BLAST®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CNA7VUXH014

- ► Formatting options
- ▶ Download

Blast report description

Nucleotide Sequence (2521 letters)

RID <u>CNA7VUXH014</u> (Expires on 02-23 13:21 pm)

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

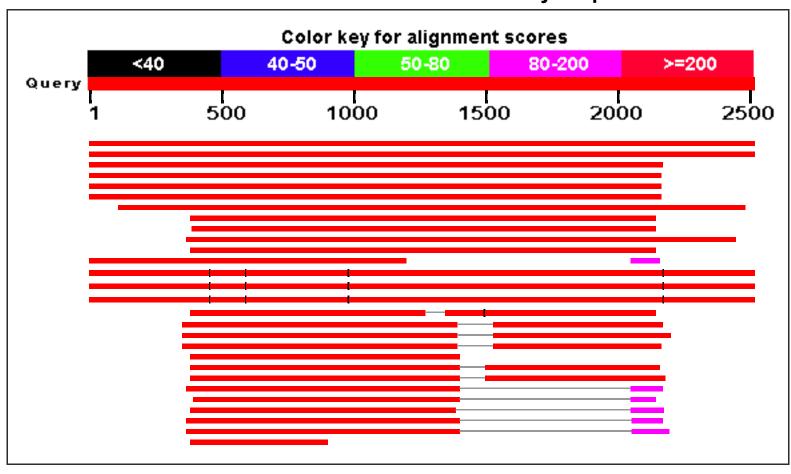
Molecule type nucleic acid

Query Length 2521

Program BLASTN 2.3.1+

□ Graphic Summary

Distribution of 53 Blast Hits on the Query Sequence



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

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila melanogaster spoonbill (spoon), transcript variant A, mRNA	4643	4643	99%	0.0	99%	NM_131993.4
Drosophila melanogaster GM14014 full length cDNA	4632	4632	99%	0.0	99%	AY051641.1
Drosophila melanogaster spoonbill (spoon), transcript variant E, mRNA	4004	4004	85%	0.0	100%	NM_001258603.2
Drosophila melanogaster spoonbill (spoon), transcript variant D, mRNA	4000	4000	85%	0.0	100%	NM_167033.3
Drosophila melanogaster spoonbill (spoon), transcript variant C, mRNA	4000	4000	85%	0.0	100%	NM_167034.2
Drosophila melanogaster RE73736 full insert cDNA	3995	3995	85%	0.0	99%	BT099605.1
Drosophila yakuba uncharacterized protein (Dyak\GE16815), mRNA	3319	3319	93%	0.0	92%	XM_002099976.2
Synthetic construct Drosophila melanogaster clone BS10696 encodes yu-RA	3249	3249	69%	0.0	99%	FJ636724.1
Synthetic construct Drosophila melanogaster clone BO11096 encodes yu-RA	3241	3241	69%	0.0	100%	FJ631998.1
Drosophila erecta uncharacterized protein (Dere\GG18497), mRNA	3037	3037	82%	0.0	93%	XM_001976927.2
Drosophila simulans GD16260 (Dsim\GD16260), mRNA	2837	2837	69%	0.0	96%	XM_002106150.1
Drosophila melanogaster LD28079 full length cDNA	2217	2217	47%	0.0	100%	AY061351.1
Drosophila melanogaster chromosome X	2194	4661	99%	0.0	99%	AE014298.5
Drosophila melanogaster X BAC RP98-7P13 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence	2194	4661	99%	0.0	99%	AC023684.4
Drosophila melanogaster X BAC RP98- 18K5 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence	2194	4661	99%	0.0	99%	AC104604.7
Drosophila sechellia GM12645 (Dsec\GM12645), mRNA	1530	2895	66%	0.0	98%	XM_002036881.1
Drosophila ananassae uncharacterized protein, transcript variant C (Dana\GF20944), mRNA	1081	1525	66%	0.0	85%	XM_014905514.1
Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF20944), mRNA	1081	1558	67%	0.0	85%	XM_014905513.1
Drosophila ananassae uncharacterized protein, transcript variant A (Dana\GF20944), mRNA	1081	1522	66%	0.0	85%	XM_001963992.2
Drosophila persimilis GL14640 (Dper\GL14640), mRNA	837	837	40%	0.0	82%	XM_002022623.1
Drosophila pseudoobscura						

pseudoobscura uncharacterized protein, transcript variant A (Dpse\GA28855), mRNA	806	1160	66%	0.0	81%	XM_002134382.2
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA28855), mRNA	806	1167	67%	0.0	81%	XM_015186614.1
Drosophila virilis uncharacterized protein (Dvir\GJ14809), mRNA	749	932	45%	0.0	80%	XM_002059478.2
Drosophila grimshawi GH24358 (Dgri\GH24358), mRNA	706	849	43%	0.0	79%	XM_001992140.1
Drosophila willistoni uncharacterized protein (Dwil\GK25472), mRNA	688	862	44%	0.0	79%	XM_002070817.2
Drosophila mojavensis uncharacterized protein, transcript variant B (Dmoj\GI11050), mRNA	684	870	45%	0.0	79%	XM_015160555.1
Drosophila mojavensis uncharacterized protein, transcript variant A (Dmoj\GI11050), mRNA	684	875	46%	0.0	79%	XM_002011490.2
Drosophila pseudoobscura pseudoobscura uncharacterized protein (Dpse\GA28909), partial mRNA	401	401	20%	3e-107	81%	XM_002134381.2
Drosophila busckii chromosome X sequence	176	176	4%	2e-39	95%	CP012528.1

□<u>Alignments</u>

Drosophila melanogaster spoonbill (spoon), transcript variant A, mRNA Sequence ID: **ref[NM_131993.4]** Length: 3341 Number of Matches: 1

Range 1	:	66	to	2582
---------	---	----	----	------

Score		Expect	Identities	Gaps	Strand	Frame
4643 bit	s(2514)	0.0()	2517/2518(99%)	1/2518(0%)	Plus/Minus	
Features	S :					
Query	4	gtgtgtgtgtg	tgtgtgtgtgtgtat	tggcgagtgtgtgtt	gtttgttatgtA	ATGATT 63
Sbjct	2582	देमदेमदेमदेमदेमदे	tgtgtgtgtgtgtat:	rtdddadddddddddd	rgttatgtt	ATGATT 2523
Query	64	AAGGGGCTCTC'	TCTGGGCTCAGTCGC	ATCTAAACAACGTAA	CAAACGTTTCAT	TTTCTT 123
Sbjct	2522	aaggggctctc	tctgggctcygtgc	AATCTAAACAACGTAA	caaacgtttcat	र्मर्मर्टममे 2463
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAG	PTCTTTTGGAATCGG	CAATTGCTATTT	GCTGTG 183
Sbjct	2462	tgttttgaggc	ctctgcacttgccag	rtcttttggaatcgg	scaattgctattt	dctdtd 240:
Query	184	TGCTACATGCT	ACATGCTAACTGCAAZ	AAGCTGCTAACGAAAT	CCTTAATCCGAA	TCCGCA 243
Sbjct	2402	tgctycyter.	Acatectaactecaa	Adctdctaacdaaat	rccttaatccgaa	rtcccch 234:
Query	244	TCTTGGAGCCT	GTTGCGCAATACTCAZ	AGCATTCCTTTTTTGT	TGCACCGCCAAG	TTGCTT 303
Sbjct	2342	tcttggagcct	ĠŦŦĠĊĠĊĀĀŦĀĊŦĊĀ	AGCATTCCTTTTTGT	rtgcyccgccyy	rtdctt 2283
Query	304	GATTTGGGTTT	GAGTGATTGTTGTTT 	AAGTTTGCTTTTAAGT	TTTCATATAGTT	CTTGGT 363
Sbjct	2282	ĠAŦŦŦĠĠĠŦŦŦ	ĠĀĠŦĠĀŦŦĠŦŦĠŦŦŦ	AAGTTTGCTTTTAAGT	rtttcatatagtt	cttggt 2223
Query	364	TGCTAGTTGAG	TTGTTCACTAAGGCT(GTTAGTCACTCATCTC	CACCCATTTGGC	GAGCTT 423
Sbjct	2222	†gctagttgag	trétrékétkágétr	stragreacted	ccacccatttgcc	dadctt 216:
Query	424	TCTGCCGACCA	GCTCCTTATTGATAA 	AGATTACATTATTGGG	SACCTAGGGATGC	GAATAA 483
Sbjct	2162	tctcccacca	ĠĊŦĊĊŦŦĀŦŦĠĀŦĀĀ	AGATTACATTATTGGG	sacctadddatdc	daataa 210:
Query	484	AAAGATTTCTG	GTAGGTTGTGACTAT	PATAGCCGGCGACTTC	TGCTTGCAAGAC	AATGCC 543
Sbjct	2102	AAAGATTTCTG	gtaggttgtgactat:	ratadccddcdacttd	stdcttdcaadac	AATGCC 2043
Query	544	TTTGGTAAGTT	TGTTGAGGATTTCGG(CCGCCTCAATGGACCA	AGGTGCCACCGAT	GGGCTC 603

Sbjct	2042	TTTGGTAAGTTTGTTGAGGATTTCGGCCGCCTCAATGGACCAGGTGCCACCGATGGGCTC	1983
Query	604	AATGTTGGACAGGATGCATTCGGTGGACTGGAAGGGCACATTCATGAAATCGGTGCGAAT	663
Sbjct	1982 664	ÄÄTĠŦŦĠĠĂĊĂĠĠĂŦĠĊĂŦŦĊĠĠŦĠĠĂĊŦĠĠĂĀĠĠĠĊĂĊĂŦŦĊĂŦĠĂĂĂŦĊĠĠŦĠĊĠĂĂŦ CTGTCGCAGTGTGTTGAAGCCGACATTCATGTAGCCACCAAAGTCAAGAAACTTGATTAC	1923 723
Query Sbjct	1922	CTGTCGCAGTGTTGAAGCCGACATTCATGTAGCCACCAAAGTCAAGAAACTTGATTAC	1863
Query	724	ĢÇĄĄÇĢÇŢÇÇŢÇĢŢÇŢÇĢĢĢĄŢÇŢĢŢĢŢÇĢĄÇĄĄŢÇŢĢĢĄÇĢÇĢĄŢĄÇÇĄÇĄÇĄŢÇĄŢŢ	783
Sbjct	1862	GCAACGCTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACACATCATT	1803
Query	784	GATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGT	843
Sbjct	1802	ĠĂŢĠĠŢĂŢĊĂĊĠĊĂĊĂĊĠĠĊĂĊŢĀĀĠĊŢĊĊĂĂĂĊŢĠĠĠĊĀĠĊĀĀŢĠĠĊĠĊĊŢĊĊĀŢĠĠŢ	1743
Query Sbjct	844 1742	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	903 1683
Query	904	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	963
Sbjct	1682	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	1623
Query	964	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT	1023
Sbjct	1622	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGAGGAACTAT	1563
Query	1024	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1083
Sbjct Query	1562 1084	ĠĠŦĊŦĠĠĠĠĂĂĠĊĠĊĂĂĂĠŦĠĠĂŦĠĊĠŦŦĠĊĂŦĠĠŦĠĂĂĠŦŦĊĠĠĂŦĂĠĊĠĊŦŦĠĠĊĊĠĠ CAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1503 1143
Sbjct	1502	CAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1443
Query	1144	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1203
Sbjct	1442	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1383
Query	1204	GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1263
Sbjct Query	1382 1264	ĠĠĊĊŦŦĠĂŦŦŦĠĠŦŦĂĂŦĂĂĂĊĠĊĊĊĠĊŦŦĠĊĠĠĊĊĠŦĂĊĂĠĠŦĠĂĊĊĂĂŦĊĂĂĠĊŦĠĂŦ CGGGAAGAGGAACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGA	1323 1323
Sbjct	1322	CGGGAAGAGGAACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGA	1263
Query	1324	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1383
Sbjct	1262	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1203
Query	1384	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	1443
Sbjct Query	1202 1444	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC CTGATCCTGCTCGAGCTCCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1143 1503
Sbjct	1142	CTGATCCTGCTCGAGCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1083
Query	1504	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1563
Sbjct	1082	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1023
Query	1564	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTGGGT	1623
Sbjct Query	1022 1624	TĠĠĊĠĀTĀTTTTĠĠĠTĠTĠĊĠĊĠTĠĠĊĊŢŢĀĀŢĊĀĊĊĠĊŢŢŢŢŢĊĊĀĊĊĠŢĊŢŢŢŢŢŢĠĠĠŢ AGCCTTACGATTGTAGAAGGATACGCGTGTATTTTACCGAATCGGGTAAATCACGTGGCGA	963 1683
Sbjct	962	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	903
Query	1684	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT	1743
Sbjct	902	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT	843
Query	1744	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCGTCC	1803
Sbjct	842 1804	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGATGCTTGCCATTTGAAGTGCGTCC ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	783 1863
Query Sbjct	782	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	723
Query	1864	СТСАТСАСТЯСТАСТТССЯСТАССЯСТТССЯСТАССЯТТААСТАААЯТТССЯТТЯАТЯТТ	1923
Sbjct	722	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTAACTAAAGTTCCGTTGATGTT	663
Query	1924	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTT	1983
Sbjct	662	ĊATĊĠAĊŦŦĠĊŦĠĠĊĊĠAĊŦĠĊŦĠŦĠĠĊAĠĊŦŦĠĊĊAŦŦĊŦĠĊAĠĠAĊŦĊĊĠŦŦĠĠĊĊŦŦ	603
Query	1984	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	2043

Sbjct	602	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	543
Query	2044	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	2103
Sbjct	542	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAAACCAAAAGACGCCGAGTATAAATGC	483
Query	2104	TACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	2163
Sbjct	482	TACACCGGGCAGTGAGAGGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	423
Query	2164	AAAGATCTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCTTTCAA	2223
Sbjct	422	AAAGATCTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCTTTCAA	363
Query	2224	AGCTATCTACTGCACACGCGAGTTGTGTATTGTTTTTTGCTTATTTGCTGGCGATTTACTG	2283
Sbjct	362	AGCTATCTACTGCACACGCGAGTTGTGTATTGTTTTTTGCTTATTTGCTGGCGATTTACTG	303
Query	2284	TCGTTTTCTCAACGCTAAAGTGCTGCACGAATTAAACACGTGTCTACGTTCCACCTTTTA	2343
Sbjct	302	tcgttttctcaacgctaaagtgctgcacgaattaaacacgtgtctacgttccacctttta	243
Query	2344	CAAATCACAATAACATGGCCGGCGTGCGGCAGTGTTGCCATGCATCCGCAAAACTCTGGC	2403
Sbjct	242	caaatcacaataacatggccggcgtgcggcagtgttgccatgcatccgcaaaactctggc	183
Query	2404	AATCGGAGCTGCCTGCTTAATCACCCGCACTCGCGATGGCCAAATCCTCGAATTACAAGA	2463
Sbjct	182	AATCGGAGCTGCCTGAATCACCCGCACTCGCGATGGCCAAATCCTCGAATTACAAGA	123
Query	2464	GCCTTTGTGCACACaaaaaaaaTATATAGAAAAATCACTTCACAGTTTGAATCGCA 2	521
Sbjct	122	GCCTTTGTGCACACAAAAAAAAAAAAATCACTTCACAGTTTGAATCGCA 6	6

Drosophila melanogaster GM14014 full length cDNA

Sequence ID: **gb|AY051641.1|** Length: 3334 Number of Matches: 1 Range 1: 40 to 2555

