVQTLPSSVQSAQQHGQSSTAQIVS				
Query	821	lptvgtvlttTAN-QPQQQHQttav L TVGTVLTT+AN QP + V			TLQQRTTAG LQQR+	GQ 657
Sbjct	2734	LATVGTVLTTSANLQPSATV				SP 2788
Query	656	SIVSMPNLGQGASPSQFQ-TQLRLA +IVSM NLG + +QFQ TQLRLA			ALQQGGKTTVI LQQGGK	PV 480
Sbjct	2789	TIVSMSNLGPSVAAAQFQATQLRLA				
Query	479	TQQSGGAHIQLYRQR-SLKVLQ T GG HIQLYRQR LKVLQ			QAGGTIIQASN A GTIIO S	
Sbjct	2837	TANVGGNQPPHIQLYRQRQQLKVLQ				
Query	314	THVTSQKVAVSGMPGTST T + QKVAV+ + +S				KQ 171 KO
Sbjct	2897	TAGGQATMQMQGQKVAVATV-SSSN				
Query	170	QLQRQVVSadgtttttaagDMLLVF	KRHNILAAQKAQ	63		

+ RQ+ DM+LVKR I A QKAQ Sbjct 2955 TIARQM-----GDDMVLVKRQVIGAHQKAQ 2979

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	Ex	cpect Method	Identities	Positives	Gaps	Frame	
117 bits((292) 7e	e-23() Compositional matrix adjust.	164/336(49%)	194/336(57%)	61/336(18%)	-1	
Features	Features:						
Query	2342	PVQTLPSVVQPQIGSGAQIVS PVQTLPS VQ Q G S AQIVS	SISSOTLPVNSS SIS QT+ + +				
Sbjct	2674	PVQTLPS VQ Q G S AQIVS PVQTLPSSVQSAQQHGQSSTAQIVS					
Query	2186	lptvgtvlttTAN-QPQQQHQttav L TVGTVLTT+AN QP + V	ttlntTMLRGQ	RIVSTAAGN	TLQQRTTAG LQQR+	GQ 2022	
Sbjct	2734	LATVGTVLTTSANLQPSATV				SP 2788	
Query	2021	SIVSMPNLGQGASPSQFQ-TQLRLA +IVSM NLG + +QFQ TQLRLA	AVPTSPATQTT	OLVTTKGIPVS	ALQQGGKTTVI LQQGGK	PV 1845	
Sbjct	2789	TIVSMSNLGPSVAAAQFQATQLRLA					
Query	1844	TQQSGGAHIQLYRQR-SLKVLQ T GG HIQLYRQR LKVLQ			QAGGTIIQASN A GTIIO S		
Sbjct	2837	TANVGGNQPPHIQLYRQRQQLKVLQ					
Query	1679	THVTSQKVAVSGMPGTST T + QKVAV+ + +S				KQ 1536 KÕ	
Sbjct	2897	TAGGQATMQMQGQKVAVATV-SSSN					
Query	1535	QLQRQVVSadgtttttaagDMLLVK + RQ+ DM+LVK	RHNILAAOKAO	1428			
Sbjct	2955	TIARQMGDDMVLVK	RQVIGAHÕKAÕ	2979			

