### **BLAST**®

## **Basic Local Alignment Search Tool**

NCBI/ BLAST/ blastn suite/ Formatting Results - CNA2V9JC014

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Blast report description

#### **Nucleotide Sequence (1141 letters)**

**RID** <u>CNA2V9JC014</u> (Expires on 02-23 13:19 pm)

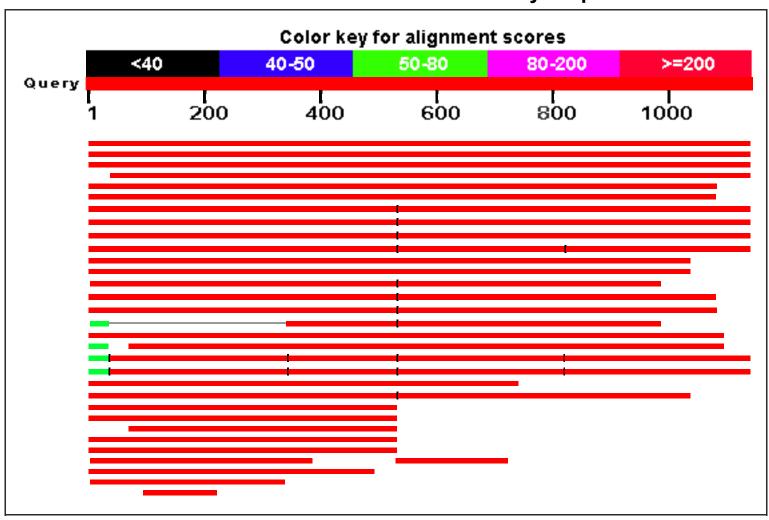
**Description** None **Description** Nucleotide collection (nt)

Molecule type nucleic acid Program BLASTN 2.3.1+

**Query Length** 1141

# **Graphic Summary**

### Distribution of 52 Blast Hits on the Query Sequence





Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant A, mRNA	2084	2084	99%	0.0	99%	NM_080220.5
Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant B, mRNA	2063	2063	99%	0.0	99%	<u>NM_167522.5</u>
Drosophila melanogaster RE23444 full insert cDNA	2063	2063	99%	0.0	99%	BT125964.1
Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant E, mRNA	2017	2017	95%	0.0	99%	NM_001298402.1
Drosophila erecta uncharacterized protein, transcript variant B (Dere\GG17966), mRNA	1762	1762	94%	0.0	96%	XM_015155246.1
Drosophila yakuba uncharacterized protein, transcript variant B (Dyak\GE17274), mRNA	1753	1753	94%	0.0	96%	XM_015190527.1
Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant C, mRNA	1112	2087	99%	0.0	99%	NM_206764.3
Drosophila melanogaster FI04456 full insert cDNA	1112	2087	99%	0.0	99%	BT088437.1
Drosophila melanogaster RH12113 full insert cDNA	1107	2081	99%	0.0	99%	BT024190.1
Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant D, mRNA	974	2091	99%	0.0	100%	NM_001298401.1
Drosophila ananassae uncharacterized protein, transcript variant C (Dana\GF19517), partial mRNA	963	963	90%	0.0	84%	XM_014904505.1
Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF19517), partial mRNA	944	944	90%	0.0	83%	XM_014904504.1
Drosophila sechellia GM13442 (Dsec\GM13442), mRNA	911	1710	85%	0.0	98%	XM_002042216.1
Drosophila yakuba uncharacterized protein, transcript variant A (Dyak\GE17274), mRNA	902	1756	94%	0.0	98%	XM_002100780.2
Drosophila erecta uncharacterized protein, transcript variant A (Dere\GG17966), mRNA	902	1765	94%	0.0	98%	XM_001977900.2
Drosophila simulans GD17286 (Dsim\GD17286), mRNA	787	1198	58%	0.0	98%	XM_002107080.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA18178), mRNA	702	702	95%	0.0	79%	XM_003736114.2
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant D (Dpse\GA18178), partial mRNA	671	671	89%	0.0	79%	XM_015186073.1

Drosophila melanogaster chromosome X	586	2099	99%	3e-163	99%	AE014298.5
Drosophila melanogaster, chromosome X, region 14C-14D, BAC clone BACR47D09, complete sequence	586	2099	99%	3e-163	99%	AC010920.11
Drosophila virilis uncharacterized protein, transcript variant C (Dvir\GJ19028), mRNA	580	580	64%	2e-161	81%	XM_015171030.1
Drosophila ananassae uncharacterized protein, transcript variant A (Dana\GF19517), partial mRNA	508	966	90%	8e-140	84%	XM_001966109.2
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant A (Dpse\GA18178), mRNA	420	420	46%	4e-113	81%	XM_001354642.3
Drosophila mojavensis uncharacterized protein (Dmoj\Gl21487), mRNA	398	398	46%	2e-106	81%	XM_002010802.2
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant C (Dpse\GA18178), partial mRNA	388	388	40%	1e-103	82%	XM_015186072.1
Drosophila virilis uncharacterized protein, transcript variant A (Dvir\GJ19028), mRNA	372	372	46%	1e-98	80%	XM_002054977.2
Drosophila virilis uncharacterized protein, transcript variant B (Dvir\GJ19028), mRNA	372	372	46%	1e-98	80%	XM_015171029.1
Drosophila persimilis GL20267 (Dper\GL20267), mRNA	340	340	33%	3e-89	83%	XM_002023253.1
Drosophila willistoni uncharacterized protein (Dwil\GK25675), mRNA	300	300	42%	5e-77	78%	XM_002071184.2
Drosophila grimshawi GH22433 (Dgri\GH22433), mRNA	270	270	29%	4e-68	81%	XM_001997807.1
Drosophila grimshawi GH24789 (Dgri\GH24789), mRNA	217	217	16%	5e-52	87%	XM_001992473.1
RNA recognition motif-type RNA-binding protein {RRM2 clone} [Drosophila melanogaster, mRNA Partial, 129 nt]	213	213	10%	7e-51	98%	<u>S51692.1</u>
Drosophila busckii chromosome X sequence	62.1	62.1	2%	3e-05	100%	<u>CP012528.1</u>

# **□** <u>Alignments</u>

Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant A, mRNA

Sequence ID: **ref|NM\_080220.5|** Length: 3898 Number of Matches: 1 Range 1: 33 to 1163

Score		Expect	Identities	Gaps	Strand	Frame	
2084 bit	s(1128)	0.0()	1130/1131(99%)	0/1131(0%)	Plus/Plus		
Feature	s:						
Query	6	CATGGCTGGAAG	GAGGTGGTTATGAACAC	GCTAGAAGCGGATTC	GGTGGGGATC	GGCATC	65
Sbjct	33	CATGGCTGGAAG	AGGTGGTTATGAACAC	GCTAGAAGCGGATTC	:GGTGGGGATC	GGCATC	92
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGTTC	ATCGCATTTGTCGGC	CAATTTGCCGC	AAGGCCT	125
Sbjct	93	caagcagttgcc	ccacegaacceccettc	Atcccatttcccc	AATTTGCCGC	AAGGCCT	152
Query	126	TGTGCAGGGCGA	TGTGATCAAAATATTC	CAGGACTTTGAGGTG	AAGTACGTGC	GCTGGT	185
Sbjct	153	TGTGCAGGGCGA	tgtgatcaaaatattc	ĊĀĠĠĀĊŦŦŦĠĀĠĠŦĊ	saagtacgtgc	GGCTGGT	212

Query	186	GAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTCGAATTCGAGACGCTGGA	245
Sbjct	213	GAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTCGAATTCGAGACGCTGGA	272
Query	246	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	305
Sbjct	273	caatctggagcggggggtagagtgcgatggtcggatcaaactggacgatctgtcggcgc	332
Query	306	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	365
Sbjct	333	gctaaggatcgacattgccgatcggagaaaaaatgatcgccctggtggcggtgttggcgg	392
Query	366	CGGCAACGGCGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCC	425
Sbjct	393	cgccaacgccatcaccccccccccccccccccccccccc	452
Query	426	ACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcgg	485
Sbjct	453	Acctcgccagggcgcagcagtcagtcagtcctacagccgggaggtcctggcactggcgg	512
Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagagatcggccggc	545
Sbjct	513	cgctcgcgacgccgccgctaatcgcgccatactactacacactacacacac	572
Query	546	TCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGTAACCAGGATCG	605
Sbjct	573	tcgtggtcggtacggcagtttcaataacgacgatcgaccattcgagcgtaaccaggatcg	632
Query	606	GGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGACGGCGATCGCTACAA	665
Sbjct	633	ggatcgcgctcagcggaaggcagctatggcaaccagtcgcgcgacggcgatcgctacaa	692
Query	666	CAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGCGA	725
Sbjct	693	caacttcaaccgccaccgcdaccgcdaccccactacaatcccaaccagcagagcga	752
Query	726	ACGTCCCAGTGGCGCATGACCGGCCTTGGCGGCGGCTCCGGCGGATCAGGAGGCCTAGG	785
Sbjct	753	AcGtcccAGtGGcGCAtGAccGGcctttGGcGGCGGCtCcGGCGGAtcAGGAGGcctAGG	812
Query	786	CGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGGCCACGTCTGCAGCT	845
Sbjct	813	cgttgccgctgcttcctcaatgcgcccattgaccaatgaccactgccacctctccacct	872
Query	846	GAAGCCACGGACCATTGCCGCGCCCCATTAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	905
Sbjct	873	GAAGCCACGGACCATTGCCGCGCCCATTAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	932
Query	906	GATCTTTGGCAACGCCAAGCCGCGCGAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	965
Sbjct	933	GATCTTTGGCAACGCCAAGCCGCGCGAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	992
Query	966	TCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCCGCAATACAATATATGCCTGATATG	1025
Sbjct	993	tcacaacgccataactagaggctggagttggtccgcaatacaatatatgcctgatatg	1052
Query	1026	ATATTTTGATGTGcgagaacgagataatccgagatagagggagagagagagggagg	1085
Sbjct	1053	ATATTTTGATGTGCGAGAACGAGATAATCCGAGATAGAGGGGAGAGAGGCGAGGAAGAGA	1112
Query	1086	agaggaggaagcagaaatagcaagggggggaggaggaggaggaggaggagga 1136	
Sbjct	1113	AGAGGAGGAAGCAGAAATAGCAAGGGGGGGGGGGGGGGG	

Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant B, mRNA Sequence ID: **ref|NM\_167522.5|** Length: 3895 Number of Matches: 1 Range 1: 33 to 1160

Score		Expect	Identities	Gaps	Strand	Frame	
2063 bits	s(1117)	0.0()	1127/1131(99%)	3/1131(0%)	Plus/Plus		
Features	S:						
Query	6	CATGGCTGGAAC	GAGGTGGTTATGAACAC	CGCTAGAAGCGGATTC	CGGTGGGGATC	GGCATC	65
Sbjct	33	CATGGCTGGAAC	GAGGTGGTTATGAACAC	CGCTAGCGGATT	CGGTGGGGATC	GGCATC	89
Query	66	CAAGCAGTTGCC	CCACGGAACCGCCGTTC	CATCGCATTTGTCGGC	CAATTTGCCGC	AAGGCCT	125
Sbjct	90	caagcagttgcd	ccacedaacceccett	catedeatttdtede	CAATTTGCCGC	AAGGCCT	149
Query	126	TGTGCAGGGCG	ATGTGATCAAAATATTC	CCAGGACTTTGAGGTO	GAAGTACGTGC(	GCTGGT	185
Sbjct	150	tgtgcagggcgz	Atgtgatcaaaatattd	ccaddactttdaddt	GAAGTACGTGC	GCTGGT	209
Query	186	GAAGGACCGGG	AAACGGATCAGTTCAA <i>I</i>	AGGCTTCTGCTACGT	CGAATTCGAGAO	CGCTGGA	245
Sbjct	210	GAAGGACCGGG	AAACGGATCAGTTCAAA	AGGCTTCTGCTACGTC	CGAATTCGAGA	CGCTGGA	269

Query	246	CAATCTGGAGCGGCCCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	305
Sbjct	270	CAATCTGGAGCGGCCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	329
Query	306	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	365
Sbjct	330	detaadgategaeattgeegategagaaaaaaatgategeeetgetgeegetgttgeege	389
Query	366	CGGCAACGGCGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCC	425
Sbjct	390	ceckakcececkatekcecececekee	449
Query	426	ACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcgg	485
Sbjct	450	acctcgccaggcgcagcagtcagtcctacagccgggaggtccttgccactggcgcgg	509
Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagagatcggccggc	545
Sbjct	510	cegtcegegegegegegegegegegegegegegegegege	569
Query	546	TCGTGGTCGGTACGCCAGTTTCAATAACGACGATCGACCATTCGAGCGTAACCAGGATCG	605
Sbjct	570	tcgtggtcggtacgcagttcaataacgacgatcgaccattcgaccattcgaccataaccaggatcg	629
Query	606	GGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGCGATCGCTACAA	665
Sbjct	630	ĠĠĀŦĊĠĊĠĠŦĊĀĠĊĠĠĠĀĀĠĠĊĀĠĊŦĀŦĠĠĊĀĀĊĊĀĠŦĊĠĊĠĀĊĠĠĊĠĀŦĊĠĊŦĀĊĀĀ	689
Query	666	CAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGCGA	725
Sbjct	690	caacttcaaccgccaccgccaccgccaccccactacaatcccaaccaccacca	749
Query	726	ACGTCCCAGTGGCGCATGACCGGCCTTGGCGGCGCTCCGGCGGATCAGGAGGCCTAGG	785
Sbjct	750	Acetcccaeteecateecateecateecateecateecat	809
Query	786	CGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGGCCACGTCTGCAGCT	845
Sbjct	810	ĊĠŤŤĠĠĊĠĠŤĠĠŤŤĊĊŤĊĂĂŤĠĠĠĊĠĊĊĂŤŤĠĂĊĠĂĊĂĂŤĠĂĠĊĠĠĊĊĂĊĠŤĊŤĠĊĀĠĊŤ	869
Query	846	GAAGCCACGGACCATTGCCGCGCCCATTAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	905
Sbjct	870	ĠAAĠĊĊAĊĠĠAĊĊAŤŤĠĊĊĠĊĠĊĊĊĀŤŤAAĊĠĊĠĠŤĠĠĊĀĠĀĠĀĊĊĀĀĠĊĀĀŤĊĠĠĊĊŤĊ	929
Query	906	GATCTTTGGCAACGCCAAGCCGCGCAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	965
Sbjct	930	ĠATĊTTTĠĠĊAAĊĠĊĊAAĠĊĊĠĊĠĊĠAAĠAĠAĠĊŦĠAAĠĠAĠĊŦĠĊAĠĊAĠAAŦĠŦĊAA	989
Query	966	TCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCCGCAATACAATATATGCCTGATATG	1025
Sbjct	990	tcacaacgccataactagaggctggagttggtccgcaatacaatatatgcctgatatg	1049
Query	1026	ATATTTTGATGTGcgagaacgagataatccgagatagagggagagagagggagg	1085
Sbjct	1050	ATATTTTGATGTGCGAGAACGAGATAATCCGAGATAGAGGGGAGAGAAGGCGAGGAAGAGA	1109
Query	1086	agaggaggaagcagaaatagcaagggggggaggaggaggaggaggaggagga 1136	
Sbjct	1110	AGAGGAGGAAGCAGAAATAGCAAGGGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	

Drosophila melanogaster RE23444 full insert cDNA

Sequence ID: **gb|BT125964.1**| Length: 1826 Number of Matches: 1 Range 1: 6 to 1133

Score		Expect	Identities	Gaps	Strand	Frame	
2063 bit	s(1117)	0.0()	1127/1131(99%)	3/1131(0%)	Plus/Plus		
Features	<b>3</b> :						
Query	6	CATGGCTGGAAG	AGGTGGTTATGAAC <i>I</i>	ACGCTAGAAGCGGATT(	CGGTGGGGATCG	GGCATC	65
Sbjct	6	categetegaad	addtadtaddadd	AccctAccccatt	CGGTGGGGATCG	GGCATC	62
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGT	CATCGCATTTGTCGG	CAATTTGCCGCA	AGGCCT	125
Sbjct	63	caaccacttccc	ccacegaaccecctd	rcatcgcatttgtcgc	caatttgccgca	Aggcct	122
Query	126	TGTGCAGGGCGA	TGTGATCAAAATAT?	CCAGGACTTTGAGGT	GAAGTACGTGCG	GCTGGT	185
Sbjct	123	tgtgcagggcga	rtgtgatcaaaatati	rccaddactttdaddt	gaagtacgtgcd	GCTGGT	182
Query	186	GAAGGACCGGGA	AACGGATCAGTTCAA	AAGGCTTCTGCTACGT(	CGAATTCGAGAC	GCTGGA	245
Sbjct	183	gyyggyggy	AACGGATCAGTTCAA	Addcttctctctacct	cgyyttçgygyç	:dctdda	242
Query	246	CAATCTGGAGCG	GGCGCTAGAGTGCG <i>I</i>	ATGGTCGGATCAAACT(	GGACGATCTGTC	GGCGCC	305
Sbjct	243	caatctggagcd	gegeetagaetee	Atggtcggatcaaact	ggycgytctgtc	:qqqqqq	302
Query	306	GCTAAGGATCGA	CATTGCCGATCGGAC	GAAAAAATGATCGCCC'	TGGTGGCGGTGT	TGGCGG	365

Sbjct	303	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	362
Query	366	CGGCAACGGCGCATGACCCGCGGCGACGGCGCAGAGACGGTTTCCAGAAGCGCGGCCC	425
Sbjct	363	CGGCAACGGCGCATGACCCGCGGCGACGGCGCAGAGACGGTTTCCAGAAGCGCGGCCC	422
Query	426	ACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcgg	485
Sbjct	423	Acctcgccagggcagcagcagtcagtcctacagccgggaggtcctggcactggcgg	482
Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagagatcggccggc	545
Sbjct	483	cegtcegeaegecegecegettaatcegeeataatcegeeataataetaeaeatcegeceaaa	542
Query	546	TCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGTAACCAGGATCG	605
Sbjct	543	tcgtggtcggtacggcagtttcaataacgacgatcgaccattcgagcgtaaccaggatcg	602
Query	606	GGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGCGATCGCTACAA	665
Sbjct	603	dgatcgcgctcagcggaaggcagctatcgcaaccagtcgcgcgacggcgatcgctacaa	662
Query	666	CAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGCGA	725
Sbjct	663	ĊĂĂĊŦŦĊĂĂĊĊĠĠĊĂĊĊĠĊĠĂĊĊĠĊĠĀĠĊĠĊĀĊĊĊĀĊŦĀĊĀĀŦĊĊĊĀĀĊĊĀĠĊĀĠĀĠĊĠĀ	722
Query	726	ACGTCCCAGTGGCGCATGACCGGCCTTGGCGGCGGCTCCGGCGGATCAGGAGGCCTAGG	785
Sbjct	723	Acetrccaed         Acetrccaed           Acetrccaed         Acetrccaed           Acetrccaed         Acetrccaed           Acetrccaed         Acetrccaed           Acetrccaed         Acetrcaed           Acetrccaed         Acetrcaed           Acetrccaed         Acetrcaed           Acetrccaed         Acetrcaed           Acetrccaed         Acetrcaed           Acetrcaed         Acetrcaed <td>782</td>	782
Query	786	CGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGGCCACGTCTGCAGCT	845
Sbjct	783	ĊĠŦŦĠĠĊĠĠŦĠĠŦŦĊĊŦĊĂĂŦĠĠĠĊĠĊĊĂŦŦĠĂĊĠĂĊĂĂŦĠĂĠĊĠĠĊĊĂĊĠŦĊŦĠĊĀĠĊŦ	842
Query	846	GAAGCCACGGACCATTGCCGCGCCCATTAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	905
Sbjct	843	ĠAAĠĊĊAĊĠĠAĊĊAŤŤĠĊĊĠĊĠĊĊĊĂŤŤAAĊĠĊĠĠŤĠĠĊAĠAĠAĊĊAAĠĊAAŤĊĠĠĊĊŤĊ	902
Query	906	GATCTTTGGCAACGCCAAGCCGCGCGAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	965
Sbjct	903	GATCTTTGGCAACGCCAAGCCGCGAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	962
Query	966	TCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCCGCAATACAATATATGCCTGATATG	1025
Sbjct	963	TĊAĊAAĊĠĠĊĠATAAĊTAĠAĠĠĠĊTGĠAĠTTĠĠTĊĊĠĊAATAĊAATA	1022
Query	1026	ATATTTTGATGTGcgagaacgagataatccgagatagagggagagagagggagg	1085
Sbjct	1023	ATATTTTGATGTGCGAGAACGAGATAATCCGAGATAGAGGGGAGAGAAGGCGAGGAAGAGA	1082
Query	1086	agaggaggaagcagaaatagcaagggggggaggaggaggaggaggaggagga 1136	
Sbjct	1083	ÁĠÁĠĠÁĠĠÁÁĠĊÁĠÁÁÁTÁĠĊÁÁĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ	

Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant E, mRNA Sequence ID: **ref|NM\_001298402.1|** Length: 2816 Number of Matches: 1 Range 1: 344 to 1438

Score		Expect	Identities	Gaps	Strand	Frame	
2017 bit	s(1092)	0.0()	1094/1095(99%)	0/1095(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	42	CGGATTCGGTGG	GGATCGGGCATCC	AGCAGTTGCCCACGGA	ACCGCCGTTCAT	CGCATT	101
Sbjct	344	cggattcggtgg	ggategggeatee <i>t</i>	Adcagttgcccacggaz	vcceccettcy1	cccatt	403
Query	102	TGTCGGCAATTT	GCCGCAAGGCCTTC	TGCAGGGCGATGTGATC	CAAAATATTCCA	GGACTT	161
Sbjct	404	TGTCGGCAATTT	GCCGCAAGGCCTTC	TGCAGGGCGATGTGAT	CAAAATATTCCA	GGACTT	463
Query	162	TGAGGTGAAGTA	CGTGCGGCTGGTG <i>I</i>	AAGGACCGGGAAACGGAT	CAGTTCAAAGG	CTTCTG	221
Sbjct	464	tgaggtgaagta	ceteceecteete	AAGGACCGGGAAACGGA	cagttcaaagd	cttctc	523
Query	222	CTACGTCGAATT	CGAGACGCTGGAC <i>I</i>	AATCTGGAGCGGGCGCT <i>I</i>	AGAGTGCGATGG	TCGGAT	281
Sbjct	524	ctacctccaatt	cgagacgctggac	AATCTGGAGCGGGCGCT/	dagtgcgatgc	steddat	583
Query	282	CAAACTGGACGA'	TCTGTCGGCGCCGC	CTAAGGATCGACATTGCC	CGATCGGAGAAA	AAATGA	341
Sbjct	584	CAAACTGGACGA'	rctgtcggcgccg	CTAAGGATCGACATTGCC	CGATCGGAGAAA	LAAATGA	643
Query	342	TCGCCCTGGTGG	CGGTGTTGGCGGCG	GCAACGGCGGCATGAC	CGCGGCGACGG	CGGCAG	401
Sbjct	644	466666466466	çqqqqqqqqqqqqqqqqqq	gcaacgccgcatgacd	ccccccccaccc	ccccac	703
Query	402	AGACGGTTTCCA	GAAGCGCGGCCCAC	CCTCGCCAGGGCGGCAG(	CAGTCAGTCCTA	CAGCCG	461

Sbjct	704	AGACGGTTTCCAGAAGCGCGGCCCACCTCGCCAGGGCGGCAGCAGTCAGT	763
Query	462	GGGAGGTCCTGGCACTggcggcggcggtcgggagggggggggggggttcgggtaatcgcgg	521
Sbjct	764	degagetectegegegegegegegegegegegegegegegegeg	823
Query	522	cgatagtagagatcggccggcAAATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCG	581
Sbjct	824	cgatagtagagatcggcggcaaatcgtggtcggtacggcagtttcaataacgacgatcg	883
Query	582	ACCATTCGAGCGTAACCAGGATCGGGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCA	641
Sbjct	884	Accattcgagcgtaaccaggatcgggatcgcggtaagcagcagctatcgcaacca	943
Query	642	GTCGCGCGACGGCGATCGCTACAACAACTTCAACCGGCACCGCGACCGCGAGCGCACCCA	701
Sbjct	944	ĠŦĊĠĊĠĊĠĂĊĠĠĊĠĂŦĊĠĊŦĂĊĂĂĊĂĂĊŦŦĊĂĂĊĊĠĠĠĊĂĊĊĠĊĠĂĊĊĠĊĠĂĠĊĠĊĀĊĊĊĀ	1003
Query	702	CTACAATCCCAACCAGCAGAGCGAACGTCCCAGTGGCGGCATGACCGGCCTTGGCGGCGG	761
Sbjct	1004	ĊŦĂĊĂĂŦĊĊĊĂĂĊĊĂĠĊĀĠĀĠĊĠĀĀĊĠŦĊĊĊĀĠŦĠĠĊĠĠĊĀŦĠĂĊĊĠĠĊĊŦŦĠĠĊĠĠĊĠĠ	1063
Query	762	CTCCGGCGGATCAGGAGGCCTAGGCGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGA	821
Sbjct	1064	ĊŢĊĊĠĠĊĠĠĂŢĊĂĠĠĂĠĠĊĊŢĀĠĠĊĠŢŢĠĠŢĠĠŢŢĊĊŢĊĂĂŢĠĠĠĊĠĊĊĂŢŢĠĀĊĠĀ	1123
Query	822	CAATGAGCGGCCACGTCTGCAGCTGAAGCCACGGACCATTGCCGCGCCCATTAACGCGGT	881
Sbjct	1124	ĊAATĠAĠĊĠĠĊĊAĊĠŦĊŦĠĊAĠĊŦĠAAĠĊĊAĊĠĠAĊĊAŦŦĠĊĊĠĊĠĊĊĊAŦŦAAĊĠĊĠĠŦ	1183
Query	882	GGCAGAGCCAAGCAATCGGCCTCGATCTTTGGCAACGCCAAGCCGCGCAAGAGAAGCT	941
Sbjct	1184 942	ĠĠĊŔĠŔĠŔĊĊŔŔĠĊŔŔŦĊĠĠĊĊŦĊĠŔŦĊŦŦŦĠĠĊŔŔĊĠĊĊŔŔĠĊĊĠĊĠĊĠŔŔĠŔĠŔŔĠĊŤ	1243 1001
Query Sbjct	1244	GAAGGAGCTGCAGCAGAATGTCAATCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCC	1303
Query	1002	GAAGGAGCTGCAGCAGAATGTCAATCACAACGGCGATAACTAGAGGGCTGGAGTTGGTCC  GÇAATAÇAATATATGÇÇTGATATGATATTTTTGATGTGCgagaacgagataatccgagata	1061
Sbjct	1304	GCAATACAATATATGCCTGATATGATATTTTGATGTGCGAGAACGAGATAATCCGAGATA	1363
Query	1062	gagggagagaaggcgaggaagagagaggaggaagcagaaatagcaagggggaggagga	1121
Sbjct	1364	GAGGGAGAGAGGCGAGGAAGAGAGAGAGGAGGAAGCAGAAATAGCAAGGGGGGAGGAGGA	1423
Query	1122	ggaggaggagga 1136	_
Sbjct	1424	[[ [	
<u>-</u> :			

Drosophila erecta uncharacterized protein, transcript variant B (Dere\GG17966), mRNA Sequence ID: **ref|XM\_015155246.1|** Length: 1402 Number of Matches: 1 Range 1: 66 to 1138

Identities

**Expect** 

Score

		=11,6000	10.0110.00	Capo			
1762 bit	s(954)	0.0()	1035/1075(96%)	2/1075(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	6	CATGGCTGGAZ	AGAGGTGGTTATGAACA(	CGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC	65
Sbjct	66	CATGGCTGGAZ	AGAGGTGGTTATGAACAG	CGCTAGAGGCGGATT	ccctccccccccccccccccccccccccccccccccccc	GGCATC	125
Query	66	CAAGCAGTTGO	CCACGGAACCGCCGTT	CATCGCATTTGTCGG	CAATTTGCCGCA	AGGCCT	125
Sbjct	126	caadcadttdd	ccacedaaccecctt	catcccatttccc	caatctgccgca	AGGCCT	185
Query	126	TGTGCAGGGC	GATGTGATCAAAATATT(	CCAGGACTTTGAGGT	GAAGTACGTGCG(	GCTGGT	185
Sbjct	186	†g†g¢aggtro	SATGTGATCAAAATATT	ccaggactttgaggt	gyygtycet	gctggt	245
Query	186	GAAGGACCGGC	GAAACGGATCAGTTCAA 	AGGCTTCTGCTACGT	CGAATTCGAGAC	GCTGGA	245
Sbjct	246	gaaggaccgg	SAAACGGATCAGTTCAA	AGGCTTCTGCTACGT	ggagttcgagaco	GCTGGA	305
Query	246	CAATCTGGAGO	CGGGCGCTAGAGTGCGA!	rggtcggatcaaact	GGACGATCTGTC	GGCGCC	305
Sbjct	306	caatctggagd	cedecectadaetecear	rddteddateaaact	ggycgy4c4g4c	gececc	365
Query	306	GCTAAGGATCO	GACATTGCCGATCGGAGA	AAAAAATGATCGCCC	TGGTGGCGGTGT	TGGCGG	365
Sbjct	366	gctgaggatro	sarattgctgatcgccc	gAAAAAtGAtCGCCC	teeteece	tęęcęę	425
Query	366	CGGCAACGGC	GCATGACCCGCGGCGA(	CGGCGGCAGAGACGG	TTTCCAGAAGCG	CGGCCC	425
Sbjct	426	cgcaacgcc	GCATGACCCGCGGCGA:	rggcggcagagacgg	tttccagaagcg	çeeçç	485
Query	426	ACCTCGCCAGO	GCGGCAGCAGTCAGTC	CTACAGCCGGGGAGG	TCCTGGCACTgg	cggcgg 	485
Sbjct	486	Acctcccado	geceecaecaecaecaecaecaecaecaecaecaecaecae	ctycycececec	<del>1</del> cc4ggcyc4gg	çeeçee	545

Gaps

**Strand** 

Frame

Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagagatcggccggc	545
Sbjct	546	CGGTCGGGAGGGCGGCGGTTCGGGTAATCGCGGCGATAGTAGAGATCGGCCGGC	605
Query	546	TCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGTAACCAGGATCG	605
Sbjct	606	teggggteggtaegeaattteaacaaegaegategaeeattegategtaaeeaggateg	665
Query	606	GGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGACGGCGATCGCTACAA	665
Sbjct	666	GGATCGCGGCCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGACGGCGATCGCTACAA	725
Query	666	CAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGCGA	725
Sbjct	726	CAACTTCAGCCGGCACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGCGA	785
Query	726	ACGTCCCAGTGGCGCATGACCGGCCTTGGCGGCGGCTCCGGCGGATCAGGAGGCCTAGG	785
Sbjct	786	AcGTCCCAGTGGCGCATGAGCGGCCTCGGCGGCGGATCCGGCGGATCAGGAGGCCTGGG	845
Query	786	CGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGGCCACGTCTGCAGCT	845
Sbjct	846	AGTTGGTGGTGGTTCCTCAATGGGCGCCATTGACGACAACGAGCGGCCACGTCTGCAGCT	905
Query	846	GAAGCCACGGACCATTGCCGCGCCCCATTAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	905
Sbjct	906	GAAGCCACGGACCATTGCCGCGCCCATAAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	965
Query	906	GATCTTTGGCAACGCCAAGCCGCGCAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	965
Sbjct	966	GATCTTTGGCAACGCCAAGCCGCGAGGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	1025
Query	966	TCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCCGCAATACAATATATGCCTGATATG	1025
Sbjct	1026	tcacaacggcgataactagagggcaggagtcggtccgcaatacaatatgcctgatatg	1083
Query	1026	ATATTTTGATGTGcgagaacgagataatccgagatagagggagagagagggagg	
Sbjct	1084	AtAttttggtgtgtgcgagaacgagggaatcggagatagagcgagagaaggagagaga	

Drosophila yakuba uncharacterized protein, transcript variant B (Dyak\GE17274), mRNA Sequence ID: **ref|XM\_015190527.1|** Length: 2094 Number of Matches: 1 Range 1: 66 to 1136

Score		Expect	Identities	Gaps	Strand	Frame	
1753 bit	s(949)	0.0()	1032/1073(96%)	2/1073(0%)	Plus/Plus		
Features	s:						
Query	6	CATGGCTGGAA	GAGGTGGTTATGAACA	CGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC	65
Sbjct	66	CATGGCTGGAA	.daggtggttatgaaca	ccctacacccccatt	cddtddddatcd	GGCATC	125
Query	66	CAAGCAGTTGC	CCACGGAACCGCCGTT	CATCGCATTTGTCGG(	CAATTTGCCGCA 	AGGCCT	125
Sbjct	126	caadcadttdc	ccacccatcaccatca	catcccatttcccc	caatctgccaca	дĠĠĊĊŢ	185
Query	126	TGTGCAGGGCG	ATGTGATCAAAATATT	CCAGGACTTTGAGGT(	GAAGTACGTGCG	GCTGGT	185
Sbjct	186	†g†g¢agg¢g	Argrgarcaaaararr	ccaccactric	ĠAAĠϮAĊĠϮĠAĠ	ĠĊŦĠĠŦ	245
Query	186	GAAGGACCGGG	AAACGGATCAGTTCAA 	AGGCTTCTGCTACGT( 	CGAATTCGAGAC 	GCTGGA	245
Sbjct	246		SAAACGGATCAGTTCAA.				305
Query	246		GGGCGCTAGAGTGCGA		GGACGATCTGTC 	GGCGCC	305
Sbjct	306		ĠĠĠĊĠĊŦĀĠĀĠŦĠĊĠĀ		GGACGATCTGTC		365
Query	306		ACATTGCCGATCGGAG				365
Sbjct	366		ATATTGCCGATCGGCG				425
Query	366		GCATGACCCGCGGCGA				425
Sbjct	426		ĠĊĂŦĠĂĊĊĊĠĊĠĠĊĠĂ				485
Query	426		GCGGCAGCAGTCAGTC 				485 545
Sbjct	486 486						545
Query Sbjct	546	CGGTCGGGAGG		taatcgcggcgatagt		GGCAAA	605
Query	546		GCGGCGGCGGTTCGGG ACGGCAGTTTCAATAA				605
Sbjct	606		ACGGCAGTTTCAATAA                'ACGGCAATTTCAACAA				665
	000	1001001001	ACCOCAMITICANCAM	COACGAICGACCAIIC	CONTEGIANCE	DOLLOG	005

Query	606	GGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGCGATCGCTACAA	665
Sbjct	666	GGATCGTGGCCAGCGGAAGGCAGCTATGGCAATCAGTCGCGACGGCGATCGCTACAA	725
Query	666	CAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGCGA	725
Sbjct	726	CAACTTCAGCCGGCACCGCGACCGCGAGCGCACCCACTACAACCCCAACCAGCAGAGCGA	785
Query	726	ACGTCCCAGTGGCGCATGACCGGCCTTGGCGGCGCTCCGGCGGATCAGGAGGCCTAGG	785
Sbjct	786	Acetcccaetegcecateaececctcegcegcectccegcegatcegeaecetege	845
Query	786	CGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGGCCACGTCTGCAGCT	845
Sbjct	846	CGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGATAATGAGCGGCCACGTCTGCAGCT	905
Query	846	GAAGCCACGGACCATTGCCGCGCCCATTAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	905
Sbjct	906	GAAGCCACGGACCATTGCCGCGCCCATCAACGCGGTGGCAGAGACCAAGCAATCGGCCTC	965
Query	906	GATCTTTGGCAACGCCAAGCCGCGCGAAGAGAAGCTGAAGGAGCTGCAGCAGAATGTCAA	965
Sbjct	966	GATCTTTGGCAACGCCAAGCCGCGCGAGGAGAAGCTGAAGGAACTGCAGCAAAATGTCAA	1025
Query	966	TCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCCGCAATACAATATATGCCTGATATG	1025
Sbjct	1026	TCACAACGGCGATAACTAGAGGGCAGGAGTCGGTCCGCAATACAATATGCCTGATATG	1083
Query	1026	ATATTTTGATGTGcgagaacgagataatccgagatagagggagagagagagggag 1078	
Sbjct	1084	ATATTTTGGTGTGCGAGAACGAGGGAAACCGAGATAGAGCGAGAGAAGGAGAG 1136	

Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant C, mRNA Sequence ID: **ref|NM\_206764.3|** Length: 2640 Number of Matches: 2 Range 1: 658 to 1262

Identities

**Expect** 

00010		Expoor	Taominioo	Gupo	Otraria	1 Tallio	
1112 bit	s(602)	0.0()	604/605(99%)	0/605(0%)	Plus/Plus		
Feature	s:						
Query	532	gatcggccggc	AAATCGTGGTCGGTAC	GGCAGTTTCAATAA	CGACGATCGACC	ATTCGAG	591
Sbjct	658	gytçggççggç	AAA†¢Ġ†ĠĠ†¢ĠĠ†A¢	ddddddddddddddddddddddddddddddddddddddd	ccaccatccacc	ATTCGAG	717
Query	592	CGTAACCAGGA	rcgggatcgcggtcag 	CGGGAAGGCAGCTA	TGGCAACCAGTC	GCGCGAC	651
Sbjct	718	ĊĠŦĀĀĊĊĀĠĠĀſ	rcgggarcgcgctag	ccccadadccccccccccccccccccccccccccccccc	.TĠĠĊAAĊĊAĠTĊ	ĠĊĠĊĠĂĊ	777
Query	652		CAACAACTTCAACCGG 				711
Sbjct	778		CAACAACTTCAACCGG				837
Query	712		CGAACGTCCCAGTGGC				771
Sbjct	838 772		ĊĠĂĂĊĠŤĊĊĊĂĠŤĠĠĊ AGGCGTTGGCGGTGGT				897 831
Query Sbjct	898		AGGCGTTGGCGGTGGT 				957
Query	832		GCTGAAGCCACGGACC				891
Sbjct	958						101
Query	892	<b>АА</b> ĢÇ <b>А</b> АТÇĢĢÇ	СТССАТСТТТСССААС	: GÇÇAAGÇÇGÇGÇGA	А <b>Ģ</b> АĢААĢСТĢАА	.ĢĢĀĢСŢĢ	951
Sbjct	1018	AAGCAATCGGC		:GCCAAGCCGCGCGA	 AGAGAAGCTGAA	 .GGAGCTG	107
Query	952	CAGCAGAATGT	CAATCACAACGGCGAT	'AACTAGAGGGCTAG	AGTTGGTCCGCA	ATACAAT	101
Sbjct	1078	cadcadaatdt	caatcacaacggcgat	'AACTAGAGGGCTGG	AGTTGGTCCGCA	Atacaat	113
Query	1012	ATATGCCTGATA	ATGATATTTTGATGTG	cgagaacgagataa 	tccgagatagag	ggagaga	107
Sbjct	1138	AtAtGCCtGAtz	Atgatattttgatgtg	ccgagaacgagataa	tccgagatagag	ĠĠĀĠĀĠĀ	119
Query	1072	aggcgaggaag	agaagaggaggaagca 	gaaatagcaagggg	ggaggaggagga	ggaggag	113
Sbjct	1198		AGAAGAGGAGGAAGCA	ĠĀĀĀŢĀĠĊĀĀĠĠĠĠ	ĠĠĀĠĠĀĠĠĀ	ĠĠĠĠĠĠĠ	125
Query	1132	gagga 1136					
Sbjct	1258	ĠĀĠĠĀ 1262					