Score		Expect	Identities	Gaps	Strand	Frame	
4632 bits	s(2508)	0.0()	2515/2518(99%)	2/2518(0%)	Plus/Minus		
Features	Features:						
Query	4	gtgtgtgtgtg	tgtgtgtgtgtatt	tggcgagtgtgtgt	gtttgttatgtA	ATGATT	63
Sbjct	2555	GTGTGTGTGTG	tgtgtgtgtgtgtatt	rtggcgagtgtgtgt	rgtttgttatgta	ATGATT	2496
Query	64	AAGGGGCTCTC	TCTGGGCTCAGTCGCA	ATCTAAACAACGTA	ACAAACGTTTCAT	TTTCTT	123
Sbjct	2495	AAGGGGCTCTC	tctgggctcagtcgca	ATCTAAACAACGTAA	Acadacetttcat	$\pm\pm\pm\pm\pm\pm\pm$	2436
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAGT	TCTTTTGGAATCGG(GCAATTGCTATTT	GCTGTG	183
Sbjct	2435	tgttttgagg	ctctgcacttgccagt	rtcttttggaatcgc	Scaattgctattt	ĠĊŦĠŦĠ	2376
Query	184	TGCTACATGCT	ACATGCTAACTGCAAA	AGCTGCTAACGAAAT	CCTTAATCCGAA	TCCGCA	243
Sbjct	2375	tgctacatgct.	Acatgctaactgcaaa	AdctdctAAcdAAA	tccttaatccgaa	tcccc	2316
Query	244	TCTTGGAGCCT	GTTGCGCAATACTCAA	GCATTCCTTTTTG7	TTGCACCGCCAAG 	TTGCTT	303
Sbjct	2315	tcttggagcct	ĠϮϮĠĊĠĊĀĀϮĀĊϮĊĀĀ	ĠĊĀŦŦĊĊŦŦŦŦŦĠſ	ttĠċaċċĠċċaaĠ	ተተĠĊተተ	2256
Query	304	GATTTGGGTTT	GAGTGATTGTTGTTTA 	AGTTTGCTTTTAAGT	TTTTCATATAGTT 	CTTGGT	363
Sbjct	2255	ĠĀŢŢŢĠĠĠŢŢŢ	ĠĀĠŦĠĀŦŦĠŦŦĠŦŦŦĀ	AGTTTGCTTTAAGT	rtttcatatagtt	ĊϮϮĠĠϮ	2196
Query	364	TGCTAGTTGAG	TTGTTCACTAAGGCTG	TTAGTCACTCATCT(CCACCCATTTGGC 	GAGCTT 	423
Sbjct	2195	†ĠĊŢĀĠŢŢĠĀĠ	††d††cactaaggc†d	rtagtcactcatct	ĊĊĀĊĊĊĀŢŢŢĠĠĊ	ĠĀĠĊϮϮ	2136
Query	424	TCTGCCGACCA	GCTCCTTATTGATAAA 	.GATTACATTATTGG(GACCTAGGGATGC	GAATAA 	483
Sbjct	2135	†c†ĠċċĠàċċà	ĠĊϮĊĊϮϮÀϮϮĠÀϮÀÀÀ	ĠÀŢŢĀĊĀŢŢĀŢŢĠĠĊ	ĠĀĊĊŦĀĠĠĠĀŦĠĊ	ĠĀĀŢĀĀ	2076
Query	484		GTAGGTTGTGACTATT 				543
Sbjct	2075	AAAGATTTCTG	ĠŦĀĠĠŦŦĠŦĠĀĊŦĀŦŦ	'ATAĠĊĊĠĠĊĠAĊTTĊ	ĠŦĠĊŦŦĠĊĂĂĠĂĊ	ÀÀTĠĊĊ	2016
Query	544	TTTGGTAAGTT	TGTTGAGGATTTCGGC	CGCCTCAATGGACC <i>I</i>	AGGTGCCACCGAT 	GGGCTC	603
Sbjct	2015	TTTGGTAAGTT	TĠTTĠAĠĠATTTĊĠĠĊ	ĊĠĊĊŦĊĂĂŦĠĠĂĊĊŹ	AĠĠŦĠĊĊĂĊĊĠĂŦ	ĠĠĠĊŦĊ	1956
Query	604	AATGTTGGACA	GGATGCATTCGGTGGA 	CTGGAAGGGCACATT	rcatgaaatcggt 	GCGAAT	663
Sbjct	1955	ÄÄTĠŤŤĠĠÄĊÄ	ĠĠÀŦĠĊÀŦŦĊĠĠŦĠĠÀ	ĊŦĠĠĂĀĠĠĠĊĀĊĀŦī	rĊATĠAAATĊĠĠŢ	ĠĊĠÀÀŤ	1896
Query	664		TGTTGAAGCCGACATT				723
Sbjct	1895	ĊŦĠŦĊĠĊĀĠŦĠ	<u> tgttgaagccgacatt</u>	ĊATĠTAĠĊĊĀĊĊĀĀĀ	AGTCAAGAAACTT	ĠAϮϮÅĊ	1836

Query	724	GCAACGCTCCTCGTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACACATCATT	783
Sbjct	1835	ĠĊĀĀĊĠĊŦĊĊŦĊĠŦĊĊŦĊĠĠĠĀŦĊŦĠŦĠŦĊĠĀĊĀĊĀĀŦĊŦĠĠĀĊĠĊĠĀŦĀĊĊĀĊĀĊĀŢĊĀŦŢ	1776
Query Sbjct	784 1775	GATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGT	843 1716
Query	844	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	903
Sbjct	1715	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	1656
Query	904	ÇĞĞĞTĞÇTĞĞATĞAAATATĞÇĞAÇÇÇAĞATAĞÇAÇÇĞÇAÇTÇAÇT	963
Sbjct	1655	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	1596
Query	964	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT	1023
Sbjct	1595	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT	1536
Query	1024	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1083
Sbjct	1535	ĠĠŤĊŤĠĠĠĠĂĂĠĊĠĊĂĂĂĠŤĠĠĂŤĠĊĠŤŤĠĊĂŤĠĠŤĠĂĂĠŤŤĊĠĠĂŤĂĠĊĠĊŤŤĠĠĊĊĠĠ	1476
Query Sbjct	1084 1475	CAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1143 1416
Query	1144	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1203
Sbjct	1415	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1356
Query	1204	GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1263
Sbjct	1355	GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1296
Query	1264	CGGGAAGAGGAACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGGCAAGCTGGA	1323
Sbjct	1295	ĊĠĠĠĀĀĠĀĠĠĀĀĊŦĊĠŦĀĠĠŦĠĠŦŦŦŦĊĀĊĠĊĠŦĠŦĊĠĊĊŦĊĊĠĀĠĊĠĊĠĠĊĀĀĠĊŦĠĠĀ	1236
Query	1324	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1383
Sbjct Query	1235 1384	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	1176 1443
Sbjct	1175	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	1116
Query	1444	СТĢАТССТĢСТСĢАĢСТССТССТĢАТСĢĢССТССТТСТТĢĢAĢĢĢСТССТССТТĢĢĢСТС	1503
Sbjct	1115	CTGATCCTGCTCGAGCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1056
Query	1504	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1563
Sbjct	1055	AĊAĠŦŦĠŦŦĠŦŦĊŦĠĊŦĊĠĊAĊŦĊĊŦŦĠŦŦĠĠŦĠŦAĠŦŦĠĠŦAŦĊĊAĠĠAAĠĠA	996
Query	1564 995	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTTGGGT	1623 936
Sbjct Query	1624	TGGCGÁTÁTTTTGGGTGTGCGCGTGGCCTTÁÁTCÁCCÁCCGGTTCCÁCCGTCTTTTGGGT AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	1683
Sbjct	935	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	876
Query	1684	СӨАТАӨАТТСТСӨАААТССТСӨТСТАТӨӨАӨСАӨАӨТӨТСТТӨТӨТТСӨӨСАТССТӨТАТ	1743
Sbjct	875	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT	816
Query	1744	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCGTCC	1803
Sbjct	815	ĊŢŢŢĠĂĊŢŢĊĂĠŢĂŢŢŢĊĠĠĂĂŢĊĠĂŢĊŢĠĊŢĠĊŢĠĂŢĠĊŢŢĠĊĊĂŢŢŢĠĂĂĠŢĠĊĠŢĊĊ	756
Query Sbjct	1804 755	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	1863 696
Query	1864	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTT	1923
Sbjct	695	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTAACTAAAGTTCCGTTGATGTT	636
Query	1924	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTT	1983
Sbjct	635	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTTGCCATTCTGCAGGACTCCGTTGGCCTT	576
Query	1984	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	2043
Sbjct	575	ĠĊĠĊĠĊĊŦĠĊĀĊĀĠŦŦĠĠŦŦĊĀĀŦĊĠĀĊĠĀĠŦĊĀŦŦĠĀŦĠĠĊĊĠĀŦĠĀĠŦĊĊŦĊĠŦĊĠŦĊ	516
Query	2044	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	2103
Sbjct Query	515 2104	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC TACACCGGGCAGTGAGAGGTAGAGTAGA	456 2163
Sbjct	455	TACACCGGGCAGTGAGAGTAGAGTAGAGGACCGCTACCATTTTCGCTGAATATTG	396
,			-

Query	2164	AAAGATCTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCTTTCAA	2223
Sbjct	395	AAAGATCTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCTTTCAA	336
Query	2224	AGCTATCTACTGCACACGCGAGTTGTGTATTGTTTTTTGCTTATTTGCTGGCGATTTACTG	2283
Sbjct	335	AGCTATCTACTGCACACGCGAGTTGTGTATTGTTTTTTGCTTATTTGCTGGCGATTTACTG	276
Query	2284	TCGTTTTCTCAACGCTAAAGTGCTGCACGAATTAAACACGTGTCTACGTTCCACCTTTTA	2343
Sbjct	275	TCGTTTTCTCAACGCTAAAGTGCTGCACGAATTAAACACGTGTCTACGTTCCACCTTTTA	216
Query	2344	CAAATCACAATAACATGGCCGGCGTGCGGCAGTGTTGCCATGCATCCGCAAAACTCTGGC	2403
Sbjct	215	CAAATCACAATAACATGGCCGGCGTGCGGCAGTGTTGCCATGCATCCGCAAAACTCTGAC	156
Query	2404	AATCGGAGCTGCCTGCTTAATCACCCGCACTCGCGATGGCCAAATCCTCGAATTACAAGA	2463
Sbjct	155	AATCGGAGCTGCCTGATTAATCACCCGCACTCGCGATGGCCAAATCCTCGAATTACAAGA	96
Query	2464	GCCTTTGTGCACACaaaaaaaaTATATAGAAAAATCACTTCACAGTTTGAATCGCA 2	521
Sbjct	95	GCCTTTGTGCACACAAAAAAAAATATAGAAAAAATCACTTCACAGTTTGAATCGCA 4	0

Drosophila melanogaster spoonbill (spoon), transcript variant E, mRNA Sequence ID: **ref[NM_001258603.2**] Length: 3179 Number of Matches: 1

Range 1: 253 to 2420

Score		Expect	Identities	Gaps	Strand	Frame	
4004 bit	s(2168)	0.0()	2168/2168(100%)	0/2168(0%)	Plus/Minus		_
Features	s:						
Query	4	gtgtgtgtgtg	tgtgtgtgtgtattt	ggcgagtgtgtgtt	gtttgttatgt A	TGATT 6	3
Sbjct	2420	GTGTGTGTGTG	+t $+$ d	œddaddddddddd	rgttagttatgta	Atgatt 2	361
Query	64	AAGGGGCTCTC	TCTGGGCTCAGTCGCAA	TCTAAACAACGTAA	CAAACGTTTCATT	TTCTT 1	.23
Sbjct	2360	AAGGGGCTCTC	rtctgggctcagtgcaa	rctaaacaacgtaa	ckaakcetttcatt	ያተተረተተ 2	301
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAGTT	CTTTTGGAATCGGG	CAATTGCTATTTC	CTGTG 1	.83
Sbjct	2300	†g††††gAggc	ctctgcacttgccagtt	ĊŦŦŦĠĠĀĀŦĊĠĠĠ	ckaarrectarre	sctgtg 2	241
Query	184		'ACATGCTAACTGCAAAA 				43
Sbjct	2240		'ACATGCTAACTGCAAAA				181
Query	244		'GTTGCGCAATACTCAAG 				03
Sbjct	2180			;CATTCCTTTTTGT			121
Query	304		'GAGTGATTGTTGTTTAA 				63
Sbjct	2120		GAGTGATTGTTGTTTAA				23
Query Sbjct	364 2060		TTGTTCACTAAGGCTGT TTGTTCACTAAGGCTGT	11111111111111			001
Query	424	ŢÇŢĢÇÇĢĄÇÇĄ	ĢСТССТТАТТĢАТА А А	; АТТАСАТТАТТGGG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	ЗААТАА 4	83
Sbjct	2000	TCTGCCGACCA	.GCTCCTTATTGATAAAG	;ATTACATTATTGGC		JIIII SAATAA 1	941
Query	484	AAAGATTTCTG	GTAGGTTGTGACTATTA	TAGCCGGCGACTTG	GTGCTTGCAAGAC <i>A</i>	ATGCC 5	43
Sbjct	1940	AAAGATTTCTG	GTAGGTTGTGACTATTA	tagccggcgactt	rtgcttgcaagaca	ATGCC 1	881
Query	544	TTTGGTAAGTT	TGTTGAGGATTTCGGCC	GCCTCAATGGACCA	GGTGCCACCGATG	GGCTC 6	03
Sbjct	1880	tttggtaagtt	rtgttgaggatttcgcc	ccctcaatcca	œqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	sddctc 1	821
Query	604	AATGTTGGACA	GGATGCATTCGGTGGAC	TGGAAGGGCACATT	CATGAAATCGGTG	GCGAAT 6	63
Sbjct	1820	AATGTTGGACA	.ĠĠAŦĠĊAŦŦĊĠĠŦĠĠAĊ	rtggaagggcacatr	'catgaaatcggtd		761
Query	664		TGTTGAAGCCGACATTC				23
Sbjct	1760		ŗĠŢŢĠĀĀĠĊĊĠĀĊĀŢŢĊ				701
Query	724		CGTCCTCGGGATCTGTG				83
Sbjct	1700		CGTCCTCGGGATCTGTG				641
Query	784		.CGCACACGGCACTAAGC				43
Sbjct	1640		ĊĠĊĀĊĀĊĠĠĊĀĊŦĀĀĠĊ				.581
Query	844	GGAGTAGCTAT	CGTACAGCTGCTTCTGC	CAGCAAAGGCAACGA	'T'GGA'TGCGAGGGA	ATGCAG 9	03