Range 2: 2674 to 2979

Score	E	xpect Method	Identities	Positives	Gaps	Frame		
117 bits	117 bits(292) 7e-23() Compositional matrix adjust. 164/336(49%) 194/336(57%) 61/336(18%) -1							
Features	Features:							
Query	977	PVQTLPSVVQPQIGSGAQIVS						
Sbjct	2674	PVQTLPS VQ Q G S AQIVS PVQTLPSSVQSAQQHGQSSTAQIVS						
Query	821	lptvgtvlttTAN-QPQQQHQttav L TVGTVLTT+AN QP + V	ttlntTMLRGQ	RIVSTAAGN RIV+ AG	TLQQRTTAG(LOOR+	GQ 657		
Sbjct	2734	LATVGTVLTTSANLQPSATV				SP 2788		
Query	656	SIVSMPNLGQGASPSQFQ-TQLRLA +IVSM NLG + +QFQ TQLRLA			ALQQGGKTTVII LQQGGK	PV 480		
Sbjct	2789	TIVSMSNLGPSVAAAQFQATQLRLA				_L 2836		
Query	479	TQQSGGAHIQLYRQR-SLKVLQ T GG HIQLYRQR LKVLQ			QAGGTIIQASNI A GTIIO S			
Sbjct	2837	TANVGGNQPPHIQLYRQRQQLKVLQ						
Query	314	THVTSQKVAVSGMPGTST T + QKVAV+ + +S						
Sbjct	2897	TAGGQATMQMQGQKVAVATV-SSSN				- - ~		
Query	170	QLQRQVVSadgtttttaagDMLLVK + RQ+ DM+LVK	KRHNILAAQKAQ KR I A QKAQ					
Sbjct	2955	TIARQMGDDMVLVK	RQVIGAHÕKAÕ	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 234		2187
Sbjct 522	PVQT+SVQ S $AQIVS+SQV+SSPQ+GSIVQTQSLPQVVSVS$ $PVQTISSTVTNQQQHHSNQVSSSTAQIVSLSPQQTIVSSSPQVGSIVQTQSLPQVVSVSQ$	581
Query 218		2019
Sbjct 582	L TVGTVLTT++ Q T VTTLNT+ LR QRIV+ ++G TLQ Q+ +AG S LATVGTVLTTSSGMQQPTATVTTLNTSALRAQRIVAASSGTTLQDVVLQQRSAGNPS	638
Query 201		1848
Sbjct 639	IVSM +LG + +Q Q TQ +LA++P+ TQ V TKGI VS+LQQG K PTIVSMSSLGTNVAQAQLQATQFQLASMPSGTQQVVTKGIRVSSLQQGQKIAAAA	693
Query 184		1689
Sbjct 694	+ HIQLYRQR LKVLQ Q LV A GTIIQ S QAGNNQQGQPHTHIQLYRQRQQLKVLQAGAPGQQGQQTVVQTASGQTALVNAQGTIIQGS	753
Query 168		1554
Sbjct 754	M T V QKVAV+ TT A VV++V Q Q R QFIKQ LMQTGSGPTTVQVVQGQKVAVATSNVAVTTPSATGVVTTVAASQVHQQQAQQTRAQFIKQ	813
Query 155	~~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	1392
Sbjct 814	+ AAGKQ + RQV DMLLVKR I AA QKA Q G +FTTTT VAAGKQTITRQVGESDMLLVKRQMISAATQQKAAQVLQQGGQIFTTTTA	862

Range 2: 522 to 848

Score	I	Expect Method	Identities	Positives	Gaps	Frame
108 bits	(271) 2	2e-20() Compositional matrix adjust.	161/345(47%)	187/345(54%) 57/345(16%) -	1
Features	S :					
Query	977	PVQTLPSVVQPQIGSGAQ				822
Sbjct	522	PVQT+ S V Q S AQ PVQTISSTVTNQQQHHSNQVSSSTAQ			QTQSLPQVVSVS QTQSLPQVVSVS(581
Query	821	lptvgtvlttTANQPQQQHQttavtt L TVGTVLTT++ Q T VTT	lntTMLRGORI	VSTAAGNTLQ	O+ +AG	
Sbjct	582	LATVGTVLTTSSGMQQPTATVTT				
Query	653	IVSMPNLGQGASPSQFQ-TQLRLA IVSM +LG + +Q Q TQ +LA	AVPTSPATQTT	OLVTTKGIPV	SALQQGGKTTVII S+LOOG K	483
Sbjct	639	PTIVSMSSLGTNVAQAQLQATQFQLA				A 693
Query	482	VTQQSGGAHIQLYRQR-SLKVL + HIQLYRQR LKVL		gsagatgatAl	NLVQAGGTIIQAS LV A GTIIO S	
Sbjct	694	QAGNNQQGQPHTHIQLYRQRQQLKVL	, QAGAPGQQGQQ	TVVQTASGQT		-
Query	323	NMATHVTSQKVAVSGMPG M T V QKVAV+	TSTTVQAGNVV	SSV(QMHGQARTQFIK(O R OFIKO	
Sbjct	754	LMQTGSGPTTVQVVQGQKVAVATSNV				
Query	188	MAAGKQQLQRQVVSadgtttttaagD	MLLVKRHNILA MI.I.VKR T A		50	
Sbjct	814	+AAGKQ + RQV D VAAGKQTITRQVGESD	MLLVKRQMISA	ATQÕKAAÕ	348	

PREDICTED: helicase domino [Musca domestica]

Sequence ID: **ref|XP_011294691.1|** Length: 2336 Number of Matches: 2 Range 1: 1601 to 1929