Gaps

Frame

Strand

Score

Score		Expect	Identities	Gaps	Strand	Frame	
974 bits	(527)	0.0()	527/527(100%)	0/527(0%)	Plus/Plus		
Features	s:						
Query	6	CATGGCTGGAAG	AGGTGGTTATGAACA	CGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC	65
Sbjct	33	categetegaad	saggtggttatgaaca	cectadaadcedatt	çeeteeeey	ggcatc	92
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGTT	CATCGCATTTGTCGG	CAATTTGCCGCA	AGGCCT	125
Sbjct	93	caadcadttdcc	ccacegaaccecett	cktckcktttckc	caatttgccgca	AĠĠĊĊŢ	152
Query	126	TGTGCAGGGCGA	TGTGATCAAAATATT	CCAGGACTTTGAGGT	GAAGTACGTGCG	GCTGGT 	185
Sbjct	153	†d†dcaddddda	rchcharch	'ccaggactttgaggt	ĠĂĀĠŦĀĊĠŦĠĊĠ	ĠĊŦĠĠŦ	212
Query	186	GAAGGACCGGGA	AACGGATCAGTTCAA	AGGCTTCTGCTACGT	CGAATTCGAGAC 	GCTGGA 	245
Sbjct	213	ĠAAĠĠAĊĊĠĠĠĀ	AAAĊĠĠATĊAĠTTĊAA	AĠĠĊŦŦĊŦĠĊŦĀĊĠŦ	ĊĠĂĂŤŤĊĠĂĠĂĊ	ĠĊŦĠĠĀ	272
Query	246	CAATCTGGAGCG	GGCGCTAGAGTGCGA 	TGGTCGGATCAAACT	GGACGATCTGTC	GGCGCC 	305
Sbjct	273			tĠĠŦĊĠĠĂŦĊĂĂĀĊŦ			332
Query	306	GCTAAGGATCGA	CATTGCCGATCGGAG	;AAAAAATGATCGCCC 	TGGTGGCGGTGT 	TGGCGG 	365
Sbjct	333	ĠĊŦĀĀĠĠĀŦĊĠĀ	\captackartccccccccccccccccccccccccccccccccc	;AAAAAATGATCGCCC	TĠĠŦĠĠĊĠĠŦĠŦ	TĠĠĊĠĠ	392
Query	366			CGGCGGCAGAGACGG.			425
Sbjct	393			.ĊĠĠĊĠĠĊĀĠĀĠĀĊĠĠ			452
Query	426			CTACAGCCGGGGAGG:			485
Sbjct	453			ĊTĀĊĀĠĊĊĠĠĠĠĀĠĠ:		ĊĠĠĊĠĠ	512
Query	486	cggtcgggaggc 	gcggcggcggttcggg 	rtaatcgcggcgatag 			
Sbjct	513	CĠĠŦĊĠĠĠĀĠĠĠ	;CGGCGGCGGTTCGGG	TAATCGCGGCGATAG	TAĠAĠ 559		

Drosophila melanogaster FI04456 full insert cDNA

Sequence ID: **gb|BT088437.1|** Length: 2647 Number of Matches: 2 Range 1: 645 to 1249

Score		Expect	Identities	Gaps	Strand	Frame	
1112 bits	s(602)	0.0()	604/605(99%)	0/605(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	532	gateggeeggeA	AATCGTGGTCGGTAC	GGCAGTTTCAATAA	.CGACGATCGACC	ATTCGAG	591
Sbjct	645	GATCGGCCGGCA	AATCGTGGTCGGTAC	GGCAGTTTCAATAA	CGACGATCGACC	ATTCGAG	704
Query	592	CGTAACCAGGAT	CGGGATCGCGGTCAG	CGGGAAGGCAGCTA	TGGCAACCAGTC	GCGCGAC	651
Sbjct	705	cdtaaccaddat	ceeeerce	ceeeyyeey	tegepayer	GCGCGAC	764
Query	652	GGCGATCGCTAC	:AACAACTTCAACCGG	CACCGCGACCGCGA	GCGCACCACTA	CAATCCC	711
Sbjct	765	GGCGATCGCTAC	dacaacttcaaccdd	ÇYÇÇÇÇYÇÇÇ	.dcdcacccacta	CAATCCC	824
Query	712	AACCAGCAGAGC	GAACGTCCCAGTGGC	GGCATGACCGGCCT	TGGCGGCGCTC	CGGCGGA	771
Sbjct	825	yyc cydd dd	cgyycgtcgyycgc	<u>ęęcytęycęęc</u>	<del>-</del> - - - - - - - - - - - - - - - - - -	ÇĞĞÇĞĞA	884
Query	772	TCAGGAGGCCTA	GGCGTTGGCGGTGGT	TCCTCAATGGGCGC	CATTGACGACAA	TGAGCGG	831
Sbjct	885	tcaccaccac	œdcette	tcctcaatgggcgc	cattgacgacaa	.tdadddd	944
Query	832	CCACGTCTGCAG	CTGAAGCCACGGACC	ATTGCCGCGCCCAT	TAACGCGGTGGC	AGAGACC	891
Sbjct	945	ccacctctctcac	ctgaagccacggacc	Attgccgcgccat	taaceceeteec	AĠĀĠĀĊĊ	1004
Query	892	AAGCAATCGGCC	TCGATCTTTGGCAAC	GCCAAGCCGCGCGA	AGAGAAGCTGAA 	GGAGCTG	951
Sbjct	1005	AAGCAATCGGCC	rtcgatctttggcaac	ęccyyęccecey ę	AGAGAAGCTGAA	ĠĠĀĠĊŦĠ	1064
Query	952	CAGCAGAATGTC	AATCACAACGGCGAT	AACTAGAGGGCTAG	AGTTGGTCCGCA	ATACAAT 	1011
Sbjct	1065	caccacaatcac	:AA†cAcAAcGGcGA†	AACTAGAGGGCTGG	AGTTGGTCCGCA	Atacaat	1124
Query	1012	ATATGCCTGATA	TGATATTTTGATGTG	cgagaacgagataa 	tccgagatagag	ggagaga 	1071
Sbjct	1125	ATATGCCTGATA	tgatattttgatgtg	ĊĠĀĠĀĀĊĠĀĠĀŦĀĀ	tccgagatagag	ĠĠĀĠĀĠĀ	1184
Query	1072	aggcgaggaaga 	gaagaggaggaagca 	gaaatagcaagggg 	ggaggaggagga	ggaggag	1131

AGGCGAGGAAGAAGAGGAGGAAGCAGAAATAGCAAGGGGGGGAGGAGGAGGAGGAG 1244 Query 1132 gagga 1136 Sbjct 1245 GAGGA 1249

Range 2: 20 to 546

Score		Expect	Identities	Gaps	Strand	Frame
974 bits	(527)	0.0()	527/527(100%)	0/527(0%)	Plus/Plus	
Feature	s:					
Query	6	CATGGCTGGAAG	AGGTGGTTATGAAC <i>I</i>	ACGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC 65
Sbjct	20	categetegaad	addtddthatdaac	\cdctadaadcddatt	çeeteeeeyte	GGCATC 79
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGTT	CATCGCATTTGTCGG	CAATTTGCCGCA 	AGGCCT 125
Sbjct	80	caagcagttgcc	ccycedyyce	tcatcgcatttgtcgg	caatttgccgca	Addcct 139
Query	126	TGTGCAGGGCGA	TGTGATCAAAATAT?	rccaggactttgaggt 	GAAGTACGTGCG 	GCTGGT 185
Sbjct	140	†Ġ†ĠĊAĠĠĠĊĠA	tgtgatcaaaatatt	rccaggactttgaggt	ĠĀĀĠŦĀĊĠŦĠĊĠ	ĠĊŦĠĠŦ 199
Query	186	GAAGGACCGGGA	AACGGATCAGTTCAA	\AGGCTTCTGCTACGT 	CGAATTCGAGAC 	
Sbjct	200	ĠAAĠĠAĊĊĠĠĠA	AAAĊĠĠATĊAĠTTĊAZ	\AĠĠĊϮϮĊϮĠĊϮAĊĠϮ	ĊĠĂĂŤŤĊĠĂĠĂĊ	ĠĊŢĠĠĀ 259
Query	246			\TGGTCGGATCAAACT 	GGACGATCTGTC 	
Sbjct	260		ĠĠĊĠĊŦĂĠĂĠŦĠĊĠ <i>Ĭ</i>			ĠĠĊĠĊĊ 319
Query	306	GCTAAGGATCGA	CATTGCCGATCGGAC	GAAAAAATGATCGCCC 	TGGTGGCGGTGT 	
Sbjct	320		ĊĂŤŤĠĊĊĠĂŤĊĠĠĂĊ		ŤĠĠŤĠĠĊĠĠŤĠŤ	
Query	366			ACGGCGGCAGAGACGG 		
Sbjct	380		ĠĊĀŦĠĀĊĊĊĠĊĠĠĠĠ			
Query	426			CCTACAGCCGGGGAGG 	TCCTGGCACT99 	
Sbjct	440	ACCTCGCCAGGG	ĠĠĠĊĀĠĊĀĠŦĊĀĠŦĊ			ĊĠĠĊĠĠ 499
Query	486	cggtcgggaggg IIIIIIIIIII	cggcggcggttcggc 		tagag 532	
Sbjct	500	CGGTCGGGAGGG	GCGCCGCCGTTCGGC	GTAATCGCGGCGATAG	TÁĠÁĠ 546	

Drosophila melanogaster RH12113 full insert cDNA

Sequence ID: **gb|BT024190.1|** Length: 2647 Number of Matches: 2 Range 1: 645 to 1249

Score		Expect	Identities	Gaps	Strand	Frame	
1107 bits	s(599)	0.0()	603/605(99%)	0/605(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	532	gatcggccggcA	AATCGTGGTCGGTAG	CGGCAGTTTCAATAA	CGACGATCGACC	ATTCGAG	591
Sbjct	645	GATCGGCCGGCA	AATCGTGGTCGGTAG	cggcagtttcaataa	cgacgatcgacc	AttcGAG	704
Query	592	CGTAACCAGGAT	CGGGATCGCGGTCA	GCGGGAAGGCAGCTA	TGGCAACCAGTC	GCGCGAC	651
Sbjct	705	CGTAACCAGGAT	cgggatcgcggtca	GCGGGAAGGCAGCTA	TGGCAACCAGTC	GCGCGAC	764
Query	652	GGCGATCGCTAC	AACAACTTCAACCG	GCACCGCGACCGCGA	GCGCACCACTA	CAATCCC	711
Sbjct	765	GGCGATCGCTAC	AACAACTTCAACCG	gcycedegy general a gan a g	gcgcaccacta	caatccc	824
Query	712	AACCAGCAGAGC	GAACGTCCCAGTGG	CGGCATGACCGGCCT	TGGCGGCGCTC	CGGCGGA	771
Sbjct	825	AACCAGCAGAGC	GAACGTCCCAGTGG	ceecateacceect	<del>t</del> eeceeceec	ÇĞĞÇĞA	884
Query	772	TCAGGAGGCCTA	GGCGTTGGCGGTGG	TTCCTCAATGGGCGC	CATTGACGACAA	TGAGCGG	831
Sbjct	885	tcaggaggccta	ĠĠĊĠŦŦĠĠĊĠĠŦĠĠ	rtcctcaatgggcgc	cattggcgacaa	TGAGCGG	944
Query	832	CCACGTCTGCAG	CTGAAGCCACGGAC	CATTGCCGCGCCCAT	TAACGCGGTGGC	AGAGACC	891
Sbjct	945	ccacdtctdcad	ctgaagccacggac	cattgccgcgccat	taaceceeteec	AGAGACC	1004
Query	892	AAGCAATCGGCC	TCGATCTTTGGCAA	CGCCAAGCCGCGCGA	AGAGAAGCTGAA 	GGAGCTG	951
Sbjct	1005	AAGCAATCGGCC	tcgatctttggcaa	cgccaagccgcga	AGAGAAGCTGAA	ggygctg	1064

Query	952	CAGCAGAATGTCAATCACAACGGCGATAACTAGAGGGCTAGAGTTGGTCCGCAATACAAT	1011
Sbjct	1065	CAGCAGAATGTCAATCACAACGGCGATAACTAGAGGGCTGGAGTTGGTCCGCAATACAAT	1124
Query	1012	ATATGCCTGATATGATATTTTGATGTGcgagaacgagataatccgagatagagggagaga	1071
Sbjct	1125	ATATGCCTGATATGATATTTGATGTGCGAGAACGAGATAATCCGAGATAGAGGGAGAGA	1184
Query	1072	aggcgaggaagaagaggaggaagcagaaatagcaaggggggaggaggaggaggaggag	1131
Sbjct	1185	AGGCGAGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1244
Query	1132	gagga 1136	
Sbjct	1245	GAGGA 1249	

Range 2: 20 to 546

Score		Expect	Identities	Gaps	Strand	Frame
974 bits	(527)	0.0()	527/527(100%)	0/527(0%)	Plus/Plus	
Features	<b>S</b> :					
Query	6	CATGGCTGGAAG	AGGTGGTTATGAAC	ACGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC 65
Sbjct	20	catggctggaag	AGGTGGTTATGAACA	Acdctadaadcddatt	CGGTGGGGATCG	GGCATC 79
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGTT	CATCGCATTTGTCGG	CAATTTGCCGCA 	AGGCCT 125
Sbjct	80	cyycycycycycycycycycycycycycycycycycycyc	cacedaaccecetr	rcatcgcatttgtcgg	caatttgccgca	Addcct 139
Query	126	TGTGCAGGGCGA	TGTGATCAAAATAT?	CCAGGACTTTGAGGT	GAAGTACGTGCG	GCTGGT 185
Sbjct	140	tgtgcygggggy	rgtgatcaaaatatr	rccaggactttgaggt	gyygtygcg	scheich 199
Query	186	GAAGGACCGGGA	AACGGATCAGTTCAA	\AGGCTTCTGCTACGT( 	CGAATTCGAGAC 	GCTGGA 245
Sbjct	200	Ġ <b>ĸ</b> ĸĠŖŖĠĠŖ	AAĊĠĠAተĊAĠተተĊAz	AAGGCTTCTGCTACGT	cgaattcgagac	dctdda 259
Query	246	CAATCTGGAGCG	GGCGCTAGAGTGCGA	ATGGTCGGATCAAACT(	GGACGATCTGTC	GGCGCC 305
Sbjct	260	caatctggagcg	ĠĠĊĠĊŦĀĠĀĠŦĠĊĠź	\rdgtcggatcaaact	ĠĠĀĊĠĀŦĊŦĠŦĊ	gegegege 319
Query	306	GCTAAGGATCGA	CATTGCCGATCGGAC	GAAAAAATGATCGCCC'	TGGTGGCGGTGT 	TGGCGG 365
Sbjct	320	ĠĊŦĀĀĠĠĀŦĊĠĀ	.cattgccgatcggac	saaaaaatgatcgccc	teeteecet	rtggcgg 379
Query	366	CGGCAACGGCGG	CATGACCCGCGGCGA	ACGGCGGCAGAGACGG'	TTTCCAGAAGCG	CGGCCC 425
Sbjct	380	çêççyyçêççê	cateacceeces	yceececycycycycycyc	tttccagaagcg	cccc 439
Query	426	ACCTCGCCAGGG	CGGCAGCAGTCAGT	CTACAGCCGGGGAGG	TCCTGGCACTgg	cggcgg 485
Sbjct	440	<b>ACCTCGCCAGGG</b>	ceecaecaetcaetc	cctycydcceeeegyde.	rcctggcactgg	cccccc 499
Query	486	cggtcgggaggg	cggcggcggttcgg	gtaatcgcggcgatag	tagag 532	
Sbjct	500	cggtcgggagg	çeeçeeçee	etaatceceeceatae	TAGAG 546	

Drosophila melanogaster RNA-binding protein 2 (Rbp2), transcript variant D, mRNA Sequence ID: **ref|NM\_001298401.1|** Length: 2730 Number of Matches: 3 Range 1: 33 to 559

Score		Expect	Identities	Gaps	Strand	Frame	
974 bits	(527)	0.0()	527/527(100%)	0/527(0%)	Plus/Plus		
Features:							
Query	6	CATGGCTGGAAC	GAGGTGGTTATGAACA	CGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC	65
Sbjct	33	categetegaad	GAGGTGGTTATGAACA	cdctadaadcddatt	ceeteeeer	GGCATC	92
Query	66	CAAGCAGTTGC	CCACGGAACCGCCGTT	CATCGCATTTGTCGG	CAATTTGCCGCA	AGGCCT	125
Sbjct	93	caadcadttdco	ccycedyycceccett	catcgcatttgtcgg	caatttgccgca	AGGCCT	152
Query	126	TGTGCAGGGCG	ATGTGATCAAAATATT(	CCAGGACTTTGAGGT	GAAGTACGTGCG	GCTGGT	185
Sbjct	153	TGTGCAGGGCGZ	Atgtgatcaaaatatt	ccaggactttgaggt	GAAGTACGTGCG	gctggt	212
Query	186	GAAGGACCGGG	AAACGGATCAGTTCAA	AGGCTTCTGCTACGT	CGAATTCGAGAC	GCTGGA	245
Sbjct	213	GAAGGACCGGG	AAACGGATCAGTTCAA	y y y y y y y y y y y y y y y y y y y	cgaattcgagac	dctdda	272

Query	246	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	305
Sbjct	273	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	332
Query	306	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	365
Sbjct	333	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	392
Query	366	CGGCAACGGCGCATGACCCGCGGCGACGGCGCAGAGACGGTTTCCAGAAGCGCGGCCC	425
Sbjct	393	CGGCAACGGCGCATGACCCGCGGCGACGGCGCAGAGACGGTTTCCAGAAGCGCGGCCC	452
Query	426	ACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcgg	485
Sbjct	453	ACCTCGCCAGGGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTGGCGGGG	512
Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagag 532	
Sbjct	513	ceetceedageedeeceetteedetaatceedeedataetaede 559	

Range 2: 1034 to 1352

Score		Expect	Identities	Gaps	Strand	Frame	
584 bits	584 bits(316) 1e-16		318/319(99%)	0/319(0%)	Plus/Plus		
Features	s:						
Query	818	ACGACAATGAGO	CGGCCACGTCTGCAGC	TGAAGCCACGGACC	ATTGCCGCGCCC	CATTAACG	877
Sbjct	1034	ACGACAATGAGO	CGGCCACGTCTGCAGC	TGAAGCCACGGACC	ATTGCCGCGCC	CATTAACG	1093
Query	878	CGGTGGCAGAG <i>F</i>	ACCAAGCAATCGGCCT	CGATCTTTGGCAAC	GCCAAGCCGCGC	CGAAGAGA	937
Sbjct	1094	CGGTGGCAGAGA	vccyydcyytcgcci	cegatetttegeeaae	<u> </u>	GAAGAGA	1153
Query	938	AGCTGAAGGAGC	CTGCAGCAGAATGTCA	ATCACAACGGCGAT	AACTAGAGGGCT	TAGAGTTG	997
Sbjct	1154	agctgaagdagd	ctdcadcadaatdtca	yatcycyyceddy	yychydd dd chan y dd y	rggagttg	1213
Query	998	GTCCGCAATAC <i>A</i>	ATATATGCCTGATAT	GATATTTTGATGTG	cgagaacgagat 	taatccga	1057
Sbjct	1214	gtccccaataca	Atatatgcctgatat	rdatattttdatdtd	¢gygyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy	raatccca	1273
Query	1058	gatagagggaga 	agaaggcgaggaagac 	gaagaggaggaagca 	gaaatagcaago	gggggagg	1117
Sbjct	1274	ĠAŦĀĠĀĠĠĀĠĀ	vgyydgggyygyy	saagaggaggaagga	ĠAAAϮAĠĊAAĠĊ	eggggygg	1333
Query	1118	aggaggaggagg	gaggagga 1136				
Sbjct	1334	<b>AGGAGGAGGAG</b>	saggagga 1352				