Sbjct	1580	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	1521
Query	904	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	963
Sbjct	1520	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	1461
Query	964	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGGAACTAT	1023
Sbjct	1460	ĠĂŢĠĊĊĊŢĊĂĂŢĊĀĠŢŢŢĊĀĠŢŢĠŢĀĠĀŢŢĠŢĀĠĀĠĠĊŢŢŢĊĠĠŢĊĠĀĀĀĠĀĠĠĀĀĊŢĀŢ	1401
Query Sbjct	1024 1400	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG 	1083 1341
Query	1084	CAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1143
Sbjct	1340		1281
Query	1144	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1203
Sbjct	1280	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1221
Query	1204	GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1263
Sbjct	1220	ĠĠĊĊŢŢĠĂŢŢŢĠĠŢŢĀĀŢĀĀĀĊĠĊĊĠĊŢŢĠĊĠĠĊĊĠŢĀĊĀĠĠŢĠĀĊĊĀĀŢĊĀĀĠĊŢĠĀŢ	1161
Query Sbjct	1264 1160	CGGGAAGAGGAACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGGCAAGCTGGA	1323 1101
Query	1324	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1383
Sbjct	1100	TCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1041
Query	1384	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	1443
Sbjct	1040	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	981
Query	1444	CTGATCCTGCTCGAGCTCCTCGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1503
Sbjct	980	ĊŢĠĂŢĊĊŢĠĊŢĊĠĀĠĊŢĊĊŢĠĀŢĊĠĠĊĊŢĊĊŢŢĊŢŢĠĠĀĠĠĠĊŢĊĊŢŢĠĠĠĊŢĊ	921
Query Sbjct	1504 920	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1563 861
Query	1564	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTGGGT	1623
Sbjct	860	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTGGGT	801
Query	1624	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	1683
Sbjct	800	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	741
Query	1684	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT	1743
Sbjct	740	ĊĠĂŤĂĠĂŤŤĊŤĊĠĂĂĂŤĊĊŤĊĠŤĊŤĂŤĠĠĂĠĊĂĠĂĠŤĠŤĊŤŤĠŤĠŤŤĊĠĠĊĂŤĊĊŤĠŤĂŤ	681
Query Sbjct	1744 680	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCGTCC	1803 621
Query	1804	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGGCTGTCCTT	1863
Sbjct	620	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	561
Query	1864	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTT	1923
Sbjct	560	ctcatcactdctacttccdctaccdcttccdctaccdttaactaaadttccdttdatdtt	501
Query	1924	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTT	1983
Sbjct	500 1984	ĊĂŢĊĠĂĊŢŢĠĊŢĠĠĊĊĠĂĊŢĠĊŢĠŢĠĠĊĂĠĊŢŢĠĊĊĂŢŢĊŢĠĊĀĠĠĂĊŢĊĊĠŢŢĠĠĊĊŢŢ GCGCGCCŢGCACAGŢŢGGŢŢCAAŢCGACGAGŢCAŢŢGAŢGGCCGAŢGAGŢCCŢCGŢC	441 2043
Query Sbjct	440	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	381
Query	2044	ĢĢĢÇŢŢĢŢÇŢĄĄĄÇĄĄŢŢŢŢŢĄŢĄŢÇŢĄÇĢÇÇĢĄĄĄÇÇĄĄĄĄĢĢÇÇÇĢĄGŢĄŢĄĄĄŢĢÇ	2103
Sbjct	380	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	321
Query	2104	TACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	2163
Sbjct	320	tacaccedecaetedadaetaeaetaeaetaeaetaeaet	261
Query	2164	AAAGATCT 2171	
Sbjct	260	AAAGATCT 253	

Range 1: 744 to 2909

Score		Expect	Identities	Gaps	Strand	Frame
4000 bits	s(2166)	0.0()	2166/2166(100%)	0/2166(0%)	Plus/Minus	
Features	S :					
Query	4	gtgtgtgtgtg		ggcgagtgtgtgtt	gtttgttatgtAAT(
Sbjct	2909 64		ŢĠŢĠŢĠŢĠŢĠŢĠŢĀŢŢŢ ŢĊŢĠĠĠĊŢĊĀĠŢĊĠĊĀĀ			
Query Sbjct	2849	AAGGGGCTCTC			CAAACGTTTCATTT 	<u> </u>
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAGTT	CTTTTGGAATCGGG	CAATTGCTATTTGC	TGTG 183
Sbjct	2789	TGTTTTGAGGC	CTCTGCACTTGCCAGTT	CTTTTGGAATCGGG	CAATTGCTATTTGC	TGTG 273
Query	184		ACATGCTAACTGCAAAA		CCTTAATCCGAATC(
Sbjct	2729		ACATGCTAACTGCAAAA			
Query Sbjct	244 2669		GTTGCGCAATACTCAAG 	CATTCCTTTTTTGT CATTCCTTTTTTGT		
Query	304		҅҅҅҅҅Ҁ҄҅҅҅҅҄҅ҀҀ҄Ҿ҇ҲҬҬҀҬҬҀҬҬҬӒӒ			
Sbjct	2609	GATTTGGGTTT		GTTTGCTTTTAAGT:	TTTCATATAGTTCT	
Query	364		TTGTTCACTAAGGCTGT			
Sbjct	2549		·TTGTTCACTAAGGCTGT		ĊĂĊĊĊĂŢŢŢĠĠĊĠĂſ	
Query Sbjct	424 2489	TCTGCCGACCA	.GCTCCTTATTGATAAAG 	ATTACATTATTGGG/ 	ACCTAGGGATGCGA 	ATAA 463 ATAA 243
Query	484	ААА ĢАТТТСТĢ	- GTAGGTTGTGACTATTA	ТАĢССĞĞСĞАСТТĞ	ГССТТССААСАСАА	
Sbjct	2429	AAAGATTTCTG		TAGCCGGCGACTTG	rgcttgcaagacaa'	 TGCC 237
Query	544		TGTTGAGGATTTCGGCC			
Sbjct	2369		rtĠttĠAĠĠAtttċĠĠċċ			
Query Sbjct	604 2309		.GGATGCATTCGGTGGAC 			
Query	664		ТĢŢŢĢĄĄĢÇÇĢĄÇĄŢŢÇ			
Sbjct	2249	CTGTCGCAGTG	TGTTGAAGCCGACATTC	ATGTAGCCACCAAA		
Query	724		CGTCCTCGGGATCTGTG			[
Sbjct	2189 784		ĊĠŦĊĊŦĊĠĠĠĂŦĊŦĠŦĠ .CGCACACGGCACTAAGC			
Query Sbjct	2129		CGCACACGGCACTAAGC 			
Query	844	GGAGTAGCTAT	· ·CGTACAGCTGCTTCTGC	[*] АĞÇAAAĞĞÇAAÇĞA'	ГССАТСССАСССАТС	GCAG 903
Sbjct	2069	GGAGTAGCTAT	CGTACAGCTGCTTCTGC	AGCAAAGGCAACGA	rggatgcgaggat	GCAG 201
Query	904		TGAAAATATGCGACCCA			
Sbjct Query	2009 964		.TGAAAATATGCGACCCA .TCAGTTTCAGTTGTAGA			
Sbjct	1949		TCAGTTTCAGTTGTAGA			
Query	1024	GGTCTGGGGAA	.GCGCAAAGTGGATGCGT	TGCATGGTGAAGTT(CGGATAGCGCTTGG	CCGG 108
Sbjct	1889	GGTCTGGGGAA	GCGCAAAGTGGATGCGT	TGCATGGTGAAGTT	CGGATAGCGCTTGG	CCGG 183
Query	1084		GGATCATGGCCAGGGCG			
Sbjct	1829 1144		ĠĠĂŦĊĂŦĠĠĊĊĂĠĠĠĊĠ .CCTTGCCCGAGTAGGGA			
Query Sbjct	1769		.CCTTGCCCGAGTAGGGA .CCTTGCCCGAGTAGGGA			
Query	1204		GGTTAATAAACGCCCGC			
Sbjct	1709	GGCCTTGATTT		TTGCGGCCGTACAG		
Query	1264		ACTCGTAGGTGGTTTTC			
Sbjct	1649	ĊĠĠĠĀĀĠĀĠĠĀ	Actcctacctacctacctacctacctacctacctacctac	ACGCGTGTCGCCTC	cgagcgcgcgcaagc	rgga 159

Query	1324	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1383
Sbjct	1589	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1530
Query	1384	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	1443
Sbjct	1529	cacattgcgcttctgattaccattgctatccaccacttcctccttcagcaccactgctc	1470
Query	1444	CTGATCCTGCTCGAGCTCCTCGTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1503
Sbjct	1469	ctgatcctgctcgagctcctgatcggcctccttctttggagggctccttcttgggctc	1410
Query	1504	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1563
Sbjct	1409	Acadttdttdttctdctcdcactccttdttdttddtadttddtatccaddaadda	1350
Query	1564	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTGGGT	1623
Sbjct	1349	tggcgatattttgggtgtgcgcgtggccttaatcaccaccggttccaccgtcttttgggt	1290
Query	1624	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	1683
Sbjct	1289	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	1230
Query	1684	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTTCGGCATCCTGTAT	1743
Sbjct	1229	cgatagattctcgaaatcctcgtctatggagcagagtgtcttgtgttctgcgcatcctgtat	1170
Query	1744	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCGTCC	1803
Sbjct	1169	ctttgacttcagtatttcgaatcgatctgctgctgatgctttgccattttgaagtgcgtcc	1110
Query	1804	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	1863
Sbjct	1109	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	1050
Query	1864	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTAACTAAAGTTCCGTTGATGTT	1923
Sbjct	1049	ctcatcactgctacttccgctaccgcttccgctaccgttaactgttaacttaaagttccgttgatgtt	990
Query	1924	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTT	1983
Sbjct	989	catcgacttgctggccgactgctgtggcagcttgccattctgcaggactccgttggcctt	930
Query	1984	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	2043
Sbjct	929	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	870
Query	2044	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	2103
Sbjct	869	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAAACCAAAAGACGCCGAGTATAAATGC	810
Query	2104	TACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	2163
Sbjct	809	TACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	750
Query	2164	AAAGAT 2169	
Sbjct	749	AAAGAT 744	

Drosophila melanogaster spoonbill (spoon), transcript variant C, mRNA Sequence ID: **ref|NM_167034.2|** Length: 4509 Number of Matches: 1 Range 1: 144 to 2309

Score		Expect	Identities	Gaps	Strand	Frame	
4000 bits(2166)		0.0()	2166/2166(100%)	0/2166(0%)	Plus/Minus		
Features	S :						
Query	4	gtgtgtgtgtg	ıtgtgtgtgtgtgtattt	ggcgagtgtgtgtt	gtttgttatgtA	ATGATT	63
Sbjct	2309	GTGTGTGTGTG	stetetetetetetet	rGGCGAGTGTGTT	GTTTGTTATGTA	ATGATT	2250
Query	64	AAGGGGCTCTC	TCTGGGCTCAGTCGCAA	ATCTAAACAACGTAA	CAAACGTTTCAT'	TTTCTT	123
Sbjct	2249	AAGGGGCTCTC	ctctgggctcagtcgcaa	ATCTAAACAACGTAA	caaacgtttcat _'	Ի դդԵդդ	2190
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAGTT	CTTTTGGAATCGGG	CAATTGCTATTT(GCTGTG	183
Sbjct	2189	TGTTTTGAGGC	ctctgcacttgccagti	rcttttggaatcggg	caattgctattt	gctgtg	2130
Query	184	TGCTACATGCT	ACATGCTAACTGCAAA	AGCTGCTAACGAAAT	CCTTAATCCGAA'	TCCGCA	243
Sbjct	2129	tectacatect	acatectaactecaaa	rectectyychy a character of the control of the cont	ccttaatcccaa	tcccc	2070
Query	244	TCTTGGAGCCT	GTTGCGCAATACTCAAG	GCATTCCTTTTTTGT	TGCACCGCCAAG'	TTGCTT	303
Sbjct	2069	tcttggagcct	dttgcgcaatactcaad	ccattccttttttct	rgcyccgccyyd,	rtgctt	2010
Query	304	GATTTGGGTTT	GAGTGATTGTTGTTTAA	AGTTTGCTTTTAAGT	TTTCATATAGTT	CTTGGT	363

Sbjct	2009	GATTTGGGTTTGAGTGATTGTTTAAGTTTGCTTTTAAGTTTTCATATAGTTCTTGGT	1950
Query Sbjct	364 1949	TGCTAGTTGAGTTGTTCACTAAGGCTGTTAGTCACTCATCTCCACCCATTTGGCGAGCTT	423 1890
Query	424	TCTGCCGACCAGCTCCTTATTGATAAAGATTACATTATTGGGACCTAGGGATGCGAATAA	483
Sbjct	1889	tctgccgaccagctccttattgataaagattacattattgggacctagggatgcgaataa	1830
Query Sbjct	484 1829	AAAGATTTCTGGTAGGTTGTGACTATTATAGCCGGCGACTTGTGCTTGCAAGACAATGCC	543 1770
Query	544	TTTGGTAAGTTTGTTGAGGATTTCGGCCGCCTCAATGGACCAGGTGCCACCGATGGGCTC	603
Sbjct	1769	tttggtaagtttgttgaggatttcggccgcctcaatggaccaggtgccaccgatggctc	1710
Query Sbjct	604 1709	AATGTTGGACAGGATGCATTCGGTGGACTGGAAGGGCACATTCATGAAATCGGTGCGAAT	663 1650
Query	664	CTGTCGCAGTGTGTTGAAGCCGACATTCATGTAGCCACCAAAGTCAAGAAACTTGATTAC	723
Sbjct	1649	ctgtcgcagtgtgttgaagccagtgtgtacattcatgtagccaccaaaagtcaagaaaagcagaagaag	1590
Query Sbjct	724 1589	GCAACGCTCCTCGTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACACATCATT	783 1530
Query	784	GATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGT	843
Sbjct	1529	GATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGT	1470
Query Sbjct	844 1469	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	903 1410
Query	904	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	963
Sbjct	1409	cgggtgctggatgaaaatatgcgacccagatagcaccgcactcact	1350
Query Sbjct	964 1349	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGGAACTAT	1023 1290
Query	1024	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1083
Sbjct	1289	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1230
Query Sbjct	1084 1229	CAAACGTTGACGGATCATGGCCAGGGCGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1143 1170
Query	1144	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1203
Sbjct	1169	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1110
Query Sbjct	1204 1109	GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1263 1050
Query	1264	CGGGAAGAGGAACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGA	1323
Sbjct	1049	cggaagagaactcgtaggtggttttcacgcgtgtcgcctccgagcgcgcaagctgga	990
Query Sbjct	1324 989	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1383 930
Query	1384	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	1443
Sbjct	929	cacattgcgcttctgattaccattgctatccaccacttcctccttcagcaccactgctc	870
Query Sbjct	1444 869	CTGATCCTGCTCGAGCTCCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1503 810
Query	1504	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1563
Sbjct	809	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	750
Query Sbjct	1564 749	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTTGGGT	1623 690
Query	1624	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	1683
Sbjct	689	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	630
Query Shict	1684	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT	1743 570
Sbjct Query	629 1744	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGCTTGTGTTCGGCATCCTGTAT	1803
-			

Sbjct	569	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCGTCC	510
Query	1804	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	1863
Sbjct	509	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	450
Query	1864	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTT	1923
Sbjct	449	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTT	390
Query	1924	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTT	1983
Sbjct	389	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTT	330
Query	1984	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	2043
Sbjct	329	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	270
Query	2044	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	2103
Sbjct	269	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	210
Query	2104	TACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	2163
Sbjct	209	TACACCGGGCAGTGAGAGGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	150
Query	2164	AAAGAT 2169	
Sbjct	149	AAAGAT 144	

Drosophila melanogaster RE73736 full insert cDNA

Sequence ID: **gb|BT099605.1|** Length: 4518 Number of Matches: 1 Range 1: 140 to 2305