Score	Ex	rpect Method	Identities	Positives	Gaps	Frame
111 bits((277) 3e	e-21() Compositional matrix adjust.	165/349(47%)	194/349(55%)	54/349(15%)	-1
Features	S :					
Query	2342	PVOTLPSVVOPOIGSGAC				
Sbjct	1601	PVQT+ S VQ Q+ S AQ PVQTISSNVQNQVAHHSQVSSSTAQ		+SS Q+GSIV ' SSSAQVGSIVH'		
Query	2183	ptvgtvlttTANQPQQQHQttavttTVGTVLTT++ Q T VTT	lntTMLRGORI	VSTAAGNTLQ-	QRTTAGGÇ Q+ TAG	S- 2019
Sbjct	1660	ATVGTVLTTSSGMQQPTGTVTT				-
Query	2018	-IVSMPNLGQGASPSQFQ-TQLRLAIVSM +LG + O O +LA		QLVTTKGIPVSZ Q V TKGI VS-		TT 1857
Sbjct	1717	TIVSMSSLGSNVGQASLQAAQFQLA				GA 1771
Query	1856	VIPVTQQSGGAHIQLYRQRSLKVLQ Q AHIQ YRQR LKVLQ			LVQAGGTIIQA LV A GTII	SN 1686
Sbjct	1772	GGTTAQGQQSAHIQSYRQRQLKVLQ				GP 1830
Query	1685	MATHVT-SQKVAVSGMPGTSTTVQA V QKV V+ TT A			FIKQM-AAGKÇ FIKQ+ A+GKÇ	
Sbjct	1831	TTVQVVQGQKVTVATSNVAVTTPSA				
Query	1529	QRQVVSadgtttttaagDMLLVKRE	INILAAQKAQ	QASGALFT	TT 1398	

Range 2: 1601 to 1910

Score	E	rpect Method	Identities	Positives	Gaps	Frame
109 bits	(272) 1e	e-20() Compositional matrix adjust.	158/330(48%)	185/330(56%)	49/330(14%)	-1
Features:						
Query	977	PVOTLPSVVQPQIGSGAC				
Sbjct	1601	PVQT+ S VQ Q+ S AQ PVQTISSNVQNQVAHHSQVSSSTAQ		+SS Q+GSIV ' SSSAQVGSIVH'		
Query	818	ptvgtvlttTANQPQQQHQttavttTVGTVLTT++ Q T VTT	lntTMLRGQRI	VSTAAGNTLQ-	QRTTAGGQS O+ TAG	
Sbjct	1660	ATVGTVLTTSSGMQQPTGTVTT	LNTSALRAQRI	VAASSGTTLQD	VVLQQRTAGNPS	
Query	653	-IVSMPNLGQGASPSQFQ-TQLRLAIVSM +LG + O O +LA	AVPTSPATQTT	QLVTTKGIPVSZ Q V TKGI VS-	ALQQGGK'	ГТ 492
Sbjct	1717	TIVSMSSLGSNVGQASLQAAQFQLA				GA 1771
Query	491	VIPVTQQSGGAHIQLYRQRSLKVLQ Q AHIQ YRQR LKVLQ			LVQAGGTIIQAS LV A GTII	SN 321
Sbjct	1772	GGTTAQGQQSAHIQSYRQRQLKVLQ				GP 1830
Query	320	MATHVT-SQKVAVSGMPGTSTTVQA V OKV V+ TT A	GNVVSSVQM VV++V QM		FIKOM-AAGKOO FIKO+ A+GKO	QL 165
Sbjct	1831	TTVQVVQGQKVTVATSNVAVTTPSA				IF 1890
Query	164	QRQVVSadgtttttaagDMLLVKRH RQV DMLLVKR	INILAA 75 I AA			
Sbjct	1891	TRQVGDSDMLLVKRQ				

PREDICTED: helicase domino [Stomoxys calcitrans]

Sequence ID: **ref|XP_013100224.1|** Length: 3504 Number of Matches: 2 Range 1: 2758 to 3096