Range 3: 658 to 945

Score		Expect	Identities	Gaps	Strand	Frame
532 bits(288)		4e-147()	288/288(100%)	0/288(0%)	Plus/Plus	
Features	s:					
Query	532	gatcggccggcA	AATCGTGGTCGGTACG	GCAGTTTCAATAAC	GACGATCGACCA	TTCGAG 591
Sbjct	658	GATCGGCCGGCA	AATCGTGGTCGGTACG	GCAGTTTCAATAAC	GACGATCGACCA	TTCGAG 717
Query	592	CGTAACCAGGAT	CGGGATCGCGGTCAGC	GGGAAGGCAGCTAT	GGCAACCAGTCG	CGCGAC 651
Sbjct	718	CGTAACCAGGAT	CGGGATCGCGGTCAGC	GGGAAGGCAGCTATO	GGCAACCAGTCG	CGCGAC 777
Query	652	GGCGATCGCTAC	AACAACTTCAACCGGC	ACCGCGACCGCGAG(	CGCACCCACTAC	AATCCC 711
Sbjct	778	ggcgatcgctac	AACAACTTCAACCGGC	ycceceycceceye.	cecycecychyc	AATCCC 837
Query	712	AACCAGCAGAGC	GAACGTCCCAGTGGCG	GCATGACCGGCCTT	GGCGGCGCTCC	GGCGGA 771
Sbjct	838	AACCAGCAGAGC	gaacgtcccagtggcg	gcatgaccggcctt	geceececte	GGCGGA 897
Query	772	TCAGGAGGCCTAG	GGCGTTGGCGGTGGTT	CCTCAATGGGCGCC	ATTGAC 819	
Sbjct	898	TCAGGAGGCCTAG	GGCGTTGGCGGTGGTT	CCTCAATGGGCGCC	ATTGAC 945	

Drosophila ananassae uncharacterized protein, transcript variant C (Dana\GF19517), partial mRNA Sequence ID: **ref|XM\_014904505.1|** Length: 2280 Number of Matches: 1 Range 1: 129 to 1181

0	F4		0	Otrono al	<b></b>
Score	Expect	Identities	Gaps	Strand	Frame

963 bits	(521)	0.0()	886/1059(84%)	37/1059(3%)	Plus/Plus	
Feature	s:					
Query	6	CATGGCTGG	AAGAGGTGGTTATGAAC	ACGCTAGAAGCGGAT	TCGGTGGGGATCGG-GC	AT 64
Sbjct	129	CATGGCTGG	:AAGAGGTGGTTATGAAC	acectaegaecegat	rtcggtggtgagcggcac	AT 188
Query	65	CCAAGCAGT	TGCCCACGGAACCGCCG	TTCATCGCATTTGTC	GGCAATTTGCCGCAAGG(	CC 124
Sbjct	189	-GAAGCAGC	teccepce	ttcatcccatcccatc	ceceptates	cc 247
Query	125	TTGTGCAGG	GCGATGTGATCAAAATA 	TTCCAGGACTTTGAG	GTGAAGTACGTGCGGCT(	G 184
Sbjct	248				ĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ	
Query	185				GTCGAATTCGAGACGCTC	
Sbjct	308				ĊĠŦĠĠĀĠŦŦĊĠĀĠĀĊĠĊŦĊ	
Query	245				CTGGACGATCTGTCGGCC	
Sbjct	368				ŢŢĠĠĂŢĠĂŢĊŢĊŢĊĠĠĊ <i>Ĭ</i>	
Query	305				CCTGGTGGCGGTGTTGGC	
Sbjct	428 365				CCTGGTGGCGGCATTGGC CGGTTTCCAGAAGCGCGGC	
Query Sbjct	488				:GG111CCAGAAGCGCGGC 	
Query	425				C-AGCC-GG-GG-AG-GTC	
Sbjct	548				GGGCCTGGAGGCGGCGG	
Query	470	СТĢĢÇ-АÇТ	'qqçqqcqqçqqtçqq	qagqqqqqqqqq	tçgggtaatçgçggçgat	a 526
Sbjct	608	GCGGCGGCA				TA 667
Query	527	gtagagato	ggccggcAAATCGTGGT	CGGTACGGCAGTTTC	CAATAACGACGATCGACC	AT 586
Sbjct	668	GTAGAGATC	GGCCGGCGAATCGAGGT	CGGTATGGAAACTTC	AACAACGACGATCGG	- <del>†</del> 724
Query	587	TCGAGCGTA	ACCAGGATCG-GGAT	CGCGGTCAGCGGGAA	AGGCAGCTATGGCAACCA	FT 643
Sbjct	725	TCGAACGGA	rycgegaptegegegyp	çeçeecçyeçeeye	sggcygctytatggcyytcy	ST 784
Query	644	CGCGCGACG	GCGATCGCTACAACAAC	TTCAACCGGCACCGC	CGACCGCGAGCGCACCCAC	T 703
Sbjct	785	ĊĠĊĠĊĠĀĊĠ	ĠŦĠĂŦĊĠĊŦĂĊĂĂĊĂĀĊ	††cágccgckarcgc	ĠĠĊĠŢĠĠĠĊĠĊĠĊĊĊ	CT 844
Query	704				ACCGGCCTTGGC-GGC	
Sbjct	845				GGCGGCGGTGGTGCCGGC	
Query	761				TCCTCAATGGGCGCCATT	
Sbjct	905				TTCCTCCATGGGTGCCATT	
Query	818				CATTGCCGCGCCCATTAAC	
Sbjct	965				ZÁŤŤĠĊŦĠĊĠĊĊĊÁŤĊÁÁŢ	
Query Sbjct	878 1025				CGCCAAGCCGCGCGAAGAC            CGCCAAGCCCCGCGAGGAC	
Query	938				'AACTAGAGGGCTAG- <i>i</i>	
Sbjct	1085				AACTAG=AGGGCTAG=A        !AACTAGGTAGTGGAAGGA	
Query	995		AATACAATATATGCCTG		1033	
Sbjct	1145	GA-GTCCGC		ATATGATATTTG	1181	

Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF19517), partial mRNA Sequence ID: **ref|XM\_014904504.1|** Length: 2259 Number of Matches: 1 Range 1: 129 to 1160

Score		Expect	Identities	Gaps	Strand	Frame	
944 bits	(511)	0.0()	870/1043(83%)	26/1043(2%)	Plus/Plus		
Features	s:						
Query	6	CATGGCTGG	AAGAGGTGGTTATGAAC	ACGCTAGAAGCGGAT'	rcggrgggarc	G-GCAT	64
Sbjct	129	CATGGCTGG	AAGAGGTGGTTATGAAC	ACGCTAGGAGCGGAT	rcggtggtgagc	GCACAT	188

Query	65	ССААĢÇAĢTTĢÇÇÇAÇĢĢAAÇÇĢÇÇGTTÇATÇĢÇATTTĢTÇĢĢÇAATTTĢÇÇÇĢÇAAĢĢÇÇ	124
Sbjct	189	-GAAGCAGCTGCCCACGGAACCGCCCTTCATCGCATTCGTCGGCAACCTGCCGCAGGGCC	247
Query	125	TTGTGCAGGGCGATGTGATCAAAATATTCCAGGACTTTGAGGTGAAGTACGTGCGGCTGG	184
Sbjct	248	TGGTGCAAGGCGATGTCATCAAAATATTCCAGGACTTTGAGGTGAAGAATGTGCGGCTGG	307
Query	185	TGAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTCGAATTCGAGACGCTGG	244
Sbjct	308	tgaaggateggaaacggateagtteaagggettetgttaegtggagttegagaegetgg	367
Query	245	ACAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGC	304
Sbjct	368	ACAATCTGGAGCGGGCGCTGGAGTGCGATGGCCGGATCAAGTTGGATGATCTCTCGGCAC	427
Query	305	CGCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCG	364
Sbjct	428	cgctrcgcatcgatatagccgatcgtcggaaaaaatgatcgccctggtggcgcattggcg	487
Query	365	GCGGCAACGGCGCATGACCCGCGCGACGGCGCAGAGACGGTTTCCAGAAGCGCGGCC	424
Sbjct	488	ĠĊĠĠŦĀĀŦĠĠĊĠĠĊĠĠŦĀŦĠĠĠŦĊĠĊĠĀŦĠĠĊĠĠĠĊĊĠĀĠĀŦĠĠĀŦŦĊĊĀĠĀĀĀĊĠĊĠĠĀĊ	547
Query	425	CACCTCGCCAGGGCGGCAGC-AGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggc	483
Sbjct	548	ĊĠĊĊŦĊĠĊĊĀĠĠĠĊĠĠ–ĀĠĊĀĀCĠĊĀĠŦĊŦŦĀŦĀĠĊĊĠŦĀĠĊĠĠĠĊĊŦĠĠĀĠĠĊĠĠĊ	606
Query	484	ggcggtcgggag-ggcggcggttcgggtaatcgcggcgatagtagagatcggccggc	542
Sbjct	607	ĠĠĊĠĠ-ĊĠĠĊĀĠĊĀĠĊĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ	662
Query	543	AAATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGTAACCAGGA	602
Sbjct	663	GAATĊĠAĠĠŦĊĠĠŦATĠĠAAACŦŦĊAACAAĊĠAĊĠAŦĊĠ——GŦŦĊĠAAĊĠGAAĊĊAĠĠA	719
Query	603	TCGG-GATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGCGATCG	659
Sbjct	720	†¢ĠCGĠCĠĂŤĊĠĊĠĠĊĊĀĠĊĠĠĠĠĠĠĊĀĠĊŤĂŤĠĠĊĀĀŤĊĀĠŤĊĠĊĠĊĠĀĊĠĠŦĠĀŤĊĠ	779
Query	660	CTACAACAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCA	719
Sbjct	780	ĊŦĀĊĀĀĊĀĀĊŦŦĊĀĠĊĊĠĠĊĀŦĊĠĊĠĀĊĊĠŦĠĀĠĊĠĊĀĊĊĀĊŦĀĊĀĀŦĊĊĊĀĀĊĊĀĠĊĀ	839
Query	720	GAGCGAACGTCCCAGTGGCGGCATGACCGGCCTTGGC-GGCGGC-TCCGGCGGATC	773
Sbjct	840	ĠĂĠĊĠĂĂĊĠŤĊĊĊĂĠĊĠĠŦĠĠŦĂŤĊĠĠĊĠĠĊĠĠĊĠĠĊĠĠĊĠĊĠĊĠĠĊĠĠŦĠĠŦĠĠ	899
Query	774	AGGAGGCCTAGGCGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGGCC	833
Sbjct	900	TĠĠŦĠĠĊĠĠŔĠĊĊĠĠŦĠĠŦĠĠŤĠĊŤĊĊŔŤĠĠĠŦĠĊĊŔŤŤĠŔŦĠŔĊŔĊĠĠŔŔĊĠĠĊĊ	959
Query	834	ACGTCTGCAGCTGAAGCCACGGACCATTGCCGCGCCCATTAACGCGGTGGCAGAGACCAA	893
Sbjct	960	GĊĠĊĊŦĠĊĀĠĊŦĠĀĀĠĊĊĠĀĠĀĀĊĊĀŦŦĠĊŦĠĊĠĊĊĀŦĊĀĀŦĠĊĠĠŦĠĠĊĊĠĀĠĀĊĠĀĀ	1019
Query	894	GCAATCGGCCTCGATCTTTGGCAACGCCAAGCCGCGCGAAGAGAAGCTGAAGGAGCTGCA	953
Sbjct	1020	ĠĊAGŤĊĠĠĊĊŤĊĊĂŤŤŤŤĊĠĠĠĂĂĊĠĊĊĂĂĠĊĊĊĊĠĊĠĂĠĠĀĠĀĠĀĀĠŤŤĠĀĀĠĠĀĠĊŤĠĊĀ	1079
Query	954	GCAGAATGTCAATCACAACGGCGATAACTAGAGGGCTAG-AGTTGGTCCGCAATACAA	1010
Sbjct	1080	ĠĊŔĠŔŔĊĠŤĊŔŔŤĊŔĊŔŔŦĠĠĊĠŔŤŔŔĊŤŔĠĠŦŔĠŦĠĠŖŔĠĠŔĠĠĸĸĠŤĊĊĠĊŔŔŤŔŦŦŔ	1138
Query	1011	TATATGCCTGATATGATATTTTG 1033	
Sbjct	1139	-ATATĠĊĊŢĠAŢAŢĠĀŢĀŢŢŢĠ 1160	

Drosophila sechellia GM13442 (Dsec\GM13442), mRNA

Sequence ID: **ref|XM\_002042216.1|** Length: 1077 Number of Matches: 2 Range 1: 1 to 526

Score		Expect	Identities	Gaps	Strand	Frame	
911 bits	(493)	0.0()	515/526(98%)	0/526(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	7	ATGGCTGGAAGA	GGTGGTTATGAACAC	GCTAGAAGCGGATTO	CGGTGGGGATCG	GGCATCC	66
Sbjct	1	ATGGCTGGAAGA	GGTGGTTATGAACAC	GCTAGAAGCGGATT	cggcgggatcg	GGCATCC	60
Query	67	AAGCAGTTGCCC	ACGGAACCGCCGTTC	ATCGCATTTGTCGG(	CAATTTGCCGCA	AGGCCTT	126
Sbjct	61	AAGCAGTTGCCC	acggaaccgcctttc	Atcecattcetce	caatttgccgca	AGGCCTT	120
Query	127	GTGCAGGGCGAT	GTGATCAAAATATTCO	CAGGACTTTGAGGT	GAAGTACGTGCG	GCTGGTG	186
Sbjct	121	GTGCAGGGCGAT	rgtgatcaaaatattc	caddactttdaddto	saagtacgtgcg:	ıçteete	180
Query	187	AAGGACCGGGAA	ACGGATCAGTTCAAA	GGCTTCTGCTACGT	CGAATTCGAGAC	GCTGGAC	246

Sbjct	181	AAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTGGAATTCGAGACGCTCGAC	240
Query	247	AATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCCG	306
Sbjct	241	AATCTGGAGCGGCGCTAGAATGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCCG	300
Query	307	CTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGGC	366
Sbjct	301	ctgagaatcgacattgctgatcgtagaaaaaaatgatcgccctggtggcggtgttggcggc	360
Query	367	GGCAACGGCGCATGACCCGCGGCGACGGCGCAGAGACGGTTTCCAGAAGCGCGGCCCA	426
Sbjct	361	GGCAACGGCGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCCA	420
Query	427	CCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcggc	486
Sbjct	421	cctcgccagggcgcagcagtcagtcctacagccgggaggtcctggcactggcgc	480
Query	487	ggtcgggagggcggcggttcgggtaatcgcggcgatagtagag 532	
Sbjct	481	ĠĠŦĊĠĠĠĠĠĠĠĠĠĠĠĠĠŦŦĊĠĠĠŦĀĀŦĊĠĊĠĠĊĠĀŦĀĠŦĀĠĀĠ 526	

Range 2: 625 to 1077

Score		Expect	Identities	Gaps	Strand	Frame	
798 bits	(432)	0.0()	446/453(98%)	0/453(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	532	gatcggccggc	AAATCGTGGTCGGT <i>I</i>	ACGGCAGTTTCAATA	ACGACGATCGAC(	CATTCGAG	591
Sbjct	625	GATCGGCCGGC	AAATCGTGGTCGGT	ACGGCAGTTTCAATA	ACGACGATCGAC	CATTCGAT	684
Query	592	CGTAACCAGGA	TCGGGATCGCGGTC	AGCGGGAAGGCAGCT.	ATGGCAACCAGT(	CGCGCGAC	651
Sbjct	685	CGTAACCAGGA	TCGGGATCGCGGCC	AGCGGGAAGGCAGCT.	ATGGCAACCAGT	CGCGCGAC	744
Query	652	GGCGATCGCTA	CAACAACTTCAACC	GCACCGCGACCGCG.	AGCGCACCCACT <i>I</i>	ACAATCCC	711
Sbjct	745	GGCGATCGCTA	CAACAACTTCAACC	TCACCGCGACCGCG.	AGCGCACCCACT	ACAATCCC	804
Query	712	AACCAGCAGAG	CGAACGTCCCAGTG	GCGGCATGACCGGCC	ттөөсөөсөөст	CCGGCGGA	771
Sbjct	805	AACCAGCAGAG	CGAACGTCCTAGTG	GCGCATGACCGGCC	rcgccgccgct	CCGGCGGA	864
Query	772	TCAGGAGGCCT	AGGCGTTGGCGGTGG	GTTCCTCAATGGGCG	CCATTGACGACA	ATGAGCGG	831
Sbjct	865	TCAGGAGGCCT	GGGCGTTGGCGGTGG	GTTCCTCAATGGGCG	CCATTGACGACAZ	ATGAGCGG	924
Query	832	CCACGTCTGCA	GCTGAAGCCACGGAG	CCATTGCCGCGCCCA	TTAACGCGGTGG	CAGAGACC	891
Sbjct	925	ccacgtctgca	GCTGAAGCCACGGAG	CCATTGCCGCGCCCA	ttaacdcddtdd	CAGAGACC	984
Query	892	AAGCAATCGGC	CTCGATCTTTGGCA	ACGCCAAGCCGCGCG.	AAGAGAAGCTGA <i>I</i>	AGGAGCTG	951
Sbjct	985	AAGCAATCGGC	CTCGATCTTTGGCAZ	ACGCCAAGCCGCGCG.	AGGAGAAGCTGA	AGGAGCTG	1044
Query	952	CAGCAGAATGT	CAATCACAACGGCG	ATAACTAG 984			
Sbjct	1045	CAGCAGAATGT	CAATCACAACGGCG	ATAACTAG 1077			

Drosophila yakuba uncharacterized protein, transcript variant A (Dyak\GE17274), mRNA Sequence ID: **ref|XM\_002100780.2|** Length: 2193 Number of Matches: 2 Range 1: 66 to 592

Score		Expect	Identities	Gaps	Strand	Frame	
902 bits	(488)	0.0()	514/527(98%)	0/527(0%)	Plus/Plus		
Feature	s:						
Query	6	CATGGCTGGAAG	GAGGTGGTTATGAACAC	CGCTAGAAGCGGATT	CGGTGGGGATC	GGCATC	65
Sbjct	66	CATGGCTGGAAG	GAGGTGGTTATGAACAC	GCTAGAGGCGGAT	rcggrgggarc	GGCATC	125
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGTTC	CATCGCATTTGTCGC	GCAATTTGCCGC <i>I</i>	AAGGCCT	125
Sbjct	126	caadcadttdcc	ccacccaaccaccrttc	catedeatttdeed	ScaatctGccacz	AAGGCCT	185
Query	126	TGTGCAGGGCGA	TGTGATCAAAATATTC	CAGGACTTTGAGG	rgaagtacgtgc(	GCTGGT	185
Sbjct	186	tgtgcyggggg	vtgtgatcaaaatattc	ckaggactttgagg	rgaagtacgtgac	schech	245
Query	186	GAAGGACCGGGA	AACGGATCAGTTCAAA	AGGCTTCTGCTACGT	rcgaattcgagad 	CGCTGGA	245

Sbjct	246	GAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTGGAGTTCGAGACGCTGGA	305
Query	246	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	305
Sbjct	306	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	365
Query	306	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	365
Sbjct	366	GCTGAGGATCGATATTGCCGATCGGCGGAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	425
Query	366	CGGCAACGGCGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCC	425
Sbjct	426	CGGCAACGGCGCATGACCCGCGGCGATGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCC	485
Query	426	ACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcgg	485
Sbjct	486	Acctcgccaggggagcagcagtcagtcctacagccgggaggtcctggcactggcgg	545
Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagag 532	
Sbjct	546	CGGTCGGGAGGCCGCGGTTCGGGTAATCGCGGCGATAGTAGAG 592	