Score		Expect	Identities	Gaps	Strand	Frame	
3995 bit	s(2163)	0.0()	2165/2166(99%)	0/2166(0%)	Plus/Minus		
Features	S :						
Query	4	gtgtgtgtgtg	tgtgtgtgtgtatt	tggcgagtgtgtgtt	gtttgttatgtA	ATGATT	63
Sbjct	2305	gtgtgtgtgtgt	rgtgtgtgtgtatt	tggcgagtgtgtgt	rgttatgtatgta	AtGATT	2246
Query	64	AAGGGGCTCTC	TCTGGGCTCAGTCGCA	ATCTAAACAACGTA <i>I</i>	ACAAACGTTTCAT'	TTTCTT	123
Sbjct	2245	AAGGGGCTCTC	tctgggctcygtgc	Atctaaacaacgtaa	Acaaacgtttcat:	ተተተረተተ	2186
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAGT	TCTTTTGGAATCGGC	CAATTGCTATTT(GCTGTG 	183
Sbjct	2185	†g††††gAggc	ĊŦĊŦĠĊĀĊŦŦĠĊĊĀĠŦ	†¢††††gĠAA†¢ĠĠĊ	scaattgctattt	ĠĊŦĠŦĠ	2126
Query	184		ACATGCTAACTGCAAA 				243
Sbjct	2125	TĠĊTĀĊĀTĠĊT.	ACATGCTAACTGCAAA	GĠĊϮĠĊϮAAĊĠAAAſ	rĊĊϮϮAAϮĊĊĠAA	rcccca	2066
Query	244		GTTGCGCAATACTCAA 				303
Sbjct	2065		ĠŦŦĠĊĠĊĂĂŦĂĊŦĊĂĂ			ŤŤĠĊŤŤ	2006
Query	304		${f GAGTGATTGTTGTTTA}$				363
Sbjct	2005		GAGTGATTGTTGTTTA				1946
Query	364		TTGTTCACTAAGGCTG				423
Sbjct	1945		ГТĠТТĊĂĊTĂĂĠĠĊTĠ GCTCCTTATTGATAAA				1886 483
Query Sbjct	424 1885	TCTGCCGACCA					1826
Query	484		GTAGGTTGTGACTATT.				543
Sbjct	1825		GTAGGTTGTGACTATT				1766
Query	544		TGTTGAGGATTTCGGC				603
Sbjct	1765						1706
Query	604	ААТĢТТĢĢĀÇĀ		Ҫҭ҃҅҅Ҫ҄҄҄҄҄҄҄҄҄ӒӒҀ҅ҪҪҪҲҪҲҬҬ	ГСАТБАААТСББТ	Ģ ÇĢĄĄŢ	663
Sbjct	1705	AATGTTGGACA	 	CTGGAAGGGCACATT	rcatgaaatcggt		1646
Query	664	CTGTCGCAGTG	TGTTGAAGCCGACATT	CATGTAGCCACCAA	AGTCAAGAAACTT(GATTAC	723
Sbjct	1645	CTGTCGCAGTG		CATGTAGCCACCAAZ	AGTCAAGAAACTT	I I I I I I GATTAC	1586
Query	724	GCAACGCTCCT	CGTCCTCGGGATCTGT	GTCGACAATCTGGA(CGCGATACCACACACACACACACACACACACACACACACA	ATCATT	783
Sbjct	1585	GCAACGCTCCT	cgtcctcgggatctgt	ĠţĊĠĸĊĸĸţĊţĠĠĸĊ	ceceataccacacac	AtcAtt	1526

Query	784 1525	GATGGGTATCACGCACACGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGT	843
Sbjct Query	844	ĠĂŦĠĠĠŦĂŦĊĂĊĠĊĂĊĂĊĠĠĊĂĊŦĂĂĠĊŦĊĊĂĂĂĊŦĠĠĠĊĂĠĊĂĂŦĠĠĊĠĊĊŦĊĊĂŦĠĠŦ GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	1466 903
Sbjct	1465	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	1406
Query	904	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	963
Sbjct	1405	cedetectedateaaaatateceaccaeataecedcactcactaccacatcettett	1346
Query	964	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT	1023
Sbjct Query	1345 1024	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1286 1083
Sbjct	1285	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1226
Query	1084	CAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1143
Sbjct	1225	caaacgttgacggatcatggccagggcgcatcaatctcgctctccgttccctcaatggt	1166
Query	1144	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1203 1106
Sbjct Query	1165 1204	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1263
Sbjct	1105	GGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGAT	1046
Query	1264	CGGGAAGAGGAACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGGCAAGCTGGA	1323
Sbjct	1045	cegeaagadetcetaegtettttcacecetetcecetecedaecececedaece	986
Query	1324	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC	1383
Sbjct Query	985 1384	TCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATC CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	926 1443
Sbjct	925	CACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTC	866
Query	1444	CTGATCCTGCTCGAGCTCCTCGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTC	1503
Sbjct	865	ctgatcctgctcgagctcctgatcggcctccttcttcgagggctcctccttcct	806
Query Sbjct	1504 805	ACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1563 746
Query	1564	TGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTGGGT	1623
Sbjct	745		686
Query	1624	AGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGA	1683
Sbjct	685	AĠĊĊŢŢĀĊĠĀŢŢĠŢĀĠĀĀĠĠĀŢĀĊĠĊĠŢĠŢĀŢŢŢĀĊĊĠĀĀŢĊĠĠĠŢĀĀĀŢĊĀĊĠŢĠĠĊĠĀ	626
Query Sbjct	1684 625	CGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTAT	1743 566
Query	1744	CTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCGTCC	1803
Sbjct	565		506
Query	1804	ATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	1863
Sbjct	505	ATTGCTCTGGATTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTT	446
Query Sbjct	1864 445	CTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTT	1923 386
Query	1924	ÇĄŢÇĢĄÇŢŢĢÇÇĢĄÇŢĢÇŢĢŢĢĢÇĄĢÇŢŢĢÇÇĄŢŢÇŢĢÇĄĢĢĄÇŢÇÇĢŢŢĢĢÇÇŢŢ	1983
Sbjct	385	CATCGACTTGCTGGCCGACTGCTGTGGCAGCTTTGCCATTCTGCAGGACTCCGTTGGCCTT	326
Query	1984	GCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTC	2043
Sbjct	325	ĠĊĠĊĠĊĊŦĠĊĀĊĀĠŦŦĠĠŦŦĊĀĀŦĊĠĀĊĠĀĠŦĊĀŦŦĠĀŦĠĠĊĊĠĀŦĠĀĠŦĊĊŦĊĠŦĊĠŦĊ	266
Query Sbjct	2044 265	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	2103 206
Query	2104	ŢĄÇĄÇÇĢĢÇĄĢŢĢĄĢĄĢŢĄĢĄĢŢĄĢĄĢĢĄÇĢĄÇÇĢĢĄŢĄÇĄŢŢŢŢÇĢÇŢĢĄĄŢĄŢŢĢ	2163
Sbjct	205	TACACCGGGCAGTGAGAGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	146
Query	2164	AAAGAT 2169 	
Sbjct	145	AAAGAT 140	

Drosophila yakuba uncharacterized protein (Dyak\GE16815), mRNA

Sequence ID: **ref|XM_002099976.2|** Length: 3785 Number of Matches: 1 Range 1: 85 to 2438

Score		Expect	Identities	Gaps	Strand	Frame
3319 bit	s(1797)	0.0()	2197/2385(92%)	47/2385(1%)	Plus/Minus	
Feature	s:					
Query	118	TTTCTTTGTTT	TG-AGGCCTCTGCAC	TTGCCAGTTCTTTTG	GAATCGGGCAATT	GCTATT 176
Sbjct	2438	$\frac{1}{2}$	rtgeegectteteer	ttgccagttctttd	GAATCGGTCAATT	GCTATA 2379
Query	177	TGCTGTGTGCT	ACATGCTACATGCTA	ACTGCAAAAGCTGCT	AACGAAATCCTTA	ATCCGA 236
Sbjct	2378	TĠĊTATĠ		AĊŢĠĊĀĀĀĀĠĊŢĠĊĀ		-тĠ- 2332
Query	237		GGAGCCTGTTGCGCA!			
Sbjct	2331	ÀTCCG-À			TTTGTTGCAC	
Query	297		TGGGTTTGAGTGATT			ĪĪĪĪĪĪ
Sbjct	2285 357		'TGGGTTTGAGTGATT 'AGTTGAGTTGTTCAC			TATAGT 2226 ATTTGG 416
Query Sbjct	2225		AGTTGAGTTGTTCAC 			
Query	417		CCGACCAGCTCCTTA			
Sbjct	2165				TTATTGGGACCTA	 GGGATG 2106
Query	477	ÇĢĄĄŢĄĄĄAĄĢ	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	ŢĢĄÇŢĄŢŢАŢĄĢÇÇĢ	ĢÇĢ Ā ÇŢŢĢŢĢÇŢŢ	ĢÇĀĀĢĀ 536
Sbjct	2105	CGAATAAATAG	ATTTCTGGTATGTTG	TGACTATTGTAGCCG	GCGACTTGTGCTT	GCAAGA 2046
Query	537	CAATGCCTTTG	GTAAGTTTGTTGAGG	ATTTCGGCCGCCTCA	ATGGACCAGGTGC	CACCGA 596
Sbjct	2045	CAATGCCTTTG	gdtaagttggttaagg	Attteggeegeeteg	AtgGACCAGGTGC	CACCGA 1986
Query	597	TGGGCTCAATG	TTGGACAGGATGCAT	TCGGTGGACTGGAAG	GGCACATTCATGA	AATCGG 656
Sbjct	1985	tdddctcaatd	sttggacaggatgcat	tcggtggcctggyyg	ĠĠĊĀĊĀŦŦĊĀŦĠĀ	AATCGG 1926
Query	657		CGCAGTGTGTTGAAG! 			
Sbjct	1925		ĊĠĊĀĠŦĠŦĠĊŦĠĀĀĠ			
Query	717		ACGCTCCTCGTCCTCG			
Sbjct Query	1865 777		ACGCTCCTCGTCCTCG GGTATCACGCACACG			
Sbjct	1805		GGTATCACGCACACG 			
Query	837		TAGCTATCGTACAGC			
Sbjct	1745	CCATGGTGGAG	TAGCTATCGTACAGC	TGCTTCTGCAGCATA	GGCAACGATGGAT	 GCGAGG 1686
Query	897	ĢĄŢĢÇĄĢÇĢĢG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	Т ĢÇĢĄСÇÇĄĢĄТĄĢÇ	АССВСАСТСАСТА	ССАСАТ 956
Sbjct	1685	GATGCAGCGGA	tgctggatgaaaaca	TGCGATCCAGAAAGC	ACCGCACTCACCA	CCACAT 1626
Query	957	CGTTGTTGATG	CCCTCAATCAGTTTC	AGTTGTAGATTGTAG	AGGCTTTCGGTCG	AAAGAG 1016
Sbjct	1625	CGTTGTTGATG	ccctcgatcacttc	AGTTGTAGATTGTAG	AGGGTTTCGTTCG	AAAGAG 1566
Query	1017	GAACTATGGTC	TGGGGAAGCGCAAAG	TGGATGCGTTGCATG	GTGAAGTTCGGAT	AGCGCT 1076
Sbjct	1565	ĠĀĀĊŢĀŢĠĠŢĊ	:tĠĠĠĠAAĠĊĠĊAAAĠ	†ggatgcgttgcatg	ĠŦĠĀĀĠŦŦĊĠĠĀŦ	
Query	1077		CGTTGACGGATCATG	11111111111111		
Sbjct	1505		\¢Ġ††ĠA¢ĠĠA†¢A†Ġ			
Query	1137		ATGCGCACCTTGCCC			
Sbjct	1445 1197	CAATGGTGCAG	GATGCGCACCTTACCC CTTGATTTGGTTAATA	ĠĂĠŦĂĠĠĠĂŦŦĊŦŦĀ		
Query Sbjct	1197		TTGATTTGGTTAATA 			
Query	1257		;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;			
Sbjct	1325		ZAAGAGGAACTCGTAG			
Query	1317		CTTGCCAGAATCGCCC			

Sbjct	1265	AGCTGGATCCTTTGCCAGAATCGCCCGATTGCACGCTGCAAATGCTCAGCGATGGACTGG	1206
Query	1377	CCGCATCCACATTGCGCTTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCG	1436
Sbjct	1205	ccccatccacattcccccttccccccccccccccccccc	1146
Query	1437	TCTGCTCCTGATCCTGCTCGAGCTCCTCCTGATCGGCCTCCTTCTTGGAGG	1487
Sbjct	1145	TCTGCTCATCCTGATCGAGCTCGAGCTCCTGATCAGCCTCCTTCTTGGAGGACTCCTCCT	1086
Query	1488	G-CTCCTCCTTGGGCTCACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGT	1541
Sbjct	1085	TGGAAĠCĊŤŢĊŤĊĊŤŤĠĠĠĊŤĊĂĊĂĠŤŤĠŤŤĠŤŤĊŤĠĊŤĊĠĊĂĊŤĊĊŤŤĠĠŤĠĠŤĠŤĀĠŤ	1026
Query	1542	TGGTATCCAGGAAGGAGTTCTCTGGCGATATTTTTGGGTGTGCGCGTGGCCTTAATCACCA	1601
Sbjct	1025	TĠĠŦĀŦĊĊĀĠĠĀĀĠĠĀĠŦŦĊŦĊŦĠĠĊĠĀŦĀŦĊŦŦĠĠĠŦĠŦĠĊĠŦĠŦĠĠĊĊŦŦĠĀŦĊĀĊĊĀ	966
Query	1602	CCGGTTCCACCGTCTTTTGGGTAGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCG	1661
Sbjct	965 1662	CCGGTTCCACCGTCTTTTGGCTAGCCTTACGATTGTGGAAGGATACGCGTGTGTTTACCG AATCGGTAAATCACGTGGCGACGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTG	906 1721
Query Sbjct	905	AATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTG	846
Query	1722	TCTTGTGTTCGGCATCCTGTATCTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGAT	1781
Sbjct	845	TCTTGTGCTCGGCGTCCTGTATCTTTGACTTCAGCATTTCGGAATCGATCTGCTGCTGAT	786
Query	1782	 Ģ СŢŢĢĊĊĄŢŢŢĢĄĄĠŢĠĊĠŢĊĊĄŢŢĠĊŢĊŢĠĠĄŢŢŢŢĠĄŢŢĠĠŢĠĊŢĠĄŢŢŢĄĊĊĄŢĄĊĄ	1841
Sbjct	785	GCTTGCCATTTGAAGTGCGTCCATTGCTCTGTATTTTGATTGGTGCTGATTTACCATACA	726
Query	1842	ACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGT	1901
Sbjct	725	ACATGGTTGTGGGACTATCCTTCTCGTCACTGCTACTTCCGTTTCCGCTCCCGCTTCCGT	666
Query	1902	TAACTAAAGTTCCGTTGATGTTCATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCAT	1961
Sbjct	665	tgactatagttccattgatgttcatcgacttgctggccggctgctgctgcdgcagtttaccat	606
Query	1962	TCTGCAGGACTCCGTTGGCCTTGCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGA	2021
Sbjct	605	tctgcaggacaccgttgccttgcccctgcacactgcctcactccactccactccactccactcccccccc	546
Query	2022	TGGCCGATGAGTCCTCGTCGGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACC	2081
Sbjct	545	TĠĠĊĊĠĂŦĠĀĠŦĊĊŦĊĠŦĊĠŦĊĠĠĠĊŦŦĠŦĊŦĀĀĀĊĠĂŦŦŦŦŦĀŦŦŦĊŦĀĊĠĊĊĠĀĀĀĊĊ	486
Query	2082	AAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGG	2141
Sbjct	485	AAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGG	426
Query	2142425	ATACCATTTTCGCTGAATATTGAAAGATCTTTGTGAACCGCTTGGGTAACTTATTTTGCT	2201 366
Sbjct Query	2202	ATACCATTTCGCTGAATATTGAAGGATCTTTGGGAACCGCTTGGGTAACTTATTTTGTT CACTATCTTTGGGTGCTTTCAAAGCTATCTACTGCACACGCGAGTTGTGTATTGTTTTTG	2261
Sbjct	365	CACTATCTTTGGGTGATTTCAATGCTATCTACCGCACACGCGTGTTGGGTATTGTTTTTG	306
Query	2262	СТТАТТТССТССССССССССССССССССССССССССССС	2321
Sbjct	305	ATTATTTACTGGCGATTTATTGTCGTTTTCTCAACGCTACGGAGCTGCACGAATTAAACA	246
Query	2322	ҪĢŢĢŢĊŢĄĊĢŢŢĊÇĄĊĊŢŢŢŢĄĊĄĄĄŢÇĄĊĄĄŢĄĄĊĄŢĢĢĊĢĢĊĢŢĠĊĢĠĊĄĠŢĠŢŢĠĊ	2381
Sbjct	245	CGTGTCTACGTTCCACCTTTTACAAATCACAATAACATGGCCGGCGTGCGGCAGTGTTGC	186
Query	2382	CATGCATCCGCAAAACTCTGGCAATCGGAGCTGCCTGCTTAATCACCCGCACTCGCGATG	2441
Sbjct	185	CATCCCTTCGCGAAACTCTGGCAATCGGAGCTGCCTGCTTAATCACGCGCACTCGCGGCA	126
Query	2442	GCCAAATCCTCGAATTACAAGAGCCTTTGTGCACACaaaaaaaaa 2486	
Sbjct	125	GTCAAATGTCCGACTTGCAAGCGCCGTGCACA-AAAAAAAA 85	