Score	Ex	xpect	Method	Identities	Positives	Gaps	Frame
103 bits(258) 6e-19() Compositional matrix adjust. 159/362(44%) 193/362(53%) 70/362(19%) -1							
Features	S :						
Query	2342		TLPSVVQPQIGSGA				
Sbjct	2758		T+ S P GS F TISSTTLPNQGSHHSQVASSSF	QIVS+S QI+ QIVSLSPQTI-	VSSSAQVGSIV	QTQSLPQVVSVS QTQSLPQVVSVS	SQ 2816
Query	2186	lpt	vgtvlttTANQPQQQHQttavt VGTVLTT++ Q V	tlntTMLRGQR	IVSTAAGNTLQ	QRTTAGG(O+ +AG	
Sbjct	2817		VGTVLTTSSGMQQPATVA				
Query	2018		VSMPNLGQGASPSQFQ-TQLRI VSM +LG + + O TO +I				
Sbjct	2873		VSM +LG + + Q TQ +I VSMSSLGTNVAQAPIQGTQFQI	ASMPAG	TQQVVTKGIRV	SSLQQGQKI	
Query	1847	VTQ	QSGGAHIQLYRQR- SGG AHIQLYRQR	-SLKVLOTTT	QAVPsgsagat Q	gatANLVQAGGT LV A GT	
Sbjct	2925	AGN	ASGGTVQGQGQAAHIQLYRQRÇ	QLKVLÕASGPG	Q QQGQQTVVQTA	SGQTALVNAQGT	
Query	1700		SNMATHVTSQKVAV + M T V QKV V			MHGQART MH Q RT	
Sbjct	2985		NIMQTSAGPTTVQVVQGQKVTV				
Query	1565	FIK	QM-AAGKQQLQRQVVSadgttt	ttaagDMLLVK	RHNILAAQKAQ	QASGALI	T 1404
Sbjct	3045	YIK	Q+ A+GKQ + RQV QVSASGKQTIARQV	GDTDMLLVK	ROMLSAATOPK.	AAQVIQQGGQIY	TT 3094
Query	1403	TT T+	1398				
Sbjct	3095	TS	3096				

Range 2: 2758 to 3077

Score	Ex	pect	Method	Identities	Positives	Gaps	Frame	_
103 bits	s(257) 9e-	-19()	Compositional matrix adjust.	155/343(45%)	184/343(53%)	65/343(18%)	-1	•
Feature	es:							
Query	977	~		QIVSISSQTLP QIVS+S QT+ v				22
Sbjct	2758		TISSTTLPNQGSHHSQVASSSA					316

Query	821	lptvgtvlttTANQPQQQHQttavttlntTMLRGQRIVSTAAGNTLQQRTTAGGQS	654
Sbjct	2817	f L TVGTVLTT++ Q V LNT+ LR QRIV+ + G TLQ Q+ +AG S LATVGTVLTTSSGMQQPATVAALNTSALRAQRIVAASGGTTLQDVVLQQRSAGNPS	2872
Query	653	IVSMPNLGQGASPSQFQ-TQLRLAAVPTSPATQTTQLVTTKGIPVSALQQGGKTTVIP	483
Sbjct	2873	IVSM + LG + + Q TQ + LA + +P TQ V TKGI VS + LQQG K I $PTIVSMSSLGTNVAQAPIQGTQFQLASMPAGTQQVVTKGIRVSSLQQGQKIA$	2924
Query	482	VTQQSGGAHIQLYRQR-SLKVLQTTTQAVPsgsagatgatANLVQAGGTI	336
Sbjct	2925	SGG AHIQLYRQR LKVLQ + Q LV A GTI AGNASGGTVQGQGQAAHIQLYRQRQQLKVLQASGPGQQGQQTVVQTASGQTALVNAQGTI	2984
Query	335	IQASNMATHVTSQKVAVSGMPGTSTTVQAGNVVSSVQMHGQARTQ	201
Sbjct	2985	${ m IQ}$ + M T	3044
Query	200	FIKQM-AAGKQQLQRQVVSadgtttttaagDMLLVKRHNILAA 75	
Sbjct	3045	+IKQ+ A+GKQ + RQV DMLLVKR + AA YIKQVSASGKQTIARQVGDTDMLLVKRQMLSAA 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		QCECGPNHSSTDTSVGGATPDR QCEC NHSSTDTSVGGATPDR				
Sbjct	2509		QCECSTNHSSTDTSVGGATPDR				

Range 2: 2509 to 2550

Score	Expect	t Method	Identities	Positives	Gaps	Frame
86.3 bits(21	2) 2e-13()) Composition-based stats.	36/42(86%)	36/42(85%)	0/42(0%)	-3
Features:						
Query 10		VQCECGPNHSSTDTSVGGATPD VQCEC NHSSTDTSVGGATPD		DAAR 892		
Sbjct 25		VQCECSTNHSSTDTSVGGATPD				