Range 2: 691 to 1235

Score		Expect	Identities	Gaps	Strand	Frame	
854 bits	(462)	0.0()	519/547(95%)	2/547(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	532	gatcggccggc	AAATCGTGGTCGGT	ACGGCAGTTTCAATA	ACGACGATCGAC	CATTCGAG	591
Sbjct	691	GATCGGCCGGC	caaatcgtggtcggtz	Acgccaatttcaaca	AcGACGATCGAC	CATTCGAT	750
Query	592	CGTAACCAGGA	ATCGGGATCGCGGTC	AGCGGGAAGGCAGCT	ATGGCAACCAGT(	CGCGCGAC	651
Sbjct	751	CGTAACCAGGA	vtcgggytcgtgcc	AGCGGGAAGGCAGCT	AtGGCAATCAGT	2GCGCGAC	810
Query	652	GGCGATCGCTA	CAACAACTTCAACC	GGCACCGCGACCGCG	AGCGCACCCACTA	ACAATCCC	711
Sbjct	811	¢¢¢¢A†¢¢¢†	caacaacttcaccc	ę c p c c c c c c c c c c c c c c c c c	y de central de la constanta d La constanta de la constanta d	ACAACCCC	870
Query	712	AACCAGCAGAG	GCGAACGTCCCAGTG(	GCGGCATGACCGGCC'	TTGGCGGCGGCT(	CCGGCGGA	771
Sbjct	871		scdaacdtccadtdc				930
Query	772	TCAGGAGGCCT	AGGCGTTGGCGGTGC	GTTCCTCAATGGGCG( 	CCATTGACGACAZ 	ATGAGCGG 	831
Sbjct	931	TĊGĠĠĀĠĠĊĊ1	:GĠĠĊĠŤŤĠĠĊĠĠŤĠ(	ĠŦŦĊĊŦĊĀĀŦĠĠĠĊĠ	ĊĊĂŢŢĠĂĊĠĂŢĀŹ	ATĠAĠĊĠĠ	990
Query	832	CCACGTCTGC#	AGCTGAAGCCACGGA( 	CCATTGCCGCGCCCA' 	TTAACGCGGTGG( 	CAGAGACC	891
Sbjct	991	ĊĊĀĊĠŦĊŦĠĊŹ	\ĠĊŦĠAAĠĊĊAĊĠĠA(	ĊĊĂŢŢĠĊĊĠĊĠĊĊĊĂ!	†CAAĊĠĊĠĠŦĠĠ(	ĊĀĠĀĠĀĊĊ	1050
Query	892	AAGCAATCGGC	CTCGATCTTTGGCA <i>I</i>	ACGCCAAGCCGCGCG/ 	AAGAGAAGCTGAA 	AGGAGCTG	951
Sbjct	1051	<b>AAĠĊAATĊĠĠĊ</b>	ĊĊŢĊĠĂŢĊŢŢŢĠĠĊĀ	ÁCGCCÁÁGCCGCGCG	ĠĠĠĠĠĠĠĠĠĠĠĠĀ	ÁĠĠĀAĊŢĠ	1110
Query	952	CAGCAGAATGT	CAATCACAACGGCGA	\TAACTAGAGGGCTA( 	GAGTTGGTCCGCA 	AATACAAT 	1011
Sbjct	1111	ĊĀĠĊĀĀĀĀŦĠſ	rcaatcacaacgcca	\takctaGaGGGCaG	ĠĀĠŦĊĠĠŦĊĊĠĊ	AATACA	1168
Query	1012	ATATGCCTGAT	CATGATATTTTGATGT	<b>[G</b> cgagaacgagata:	atccgagataga 	gggagaga 	1071
Sbjct	1169	AtAtGCCTGA1	rAtGAtAttttGGtG	tĠĊĠAĠAAĊĠAĠGGA:	AACCGAGATAGA(	3CGAGAGA	1228
Query	1072	aggcgag 10	078				
Sbjct	1229	AGGAGAG 12	235				

Drosophila erecta uncharacterized protein, transcript variant A (Dere\GG17966), mRNA Sequence ID: **ref|XM\_001977900.2|** Length: 1502 Number of Matches: 2 Range 1: 67 to 593

Score		Expect	Identities	Gaps	Strand	Frame	
902 bits	(488)	0.0()	514/527(98%)	0/527(0%)	Plus/Plus		
Feature	s:						
Query	6	CATGGCTGGAAG	AGGTGGTTATGAACAC	CGCTAGAAGCGGAT'	CGGTGGGGATC	GGCATC	65
Sbjct	67	CATGGCTGGAAG	addredthatdaacad	cgctagaggcggat	rcggtgggatc	GGCATC	126
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGTTC	CATCGCATTTGTCG	GCAATTTGCCGC	AAGGCCT	125
Sbjct	127	caagcagttgcc	ckacggaaccgcccttd	catedeathtdeed	gcaatctgccgcz	AAGGCCT	186

Query	126	ŢĠŢĠĊŖĠĠĠĠŖŢĠŢĠŖŢĊŖŖŖŖŦŢŢĊĊŖĠĠŖĊŢŢŢĠŖĠĠŢĠŖŖĠŢŖĊĠŦĠĊĠĠĊŢĠĠŢ	185
Sbjct	187	TGTGCAGGGTGATGTGATCAAAATATTCCAGGACTTTGAGGTGAAGTACGTGCGGCTGGT	246
Query	186	GAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTCGAATTCGAGACGCTGGA	245
Sbjct	247	GAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTGGAGTTCGAGACGCTGGA	306
Query	246	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	305
Sbjct	307	CAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCC	366
Query	306	GCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	365
Sbjct	367	GCTGAGGATTGATATTGCTGATCGGCGGAAAAATGATCGCCCTGGTGGCGGTGTTGGCGG	426
Query	366	CGGCAACGGCGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCC	425
Sbjct	427	CGGCAACGGCGGCATGACCCGCGGCGATGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCC	486
Query	426	ACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcgg	485
Sbjct	487	ACCTCGCCAGGGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTGGCGCGG	546
Query	486	cggtcgggagggcggcggttcgggtaatcgcggcgatagtagag 532	
Sbjct	547	CGGTCGGGAGGGCGGCGGTTCGGGGTAATCGCGGCGATAGTAGAG 593	

Range 2: 692 to 1238

Score		Expect	Identities	Gaps	Strand	Frame	
863 bits	(467)	0.0()	522/549(95%)	2/549(0%)	Plus/Plus		
Feature	s:						
Query	532	gatcggccggc	AAATCGTGGTCGGTAG	CGGCAGTTTCAATA	ACGACGATCGACO	CATTCGAG	591
Sbjct	692	GATCGGCCGGC	CAAATCGGGGTCGGTAG	CGGCAATTTCAACA	ACGACGATCGACC	CATTCGAT	751
Query	592	CGTAACCAGGA	TCGGGATCGCGGTCA	GCGGGAAGGCAGCTA	ATGGCAACCAGT(	CGCGCGAC	651
Sbjct	752	cgtaaccagga	rtcgggytcgcggccy	gcgggaaggcagctz	Atggcaaccagtd	GCGCGAC	811
Query	652	GGCGATCGCTA	ACAACAACTTCAACCG(	GCACCGCGACCGCG2	AGCGCACCCACT <i>A</i>	CAATCCC	711
Sbjct	812	ggcgytcgcty	rcyycytage	acycededyceded a communication of the communication	ygcgcycccycty	cyytccc	871
Query	712	AACCAGCAGAG	GCGAACGTCCCAGTGG(	CGGCATGACCGGCC	TTGGCGGCGCTC	CGGCGGA	771
Sbjct	872	AACCAGCAGAG	scgyycetccyddae	pggcytgygggcp.	rcddddddddard	ccgccgda	931
Query	772	TCAGGAGGCCT	AGGCGTTGGCGGTGGT	TTCCTCAATGGGCG(	CCATTGACGACAA	TGAGCGG	831
Sbjct	932	†caggaggcc1	reddadttddtddtddr	ttcctcaatgggcg	ccattgacgacaa	rcgygcgg	991
Query	832	CCACGTCTGCA	AGCTGAAGCCACGGAC	CATTGCCGCGCCCAT	TTAACGCGGTGGC	CAGAGACC	891
Sbjct	992	ccacetcteca	ręctęyyęccycegyc	catteccecece	taaaceceeteec	cagagacc	1051
Query	892	AAGCAATCGGC	CTCGATCTTTGGCAA(	CGCCAAGCCGCGCGA	AAGAGAAGCTGA <i>A</i>	GGAGCTG	951
Sbjct	1052	AAGCAATCGGC	cctcgatctttggcaac	page page page page page page page page	<sup>A</sup> GĠAĠAAĠĊŦĠA <i>A</i>	ddadctd	1111
Query	952	CAGCAGAATGT	CAATCACAACGGCGAT	TAACTAGAGGGCTA(	GAGTTGGTCCGC <i>P</i>	ATACAAT	1011
Sbjct	1112	caccacaatct	ccyytcycyycyc	taactagagggcagc	gygtcggtccgcy	ATACA	1169
Query	1012	ATATGCCTGAT	ATGATATTTTGATGT(	Gcgagaacgagataa	atccgagatagac	ggagaga 	1071
Sbjct	1170	AtAtdcctdat	ratgatattttggtgtc	ecgygyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy	Atcegagatagad	cgagaga	1229
Query	1072	aggcgagga 	1080				
Sbjct	1230	AGCAGAGGA	1238				

Drosophila simulans GD17286 (Dsim\GD17286), mRNA

Sequence ID: **ref|XM\_002107080.1|** Length: 771 Number of Matches: 3 Range 1: 319 to 771

Score	Expect	Identities	Gaps	Strand	Frame
787 bits(426)	0.0()	444/453(98%)	0/453(0%)	Plus/Plus	
Features:					

Query	532	gatcggccggcAAATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAG	591
Sbjct	319	GATCGGCCGGCAAATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAT	378
Query	592	CGTAACCAGGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGAC	651
Sbjct	379	CGTAACCAGGATCGCGGCCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGAC	438
Query	652	GGCGATCGCTACAACAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCC	711
Sbjct	439	GGCGATCGCTACAACAACTTCAACCGTCACCGCGACCGCGAGCGCACCCACTACAATCCT	498
Query	712	AACCAGCAGAGCGAACGTCCCAGTGGCGGCATGACCGGCCTTGGCGGCGGCTCCGGCGGA	771
Sbjct	499	AACCAGCAGAGCGAACGTCCTAGTGGCGGCATGACCGGCCTCGGCGGCGGGTCCGGCGGA	558
Query	772	TCAGGAGGCCTAGGCGTTGGCGGTGGTTCCTCAATGGGCGCCATTGACGACAATGAGCGG	831
Sbjct	559	tcaggaggcctgggcgttggttcctcaatgggcgccattgacgacaatgagcgg	618
Query	832	CCACGTCTGCAGCTGAAGCCACGGACCATTGCCGCGCCCATTAACGCGGTGGCAGAGACC	891
Sbjct	619	CCACGTCTGCAGCTGAAGCCACGGACCATTGCCGCGCCCATTAACGCGGGTGGCAGAGACC	678
Query	892	AAGCAATCGGCCTCGATCTTTGGCAACGCCAAGCCGCGCGAAGAGAAGCTGAAGGAGCTG	951
Sbjct	679	AAGCAATCGGCCTCGATCTTTGGCAACGCCAAGCCGCGCGAGGAGAAGCTGAAGGAGCTG	738
Query	952	CAGCAGAATGTCAATCACAACGGCGATAACTAG 984	
Sbjct	739	cagcagaatgtcaatcacaacggcgataactag 771	

Range 2: 32 to 220

Score		Expect	Identities	Gaps	Strand	Frame	
350 bits	(189)	5e-92()	189/189(100%)	0/189(0%)	Plus/Plus		
Features	<b>S</b> :						
Query	344	GCCCTGGTGG	CGGTGTTGGCGGCGGCA	ACGGCGGCATGACCC	GCGGCGACGGCG	GCAGAG	403
Sbjct	32	GCCCTGGTGG	CGGTGTTGGCGGCGCA	ACGGCGGCATGACCC	GCGGCGACGGCG	GCAGAG	91
Query	404	ACGGTTTCCAC	GAAGCGCGGCCCACCTC	GCCAGGGCGGCAGCA	GTCAGTCCTACA	AGCCGGG	463
Sbjct	92	Accentracca	gaagegegeeekete	gccagggggggggg	gtcagtcctaca	7GCCGGG	151
Query	464	GAGGTCCTGG	CACTggcggcggcggtc	gggagggcggcggcg	gttegggtaate 	geggeg	523
Sbjct	152	ĠĀĠĠŦĊĊŦĠĠ	cactedces	ęęęyęęęçęęç <sub></sub>	ĠŦŦĊĠĠĠŦĂĂŦĊ	c q q q q q q	211
Query	524	atagtagag 	532				
Sbjct	212	ATAGTAGAG	220				

Range 3: 1 to 32

Score		Expect	Identities	G	aps	Strand	Frame
60.2 bits(32)		9e-05()	32/32(100%)	0/	/32(0%)	Plus/Plus	
Features	s:						
Query	7	ATGGCTGGAAGAG	GTGGTTATGAACACGC	TAG	38		
Sbjct	1	ATGGCTGGAAGAG	GTGGTTATGAACACGC	TAG	32		

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA18178), mRNA Sequence ID: **ref|XM\_003736114.2|** Length: 2805 Number of Matches: 1 Range 1: 73 to 1181

Score		Expect	Identities	Gaps	Strand	Frame	
702 bits	(380)	0.0()	889/1128(79%)	62/1128(5%)	Plus/Plus		
Feature	s:						
Query	6	CATGGCTGG	AAGAGGTGGTTATGAAC	ACGCTAGAAGCGGAT'	тсөөтөөөөлгө	GGGCA-T	64
Sbjct	73	CATGGCTGG	Adaggtggttatgaac	ACGCTAGGGGGGAT	TTGGCGGTGAAC	GC-CAGA	131
Query	65	CCAAGCAGT	rgcccacggaaccgcc	TTCATCGCATTTGTC	GGCAATTTGCCG	CAAGGCC	124

Sbjct	132	TGAAGGTACTGCCAACGGAACCGCCCTTTTTTGGCCTTTGTGGGCAACCTGCCCCAGGGCC	191
Query	125	TTGTGCAGGGCGATGTGATCAAAATATTCCAGGACTTTGAGGTGAAGTACGTGCGGCTGG	184
Sbjct	192	tcgtccagggcgatgtaatgaaaatatttcaagactttgaggtgaagaacgtgaggctgg	251
Query	185	TGAAGGACCGGGAAACGGATCA-GTTCAAAGGCTTCTGCTACGTCGAATTCGAGACGCTG	243
Sbjct	252	TAAAGGATCGGGAAACGGA-CATGTTCAAAGGCTTTTGCTACGTGGAATTCGAAACGCTA	310
Query	244	GACAATCTGGAGCGGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCG	303
Sbjct	311	GAGAATCTGGAGCGGGCACTCGAGTTCGATGGTCGTATCAAACTGGACGATCTGTCGGCG	370
Query	304	CCGCTAAGGATCGACATTGCCGATCGGAGAAAAATGATCGCCCTGGTGGCGGTGTTGGC	363
Sbjct	371	cccctgccccccccccccccccccccccccccccccccc	430
Query	364	GGCGGCAACGGCGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGC	423
Sbjct	431	ĠĠŦĠĠĊĀĀŦĠĠĀĠĠĊĀŦĠĀĊĊĊĠĊĠĀŦĠĠŦĠĠĀĀĠĀĠĀĊĠĠŦŦŦĊĊĀĠĀĀĠĊĠŦĠĠĀ	487
Query	424	CCACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggc	483
Sbjct	488	ccccccccccccccccccccccccccccccccccccccc	547
Query	484	ggcggtcgg-gagggcggcggcggttcgggtaatcgcggcgatagtagagat	534
Sbjct	548	AACĠĠĊĠĠAGGŦĠĠTĊĠĊĠĠĠĠĠĠĠĠĠĠĠĊĠĠĊĠĠŦĀĀŦĊĠĊĠĊĊĠĀŦĀĠŦĀĠĀĠĀŦ	607
Query	535	cggccggcAAATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGT	594
Sbjct	608	ĊĠĠĊĊĠĠĊĠÀĀŢĊĠŢĠĠĊĊĠĠŢĀŢĠĠAĀAĊŢŢĊĀĀĊĀĀŢĠĀŢĠĀĊĊĠĠŢ—ŢŢŢĠĀĠĊĠĠ	664
Query	595	AACCAGGATCGGGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGC	654
Sbjct	665	AACCAGGACCGTGACCGGGGGCAGCGTGAGGGAAGTTATGGCAATCAGTCGCGCGACGGT	724
Query	655	GATCGCTACAACAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAAC	714
Sbjct	725	ĠACĊĠĊŦAĊAAĊAAĊŦŦĊAGĊAĠĠĊAĊĊĠŦĠAĊĊĠĊĠAĠĊĠŦAĊĊĊAĊŦAĊAAŦĊĊĊAAĊ	784
Query	715	CAGCAGAGCGAACGTCCCAGTGGCGGCAT-GA-CCGGCCTTGGCGGCGGC	762
Sbjct	785	ĊĂĠĊĂĠĂĠŦĠĂĂĊĠŤĊĊŦĂĠĊĠĠĊĠĠĊĊŤŦĠGŦĠĠĀĠĠĊĠĠĊĠĠĊĊŤŦĠĠĠĠĠĊĀĠĊ	844
Query	763	TCCGGCGGAT-CAGGAGGCC-TAGGCG-TTGGCGGTGGTTCC-TCAAT	806
Sbjct	845	GGĊĠĠĊCTTĠĠAGGĊAĠC-ĠĠĊAAĊCŤĊĠĠŤĠGŤĠĠŤĠĠŤĠĠĊĠĠĊĠĠŤĠĠŤĠĊAŤĊĠĀŤ	903
Query	807	GGGCGCCATTGACGACAATGAGCGGCCACGTCTGCAGCTGAAGCCACGGACCATTGCCGC	866
Sbjct	904	TĠĠĊĠĊĊĂŤAĠĀĊĠĀĊĀCĠĠĀĠĀĠĠĊĊĀĊĠĊĊŤĠĊĀĠĊŤĠĊĀĠĊĊĀĊĠŦĀĊĊĀŤŤĠĊŦĠĊ	963
Query	867	GCCCATTAACGCGGTGGCAGAGCCAAGCAATCGGCCTCGATCTTTGGCAACGCCAAGCC	926
Sbjct	964	ĠĊĊAĂŢĊĂĂŢĠĊĠĠŢĠĠĊĊĠĂAĂĊĊĂĂAĊĂĠŢĊĠĠĊAŢĊĊĂŢŢŢŢĊĠĠĊĂĂŢĠĊĊĂĀĠĊĊ	1023
Query	927	GCGCGAAGAGCTGAAGGAGCTGCAGCAGAATGTCAATCACAACGGCGATAACTAGAG	986
Sbjct	1024	ĠĊĠĊĠĀĠĠĀĠĀĀĀŦŤĠĀĀĠĠĀĠĊŤĠĠĀĠĊĀĠĀĀŤĠŤĊŦĊŤĊĀĊĀĀŦĠĠĊĠĀĊĀŦĊŤĀĀĀĠ	1083
Query	987	GGCTAGAGT-TGG-TCCGCAATACAATATATGCCTGATATGATA	1044
Sbjct	1084	TĠĊ-AĠĠĠAAŤĊĠAŤĊĊĠĊĀĀŤĀ-ĀĀĠĊĊŤĠĀŤĀŤĠĀŤĀŤŤŤŤĠĊŤĠ-ĠŤĠĀĠĀĠ	1135
Query	1045	cgagataatccgagatagagggagagaaggcgaggaagagaagagg 1090	
Sbjct	1136	TĠÁĠÁCÁGAGAĠÁĠÁĠÁĠÁĠÁĠÁĠÁĠÁĠĠ-ĠÁĠAÁĊĠTCÁĠÁÁĠÁĠĠ 1181	