Synthetic construct Drosophila melanogaster clone BS10696 encodes yu-RA Sequence ID: **gb|FJ636724.1|** Length: 1790 Number of Matches: 1 Range 1: 17 to 1778

Score		Expect	Identities	Gaps	Strand	Frame	
3249 bits(1759)		0.0()	1761/1762(99%)	0/1762(0%)	Plus/Minus		
Features	S :						
Query	387	GCTGTTAGTCA	CTCATCTCCACCCATTT	GGCGAGCTTTCTGC	CCGACCAGCTCCTT	'ATTGA 	446

Sbjct	1778	GCTTTTAGTCACTCATCTCCACCCATTTGGCGAGCTTTCTGCCGACCAGCTCCTTATTGA	1719
Query	447	TAAAGATTACATTATTGGGACCTAGGGATGCGAATAAAAAGATTTCTGGTAGGTTGTGAC	506
Sbjct	1718	TAAAGATTACATTATTGGGACCTAGGGATGCGAATAAAAAAGATTTCTGGTAGGTTGTGAC	1659
Query Sbjct	507 1658	TATTATAGCCGGCGACTTGTGCTTGCAAGACAATGCCTTTGGTAAGTTTGTTGAGGATTT	566 1599
Query	567	CGGCCGCCTCAATGGACCAGGTGCCACCGATGGGCTCAATGTTGGACAGGATGCATTCGG	626
Sbjct	1598	CGGCCGCTCAATGGACCAGGTGCCACCGATGGGCTCAATGTTGGACAGGATGCATTCGG	1539
Query	627	TGGACTGGAAGGGCACATTCATGAAATCGGTGCGAATCTGTCGCAGTGTGTTGAAGCCGA	686
Sbjct	1538	tegactegaaegecacatteateaaateegeteegaateteteteegetetetete	1479
Query	687	CATTCATGTAGCCACCAAAGTCAAGAAACTTGATTACGCAACGCTCCTCGTCCTCGGGAT	746
Sbjct Query	1478 747	CATTCATGTAGCCACCAAAGTCAAGAAACTTGATTACGCAACGCTCCTCGTCCTCGGGAT CTGTGTCGACAATCTGGACGCGATACCACACATCATTGATGGGTATCACGCACACGCAC	1419 806
Sbjct	1418	CTGTGTCGACAATCTGGACGCGATACCACACATCATTGATGGGTATCACGCACACGCAC	1359
Query	807	ТААĢСТССАААСТĢĢĢCAĢCAATĢĢCĢCCTCCATĢĢTĢĢAĢTAĢCTATCĢTACAĢCTĢCT	866
Sbjct	1358	TAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGTGGAGTAGCTATCGTACAGCTGCT	1299
Query	867	TCTGCAGCAAAGGCAACGATGGATGCGAGGGATGCAGCGGGTGCTGGATGAAAATATGCG	926
Sbjct	1298 927	TCTGCAGCAAAGGCAACGATGGATGCGAGGGATGCAGCGGGTGCTGGATGAAAATATGCG ACCCAGATAGCACCGCACTCACTACCACATCGTTGTTGATGCCCTCAATCAGTTTCAGTT	1239 986
Query Sbjct	1238	ACCAGATAGCACCGCACTCACTACCACATCGTTGTTGATGCCCTCAATCAGTTTCAGTT	1179
Query	987	ĢŢĄĢĄŢŢĢŢĄĢĄĢĢÇŢŢŢÇĢĢŢÇĢĄĄĄĢĢĄĄÇŢĄŢĢĢŢÇŢĢĢĢĢĄĄĢÇĢÇĄĄĄĢŢĢĢĄ	1046
Sbjct	1178	GTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTATGGTCTGGGGAAGCGCAAAGTGGA	1119
Query	1047	TGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGGCAAACGTTGACGGATCATGGCCA	1106
Sbjct	1118	ŤĠĊĠŤŤĠĊĂŤĠĠŤĠĂĂĠŤŤĊĠĠĂŤĂĠĊĠĊŤŤĠĠĊĊĠĠĊĂĂĂĊĠŤŤĠĂĊĠĠĂŤĊĂŤĠĠĊĊĀ	1059
Query Sbjct	1107 1058	GGGCGCATCAATCTCGCTCTCCGTTCCCTCAATGGTACAGATGCGCACCTTGCCCGAGT	1166 999
Query	1167	ĄĢĢĢĀTTÇTTĢÇÇTĀÇĀĢĀÇĀÇĢÇTĢĢÇÇĀĢĢGTÇTTĢĢCÇTTĢĀTTTĢĢTTĀĀTĀĀĀÇĢ	1226
Sbjct	998	AGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTTGGCCTTGATTTGGTTAATAAACG	939
Query	1227	CCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGATCGGGAAGAGGAACTCGTAGGTGG	1286
Sbjct	938	ccccctrcccccccccccccccccccccccccccccccc	879
Query Sbjct	1287 878	TTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGATCCCTTGCCAGAATCGCCCGATT	1346 819
Query	1347	GCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTACCAT	1406
Sbjct	818	GCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTACCAT	759
Query	1407	TGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTCCTGATCCTGCTCGAGCTCCTCCT	1466
Sbjct	758	tĠċtAtċċAċċAċttċċttċċttċAĠċAċċĠtċtĠċtċċtĠAtċċtĠċĠĠĠċtċċtċċt	699
Query	1467 698	GATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTCACAGTTGTTGTTCTGCTCGCACT	1526 639
Sbjct Query	1527	GATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTCACAGTTGTTGTTCTGCTCGCACT CCTTGTTGGTGTAGTTGGTATCCAGGAAGGAGTTCTCTGGCGATATTTTGGGTGTGCGCG	1586
Sbjct	638	CCTTGTTGGTGTAGTTGGTATCCAGGAAGGAGTTCTCTGGCGATATTTTGGGTGTGCGCG	579
Query	1587	TGGCCTTAATCACCACCGGTTCCACCGTCTTTTTGGGTAGCCTTACGATTGTAGAAGGATA	1646
Sbjct	578	tggccttaatcaccaccgttccaccgtcttttgggtagccttacgattgtagaaggata	519
Query	1647	CGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAATCCTCGT	1706
Sbjct Query	518 1707	CGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAATCCTCGT CTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTATCTTTGACTTCAGTATTTCGGAAT	459 1766
Sbjct	458	CTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTATCTTTGACTTCAGTATTTCGGAAT	399
Query	1767	CGATCTGCTGATGCTTGCCATTTGAAGTGCGTCCATTGCTCTGGATTTTGATTGGTG	1826
Sbjct	398	cgatctgctgctgatgctttgccatttgaagtgcgtccattgctctggattttgattggtg	339
Query	1827	CTGATTTACCATACAACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTACTTCCGCTAC	1886
Sbjct	338	ĊŦĠĂŦŦŦĂĊĊĂŦĂĊĂĂĊĂŦĠĠŦĂĠŦĠĠĠĠĊŦĠŦĊĊŦŦĊŦĊĂŦĊĂĊŦĠĊŦĂĊŦŦĊĊĠĊŦĂĊ	279

Query	1887	CGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTTCATCGACTTGCTGGCCGACTGCT	1946
Sbjct	278	cccttcccctacccttaactaaacttcccttcatctatccacttcctcc	219
Query	1947	GTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTTGCGCGCCCTGCACAGTTGGTTCAA	2006
Sbjct	218	GTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTTGCGCGCCCTGCACAGTTGGTTCAA	159
Query	2007	TCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAACAATTTTTAT	2066
Sbjct	158	TCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAACAATTTTTAT	99
Query	2067	ATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGAGGTAGA	2126
Sbjct	98	Atctacccccaaaaccaaaacccccaactataaatcctacacccccc	39
Query	2127	GTAGAGGACGACCGGATACCAT 2148	
Sbjct	38	GTAGAGGACGACCGGATACCAT 17	

Synthetic construct Drosophila melanogaster clone BO11096 encodes yu-RA

Sequence ID: **gb|FJ631998.1|** Length: 1789 Number of Matches: 1 Range 1: 17 to 1771

Score		Expect	Identities	Gaps	Strand	Frame	
3241 bit	ts(1755)	0.0()	1755/1755(100%)	0/1755(0%)	Plus/Minus		
Feature	s:						
Query	394	GTCACTCATCT	CCACCCATTTGGCGAG	CTTTCTGCCGACCAG	CTCCTTATTGAT	AAAGAT	453
Sbjct	1771	GTCACTCATCT	ccacccatttggcgag	ctttctgccgaccag	ctccttattgatz	AAAGAT	1712
Query	454	TACATTATTGG	GACCTAGGGATGCGAA'	TAAAAAGATTTCTGG 	TAGGTTGTGACT	ATTATA 	513
Sbjct	1711	tacattattgg	ĠĸĊĊŦĸĠĠĠĸŦĠĊĠĸĸ	taaaaagatttctgg	taggttgtgagt	Aተተልተል	1652
Query	514	GCCGGCGACTT	GTGCTTGCAAGACAAT	GCCTTTGGTAAGTTT 	GTTGAGGATTTC(573
Sbjct	1651		ĠŦĠĊŦŦĠĊĀĀĠĀĊĀĀŦ				1592
Query	574		AGGTGCCACCGATGGG	11111111111111			633
Sbjct	1591		AĠĠŦĠĊĊĂĊĊĠĂŦĠĠĠ				1532
Query	634		TCATGAAATCGGTGCG.	11111111111111			693
Sbjct	1531		rtcatgaaatcggtgcg.				1472753
Query Sbjct	694 1471		AGTCAAGAAACTTGAT' AGTCAAGAAACTTGAT'	11111111111111			1412
Query	754		.CGCGATACCACACATC				813
Sbjct	1411			11111111111111			1352
Query	814	ҪӒӒӒҪҬ҅Ҫ҄ҪҪӒ	ĢÇĄĄТĢĢÇĢÇÇТÇÇĄТ	ĢĢŢĢĢĀĢŢĀĢÇŢĀŢÇ	Ģ ŢĀÇĀĢÇŢĢÇŢŢ(СТССАС	873
Sbjct	1351	CAAACTGGGCA	GCAATGGCGCCTCCAT		GTACAGCTGCTT0		1292
Query	874	CAAAGGCAACG	ATGGATGCGAGGGATG	CAGCGGGTGCTGGAT	GAAAATATGCGAG	CCCAGA	933
Sbjct	1291	CAAAGGCAACG	ATGGATGCGAGGGATG	L L L L L L L L L L L L L L L L L L L	GAAAATATGCGAG	CCAGA	1232
Query	934	TAGCACCGCAC	TCACTACCACATCGTT	GTTGATGCCCTCAAT	CAGTTTCAGTTG	PAGATT	993
Sbjct	1231	† A G C A C C G C A C	tcactaccacatcgtt	gttgatgccctcaat	cagtttcagttg:	ragatt	1172
Query	994	GTAGAGGCTTT	CGGTCGAAAGAGGAAC'	TATGGTCTGGGGAAG 	CGCAAAGTGGAT(GCGTTG 	1053
Sbjct	1171	ĠŦĀĠĀĠĠĊŦŦŦ	'ĊĠĠϮĊĠAAAĠAĠĠAAĊ'	tatĠĠtĊtĠĠĠĠāaĠ	ĊĠĊAAAĠŦĠĠAŦŒ		1112
Query	1054	CATGGTGAAGT	TCGGATAGCGCTTGGC	CGGCAAACGTTGACG 	GATCATGGCCAG(1113
Sbjct	1111		TĊĠĠÀTÄĠĊĠĊŦŦĠĠĊ				1052
Query	1114		TCTCCGTTCCCTCAAT	11111111111111			1173
Sbjct	1051		TCTCCGTTCCCTCAAT				992
Query	1174		ACACGCTGGCCAGGGT	11111111111111			1233
Sbjct	991		·ACACGCTGGCCAGGGT				932
Query	1234		.GGTGACCAATCAAGCT(.CCTCACCAATCAACCT				1293
Sbjct	931	GCGGCCGTACA	.GGTGACCAATCAAGCT(AAJJAJAAJJJJIAJ	CICGTAGGTGGT.	LIICAC	872

Query	1294	GCGTGTCGCCTCCGAGCGCGGCAAGCTGGATCCCTTGCCAGAATCGCCCGATTGCACACT	1353
Sbjct	871	GCGTGTCGCCTCCGAGCGCGCAAGCTGGATCCCTTGCCAGAATCGCCCGATTGCACACT	812
Query	1354	GCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTACCATTGCTATC	1413
Sbjct	811	GCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTACCATTGCTATC	752
Query	1414	CACCACTTCCTCCTTCAGCACCGTCTGCTCCTGATCCTGCTCGAGCTCCTCCTGATCGGC	1473
Sbjct	751	caccacttcctcctcaccaccactctcctcctcatcctcacctcacctcct	692
Query	1474	CTCCTTCTTGGAGGGCTCCTCCTTGGGCTCACAGTTGTTGTTCTGCTCGCACTCCTTGTT	1533
Sbjct	691	ctccttcttggagggctctcttgggctcacagttgttgttctgctccctcc	632
Query	1534	GGTGTAGTTGGTATCCAGGAAGGAGTTCTCTGGCGATATTTTGGGTGTGCGCGTGGCCTT	1593
Sbjct	631	ĠĠŦĠŦĀĠŦŦĠĠŦĀŦĊĊĀĠĠĀĀĠĠĀĠŦŦĊŦĊŦĠĠĊĠĀŦĀŦŦŦŦĠĠĠŦĠŦĠĊĠĊĠŦĠĠĊĊŦŦ	572
Query	1594	AATCACCACCGGTTCCACCGTCTTTTGGGTAGCCTTACGATTGTAGAAGGATACGCGTGT	1653
Sbjct	571	AATCACCACCGGTTCCACCGTCTTTTGGGTAGCCCTTACGATTGTAGAAGGATACGCGTGT	512
Query	1654	ATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAATCCTCGTCTATGGA	1713
Sbjct	511	ATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAATCCTCGTCTATGGA	452
Query	1714	GCAGAGTGTCTTGTGTTCGGCATCCTGTATCTTTGACTTCAGTATTTCGGAATCGATCTG	1773
Sbjct	451	ĠĊĀĠĀĠŦĠŦĊŦŦĠŦĠŦŦĊĠĠĊĀŦĊĊŦĠŦĀŦĊŦŦŦĠĀĊŦŦĊĀĠŦĀŦŦŦĊĠĠĀĀŦĊĠĀŦĊŦĠ	392
Query	1774	CTGCTGATGCTTGCCATTTGAAGTGCGTCCATTGCTCTGGATTTTGATTGGTGCTGATTT	1833
Sbjct	391	ĊŦĠĊŦĠĂŦĠĊŦŦĠĊĊĂŦŦŦĠĂĂĠŦĠĊĠŦĊĊĂŦŦĠĊŦĊŦĠĠĂŦŦŦŦĠĂŦŦĠĠŦĠĊŦĠĂŦŦŦ	332
Query	1834	ACCATACAACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTACTTCCGCTACCGCTTCC	1893
Sbjct	331	ACCATACAACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTACTTCCGCTACCGCTTCC	272
Query	1894	GCTACCGTTAACTAAAGTTCCGTTGATGTTCATCGACTTGCTGGCCGACTGCTGTGGCAG	1953
Sbjct	271	ĠĊŦĂĊĊĠŦŦĂĂĊŦĂĂĂĠŦŦĊĊĠŦŦĠĂŦĠŦŦĊĂŦĊĠĂĊŦŦĠĊŦĠĠĊĊĠĂĊŦĠĊŦĠŦĠĠĊĀĠ	212
Query	1954	CTTGCCATTCTGCAGGACTCCGTTGGCCTTGCGCGCCTGCACAGTTGGTTCAATCGACGA	2013
Sbjct	211	cttgccattctgcaggactcgcttgcccttgcacagttgcacagttcacagtcgacga	152
Query	2014	GTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAACAATTTTTATATCTACG	2073
Sbjct	151	ĠŦĊĂŦŦĠĂŦĠĠĊĊĠĂŦĠĂĠŦĊĊŦĊĠŦĊĠŦĊĠĠĠĊŦŦĠŦĊŦĂĂĂĊĂĂŦŦŤŦŦĀŦĀŦĊŦĀĊĠ	92
Query	2074	CCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGAGGTAGAGTAGAGG	2133
Sbjct	91	CCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGAGGTAGAGTAGAGG	32
Query	2134	ACGACCGGATACCAT 2148	
Sbjct	31	AcGAccGGATACCAT 17	