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant D (Dpse\GA18178), partial mRNA Sequence ID: **ref|XM\_015186073.1**| Length: 2834 Number of Matches: 1 Range 1: 170 to 1210

Score		Expect	Identities	Gaps	Strand	Frame	
671 bits	(363)	0.0()	837/1059(79%)	60/1059(5%)	Plus/Plus		
Features	<b>S</b> :						
Query	74	TGCCCACGGA	ACCGCCGTTCATCGC	ATTTGTCGGCAATTTG	CCGCAAGGCCTT	GTGCAGG	133
Sbjct	170	TGCCAACGGA	Acceccttrreed	ctttgtgggcaacctg	cccagggcctc	GTCCAGG	229
Query	134	GCGATGTGAT	'CAAAATATTCCAGG <i>A</i>	CTTTGAGGTGAAGTAC	GTGCGGCTGGTG	AAGGACC	193
Sbjct	230	GCGATGTAAT	'GAAAATATTTCAAGA	CTTTGAGGTGAAGAAC	GTGAGGCTGGTA	AAGGATC	289
Query	194	GGGAAACGGA	TCA-GTTCAAAGGCT	TCTGCTACGTCGAATT	CGAGACGCTGGA	CAATCTG	252
Sbjct	290	GGGAAACGGA	-cardttcaaaddct	rtrtgctacgtggaatt	CGAAACGCTAGA	.gAAtctg	348

Query	253	GAGCGGCCCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGCCCCTAAGG	312
Sbjct	349	ĠAĠĊĠĠĠĊAĊŦĊĠAĠŦŦĊĠAŦĠĠŦĊĠŦAŦĊAAAĊŦĠĠAĊĠAŦĊŦĠŦĊĠĠĊĠĊĊĠĊŦĠĊĠĊ	408
Query	313	ATCGACATTGCCGATCGGAGAAAAATGATCGCCCTGGTGGCGGTGTTGGCGGCGGCAAC	372
Sbjct	409	AtcGATATAGCTGACCGGAAGAAAAACGATCGGCCCGGTGGCGGTATCGGCGGTGGCAAT	468
Query	373	GGCGGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGAAGCGCGGCCCACCTCGC	432
Sbjct	469	GGAGGCATGACCCGCGATGGTGGAAGAGACGGTTTCCAGAAGCGTGGACCGCCCGA	525
Query	433	CAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcggcggcgg-	488
Sbjct	526	cagggggtacgagccaatcctatagtcggggcggtcccgggactggcggcaacggcgga	585
Query	489	tcgg-gagggcggcggttcgggtaatcgcggcgatagtagagatcggccggc	543
Sbjct	586	ggtggtcgcgaggtggcgcgctctggtaatcgcgccgatagtagagatcgccg	645
Query	544	AATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGTAACCAGGAT	603
Sbjct	646	AATCGTGGCCGGTATGGAAACTTCAACAATGATGACCGGTTT-GAGCGGAACCAGGAC	702
Query	604	CGGGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGCGATCGCTAC	663
Sbjct	703	cgrgaccggggcagcggaagttatggcaarcagtcgcgcgacggtgaccgctac	762
Query	664	AACAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACCAGCAGAGC	723
Sbjct	763	AACAACTTCAGCAGGCACCGTGACCGCGAGCGTACCCACTACAATCCCAACCAGCAGAGT	822
Query	724	GAACGTCCCAGTGGCGCAT-GA-CCGGCCTTGGCGGCGCTCCGGC	768
Sbjct	823	GAACGTCCTAGCGGCGGCCTTGGTGGAGGCGGCGGCGGCCTTTGGGGGGCAGCGGCGGCCTT	882
Query	769	GGAT-CAGGAGGCC-TAGGCG-TTGGCGGTGGTTCC-TCAATGGGCGCCAT	815
Sbjct	883	ddagcadc-ddcaacctcddtdgtgdtddtgcddcddtgctdtgctatcdattddcdcdcat	941
Query	816	TGACGACAATGAGCGGCCACGTCTGCAGCTGAAGCCACGGACCATTGCCGCGCCCATTAA	875
Sbjct	942	agacgacacgagagaggccacctgcagctgcagccacctaccattgctgccaatcaa	1001
Query	876	CGCGGTGGCAGAGCCAAGCAATCGGCCTCGATCTTTGGCAACGCCAAGCCGCGCAAGA	935
Sbjct	1002	TGCGGTGGCCGAAACCAAACAGTCGGCATCCATTTTCGGCAATGCCAAGCCGCGCGAGGA	1061
Query	936	GAAGCTGAAGGAGCTGCAGCAGAATGTCAATCACAACGGCGATAACTAGAGGGCTAGAGT	995
Sbjct	1062	GAAATTGAAGGAGCTGGAGCAGAATGTCTCTCACAATGGCGACATCTAAAGTGC-AGGGA	1120
Query	996	-TGG-TCCGCAATACAATATATGCCTGATATGATATTTTTGATGTGcgagaacgagataat	1053
Sbjct	1121	ATCGATCCGCAATA-AAGCCTGATATGATATTTTGCTG-GTGAGAGTGAGACAGA	1173
Query	1054	ccgagatagagggagaaggcgaggaagagaagagg 1090	
Sbjct	1174	GAGAGAGAGAGAGA-GG-GAGAACGTCAGAAGAGG 1210	

Drosophila melanogaster chromosome X

Sequence ID: **gb|AE014298.5|** Length: 23542271 Number of Matches: 5 Range 1: 16451918 to 16452237

Score		Expect	Identities	Gaps	Strand	Frame	
586 bits(	(317)	3e-163()	319/320(99%)	0/320(0%)	Plus/Plus		
Features RNA-bin	s: iding protei	n 2, isoform	DRNA-binding prot	ein 2, isoform B			
Query	817	GACGACA	TGAGCGGCCACGTCT	GCAGCTGAAGCCAC	GGACCATTGCCG	CGCCCATTAAC	876
Sbjct	16451918	GACGACA	tgageggeeaegtete	GCAGCTGAAGCCAC	GGACCATTGCCG	CGCCCATTAAC	1645197
Query	877	GCGGTGGC	CAGAGACCAAGCAATC	GGCCTCGATCTTTG	GCAACGCCAAGC	CGCGCGAAGAG	936
Sbjct	16451978	GCGGTGGC	CAGAGACCAAGCAATC	GGCCTCGATCTTTG	GCAACGCCAAGC	CGCGCGAAGAG	1645203
Query	937	AAGCTGA <i>P</i>	GGAGCTGCAGCAGAA'	rgtcaatcacaacg	GCGATAACTAGA	GGGCTAGAGTT	996
Sbjct	16452038	AAGCTGAA	dgagctgcagcagaa'	rgtcaatcacaacg	GCGATAACTAGA	GGGCTGGAGTT	1645209
Query	997	GGTCCGC <i>P</i>	ATACAATATATGCCT	GATATGATATTTG	ATGTGcgagaac	gagataatccg	1056
Sbjct	16452098	GGTCCGC	ATACAATATATGCCT	GATATGATATTTG	ATGTGCGAGAAC	GAGATAATCCG	1645215
Query	1057	agatagaç	ggagagaaggcgagg	aagagaagaggagg	aagcagaaatag	caagggggag	1116
Sbjct	16452158	AGATAGAC	GGAGAGAAGGCGAGG	AAGAGAAGAGGAGG	AAGCAGAAATAG	CAAGGGGGAG	1645221

Query 1117 gaggaggaggaggaggagga 1136 Sbjct 16452218 GAGGAGGAGGAGGAGGA 16452237

#### Range 2: 16449872 to 16450179

Score		Expect	Identities	Gaps	Strand	Frame	
569 bits	(308)	3e-158()	308/308(100%)	0/308(0%)	Plus/Plus		
Features RNA-bir	eatures: NA-binding protein 2, isoform DRNA-binding protein 2, isoform B						
Query	37	AGAAGCGG	ATTCGGTGGGGATCGG	GCATCCAAGCAGT	rgcccacggaac	CGCCGTTCATC	96
Sbjct	16449872	AGAAGCGG	ATTCGGTGGGGATCGG	catccaagcagt:	reccaceeaac	cdccdttcatc	16449931
Query	97	GCATTTGT	CGGCAATTTGCCGCAAG	GGCCTTGTGCAGG	GCGATGTGATCA	AAATATTCCAG	156
Sbjct	16449932	GCATTTGT	cggcaatttgccgcaad	egccttgtgcagg	GCGATGTGATCA	AAATATTCCAG	16449991
Query	157	GACTTTGA(	GGTGAAGTACGTGCGGC	CTGGTGAAGGACC(	GGAAACGGATC	AGTTCAAAGGC	216
Sbjct	16449992	GACTTTGAG	GGTGAAGTACGTGCGGC	ctggtgaaggacc	GGAAACGGATC	AGTTCAAAGGC	16450051
Query	217	TTCTGCTA	CGTCGAATTCGAGACGC	CTGGACAATCTGGA	AGCGGGCGCTAG	AGTGCGATGGT	276
Sbjct	16450052	ttctcctac	cgtcgaattcgagacgd	ctggacaatctgg	ygcgggcgctyg	AGTGCGATGGT	16450111
Query	277	CGGATCAAZ	ACTGGACGATCTGTCGG	GCGCCGCTAAGGA	rcgacattgccg	ATCGGAGAAAA	336
Sbjct	16450112	CGGATCAA	Actedaceateteted	ececeetaaeea.	rcgacattgccg.	AtcGGAGAAAA	16450171
Query	337	AATGATCG	344				
Sbjct	16450172	AATGATCG	16450179				

Range 3: 16451273 to 16451559

Score		Expect	Identities	Gaps	Strand	Frame				
531 bits(	(287)	2e-146()	287/287(100%)	0/287(0%)	Plus/Plus					
Features: RNA-binding protein 2, isoform DRNA-binding protein 2, isoform B										
Query	531	agatcgg	ccggcAAATCGTGGTC	GGTACGGCAGTTTC	AATAACGACGAT	CGACCATTCGA	590			
Sbjct	16451273	AGATCGG	CCGGCAAATCGTGGTC	GGTACGGCAGTTTC	AATAACGACGA1	rcgaccattcga	16451			
Query	591	GCGTAAC	CAGGATCGGGATCGCG	GTCAGCGGGAAGGC	AGCTATGGCAAC	CAGTCGCGCGA	650			
Sbjct	16451333	GCGTAAC	caddatcdddatcdcd	GTCAGCGGGAAGGC	AGCTATGGCAAC	ccagtcgcgcga	16451			
Query	651	CGGCGAT	CGCTACAACAACTTCA	ACCGGCACCGCGAC	CGCGAGCGCACC	CACTACAATCC	710			
Sbjct	16451393	сĠĠċĠĀт	cectycyycyycy certycy (cectycy)	ycceecyce a character of the control	cgcgagcgcacd	ccactacaatcc	16451			
Query	711	CAACCAG 	CAGAGCGAACGTCCCAC	GTGGCGGCATGACC(	GGCCTTGGCGGC	GGCTCCGGCGG	770			
Sbjct	16451453	ĊAAĊĊAĠ	cadadcdaacdtcccac	gtggcggcytgycc	ĠĠĊĊŦŦĠĠĊĠĠĊ	ceectee	16451			
Query	771	ATCAGGA	GGCCTAGGCGTTGGCG(	GTGGTTCCTCAATG(	GGCGCCATTG	817				
Sbjct	16451513	Atcacca	ĠĠĊĊŦĀĠĠĊĠŦŦĠĠĊĠŒ	ĠŦĠĠŦŦĊĊŦĊĂĂŦĠŒ	ĠĠĠĠĊĠĦŦĠ	16451559				

Range 4: 16450313 to 16450501

Score		Expect	Identities	Gaps	Strand	Frame	
350 bits(	(189)	5e-92()	189/189(100%)	0/189(0%)	Plus/Plus		
Features RNA-bin		n 2, isoforı	n DRNA-binding prot	ein 2, isoform B			
Query	344	GCCCTGG	;TGGCGGTGTTGGCGGC	GGCAACGGCGGCAT	GACCCGCGGCG <i>I</i>	ACGGCGGCAGAG	40
Sbjct	16450313	GCCTGG	rtggcggtgttgcgcgc	GCAACGGCGGCAT	GACCCGCGGCGZ	ACGGCGGCAGAG	16
Query	404	ACGGTTT	CCAGAAGCGCGGCCCA	CCTCGCCAGGGCGG	CAGCAGTCAGTC	CCTACAGCCGGG	46
Sbjct	16450373	ACGGTTT	CCAGAAGCGCGGCCA	CCTCGCCAGGGCGG	CAGCAGTCAGT	CTACAGCCGGG	16
Query	464	GAGGTCC	TGGCACTggcggcggc	ggtcgggagggcgg	caacaattcaa	gtaatcgcggcg	52
Sbjct	16450433	GAGGTCC	TGGCACTGGCGGCGGC	GTCGGGAGGGCGG	ceeceetteec	STAATCGCGGCG	164

Query 524 atagtagag 532 Sbjct 16450493 ATAGTAGAG 16450501

Range 5: 16448697 to 16448729

Score		Expect Identities		Gaps	Strand	Frame
62.1 bits	s(33)	3e-05()	33/33(100%)	0/33(0%)	Plus/Plus	
Features RNA-bir	s: nding proteir	n 2, isoforn	n DRNA-binding pro	otein 2, isoform	В	
Query	6	CATGGCT	GGAAGAGGTGGTTATO	GAACACGCTAG	38	
Sbjct	16448697	CATGGCT	GGAAGAGGTGGTTATO	SAACACGCTAG	16448729	

Drosophila melanogaster, chromosome X, region 14C-14D, BAC clone BACR47D09, complete sequence Sequence ID: **gb|AC010920.11|AC010920** Length: 166935 Number of Matches: 5 Range 1: 99829 to 100148

Score		Expect	Identities	Gaps	Strand	Frame	_
586 bits	(317)	3e-163()	319/320(99%	%) 0/320(0%)	Plus/Plus		_
Feature	s:						
Query	817	GACGACAAT(	GAGCGGCCACGT	CTGCAGCTGAAGCCACG	GACCATTGCCGCG	CCCATTAAC	876
Sbjct	99829	GACGACAAT	GAGCGGCCACGT	CTGCAGCTGAAGCCACG	GACCATTGCCGCG	CCCATTAAC	99888
Query	877	GCGGTGGCA	GAGACCAAGCAA	TCGGCCTCGATCTTTGG	GCAACGCCAAGCCG	CGCGAAGAG	936
Sbjct	99889	GCGGTGGCA	GAGACCAAGCAA	tcggcctcgatctttg	caacgccaagccg	CGCGAAGAG	99948
Query	937	AAGCTGAAG(	GAGCTGCAGCAG	AATGTCAATCACAACGG	GCGATAACTAGAGG	GCTAGAGTT	996
Sbjct	99949	AAGCTGAAG	GAGCTGCAGCAG	sAATGTCAATCACAACGG	scdataactadadd	GCTGGAGTT	100008
Query	997	GGTCCGCAA!	TACAATATATGC	CTGATATGATATTTTGA	ATGTGcgagaacga	gataatccg	1056
Sbjct	100009	GGTCCGCAA	racaatatatgo	CTGATATGATATTTTGA	ATGTGCGAGAACGA	GATAATCCG	100068
Query	1057	agatagagg	gagagaaggcga	.ggaagagaagaggagga	agcagaaatagca	aggggggag	1116
Sbjct	100069	AGATAGAGG	gagagaaggcga	.ggaagagaagaggagga	y y y y y y y y y y y y y y y y y y y	AGGGGGAG	100128
Query	1117	gaggaggag	gaggaggagga	1136			
Sbjct	100129	GAGGAGGAGG	GAGGAGGA	100148			

Range 2: 97783 to 98090

Score		Expect	Identities	Gaps	Strand	Frame	
569 bits	(308)	3e-158()	308/308(100%)	0/308(0%)	Plus/Plus		
Features	3:						
Query	37	AGAAGCGGAT'	TCGGTGGGGATCGGG	CATCCAAGCAGTTGC	CCACGGAACCGC	CGTTCATC	96
Sbjct	97783	AGAAGCGGAT	TCGGTGGGGATCGGGC	catccaagcagttgc	CCACGGAACCGC	CGTTCATC	97842
Query	97	GCATTTGTCG	GCAATTTGCCGCAAGG	CCTTGTGCAGGGCG	ATGTGATCAAAA	TATTCCAG	156
Sbjct	97843	GCATTTGTCG	GCAATTTGCCGCAAGG	CCTTGTGCAGGGCG	ATGTGATCAAAA	TATTCCAG	97902
Query	157	GACTTTGAGG	TGAAGTACGTGCGGCT	GGTGAAGGACCGGG	AAACGGATCAGT	TCAAAGGC	216
Sbjct	97903	GACTTTGAGG	tgaagtacgtgcgct	deppyyddyng a gaeth a g	AAACGGATCAGT	tcaaaggc	97962
Query	217	TTCTGCTACG	TCGAATTCGAGACGCT	GGACAATCTGGAGC	GGCGCTAGAGT	GCGATGGT	276
Sbjct	97963	TTCTGCTACG	tcgyyttcgygycgct	rddacaatctddadco	gggcgctagagt	GCGATGGT	98022
Query	277	CGGATCAAAC'	TGGACGATCTGTCGGC	GCCGCTAAGGATCG	ACATTGCCGATC	GGAGAAAA	336
Sbjct	98023	CGGATCAAAC	tggacgatctgtcggc	ccccctaaccatcc	Acattdccdatc	GGAGAAAA	98082
Query	337	AATGATCG	344				
Sbjct	98083	AATGATCG	98090				

Range 3: 99184 to 99470

Score		Expect	Identities	Gaps	Strand	Frame	
531 bits	(287)	2e-146()	287/287(100%)	0/287(0%)	Plus/Plus		
Feature	s:						
Query	531	agatcggccg	gcAAATCGTGGTCGGT	ACGGCAGTTTCAATA	AACGACGATCGA	CCATTCGA	590
Sbjct	99184	AGATCGGCCG	GCAAATCGTGGTCGGTZ	Acgccagtttcaatz	AACGACGATCGA	CCATTCGA	99243
Query	591	GCGTAACCAG	GATCGGGATCGCGGTC	AGCGGGAAGGCAGC	TATGGCAACCAG	TCGCGCGA	650
Sbjct	99244	GCGTAACCAG	gatcgggatcgcggtc <i>i</i>	/qqqqqqqqqqqq	ratggcaaccag	†cdcdcda	99303
Query	651	CGGCGATCGC	TACAACAACTTCAACCO	GCACCGCGACCGC	GAGCGCACCCAC	TACAATCC	710
Sbjct	99304	cgccgatcgc	†AĊAAĊAAĊ††ĊAAĊĊ	s d c d c d c d d c d c d c d c d c d c	ĠĀĠĊĠĊĀĊĊĊĀĊ	tacaatcc	99363
Query	711	CAACCAGCAG	AGCGAACGTCCCAGTG(	GCGGCATGACCGGC(	CTTGGCGGCGGC 	TCCGGCGG	770
Sbjct	99364	caaccagcag	AĠĊĠAAĊĠŦĊĊĊAĠŦĠŒ	ĠĊĠĠĊĀŦĠĀĊĊĠĠĊŒ	ċŦŦĠĠĊĠĠĊĠĠĊ	tccccccc	99423
Query	771	ATCAGGAGGC	CTAGGCGTTGGCGGTG(	GTTCCTCAATGGGC(	GCCATTG 817		
Sbjct	99424	ATCAGGAGGC	ĊŦĀĠĠĊĠŦŦĠĠĊĠĠŦĠĊ	ĠŦŦĊĊŦĊĂĂŦĠĠĠĊŒ	SCCATTG 994	70	