Drosophila erecta uncharacterized protein (Dere\GG18497), mRNA Sequence ID: **ref|XM_001976927.2|** Length: 2106 Number of Matches: 1 Range 1: 23 to 2106

Score		Expect	Identities	Gaps	Strand	Frame	
3037 bit	s(1644)	0.0()	1945/2090(93%)	21/2090(1%)	Plus/Minus		
Features	S:						
Query	374	GTTGTTCACTA	AGGCTGTTAGTCACTC	ATCTCCACCCATTTG	GCGAGCTTTCTG	CCGACC	433
Sbjct	2106	GTTGTTCACTA	AGGCTGTTAGTCACGC	Atctccaccactr	ĠĊĠĀĠĠŦŦŦĊŦĠ	GCGACC	2047
Query	434	AGCTCCTTATT	GATAAAGATTACATTA	TTGGGACCTAGGGAT	GCGAATAAAAAG	ATTTCT	493
Sbjct	2046	AGCTCCTTATT	gataaagattacatta	ttgggycctygggy	gcgyytyyy	Atttct	1987
Query	494	GGTAGGTTGTG	ACTATTATAGCCGGCG	ACTTGTGCTTGCAAG	ACAATGCCTTTG	GTAAGT 	553
Sbjct	1986	ĠĠŦĀŦĠŦŦĀŦĠ	actattgtagccgcc	sacttgtgcttgcaag	sacaatgcctttg	ĠţaaĠţ	1927
Query	554	TTGTTGAGGAT	TTCGGCCGCCTCAATG	GACCAGGTGCCACCG	ATGGGCTCAATG	TTGGAC	613
Sbjct	1926	tgĠttĠAĠĠAt	rttcggccgcctcgate	ĠĸĊĊĸĠĠŦĠĊĊĸĊĊĠ	atgggctcaatg	ttĠĠĀĊ	1867
Query	614	AGGATGCATTC	GGTGGACTGGAAGGGC	CACATTCATGAAATCG	GTGCGAATCTGT	CGCAGT	673
Sbjct	1866	AĠĠĀŦĠĊĀŦŦĊ	deddeddaddeddaddaddaddadddadddadddaddda	zacarrcargaaarcg	sgtgcggatctgt	ĊĠĊĀĠŦ	1807
Query	674	GTGTTGAAGCC	GACATTCATGTAGCCA	CCAAAGTCAAGAAAC	TTGATTACGCAA	CGCTCC	733

Sbjct	1806	GTGCTGAAACCGACATTCATGTAGCCACCAAAGTCGAGGAATTTGACCAGGCAACGCTCC	1747
Query Sbjct	734 1746	TCGTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACACATCATTGATGGGTATC	793 1687
Query	794	AÇĢÇAÇAÇĢĢÇAÇTAAGÇTÇÇAAAÇTĢĢĢÇAĢÇAATĢĢÇĢÇÇÇTÇÇATĢĢTĢĢAĢTAĢÇTA	853
Sbjct	1686	ACGCATACGGCACTGACCTCCAAACTGGGCAGCAAGGGCGCCTCCATGGTGGAGTAGCTA	1627
Query	854	TCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATGCGAGGGATGCAGCGGGTGCTGG	913
Sbjct Query	1626 914	TĊĠŦĀĊĀĠĊŦĠĊŦŦĊŦĠĊĀĠĊĀŦĀĠĠĊĀĀĊĠĀŦĠĠĀŦĠĊĠĀĀĠĠĀŦĠĊĀĠĊĠĠĠŦĠĊŦĠĠ ATGAĀĀĀTĀTGCGĀCCCĀGĀTĀGCĀCCGCĀCTĀCCĀCĀCĀTGTTGTTGĀTGCCCTCĀ	1567 973
Sbjct	1566	ATGAAAACATGCGACCAGAAAGCACCGCACTAACCACCACATCGTTGATGCCCTCG	1507
Query	974	ATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTATGGTCTGGGGA	1033
Sbjct	1506	Atcachttcachtchcatachtchachcccatachtccachtccachachccachachccachachccachachccachach	1447
Query Sbjct	1034 1446	AGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGGCAAACGTTGA 	1093 1387
Query	1094	CGGATCATGGCCAGGGCGCATCAATCTCGCTCTCCGTTCCCTCAATGGTACAGATGCGC	1153
Sbjct	1386	CGGATCATGGCCAGAGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGTGCAGATGCGC	1327
Query	1154 1326	ACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTTGGCCTTGATT	1213 1267
Sbjct Query	1214	TGGTTAATAAACGCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGATCGGGAAGAGG	1207
Sbjct	1266	TGGTTTATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAGGCTGATAGGGAAGAGG	1207
Query	1274	AACTCGTAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGGCAAGCTGGATCCCTTGCCA	1333
Sbjct Query	1206 1334	ÄÄĊTĊĠTÄACTĠĠTCTTĊÄĊĠĊĠTĠTĊĠĊĊŤĊĊĠÄĠĊĠĊĠĠĊÄÄĠĊTĠĠÄTĊĊTTTĠĊĊÄ GAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGC	1147 1393
Sbjct	1146	GAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGC	1087
Query	1394	TTCTGATTACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTCCTGATCCTGC	1453
Sbjct	1086	††c†gg††gcca††gc†a†ccaccacacacacacacacac	1027
Query Sbjct	1454 1026	TCGAGCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGG	1499 967
Query	1500	-GCTCACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1558
Sbjct	966	GGCTCACAATTGTTTTTGCTCACACTCCTTTGTGGCATAGTTGGTATCCAGGAAAGAG	907
Query Sbjct	1559 906	TTCTCTGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTT	1618 847
Query	1619	TGGGTAGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGT	1678
Sbjct	846	TGGCTAGTCTTACGATTGTGGAAGGATACGCGTGTGTTTACCGAATCGGGTAAATCGCGT	787
Query Sbjct	1679 786	GGCGACGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCC	1738 727
Query	1739	TGTATCTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTG	1798
Sbjct	726	tgtatctttgacttcagcatttctgaatcaatctgctgctgatgtttgccatttgaagtg	667
Query Sbjct	1799 666	CGTCCATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTG	1858 607
Query	1859	ŢĊĊŢŢĊŢĊĄŢĊĄĊŢĠĊŢĄĊŢŢĊĊĠĊŢAĊĊĠĊŢŢĊĊĠĊŢĄĊĊĠŢŢAĄĊŢĄĄĄĠŢŢĊĊĠŢŢĠ	1918
Sbjct	606	TCCTTCTCATCACTGCTACTTCCGCTTCCGCTTCCGTTGCCTAAAGTTCCATTA	553
Query	1919	ATGTTCATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTG	1978
Sbjct Query	552 1979	ATGTTCATCGACTTGCTGGCCGGCTGCTGTGGCAGCTTACCATTCTGCAGGACACCGTTG GCCTTGCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCG	493 2038
Sbjct	492	GCCTTGCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCG	433
Query	2039	TCGTCGGGCTTGTCTAAACAATTTTTATATCTACGCCGAAAACCAAAAGACGCCGAGTATA	2098
Sbjct	432	†cdtcdddcttdtctAAAcGAttttttAtttctAcdccdAAAAcCAAAAdAcdccdAdatAtA	373
Query	2099	AATGCTACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAA	2158

Sbjct	372	AATGCTACACCGGGCAGTGAAAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAA	313
Query	2159	TATTGAAAGATCTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCT	2218
Sbjct	312	tattgaaggatetttgggaaeegettgggtaaettatattgeteaetattttgggtget	253
Query	2219	TTCAAAGCTATCTACTGCACACGCGAGTTGTGTATTGTTTTTTTT	2278
Sbjct	252	TTCAATGCTATCGACTGCACACGCGTGTTGTGTATTGTTTTTTGCTTATTTACTGGCGATG	193
Query	2279	TACTGTCGTTTTCTCAACGCTAAAGTGCTGCACGAATTAAACACGTGTCTACGTTCCACC	2338
Sbjct	192	tAGTGTGGTTTTTTCAACGTTACAGAGCTGCACGAATTAAACACGTGTCTACGTTCCACC	133
Query	2339	TTTTACAAATCACAATAACATGGCCGGCGTGCGGCAGTGTTGCCATGCATCCGCAAAACT	2398
Sbjct	132	ttttacaaatcacaataacatggccggcgtgcggcagtgttgccatccctttgcgaaact	73
Query	2399	CTGGCAATCGGAGCTGCCTGCTTAATCACCCGCACTCGCGATGGCCAAAT 2448	
Sbict	72	CTGGCAATCGGAGCTGCCTGATCACGCGCACTCGCGGCAGCCAAAT 23	

Drosophila simulans GD16260 (Dsim\GD16260), mRNA

Sequence ID: **ref|XM_002106150.1|** Length: 1782 Number of Matches: 1 Range 1: 1 to 1782

Score		Expect	Identities	Gaps	Strand	Frame	
2837 bit	s(1536)	0.0()	1710/1788(96%)	36/1788(2%)	Plus/Minus		
Feature	s:						
Query	391	TTAGTCACTCA	TCTCCACCCATTTGGC	GAGCTTTCTGCCGAC	CCAGCTCCTTATTO	GATAAA	450
Sbjct	1782	TTAGTCACTCA	TCTCCACCCAATTTGC	GAGCTTTCTGCCGAC	ccacctccttattc	SATAAA	1723
Query	451	GATTACATTAT	TGGGACCTAGGGATGC	GAATAAAAAGATTTC	TGGTAGGTTGTG	ACTATT	510
Sbjct	1722	GATTACATTAT	rtgggacctagggatgc	GAATAAAAAGATCTC	ctggtargttgtg	Actatt	1663
Query	511	ATAGCCGGCGA	CTTGTGCTTGCAAGAC	AATGCCTTTGGTAAG	GTTTGTTGAGGATT	TTCGGC	570
Sbjct	1662		.ctrgtgcttgcaagac				1603
Query	571		ACCAGGTGCCACCGAT				630
Sbjct	1602		ACCAGGTGCCATCGAT				1543
Query	631		.CATTCATGAAATCGGT CATTCATGAAATCGGT				690 1483
Sbjct Query	1542 691		CAAAGTCAAGAAACTT		ĠŦĠŦĠŦŦĠĂĂĠĊĊŒ ĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ		750
Sbjct	1482		CAAAGTCAAGAAACTT 				1423
Query	751		GGACGCGATACCACAC				810
Sbjct	1422	GTCGACAATCT		 ATCATTGATGGGTAT	CACGCACACGGC	 ACTGAG	1363
Query	811	СТССАААСТСС	- - - - - - - - - - - - - - - - - - -	Ҫ҅҇Ҳҭ҅҄҅҄҅҄҄Ҿҭҫ҄ҫѧҫҭѧҫҁҭ	гатсетасаесте	СТТСТБ	870
Sbjct	1362	CTCCAAACTGG	GCAGCAATGGCGCCTC	CATGGTGGAGTAGCT	TATCGTACAGCTG	 CTTCTG	1303
Query	871	CAGCAAAGGCA	ACGATGGATGCGAGGG	ATGCAGCGGGTGCTG	GATGAAAATATGG	CGACCC	930
Sbjct	1302	CAGCAAAGGCA	AcGATGGATGCGAGGG	Atgcagcgggtgctd	sdatdaaaaatatdo	CGACCC	1243
Query	931	AGATAGCACCG	CACTCACTACCACATC	GTTGTTGATGCCCTC	CAATCAGTTTCAGT	TTGTAG	990
Sbjct	1242	AGATAGCACCG	cyctcyccycycytc	ĠŦŦĠŦŦĠĂŦĠĊĊĊŦĊ	cgatcagtttcag	rtgtag	1183
Query	991	ATTGTAGAGGC	TTTCGGTCGAAAGAGG	AACTATGGTCTGGGG	GAAGCGCAAAGTG(GATGCG 	1050
Sbjct	1182		ŤŤŤĊĠĠŤĊĠĂÄÄĠÄĠĠ				1123
Query	1051		AGTTCGGATAGCGCTT				1110
Sbjct	1122		AGTTĊĠĠATAĠĊĠĊŦŢ				1063
Query	1111		CGCTCTCCGTTCCCTC				11701003
Sbjct Query	1062 1171		ĊĠĊŦĊŦĊĊĠŦŦĊĊĊŦĊ .CAGACACGCTGGCCAG				1230
Sbjct	1002		CAGACACGC IGGCCAG GAGACACGCTGGCCAG				943
Query	1231		'ACAGGTGACCAATCAA				1290
Sbjct	942		ACAAGTGACCAATCAG				883

Query	1291	CACGCGTGTCGCCTCCGAGCGCGGCAAGCTGGATCCCTTGCCAGAATCGCCCGATTGCAC	1350
Sbjct	882	ĊĂĊĠĊĠŦĠŦĊĠĊĊŦĊĊĠĀĠĊĠĊĠĠĊĀĀĠĊŦĠĠĀŦĊĊĊŦŦĠĊĊĀĠĀĀŦĊĠĊĊĊĠĀŦŦĠĊĀĊ	823
Query	1351	ACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTACCATTGCT	1410
Sbjct	822	Actigcaaatigctcagcgatggactiggccgcatccacattgcgctttctgattgccattgt	763
Query	1411	ATCCACCACTTCCTCCTTCAGCACCGTCTGCTCCTGATCCTGCTCGAGCTCCTCCTGATC	1470
Sbjct	762	Atcaaccacttccttcaccaccatctcctcctcatctctctcacctctctcatc	703
Query	1471	GGCCTCCTTCTTGGAGGGCTCCTTGGG	1500
Sbjct	702	GGCCTCCTTGGAGGACTCCTCCTTGGCGGGCTCCTCCTTGGCGGGCTCCTCCTTGGC	643
Query	1501	CTCACAGTTGTTGTTCTGCTCGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGA	1560
Sbjct	642	ctcacagttgttgttctgctcgcactccttgttggtgtagttggtattccaggaagga	583
Query	1561	CTCTGGCGATATTTTGGGTGTGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTG	1620
Sbjct	582	ctctggcgatattttgggtgtgcgcgtggccttaatcaccaccggttccaccgtcttctg	523
Query	1621	GGTAGCCTTACGATTGTAGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGG	1680
Sbjct	522	GCTAGTCTTACGATTGTAGAACGAGATGCGTGTGTTTACCGAATCGGGTAAATCACGTGG	463
Query	1681	CGACGATAGATTCTCGAAATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTG	1740
Sbjct	462	cdacdatadattctcdaaatcctcdtctattdadcadadtdtcttdtctcdcctcd	403
Query	1741	TATCTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGTGCG	1800
Sbjct	402	TATCTTTGACTTCAGTATTTCGGAATCGATCTGCTGCTGATGCTTGCCATTTGAAGAGCG	343
Query	1801	TCCATTGCTCTGGATTTTGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTC	1860
Sbjct	342	tccattgctctggattttgatgggtgctgatttaccatacaacatggtagtggactgtc	283
Query	1861	CTTCTCATCACTGCTACTTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGAT	1920
Sbjct	282	cttctcatcactdctacatccdctaccdcttccdttaactaaadttccdtcdat	229
Query	1921	GTTCATCGACTTGCTGGCCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGC	1980
Sbjct	228	GTTCATCGACTTGCTGGCCGGCTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGC	169
Query	1981	CTTGCGCGCCTGCACAGTTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTC	2040
Sbjct	168	cttgcgcgcctgcacagtgggttcaatcgacgagtcattgatggccgatgagtcctcgtc	109
Query	2041	GTCGGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAA	2100
Sbjct	108	GTCGGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAA	49
Query	2101	TGCTACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCAT 2148	
Sbjct	48	TGCTACACCGGGCAGTGAGAGGTAGAGGACGACCGGATACCAT 1	

Drosophila melanogaster LD28079 full length cDNA

Sequence ID: **gb|AY061351.1|** Length: 1491 Number of Matches: 1 Range 1: 1 to 1200

Score		Expect	Identities	Gaps	Strand	Frame	
2217 bits	s(1200)	0.0()	1200/1200(100%)	0/1200(0%)	Plus/Minus		
Features	S:						
Query	4	gtgtgtgtgtg	tgtgtgtgtgtatt	tggcgagtgtgtgtt	gtttgttatgtA	ATGATT	63
Sbjct	1200	gtgtgtgtgtg	rtgtgtgtgtgtgtatt	rtggcgagtgtgtgtt	stttgttatgta	AtGAtt	1141
Query	64	AAGGGGCTCTC	TCTGGGCTCAGTCGCA	ATCTAAACAACGTAA(CAAACGTTTCAT	TTTCTT	123
Sbjct	1140	AAGGGGCTCTC	tctgggctcagtcgca	Adtetaaaeaaegtaa	CAAACGTTTCAT	դդդ сդդ	1081
Query	124	TGTTTTGAGGC	CTCTGCACTTGCCAGT	TCTTTTGGAATCGGG	CAATTGCTATTT	GCTGTG	183
Sbjct	1080	tgttttgagg	ctctgcacttgccagt	rtcttttggaatcggg	caattgctattt	gctgtg	1021
Query	184	TGCTACATGCT	'ACATGCTAACTGCAAA	AGCTGCTAACGAAAT	CCTTAATCCGAA	TCCGCA	243
Sbjct	1020	tgctycytgct	acatectaactecaaa	ryddagaeth	ccttaatccdaa	tcccc	961
Query	244	TCTTGGAGCCT	GTTGCGCAATACTCAA	GCATTCCTTTTTTGT	rgcaccgccaag	TTGCTT	303
Sbjct	960	TCTTGGAGCCT	GTTGCGCAATACTCAA	ſĠĊŖŦŦĊĊŦŦŦŦŦŦĠŦ	rgcaccgccaag	ŦŦĠĊŦŦ	901

Query	304	GATTTGGGTTTGAGTGATTGTTTAAGTTTTGCTTTTAAGTTTTCATATAGTTCTTGGT	363
Sbjct	900	GATTTGGGTTTGAGTGATTGTTTAAGTTTGCTTTTAAGTTTTCATATAGTTCTTGGT	841
Query	364	TGCTAGTTGAGTTGTTCACTAAGGCTGTTAGTCACTCATCTCCACCCATTTGGCGAGCTT	423
Sbjct	840	tgctagttgagttgttcactaaggctgttagtcactcatctccaccattttggcgagctt	781
Query	424	TCTGCCGACCAGCTCCTTATTGATAAAGATTACATTATTGGGACCTAGGGATGCGAATAA	483
Sbjct	780	tctgccgaccagctccttattgataaagattacattattgggacctagggatgcgaataa	721
Query	484	AAAGATTTCTGGTAGGTTGTGACTATTATAGCCGGCGACTTGTGCTTGCAAGACAATGCC	543
Sbjct	720	AAAGATTTCTGGTAGGTTGTGACTATTATAGCCGGCGACTTGTGCTTGCAAGACAATGCC	661
Query	544	TTTGGTAAGTTTGTTGAGGATTTCGGCCGCCTCAATGGACCAGGTGCCACCGATGGGCTC	603
Sbjct	660	††††† †††† †††† ††† ††† †† †† †† †† †† †† †† †† † †	601
Query	604	AATGTTGGACAGGATGCATTCGGTGGACTGGAAGGGCACATTCATGAAATCGGTGCGAAT	663
Sbjct	600	AATGTTGGACAGGATGCATTCGGTGGACTGGAAGGGCACATTCATGAAATCGGTGCGAAT	541
Query	664	CTGTCGCAGTGTTGAAGCCGACATTCATGTAGCCACCAAAGTCAAGAAACTTGATTAC	723
Sbjct	540	ĊŢĠŢĊĠĊĀĠŢĠŢĠŢŢĠĀĀĠĊĊĠĀĊĀŢŢĊĀŢĠŢĀĠĊĊĀĊĊĀĀĀĠŢĊĀĀĠĀĀĀĊŢŢĠĀŢŢĀĊ	481
Query	724	GCAACGCTCCTCGTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACACATCATT	783
Sbjct	480	ĠĊĂĂĊĠĊŦĊĊŦĊĠŦĊĊŦĊĠĠĠĂŦĊŦĠŦĠŦĊĠĂĊĂĂŦĊŦĠĠĂĊĠĊĠĂŦĂĊĊĂĊĂĊĂŦĊĂŦŦ	421
Query	784	GATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGT	843
Sbjct	420	ĠĂŤĠĠĠŤĂŤĊĂĊĠĊĂĊĂĊĠĠĊĂĊŤĂĂĠĊŤĊĊĂĂĂĊŤĠĠĠĊĂĠĊĀĂŤĠĠĊĠĊĊŤĊĊĂŤĠĠŤ	361
Query	844	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	903
Sbjct	360	GGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	301
Query	904	CGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	963
Sbjct	300	ĊĠĠĠŦĠĊŦĠĠĀŦĠĀĀĀĀŦĀŦĠĊĠĀĊĊĊĀĠĀŦĀĠĊĀĊĠĊĀĊ	241
Query	964	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT	1023
Sbjct	240	GATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTAT	181
Query	1024	GGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGG	1083
Sbjct	180	ĠĠŤĊŤĠĠĠĠĂĂĠĊĠĊĂĂĂĠŤĠĠĂŤĠĊĠŤŤĠĊĂŤĠĠŤĠĂĂĠŤŤĊĠĠĂŤĂĠĊĠĊŤŤĠĠĊĊĠĠ	121
Query	1084	CAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGT	1143
Sbjct	120	ĊAAAĊĠŤŤĠĂĊĠĠĂŤĊĂŤĠĠĊĊĀĠĠĠĊĠĠĊĂŤĊĂĂŤĊŤĊĠĊŤĊŤĊĊĠŤŤĊĊĊŤĊĂĂŤĠĠŤ	61
Query	1144	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1203
Sbjct	60	ACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAGACACGCTGGCCAGGGTCTT	1

Drosophila melanogaster chromosome X

Sequence ID: **gb|AE014298.5|** Length: 23542271 Number of Matches: 5 Range 1: 5416186 to 5417376

Score		Expect	Identities	Gaps	Strand	Frame	
2194 bit	s(1188)	0.0()	1190/1191(99%)	0/1191(0%)	Plus/Plus		
Features spoonb		Aspoonbill, i	isoform E				
Query	981	TCAGTTGTA	GATTGTAGAGGCTTTC	GGTCGAAAGAGGAAC	CTATGGTCTGGG	GAAGCGCAA	1040
Sbjct	5416186	tcacttgt	\dattgtagaggettte	ggtcgaaagaggaad	ctateetcteec	GAAGCGCAA	54162
Query	1041	AGTGGATGC	GTTGCATGGTGAAGTT	CGGATAGCGCTTGGC	CGGCAAACGTT	GACGGATCA	1100
Sbjct	5416246	AGTGGATGC	cdttdcatddtdaadtt	CGGATAGCGCTTGGC	CCGCCAAACGTT	GACGGATCA	54163
Query	1101	TGGCCAGGG	GCGGCATCAATCTCGCT(CTCCGTTCCCTCAAT	GGTACAGATGC	GCACCTTGC	1160
Sbjct	5416306	TGGCCAGGC	scggcatcaatctcgct	ctcccttcaat	rggtacagatgc	dcaccttdc	54163
Query	1161	CCGAGTAGO	GATTCTTGCCTACAGA	CACGCTGGCCAGGGT	CTTGGCCTTGA	TTTGGTTAA	1220
Sbjct	5416366	ccgagtagd	sgyttgcptychtgc	cycetteecpye	ccttggccttg	tttggttaa	54164
Query	1221	TAAACGCCC	CGCTTGCGGCCGTACAG	GTGACCAATCAAGCT	GATCGGGAAGA	GGAACTCGT	1280
Sbjct	5416426	TAAACGCCC	cdcttdcddccdtacad	gtgaccaatcaagci	rgatcgggaaga	.ĠĠÅÅĊ†ĊĠ†	54164

Query	1281	AGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGATCCCTTGCCAGAATCGC	1340
Sbjct	5416486	AGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGATCCCTTGCCAGAATCGC	5416545
Query	1341	CCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGAT	1400
Sbjct	5416546	ccgattgcacactgcaaatgctcagcgatggactggccgcatccacattgcgcttctgat	5416605
Query	1401	TACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTCCTGATCCTGCTCGAGCT	1460
Sbjct	5416606	taccattgctatccaccacttccttccttcagcaccgtctgctcctgatcctgctcgagct	5416665
Query	1461	CCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTCACAGTTGTTCTGCT	1520
Sbjct	5416666	cctcctgatcggcctccttcttggagggctcctccttgggctcacagttgttctgct	5416725
Query	1521	CGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGAGTTCTCTGGCGATATTTTGGGTG	1580
Sbjct	5416726	cccactccttcttcttcctccccct	5416785
Query	1581	TGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTTGGGTAGCCTTACGATTGTAGA	1640
Sbjct	5416786	tgcgcgtggccttaatcaccaccggttcaccgtcttttgggtagccttacgattgtaga	5416845
Query	1641	AGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAAT	1700
Sbjct	5416846	AGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAAT	5416905
Query	1701	CCTCGTCTATGGAGCAGAGTGTCTTGTGTTTCGGCATCCTGTATCTTTGACTTCAGTATTT	1760
Sbjct	5416906	cctcgtctatggagcagagtgtcttgtgttctcgccatcctgtatcttttgacttcagtattt	5416965
Query	1761	CGGAATCGATCTGCTGATGCTTGCCATTTGAAGTGCGTCCATTGCTCTGGATTTTGA	1820
Sbjct	5416966	cccahrcccarccccarcccccccccccccccccccccc	5417025
Query	1821	TTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTACTTC	1880
Sbjct	5417026	tregregeter	5417085
Query	1881	CGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTTCATCGACTTGCTGGCCG	1940
Sbjct	5417086	ccctacccctrtcccctaccctrtaactaaactrtccctrtcatctatccacttccccc	5417145
Query	1941	ACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTTGCGCGCCTGCACAGTTG	2000
Sbjct	5417146	Actigctigtiggcagettigccattictigcaggacticcigtiggccttigccigcctigcacagtigg	5417205
Query	2001	GTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAACAAT	2060
Sbjct	5417206	gttcaatcgacgagtcattgatggccgatgagtcctcgtcgtcggccttgtctaaacaat	5417265
Query	2061	TTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGA	2120
Sbjct	5417266	ttttatatetaeeeeeekeeseeeeeeeeeeeeeeeeeee	5417325
Query	2121	GGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTGAAAGATCT 2171	
Sbjct	5417326	ĠĠŦĀĠĀĠŦĀĠĀĠĠĀĊĠĀĊĊĠĠĀŦĀĊĊĀŦŦŦŦĊĠĊŦĠĀĀŦĀŦŦĠĀĀĀĠĀŦĊŦ 5417376	

Range 2: 5414586 to 5415041

Score		Expect	Identities	Gaps	Strand	Frame	
843 bits	(456)	0.0()	456/456(100%)	0/456(0%)	Plus/Plus		
Features spoonb	s: ill, isoform	Aspoonbill	, isoform E				
Query	4	gtgtgtgt	gtgtgtgtgtgtgt	atttggcgagtgtg	tgttgtttgtta	atgtAATGATT	63
Sbjct	5414586	gtgtgtgt	retetetetetetetetet	Atttggcgagtgtg	Ϯ ĠϮϮĠϮϮϮĠϮϮ <i>ϳ</i>	Atgtaatgatt	54146
Query	64	AAGGGGCT	CTCTCTGGGCTCAGTC	GCAATCTAAACAAC	GTAACAAACGT7	TCATTTTCTT	123
Sbjct	5414646	AAGGGGCT	CTCTCTGGGCTCAGTC	GCAATCTAAACAAC	GTAACAAACGT1	rtcattttctt	5414
Query	124	TGTTTTGA	AGGCCTCTGCACTTGCC	AGTTCTTTTGGAAT	CGGGCAATTGC	PATTTGCTGTG	183
Sbjct	5414706	†G††††G	decctctecketteck	AGTTCTTTTGGAAT	cdddcaattdci	rAtttgctgtg	5414
Query	184	TGCTACAT	GCTACATGCTAACTGC	AAAAGCTGCTAACG	AAATCCTTAATC	CCGAATCCGCA	243
Sbjct	5414766	†GC†ACA†	rdctacatdctaactdc	AAAAGCTGCTAACG.	AAA+cc++AA+c	ccdaatccdca	54148
Query	244	TCTTGGAG	CCTGTTGCGCAATACT	CAAGCATTCCTTTT	TTGTTGCACCGC	CCAAGTTGCTT	303
Sbjct	5414826	TCTTGGA	CCTGTTGCGCAATACT	CAAGCATTCCTTTT	TTGTTGCACCGC	CCAAGTTGCTT	54148
Query	304	GATTTGGG	TTTGAGTGATTGTTGT	TTAAGTTTGCTTTT	AAGTTTTCATAT	CAGTTCTTGGT	363
Sbjct	5414886	GATTTGGG	strtgagtgattgttgt	ተተልልĠተተተĠċተተተተ	AAGTTTTCATAT	rAGTTCTTGGT	5414
Query	364	TGCTAGTT	GAGTTGTTCACTAAGG	CTGTTAGTCACTCA	TCTCCACCCATT	TGGCGAGCTT	423