Range 4: 98224 to 98412

Score		Expect	Identities	Gaps	Strand	Frame	
350 bits	(189)	5e-92()	189/189(100%)	0/189(0%)	Plus/Plus		
Features	S:						
Query	344	GCCCTGGTGG	СССТСТТСССССССССССССССССССССССССССССССС	GCAACGGCGGCATGAC	CCGCGGCGACGG	GCGGCAGAG	403
Sbjct	98224	GCCCTGGTGG	ceererreecece	GCAACGGCGGCATGAC	cccccccccq	SCGGCAGAG	98283
Query	404	ACGGTTTCCA	GAAGCGCGGCCCAC	CTCGCCAGGGCGGCAG	CAGTCAGTCCTA	CAGCCGGG	463
Sbjct	98284	ACGGTTTCCA	GAAGCGCGGCCCAC	ctcgccagggcgcag	cagtcagtcct	ACAGCCGGG	98343
Query	464	GAGGTCCTGG	CACTggcggcggcg	gtcgggagggcggcgg	cggttcgggtaa	tcgcggcg	523
Sbjct	98344	GAGGTCCTGG	çyç4çeççeççe	gtcggggggggggg	ccettrccct	74çeçeçeçe	98403
Query	524	atagtagag 	532				
Sbjct	98404	ATAGTAGAG	98412				

Range 5: 96608 to 96640

Score		Expect	Identities	Gaps		Strand	Frame
62.1 bits	s(33)	3e-05()	33/33(100%)	0/33(0	%)	Plus/Plus	_
Features	3:						
Query	6	CATGGCTGGAAGAGGTGGTTATGAACACGCTAG			38		
Sbjct	96608	cateecteea	AGAGGTGGTTATGAAG	CACGCTAG	96640		

Drosophila virilis uncharacterized protein, transcript variant C (Dvir\GJ19028), mRNA Sequence ID: **ref|XM\_015171030.1|** Length: 1625 Number of Matches: 1 Range 1: 177 to 910

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
580 bits	(314)	2e-161()	605/745(81%)	22/745(2%)	Plus/Plus		
Feature	s:						
Query	6	CATGGCTGGAAG	AGGTGGTTATGAACA(	CGCTAGAAGCGGATT	СĢĢТĢĢGĢĀТÇĢ	GCATC	65
Sbjct	177	CATGGCTGGAAG	AGGTGGTTATGAACAG	CGCTAGAGGTGGCTT	TGGAGGCGAACGG	J-CATG	235
Query	66	C-AAGCAGTTGC	CCACGGAACCGCCGT	CATCGCATTTGTCG	GCAATTTGCCGCA	AAGGCC	124

Sbjct	236	TGAAGCAAATGCCAACGGAACCCCCATTTATTGCGTACGTGGGCAACTTGCCACAGGGTC	295
Query	125	TTGTGCAGGGCGATGTGATCAAAATATTCCAGGACTTTGAGGTGAAGTACGTGCGGCTGG	184
Sbjct	296	TCGTTCAGGGAGATGTTATGAAAATATTTAATGACTTCGAGGTGAAAAACGTGCGACTTG	355
Query	185	TGAAGGACCGGGAAACGGATCAGTTCAAAGGCTTCTGCTACGTCGAATTCGAGACGCTGG	244
Sbjct	356	TCAAGGATCGCGAAACGGATCAGTTTAAGGGCTTCTGTTATGTGGAGTTCGAGACGTTGG	415
Query	245	ACAATCTGGAGCGGCGCTAGAGTGCGATGGTCGGATCAAACTGGACGATCTGTCGGCGC	304
Sbjct	416	ACAATTTGGAGCGTGCCCTCGAATGTGATGGTCGAATAAAGTTGGATGATCTGTCGGCCC	475
Query	305	CGCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCG	364
Sbjct	476	CGCTGCGGATAGACATTGCTGATCGCAGGAAAAATGAACGCCCTGGAGGCGGCATTGGCG	535
Query	365	GCGGCAACGGCGGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGA	415
Sbjct	536	GCGGCGGCGATGGCGCGCGATGGCGGTCGAGATGGCTTCCAGA	592
Query	416	AGCGCGGCCCACCTCGCCAGGGCGGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCA	475
Sbjct	593	AACGGGGACCACCACGTCAGGGCGCAGCAGTCAATCGTATAGCCGAGGCGTCCCTGGCA	652
Query	476	CTggcggcggcggtcgggagggcggcggttcgggtaatcgcggcgatagtagagatc	535
Sbjct	653	ccgccgccgctcgccgacgccgccgcctctgctaatcgtgccgatagtacatc	709
Query	536	ggccggcAAATCGTGGTCGGTACGGCAGTTTCAATAACGACGATCGACCATTCGAGCGTA	595
Sbjct	710	GCCCGGCAAATCGTGGCCGTTATGGTAATTTCAACAATGACGAGCG-CT-TT-GATCGCA	766
Query	596	ACCAGGATCGCGGTCAGCGGGAAGGCAGCTATGGCAACCAGTCGCGCGACGGCG	655
Sbjct	767	ATCAGGATCGGGATCGTGGCCAACGCGAAGGCAGCTATGGTAACCAGTCGCGCGATGGCG	826
Query	656	ATCGCTACAACAACTTCAACCGGCACCGCGACCGCGAGCGCACCCACTACAATCCCAACC	715
Sbjct	827	AtcGGTATAACAACTTCAGCCGGCATCGTGACCGCGAGCGCACCCACTATAATCCCAACC	886
Query	716	AGCAG-AGCGAACGTCCCAGTGGCG 739	
Sbjct	887	AGCAGCAG-GAACGTCCCAGCGGCG 910	

Drosophila ananassae uncharacterized protein, transcript variant A (Dana\GF19517), partial mRNA Sequence ID: **ref|XM\_001966109.2|** Length: 2388 Number of Matches: 2 Range 1: 129 to 673

Score		Expect	Identities	Gaps	Strand	Frame	
508 bits	(275)	8e-140()	459/546(84%)	20/546(3%)	Plus/Plus		
Features	<b>S</b> :						
Query	6	CATGGCTGGAAG	AGGTGGTTATGAAC.	ACGCTAGAAGCGGATT	TCGGTGGGGATCG	GG-CAT	64
Sbjct	129	catedctedaada	AGGTGGTTATGAAC	ACGCTAGGAGCGGAT	rcddrddrdadcd	GCACAT	188
Query	65	CCAAGCAGTTGC(	CCACGGAACCGCCG'	TTCATCGCATTTGTC(	GGCAATTTGCCGC	AAGGCC	124
Sbjct	189	g-AAGCAGCTGC	ccyced y y ccycec	ttcatcccattcctc	ggcaacctgccgc	AGGGCC	247
Query	125	TTGTGCAGGGCGA	ATGTGATCAAAATA' 	TTCCAGGACTTTGAG(	GTGAAGTACGTGC	GGCTGG 	184
Sbjct	248	tgĠtĠċAaĠĠċĠ <i>i</i>	Atgtcatcaaaaata	ttccaggactttgag	stgaagaatgtgc	ффффф	307
Query	185	TGAAGGACCGGGA	AAACGGATCAGTTC.	AAAGGCTTCTGCTAC(	GTCGAATTCGAGA	CGCTGG 	244
Sbjct	308	†ĠAAĠĠATĊĠĠĠ <i>I</i>	AAAĊĠĠA中ĊAĠ中中Ċ.	AAGĠĠĊϮϮĊϮĠτϮAĊĊ	stggagttcgaga s	¢¢¢†¢¢	367
Query	245	ACAATCTGGAGCO	GGCGCTAGAGTGC	GATGGTCGGATCAAA( 	CTGGACGATCTGT	CGGCGC	304
Sbjct	368	AĊĀĀŦĊŦĠĠĀĠĊŒ	ĠĠĠĊĠĊϮĠĠĀĠϮĠĊ	ĠÀŦĠĠĊĊĠĠÀŦĊÀÀGŢ	rtĠĠĀTĠĀtĊtCt	ĊĠĠĊAĊ	427
Query	305	CGCTAAGGATCGA	ACATTGCCGATCGG. 	AGAAAAAATGATCGCO	CCTGGTGGCGGTG 	TTGGCG	364
Sbjct	428	¢Ġ¢ttcĠcAt¢Ġz	ATATAĠĊĊĠATĊĠT	cĠĠĀĀĀĀĀŤĠĀŤĊĠĊĊ	cctgctgcca	ttĠĠĊĠ	487
Query	365	GCGGCAACGGCGC	GCATGACCCGCGGC	GACGGCGGCAGAGAC(	GGTTTCCAGAAGC	GCGGCC	424
Sbjct	488	ĠĊĠĠŦĂĂŦĠĠĊĠŒ	gcentare de la company de la c	ĠĀŦĠĠĊĠĠĊĊĠĀĠĀŦŒ	g gattccagaaac	ĠĊĠĠAĊ	547
Query	425	CACCTCGCCAGG	GCGGCAGCAG'	TCA-GTCC-TA-CA	AG-CC-GG-GGAG	GTC-	469
Sbjct	548	çeççtçeççyeç	gcggagcaacgcag,	tcttatagccgtagcc	gggcctggaggcg	qceeçe	607
Query	470	-CTG-G-CACTgg	gcggcggcggtcgg	gagggcggcggtt 	tcgggtaatcgcg 	gcgata 	526
Sbjct	608	gcgccgccyccac	<del>c</del> cededecededecedecedecedecedecedecedece	ĠĂĀĠĠĠĠĠĠĠĠĠĠ	tcgggtaatcgcg	ĠĊĠĀŦĀ	667

Range 2: 781 to 1289

Score		Expect	Identities	Gaps	Strand	Frame	
457 bits	(247)	3e-124()	428/514(83%)	17/514(3%)	Plus/Plus		
Feature	s:						
Query	532	gatcggccggc	AAATCGTGGTCGGTA	CGGCAGTTTCAATAA	.CGACGATCGACC	ATTCGAG	591
Sbjct	781	GATCGGCCGGC	GAATCGAGGTCGGTA	rggaaacttcaacaa	.cdacdatcd	GTTCGAA	837
Query	592	CGTAACCAGGA	TCGG-GATCGCGG'	rcagcgggaaggcag	CTATGGCAACCA	GTCGCGC	648
Sbjct	838	cggaaccagga	tcgcggcgatcgcgg	ccadcdddadddcad	ctatggcaarca	'q4çqçqç	897
Query	649	GACGGCGATCG	CTACAACAACTTCAA(	CCGGCACCGCGACCG	CGAGCGCACCCA	CTACAAT	708
Sbjct	898	GACGGTGATCG	ctacaacaacttcag	cceccarceceacce	TGAGCGCACCCA	.ctacaat	957
Query	709	CCCAACCAGCA	GAGCGAACGTCCCAG'	IGGCGGCATGACCGG	CCTTGGC-GG	CGGC-TC	764
Sbjct	958	CCCAACCAGCA	.gagcgaacgtcccag	cddrddratcgddd	cededateced	CGGCATC	1017
Query	765	CGGCGGATC	AGGAGGCCTAGGCGT	rggcggtggttcctc	AATGGGCGCCAT	TGACGAC	822
Sbjct	1018	сесестест	rggregeder	rddrddtddthe	cateeerectat	rtgatgac	1077
Query	823	AATGAGCGGCC	ACGTCTGCAGCTGAA	GCCACGGACCATTGC	CGCGCCCATTAA	CGCGGTG	882
Sbjct	1078	AcgGAAcGGCC	GCGCCTGCAGCTGAA	gccgagaaccattgc	rdcdcccatcaa	receere	1137
Query	883	GCAGAGACCAA	GCAATCGGCCTCGAT(	CTTTGGCAACGCCAA	.GCCGCGCGAAGA	GAAGCTG	942
Sbjct	1138	GCCGAGACGAA	.dcagtcggcctccat	rttcgggaacgccaa	.dcccdcdagda	GAAGTTG	1197
Query	943	AAGGAGCTGCA	GCAGAATGTCAATCA	CAACGGCGATAACTA	.GAGGGCTAG-	AGTTGGT	999
Sbjct	1198	AAGGAGCTGCA	.dcadaacdtcaatca	caarddcdataacta	.dgtadtdgaadg	AGGA-GT	1256
Query	1000	CCGCAATACAA	TATATGCCTGATATG	ATATTTTG 1033			
Sbjct	1257	ccccaatatra	Atatgcctgatatg	ATATTTTG 1289			

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant A (Dpse\GA18178), mRNA Sequence ID: **ref|XM\_001354642.3|** Length: 2904 Number of Matches: 1 Range 1: 73 to 605

Score		Expect	Identities	Gaps	Strand	Frame	·
420 bits	(227)	4e-113()	437/538(81%)	16/538(2%)	Plus/Plus		
Features:							
Query	6	CATGGCTGGAAGA	AGGTGGTTATGAACA	CGCTAGAAGCGGATT	CGGTGGGGATCG	GGCA-T	64
Sbjct	73	catecetecada	AGGTGGTTATGAACA	ccctaggggggatt:	rddcddtdaadd	C-CAGA	131
Query	65	CCAAGCAGTTGC	CCACGGAACCGCCGT	TCATCGCATTTGTCG	GCAATTTGCCGC	AAGGCC	124
Sbjct	132	TGAAGGTACTGC	caacggaaccgccct	rtrrtggcctttggg	gcaacctgcccc	AGGGCC	191
Query	125	TTGTGCAGGGCG	ATGTGATCAAAATAT	TCCAGGACTTTGAGG	rgaagtacgtgc	GGCTGG	184
Sbjct	192	TCGTCCAGGGCGA	Atgtaatgaaaatat	TTCAAGACTTTGAGG	rgaagaacgtga	ggctgg	251
Query	185	TGAAGGACCGGG	AAACGGATCA-GTTC	CAAAGGCTTCTGCTAC	GTCGAATTCGAG	ACGCTG	243
Sbjct	252	tadaggateggg	AAAcGGA-cATGTTC	caaaggettttgetae	stggaattegaa	Acccta	310
Query	244	GACAATCTGGAG(	CGGGCGCTAGAGTGC	GATGGTCGGATCAAA(	CTGGACGATCTG	TCGGCG	303
Sbjct	311	GAGAATCTGGAGG	cdddactcdadtro	cdatddtcdtatcaaa	ctggacgatctg	tcggcg	370
Query	304	CCGCTAAGGATC(	GACATTGCCGATCGC	GAGAAAAATGATCGC	CCTGGTGGCGGT	GTTGGC	363
Sbjct	371	ccccatcc	SATATAGCTGACCGG	saagaaaaaacgatcgg	ccceqteeceet	atcddc	430
Query	364	GGCGGCAACGGC	GCATGACCCGCGGC	GACGGCGGCAGAGAC	GGTTTCCAGAAG	CGCGGC	423
Sbjct	431	GGTGGCAATGGAG	ggcatgacccgc	cdarddrddaddddddddd	GGTTTCCAGAAG	СĠтĠĠА	487

Query	424	ҪҪѦҪҪҭҪ҅҅҅ҀҪѦ҅҅Ҁ҇ҿ҇ҀҪ҅҅Ҁ҇ҾҀѦ҅Ҁ҄҅ҀӒҾҭҪӒҾҭҪҀҭѧ҅ҪѦ҅ҪҪ҅҅Ҁ҅҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ҅Ҁ	483
Sbjct	488	CCACCTCGCCAGGGCGCAGCAGTCAGTCCTACAGCCGGGAGGTCCTGGCACTggcggc	547
Query	484	ggcggtcgg-gagggcggcggcggttcgggtaatcgcggcgatagtagag 5 AACGGCGGAGGTGGCGAGGGTGGCGCGCCGCTCTGGTAATCGCGCCGATAGTAGAG 6	32
Sbjct	548	AACGGCGGAGGTGGCGAGGGTGGCGGCGCTCTGGTAATCGCGCCGATAGTAGAG 6	05

Drosophila mojavensis uncharacterized protein (Dmoj\Gl21487), mRNA Sequence ID: **ref|XM\_002010802.2|** Length: 1263 Number of Matches: 1 Range 1: 278 to 804

Score		Expect	Identities	Gaps	Strand	Frame
398 bits	(215)	2e-106()	431/535(81%)	16/535(2%)	Plus/Plus	
Features	<b>S</b> :					
Query	6	CATGGCTGGAAG	AGGTGGTTATGAAC	ACGCTAGAAGCGGATT	CGGTGGGGATCG	GGCAT- 64
Sbjct	278	CATGGCTGGAAGA	AGGTGGTTATGAAC	ACGCTAGAGGTGGCTT	TGGAGGAGAGCG	-TCATG 336
Query	65	CCAAGCAGTTGC	CCACGGAACCGCCG	TTCATCGCATTTGTCG	GCAATTTGCCGC	AAGGCC 124
Sbjct	337	TGAAGCAATTGC	caacddaaccdcca	ttratrdcgtacdtgd	dcaatttdccac	AAGGTC 396
Query	125	TTGTGCAGGGCG	ATGTGATCAAAATA	TTCCAGGACTTTGAGG	TGAAGTACGTGC	GGCTGG 184
Sbjct	397	†cg††caaggcg <i>i</i>	Atgttatgaaaata	ttcaatgactttgagg	tgaaaaacgtgc	GATTGG 456
Query	185	TGAAGGACCGGGA	AAACGGATCAGTTC.	AAAGGCTTCTGCTACG	TCGAATTCGAGA	CGCTGG 244
Sbjct	457	тта́аĠĠ́атċĠаĠ́а	AAACGGATCAGTTT.	<u>AAAĠĠĊ</u> ŦŦĊŦĠĊŦĀĊĠ	†GĠÅG††TĠÅAÅ	ĊĠĊ <b>†</b> ТĠ 516
Query	245	ACAATCTGGAGCO	GGCGCTAGAGTGC	GATGGTCGGATCAAAC 	TGGACGATCTGT	CGGCGC 304
Sbjct	517	ACAACTTGGAACC	<del>S</del> AGCTCTGGAATGC	ĠĀŢĠĠĀĊĠŢĀŢĊĀĀĀŢ	tĠĠĀTĠĀCĊŦĀŤ	င် <del>ဖ်</del> ဖ်င်ငင် 576
Query	305	CGCTAAGGATCGA	ACATTGCCGATCGG	AGAAAAAATGATCGCC	CTGGTGGCGGTG	TTGGCG 364
Sbjct	577	ĊĠĊŦĀĀĠĠĀŦĀĠ	Acattecaeatece	AAGAGAAATGACCGCC	ctggtggcggaa	र्ममेंदेदेदे 636
Query	365	GCGGCAACGGCGC	GC-ATGACCCGCGG	CG-A-CG-G-CGGC 	AGAGACGGTTTC	CAGAAG 417
Sbjct	637	ĠĊĠĠ===TĠĠĊĠĠ	scaatg-gcggcgg	ĊATĠAÁTĊĠCĠATĠĠT	cĠĠĠĀŦĠĠĠŦŦĊ	ĊAĠAAĠ 692
Query	418	CGCGGCCCACCTC	CGCCAGGGCGGCAG	CAGTCAGTCCTACAGC	CGGGGAGGTCCT	GGCACT 477
Sbjct	693	¢¢¢¢åc¢å¢¢g¢	cgrcyggggggggggg	cagtcaatcgtatagc	cgaggcggccct	ĠĠĊĀĊ <b>–</b> 751
Query	478	ggcggcggcggt	cgggagggcggcgg	cggttcgggtaatcgc	ggcgatagtaga	g 532
Sbjct	752	çççççççцç	ceceyeccece	ceectereetaateec	ĠĠĊĠĂŦĀĠŦĀĠĀ	Ġ 804

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant C (Dpse\GA18178), partial mRNA Sequence ID: **ref|XM\_015186072.1|** Length: 2933 Number of Matches: 1 Range 1: 170 to 634

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
388 bits	(210)	1e-103()	385/469(82%)	14/469(2%)	Plus/Plus		
Features	s:						
Query	74	TGCCCACGGAAC	CGCCGTTCATCGCAT	TTGTCGGCAATTTGC	CGCAAGGCCTTG	TGCAGG	133
Sbjct	170	TGCCAACGGAAC	cdcccttrrtgdcct	TTGTGGGCAACCTGC	cccagggcttcg	tccagg	229
Query	134	GCGATGTGATCA	AAATATTCCAGGACT	TTGAGGTGAAGTACG	TGCGGCTGGTGA	AGGACC	193
Sbjct	230	GCGATGTAATGA	AAATATTCAAGACT	ttgaggtgaagaacg	tgaggctggtaa	AGGATC	289
Query	194	GGGAAACGGATC.	A-GTTCAAAGGCTTC	TGCTACGTCGAATTC	GAGACGCTGGAC	AATCTG	252
Sbjct	290	GGGAAACGGA-C	Argttcaaaggcttr	TGCTACGTGGAATTC	GAAACGCTAGAG	SAATCTG	348
Query	253	GAGCGGGCGCTA	GAGTGCGATGGTCGG	ATCAAACTGGACGAT	CTGTCGGCGCCG	CTAAGG	312
Sbjct	349	GAGCGGGCACTC	gagtregategtegr	Atcaaactggacgat	ç4q4çqqçqçqq	ctecec	408
Query	313	ATCGACATTGCC	GATCGGAGAAAAAT	GATCGCCCTGGTGGC	GGTGTTGGCGGC	GGCAAC	372
Sbjct	409	AtcGATATAGCT	GACCGGAAGAAAAC	gytcegecegetege	ggtatcggcggt	GGCAAT	468
Query	373	GGCGGCATGACC	CGCGGCGACGGCGGC	AGAGACGGTTTCCAG	AAGCGCGGCCCA	CCTCGC	432

Sbjct	469	GGAGGCATGACCCGCGATGGTGGAAGAGACGGTTTCCAGAAGCGTGGA	.CCGCCCGA	525
Query	433	CAGGGCGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCACTggcgg	ggcgg-	488
Sbjct	526	CAGGGCGTACGAGCCAATCCTATAGTCGGGGCGGTCCCGGGACTGGCGGC	AACGGCGGA	585
Query	489	tcgg-gagggcggcggttcgggtaatcgcggcgatagtagag	532	
Sbjct	586	ggtggtcgcgagggtggcggctctggtaatcgcgccgatagtagag	634	

Drosophila virilis uncharacterized protein, transcript variant A (Dvir\GJ19028), mRNA Sequence ID: **ref|XM\_002054977.2|** Length: 1646 Number of Matches: 1 Range 1: 177 to 706

Score		Expect	Identities	Gaps	Strand	Frame	
372 bits	(201)	1e-98()	428/537(80%)	17/537(3%)	Plus/Plus		
Features	s:						
Query	6	CATGGCTGGAAG	GAGGTGGTTATGAAC	ACGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC	65
Sbjct	177	catggctggaad	SAGGTGGTTATGAAC	Accctacacct	rtggaggcgaacg	G-CATG	235
Query	66	C-AAGCAGTTGC	CCACGGAACCGCCG	TTCATCGCATTTGTC	GCAATTTGCCGC.	AAGGCC 	124
Sbjct	236	TGAAGCAAATGC	ccaacggaaccccca	ttratrecetacetec	sgcaacttgccac	AGĠĠŦĊ	295
Query	125	TTGTGCAGGGC	GATGTGATCAAAATA	TTCCAGGACTTTGAGO	GTGAAGTACGTGC	GGCTGG 	184
Sbjct	296	tcgttcagggad	SATGTTATGAAAATA	ttraatgacttcgago	stgaaaaacgtgc	ĠAĊŢŢĠ	355
Query	185	TGAAGGACCGGG	GAAACGGATCAGTTC	AAAGGCTTCTGCTACC	GTCGAATTCGAGA 	CGCTGG 	244
Sbjct	356	†cáággátcgcó	SAAACGGATCAGTTT	AAGGGCTTCTGTTATC	ĠŦĠĠĠĠŦŦĊĠĠĠĠ	сфттфф	415
Query	245	ACAATCTGGAGO	CGGGCGCTAGAGTGC	GATGGTCGGATCAAA(	CTGGACGATCTGT	CGGCGC 	304
Sbjct	416	Acaatttccacc	cgrecctceaater	ĠĀŢĠĠŢĊĠĀĀŢĀĀĀĠŢ	rtĠĠATĠAtĊtĠt	ççççcç	475
Query	305	CGCTAAGGATCG	GACATTGCCGATCGG	AGAAAAAATGATCGCC	CCTGGTGGCGGTG'	TTGGCG	364
Sbjct	476	ĊĠĊϮGCĠĠĀϮĀĠ	SACATTGCTGATCGC	AGGAAAAATGAACGCC	cctggaggcggca	ttĠĠĊĠ	535
Query	365	GCGGC <i>F</i>	\ACGGCGGCATG 	ACCCGCGGCGACGGCC	GCAGAGACGGTT'	TCCAGA 	415
Sbjct	536	ĠĊĠĠĊGGCGGC <i>i</i>	\ATGGĊĠĠĊĠĠĊĀŦĠ	ÁGĆĆĠĆĠ––ATĠĠĊĊ	ĠĠŦĊĠĀĠĀŦĠĠĊŤ	tccaga	592
Query	416	AGCGCGGCCCAC	CCTCGCCAGGGCGGC	AGCAGTCAGTCCTACA	AGCCGGGGAGGTC 	CTGGCA 	475
Sbjct	593	<b>AAĊĠĠĠĠAĊĊĀĊ</b>	ccacercaeeecec	AĠĊĀĠŦĊĀĀŦĊĠŦĀŦĀ	AĠĊĊĠAĠĠĊĠŦĊĊ	ctgck	652
Query	476	CTggcggcggc	ggtcgggagggcggc	ggcggttcgggtaato	cgcggcgatagta 	gag 532 	2
Sbjct	653	çç <u></u> ççççççç	ĠĠŦĊĠĊĠĀĠĠĊĊĠĠĊ	ĠĠĊĠĠĊŢĊŢĠĠŢĀĀŢĊ	cĠŦĠĠĊĠĂŦĀĠŦĀ	ĠĀĠ 706	5

Drosophila virilis uncharacterized protein, transcript variant B (Dvir\GJ19028), mRNA Sequence ID: **ref|XM\_015171029.1|** Length: 1714 Number of Matches: 1 Range 1: 185 to 714

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
372 bits	(201)	1e-98()	428/537(80%)	17/537(3%)	Plus/Plus		
Features:							
Query	6	CATGGCTGGAAC	GAGGTGGTTATGAAC	ACGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC	65
Sbjct	185	CATGGCTGGAAG	GAGGTGGTTATGAAC	ACGCTAGAGGTGGCT	TGGAGGCGAACG	G-CATG	243
Query	66	C-AAGCAGTTGO	CCACGGAACCGCCG	TTCATCGCATTTGTCG	GCAATTTGCCGC	AAGGCC	124
Sbjct	244	TGAAGCAAATGO	ccaacggaaccccca	ttratrdegtaedtgd	sdcaacttdccac	AGGGTC	303
Query	125	TTGTGCAGGGC	GATGTGATCAAAATA	TTCCAGGACTTTGAGG	TGAAGTACGTGC	GGCTGG	184
Sbjct	304	TCGTTCAGGGA	GATGTTATGAAAATA	TTTAATGACTTCGAGG	TGAAAAACGTGC	GACTTG	363
Query	185	TGAAGGACCGG	GAAACGGATCAGTTC	AAAGGCTTCTGCTACG	TCGAATTCGAGA	.CGCTGG	244
Sbjct	364	TCAAGGATCGCC	GAAACGGATCAGTTT	AAGGGCTTCTGTTATC	stgdagttcdada	cgttgg	423
Query	245	ACAATCTGGAG(	CGGGCGCTAGAGTGC	GATGGTCGGATCAAAC	TGGACGATCTGT	CGGCGC	304

Sbjct	424	ACAATTTGGAGCGTGCCCTCGAATGTGATGGTCGAATAAAGTTGGATGATCTGTCGGCCC	483
Query	305	CGCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCG	364
Sbjct	484	CGCTGCGGATAGACATTGCTGATCGCAGGAAAAATGAACGCCCTGGAGGCGGCATTGGCG	543
Query	365	GCGGCAACGGCGGCATGACCCGCGGCGACGGCGGCAGAGACGGTTTCCAGA	415
Sbjct	544	GCGGCGGCATGGCGCGCATGAGCCGCGATGGCGGTCGAGATGGCTTCCAGA	600
Query	416	AGCGCGGCCCACCTCGCCAGGGCGGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCTGGCA	475
Sbjct	601	AACGGGGACCACCACGTCAGGGCGCAGCAGTCAATCGTATAGCCGAGGCGTCCCTGGCA	660
Query	476	CTggcggcggcggtcgggaggggggggttcgggtaatcgcggcgatagtagag 53	2
Sbjct	661	ccgccgcgctcgcgaggccggcggctctggtaatcgtggcgatagtagag 71	4

Drosophila persimilis GL20267 (Dper\GL20267), mRNA

Sequence ID: ref|XM\_002023253.1| Length: 903 Number of Matches: 1

Range 1: 1 to 382

Score		Expect	Identities	Gaps	Strand	Frame	
340 bits	(184)	3e-89()	318/384(83%)	4/384(1%)	Plus/Plus		
Features	<b>S</b> :						
Query	7	ATGGCTGGAAGA	.GGTGGTTATGAACA	CGCTAGAAGCGGATTC	CGGTGGGGATCG	GGCA-TC	65
Sbjct	1	ATGGCTGGAAGA	.ddfddftafdadd	CGCTAGGGGGGATTI	GGCGGTGAACG	C-CAGAT	59
Query	66	CAAGCAGTTGCC	CACGGAACCGCCGT	TCATCGCATTTGTCGC	GCAATTTGCCGC	AAGGCCT	125
Sbjct	60	GAAGGTACTGCC	AACGGAACCGCCCT	trrtggcrtttggg	caacctdccc2	AGGGCCT	119
Query	126	TGTGCAGGGCGA	TGTGATCAAAATAT	TCCAGGACTTTGAGG7	GAAGTACGTGC	GCTGGT	185
Sbjct	120	CGTCCAGGGCGA	tgtaatgaaaatat	TTCAAGACTTTGAGG	GAAGAACGTGAG	GCTGGT	179
Query	186	GAAGGACCGGGA	AACGGATCA-GTTC	AAAGGCTTCTGCTACG	TCGAATTCGAG	ACGCTGG	244
Sbjct	180	AAAGGATCGGGA	AACGGA-CATGTTC	AAAGGCTTTTGCTACC	stggaattcgaaz	ACGCTAG	238
Query	245	ACAATCTGGAGC	GGGCGCTAGAGTGC	GATGGTCGGATCAAAC	TGGACGATCTG	rcggcgc	304
Sbjct	239	AGAATCTGGAGC	dggcactcgagttc	gatggtcgtatcaaad	ctddacdatctdc	rcggcgc	298
Query	305	CGCTAAGGATCG	ACATTGCCGATCGG	AGAAAAAATGATCGCC	CTGGTGGCGGT	GTTGGCG	364
Sbjct	299	ccctccccatcc	ATATAGCTGACCGG	AAGAAAAACGATCGGC	cccddtddcddt	ATCGGCG	358
Query	365	GCGGCAACGGCG	GCATGACCCGCG	388			
Sbjct	359	GTGGCAATGGAG	gcatgacccgcg	382			

Drosophila willistoni uncharacterized protein (Dwil\GK25675), mRNA Sequence ID: ref|XM\_002071184.2| Length: 1121 Number of Matches: 1 Range 1: 64 to 561

Score		Expect	Identities	Gaps	Strand	Frame	
300 bits(162)		5e-77()	391/501(78%)	17/501(3%)	Plus/Plus		
Features:							
Query	6	CATGGCTGGAAC	GAGGTGGTTATGAAC	ACGCTAGAAGCGGATT	CGGTGGGGATCG	GGCATC 6	55
Sbjct	64	CATGGCTGGAAG	JAGGTGGTTATGAAC	ACGCTAGAGGCGGATT	TGGCGGTGAGCG	G-CATG 1	22
Query	66	C-AAGCAGTTGO	CCACGGAACCGCCG	TTCATCGCATTTGTCG	GCAATTTGCCGC	AAGGCC 1	24
Sbjct	123	TAAAGCAATTGO	CCACGGAACCGCCC	ttctrcctrccttd	sggyytctgccc	AGGGAC 1	.82
Query	125	TTGTGCAGGGC	GATGTGATCAAAATA	TTCCAGGACTTTGAGG	TGAAGTACGTGC	GGCTGG 1	84
Sbjct	183	ttgtccagggc	GATGTTATTAAAATA	tttcaagactttgaad	straaaaatgtgc	GATTGG 2	42
Query	185	TGAAGGACCGG	GAAACGGATCAGTTC	AAAGGCTTCTGCTACG	TCGAATTCGAGA	CGCTGG 2	44
Sbjct	243	TCAAAGATCGGC	GAAACGGATCAATTT	AAAGGATTTTGTTATC	stcgaatttgaga	CGCTGG 3	02
Query	245	ACAATCTGGAGG	CGGGCGCTAGAGTGC	GATGGTCGGATCAAAC	CTGGACGATCTGT	CGGCGC 3	04
Sbjct	303	Acaatctggaaz	aggcactggaatgc	GATGGGCGTATCAAA1	rtggargatrtgt	CAGACC 3	62

Query	305	CGCTAAGGATCGACATTGCCGATCGGAGAAAAAATGATCGCCCTGGTGGCGGTGTTGGCG	364
Sbjct	363	CATTGCGTATAGATATTGCTGATCGCAGGAAAAATGACCGCCCTGGCGGCGCGTTGGCG	422
Query	365	GCGGCAACGGCGCA-TGACCCGCGGCGACG-GC-GGCAGAGACGGTTTCCAG	414
Sbjct	423	GCGGCGGTGGTGGCAATGGCGGG-GGCATGAATCGTGATGGCGGTCGGGATGGCTTCCAG	481
Query	415	AAGCGCGGCCCACCTCGCCAGGGCGGCAGCAGTCAGTCCTACAGCCGGGGAGGTCCT	471
Sbjct	482	AAACGTGGACCACCACGGCAGGGTGGCGGTAGCAGTCAGT	541
Query	472	GGCACTggcggcggtcgg 492	
Sbjct	542	GGCACGGGTGGTGGCGG 561	

Drosophila grimshawi GH22433 (Dgri\GH22433), mRNA

Sequence ID: ref|XM\_001997807.1| Length: 342 Number of Matches: 1

Range 1: 1 to 335

Score		Expect	Identities	Gaps	Strand	Frame	
270 bits	(146)	4e-68()	274/337(81%)	4/337(1%)	Plus/Plus		
Features	s:						
Query	7	ATGGCTGGAAGA	GGTGGTTATGAACAC	GCTAGAAGCGGATT	CGGTGGGGATCGG	GCATCC	66
Sbjct	1	ATGGCTGGAAGA	.ggtggttatgaacac	dctagaggregatt	TGGAGGCGAACGG	-CATGT	59
Query	67	-AAGCAGTTGCC	CACGGAACCGCCGTT	CATCGCATTTGTCG	GCAATTTGCCGC <i>E</i>	AGGCCT	125
Sbjct	60	gaagcaattgcc	gacggaaccgccatt	TATTGCGTACGTGG	GCAACTTGCCGCA	сффтст	119
Query	126	TGTGCAGGGCGA	TGTGATCAAAATATT	CCAGGACTTTGAGG	TGAAGTACGTGCG	GCTGGT	185
Sbjct	120	cdtccadddcda	tgttatgaaaatatt	TAACGATTTCGAAG	tgaagaatgtgcd	cctddt	179
Query	186	GAAGGACCGGGA	AACGGATCA-GTTCA	AAGGCTTCTGCTAC	GTCGAATTCGAG <i>A</i>	CGCTGG	244
Sbjct	180	CAAGGATCGGGA	.cacgga-cargttca	AGGGCTTCTGTTAC	GTGGAGTTCGAGA	rcectce	238
Query	245	ACAATCTGGAGC	GGGCGCTAGAGTGCG	ATGGTCGGATCAAA	CTGGACGATCTGT	CGGCGC	304
Sbjct	239	Acaatttggagc	grgcactcgagtgcg	atggtcgcattaaa	.ctcgatgatcttd	cedecce	298
Query	305	CGCTAAGGATCG	ACATTGCCGATCGGA	GAAAAAATGA 34	1		
Sbjct	299	cccccatac	ATATTGCTGATCGTA	.dgaaaaaatda 33	5		

Drosophila grimshawi GH24789 (Dgri\GH24789), mRNA

Sequence ID: ref|XM\_001992473.1| Length: 438 Number of Matches: 1

Range 1: 29 to 216

Score		Expect	Identities	Gaps	Strand	Frame	
217 bits(117)		5e-52()	167/191(87%)	4/191(2%)	Plus/Plus		
Features:							
Query	531	agatcggcc-gg	CAAATCGTGGTCGGT	ACGGCAGTTTCAATA	ACGACGATCGA	CCATTCG	589
Sbjct	29	AGATCGCCCGGG	CAAATCGCGGCCGT1	racgcaatttcaata	ATGACGAA	CGATTCG	85
Query	590	AGCGTAACCAGG	ATCGGGATCGCGGTC	CAGCGGGAAGGCAGC	TATGGCAACCAG'	TCGCGCG	649
Sbjct	86	AACGCAATCAGG	AtcGTGACCGTGGtC	cydddaegddaed	rateecaarcae	tçeçeçe	145
Query	650	ACGGCGATCGCT.	ACAACAACTTCAACC	CGGCACCGCGACCGCG	GAGCGCACCCAC'	TACAATC	709
Sbjct	146	aceeceatcect.	acaacaacttcagcc	cęęcyrceeeycee	sądędtąccy.	racaatc	205
Query	710	CCAACCAGCAG	720				
Sbjct	206	ççyyççyçyç	216				

RNA recognition motif-type RNA-binding protein {RRM2 clone} [Drosophila melanogaster, mRNA Partial, 129 nt] Sequence ID: **gb|S51692.1**| Length: 129 Number of Matches: 1

Range 1: 1 to 124

Score		E	Expect	Identities	Gaps	Strand	Frame	_
213 bits(115)		7	e-51()	121/124(98%)	0/124(0%)	Plus/Plus		
Feature	s:							
Query	100	TTTGT	CGGCAA'	PTTGCCGCAAGGCCT"	FGTGCAGGGCGATGT(	GATCAAAATATT(	CCAGGAC	159
Sbjct	1	TTTGT	CGGGAA'	TCTGCCGCAAGGCCT:	rgtgcagggcgatgt(	GATCAAAATATT	CCAGGAC	60
Query	160	TTTGA	GGTGAA(	GTACGTGCGGCTGGT	GAAGGACCGGGAAAC	GGATCAGTTCAA	AGGCTTC	219
Sbjct	61	TTTGA	GGTGAA	gtaceteceecteet	SAAGGACCGGGAAAC	ggatcagttcaa	AGGCTTC	120
Query	220	TGCT	223					
Sbjct	121	GGСТ	124					

Drosophila busckii chromosome X sequence

Sequence ID: **gb|CP012528.1|** Length: 23724088 Number of Matches: 1 Range 1: 19017975 to 19018007

Score	Expect	Identities	Gaps	Strand	Frame
62.1 bits(33)	3e-05()	33/33(100%)	0/33(0%)	Plus/Minus	_
Features:					

Features: 665 bp at 5' side: Rbp2614 bp at 3' side: elF-2alpha

Query 6 CATGGCTGGAAGAGGTGGTTATGAACACGCTAG 38
Sbjct 19018007 CATGGCTGGAAGAGGTGGTTATGAACACGCTAG 19017975