Sbjct 5414946 TGCTAGTTGAGTTGTTCACTAAGGCTGTTAGTCACTCATCTCCACCCATTTGGCGAGCTT 5415005

5415041

Range 3: 5415525 to 5415918

Score		Expect	Identities	Gaps	Strand	Frame	
728 bits	728 bits(394) 0.		394/394(100%)	0/394(0%)	Plus/Plus		
Feature spoonb	s: ill, i soform	Aspoonbill	, isoform E				
Query	591	CACCGATO	GGCTCAATGTTGGACAC	GGATGCATTCGGTG	GACTGGAAGGGC	ACATTCATGA	650
Sbjct	5415525	CACCGATO	GGCTCAATGTTGGACAC	GATGCATTCGGTG	GACTGGAAGGGC	ACATTCATGA	5415584
Query	651	AATCGGTG	CGAATCTGTCGCAGTG	rgttgaagccgaca'	TTCATGTAGCCA	CCAAAGTCAA	710
Sbjct	5415585	AATCGGTG	ccaatctctcccactc	rgttgaagccgaca	ttcatgtagcca	ccaaagtcaa	5415644
Query	711	GAAACTTG	ATTACGCAACGCTCCT(CGTCCTCGGGATCT	GTGTCGACAATC	TGGACGCGAT	770
Sbjct	5415645	GAAACTTG	attacccaaccctcctc	cetecteeee	gtgtcgacaatc	TGGACGCGAT	5415704
Query	771	ACCACACA	TCATTGATGGGTATCA	CGCACACGGCACTA.	AGCTCCAAACTG	GGCAGCAATG	830
Sbjct	5415705	ACCACACA	tcattgatgggtatcac	cdcacacddcacta.	AGCTCCAAACTG	GGCAGCAATG	5415764
Query	831	GCGCCTCC	ATGGTGGAGTAGCTAT(CGTACAGCTGCTTC	TGCAGCAAAGGC	AACGATGGAT	890
Sbjct	5415765	gcgcctcc	atggtggagtagctato	cetacaectecttc	tecaecaaaec	AACGATGGAT	5415824
Query	891	GCGAGGGA	TGCAGCGGGTGCTGGAT	rgaaaatatgcgac	CCAGATAGCACC	GCACTCACTA	950
Sbjct	5415825	GCGAGGGA	rtecaeceeetecteear	rgaaaatatgcgac	ccagatagcacc	GCACTCACTA	5415884
Query	951	CCACATCG	TTGTTGATGCCCTCAAT	CAGTTTCAG 98	4		
Sbjct	5415885	CCACATCG	rtgttgatgccctcaar	rcagtttcag 54	15918		

Range 4: 5420452 to 5420802

Score	Expect	Identities	Gaps	Strand	Frame
643 bits(348)	4e-180()	351/352(99%)	1/352(0%)	Plus/Plus	_

Features:

214 bp a	at 5' side: s _l	poonbill, isoform C1820 bp at 3' side: ubiquitin specific protease 16/45, isoform	ı D
Query	2170	CTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCTTTCAAAGCTAT	2229
Sbjct	5420452	CTTTGTGAACCGCTTGGGTAACTTATTTTGCTCACTATCTTTGGGTGCTTTCAAAGCTAT	5420511
Query	2230	CTACTGCACACGCGAGTTGTGTATTGTTTTTGCTTATTTGCTGGCGATTTACTGTCGTTT	2289
Sbjct	5420512	chachdeacacacachtartartartartartartartachachdeachartartachdeachdeachdeachdeachdeachdeachdeachde	5420571
Query	2290	TCTCAACGCTAAAGTGCTGCACGAATTAAACACGTGTCTACGTTCCACCTTTTACAAATC	2349
Sbjct	5420572	tctcaacgctaaagtgctgcacgaattaaacacgtgtctacgttccaccttttacaaatc	5420631
Query	2350	ACAATAACATGGCCGGCGTGCGGCAGTGTTGCCATGCATCCGCAAAACTCTGGCAATCGG	2409
Sbjct	5420632	Acaataacategecegeceteegecaetetteeceatecatececaaaactecegeaatege	5420691
Query	2410	AGCTGCCTGCTTAATCACCCGCACTCGCGATGGCCAAATCCTCGAATTACAAGAGCCTTT	2469
Sbjct	5420692	AGCTGCCTGCTTAATCACCCGCACTCGCGATGGCCAAATCCTCGAATTACAAGAGCCTTT	5420751
Query	2470	GTGCACACaaaaaaaaTATATAGAAAAAATCACTTCACAGTTTGAATCGCA 2521	
Sbjct	5420752	ĠŦĠĊAĊAĊAAAAAAAA-ATATAĠAAAAATĊAĊŦŦĊAĊAĠŦŦŦĠAAŦĊĠĊA 5420802	

Range 5: 5415322 to 5415456

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(135)	1e-61()	135/135(100%)	0/135(0%)	Plus/Plus	_

Features: spoonbill, isoform Aspoonbill, isoform E

Sbjct	5415322	ATTGGGACCTAGGGAT	GCGAATAAAAAGATTTCTGGTAGGTTGTGACTATTATAGCCGGC	5415381
Query	520	GACTTGTGCTTGCAAG	ACAATGCCTTTGGTAAGTTTGTTGAGGATTTCGGCCGCCTCAAT	579
Sbjct	5415382	GACTTGTGCTTGCAAG	ACAATGCCTTTGGTAAGTTTGTTGAGGATTTCGGCCGCCTCAAT	5415441
Query	580	GGACCAGGTGCCACC	594	
Sbjct	5415442	GGACCAGGTGCCACC	5415456	

Drosophila melanogaster X BAC RP98-7P13 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence Sequence ID: **gb|AC023684.4|** Length: 178077 Number of Matches: 5 Range 1: 172050 to 173240

Score		Expect	Identities	Gaps	Strand	Frame
2194 bit	ts(1188)	0.0()	1190/1191(99%)	0/1191(0%)	Plus/Minus	
Feature	s:					
Query	981	TCAGTTGTA	GATTGTAGAGGCTTTC 	GGTCGAAAGAGGAA(CTATGGTCTGGG(GAAGCGCAA
Sbjct	173240		ĠÀŦŦĠŦĀĠĀĠĠĊŦŦŦĊ			
Query	1041		$\operatorname{GTTGCATGGTGAAGTT}$			
Sbjct Query	173180 1101		ĠϮϮĠĊĂϮĠĠϮĠĂĂĠϮϮ CGGCATCAATCTCGCT			
Sbjct	173120		CGGCATCAATCTCGCT			
Query	1161		Ģ ĀŢŢĊŢŢĢĊĊŢĀĊĀĢĀ			
Sbjct	173060	CCGAGTAGG				
Query	1221	TAAACGCCC	GCTTGCGGCCGTACAG	GTGACCAATCAAGC	TGATCGGGAAGA(GGAACTCGT
Sbjct	173000	TAAACGCCC	gc44gcggccg4ycyg	gtgyccyytcyygc.	rgatcgggaagac	GGAACTCGT
Query	1281		TCACGCGTGTCGCCTC			
Sbjct Query	172940 1341		TCACGCGTGTCGCCTC CACTGCAAATGCTCAG			
Sbjct	172880		CACTGCAAATGCTCAG 			
Query	1401		ТАТССАССАСТТССТС			
Sbjct	172820	TACCATTGC	TATCCACCACTTCCTC	CTTCAGCACCGTCTC	GCTCCTGATCCT	
Query	1461	CCTCCTGAT	CGGCCTCCTTCTTGGA	GGGCTCCTCCTTGG(GCTCACAGTTGT	rgttctgct
Sbjct	172760	cctcctgat	ċĠĠċċŧċċŧŧċŧŧĠĠĀ	ĠĠĠĊŦĊĊŦĊĊŦŦĠĠŒ	sctcacagttgt	tgttctgct
Query	1521		TGTTGGTGTAGTTGGT			
Sbjct Query	172700 1581		TGTTGGTGTAGTTGGT CCTTAATCACCACCGG			
Sbjct	172640					
Query	1641	А ĢĢ А Ţ А ÇĢÇ	<mark>Ģ</mark> ŢĢŢĄŢŢŢĄÇÇĢĄĄŢÇ	<mark>ĢĢĢŢ</mark> ĄĄĄŢÇĄÇĢŢĢ¢	GCGACGATAGATT	ГСТССАААТ
Sbjct	172580	AGGATACGC	GTGTATTTACCGAATC	GGGTAAATCACGTG	GCGACGATAGAT	rctcgaaat
Query	1701	CCTCGTCTA	TGGAGCAGAGTGTCTT 	GTGTTCGGCATCCT(GTATCTTTGACTT	CAGTATTT
Sbjct	172520		tĠĠĀĠĊĀĠĀĠŦĠŦĊŦŦ			
Query	1761		$ ext{TCTGCTGCTGATGCTT} ig ig ig ig ig ig ig ig $			
Sbjct Query	172460 1821		TCTGCTGCTGATGCTT ATTTACCATACAACAT			
Sbjct	172400		TTTTACCATACAACAT			
Query	1881		ТТСССТАСССТТААС			
Sbjct	172340	CGCTACCGC		TAAAGTTCCGTTGA		 rgctggccg
Query	1941	ACTGCTGTG	GCAGCTTGCCATTCTG	CAGGACTCCGTTGG	CCTTGCGCGCCTC	GCACAGTTG
Sbjct	172280	Actdctdtd	gcygctagc	caggactcccttgc	ccttgcgcgcct	Scacagttg
Query	2001	GTTCAATCG.	ACGAGTCATTGATGGC 	CGATGAGTCCTCGTC	CGTCGGGCTTGT(CTAAACAAT

Sbjct	172220	GTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAACAAT	172161
Query	2061	TTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGA	2120
Sbjct	172160	TTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGA	172101
Query	2121	GGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTGAAAGATCT 2171	
Sbjct	172100	GGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTGAAAGATCT 172050	

Range 2: 174385 to 174840

Score		Expect	Identities	Gaps	Strand	Frame	_
843 bits	(456)	0.0()	456/456(100%)	0/456(0%)	Plus/Minus		_
Features	s:						
Query	4	gtgtgtgt	gtgtgtgtgtgtgtgt	atttggcgagtgtg	tgttgtttgtta	tgtAATGATT	63
Sbjct	174840	ĠŦĠŦĠŦĠŦ	ĠŦĠŦĠŦĠŦĠŦĠŦĠŦĠŦ	Atttggcgagtgtg	tĠttĠtttĠttA:	rgtaatgatt	174781
Query	64	AAGGGGCT	CTCTCTGGGCTCAGTC	GCAATCTAAACAAC	GTAACAAACGTT'	CATTTTCTT	123
Sbjct	174780	AAGGGGCT	ctctctgggctcagtc	GCAATCTAAACAAC	gtaacaaacgtt:	rcattttctt	174721
Query	124	TGTTTTGA	GGCCTCTGCACTTGCC	AGTTCTTTTGGAAT	CGGGCAATTGCT	ATTTGCTGTG	183
Sbjct	174720	TGTTTTGA	.ggcctctgcacttgccz	AGTTCTTTTGGAAT	CGGGCAATTGCT	ATTTGCTGTG	174661
Query	184	TGCTACAT	GCTACATGCTAACTGC	AAAAGCTGCTAACG	AAATCCTTAATC	CGAATCCGCA	243
Sbjct	174660	TGCTACAT	GCTACATGCTAACTGC	AAAAGCTGCTAACG	AAATCCTTAATC	CGAATCCGCA	174601
Query	244	TCTTGGAG	CCTGTTGCGCAATACT	CAAGCATTCCTTTT	TTGTTGCACCGC	CAAGTTGCTT	303
Sbjct	174600	TCTTGGAG	cctgttgcgcaatacto	CAAGCATTCCTTT	ttgttgcaccgc	CAAGTTGCTT	174541
Query	304	GATTTGGG	TTTGAGTGATTGTTGT	TTAAGTTTGCTTTT	AAGTTTTCATAT	AGTTCTTGGT	363
Sbjct	174540	GATTTGGG	trtgagtgartgrtgr	rtaagtttgettt	AAGTTTTCATAT	AGTTCTTGGT	174481
Query	364	TGCTAGTT	'GAGTTGTTCACTAAGG(CTGTTAGTCACTCA	TCTCCACCCATT	TGGCGAGCTT	423
Sbjct	174480	TGCTAGTT	GAGTTGTTCACTAAGG	CTGTTAGTCACTCA	TCTCCACCCATT		174421
Query	424	TCTGCCGA	.CCAGCTCCTTATTGAT	AAAGATTACATT	459		
Sbjct	174420	TCTGCCGA	.ccagctccttattgatz	AAGATTACATT	174385		

Range 3: 173508 to 173901

Score		Expect	Identities	Gaps	Strand	Frame	_
728 bits	(394)	0.0()	394/394(100%)	0/394(0%)	Plus/Minus		_
Features	S :						
Query	591	CACCGATG	GGCTCAATGTTGGACAG	GATGCATTCGGTG	GACTGGAAGGGCA	CATTCATGA	650
Sbjct	173901	CACCGATG	GGCTCAATGTTGGACAG	GATGCATTCGGTG	GACTGGAAGGGCA	CATTCATGA	173842
Query	651	AATCGGTG	CGAATCTGTCGCAGTGT	GTTGAAGCCGACA	TTCATGTAGCCAC	CAAAGTCAA	710
Sbjct	173841	AATCGGTG	cgaatctgtcgcagtgt	gttgaageegaea	ttcatgtagccac	CAAAGTCAA	173782
Query	711	GAAACTTG	ATTACGCAACGCTCCTC	GTCCTCGGGATCT	GTGTCGACAATCT	GGACGCGAT	770
Sbjct	173781	GAAACTTG	AttAcccAAccctcctc	gtcctcgggatct	ĠŦĠŦĊĠĂĊĂĂŦĊŦ	GGACGCGAT	173722
Query	771	ACCACACA	TCATTGATGGGTATCAC	GCACACGGCACTA	AGCTCCAAACTGG	GCAGCAATG	830
Sbjct	173721	ACCACACA	TCATTGATGGGTATCAC	GCACACGGCACTA	AGCTCCAAACTGG	GCAGCAATG	173662
Query	831	GCGCCTCC	ATGGTGGAGTAGCTATC	GTACAGCTGCTTC	TGCAGCAAAGGCA	ACGATGGAT	890
Sbjct	173661	gcgcctcc	AtGGtGGAGTAGCTATC	gtacagctgcttc	tgcygcyyydd	ACGATGGAT	173602
Query	891	GCGAGGGA	TGCAGCGGGTGCTGGAT	GAAAATATGCGAC	CCAGATAGCACCG	CACTCACTA	950
Sbjct	173601	GCGAGGGA	tgcygcgggtgctggyt	gaaaatatgcgac	ççyeytyeçyççe	cactcacta	173542
Query	951	CCACATCG	TTGTTGATGCCCTCAAT	CAGTTTCAG 98	4		
Sbjct	173541	ccacatcg	ttgttgatgccctcaat	cagtttcag 17	3508		

Range 4: 168624 to 168974

Score		Expect	Identities	Gaps	Strand	Frame	
643 bits	(348)	4e-180()	351/352(99%)	1/352(0%)	Plus/Minus		_
Features	S :						
Query	2170	CTTTGTGAA	.CCGCTTGGGTAACTTA	TTTTGCTCACTAT	CTTTGGGTGCTTT	CAAAGCTAT	2229
Sbjct	168974	ctttgtgaa	.ccccttccctakctta	.ተተተተ <mark></mark> ፈተተ	$c\mathtt{t}\mathtt{t}\mathtt{t}ddddtdctttd$	CAAAGCTAT	168915
Query	2230	CTACTGCAC	ACGCGAGTTGTGTATT	GTTTTTGCTTATT	TGCTGGCGATTTA	CTGTCGTTT	2289
Sbjct	168914	CTACTGCAC	ACGCGAGTTGTGTATT	ĠŦŦŦŦĠĊŦŦĀŦŦ	tgctggcgattta	ctgtcgttt	168855
Query	2290	TCTCAACGC	TAAAGTGCTGCACGAA	TTAAACACGTGTC	TACGTTCCACCTT	TTACAAATC	2349
Sbjct	168854	tctcaacgc	taaagtgctgcacgaa	ttaaacacgtgtc	tacettccacctt	rttacaaatc	168795
Query	2350	ACAATAACA	TGGCCGGCGTGCGGCA	GTGTTGCCATGCA	TCCGCAAAACTCT	GGCAATCGG	2409
Sbjct	168794	Acaataaca	rteecceeceter	dtgttgccatgca.	tccccaaaactct	ggcaatcgg	168735
Query	2410	AGCTGCCTG	CTTAATCACCCGCACT	CGCGATGGCCAAA'	TCCTCGAATTACA	AGAGCCTTT	2469
Sbjct	168734	AGCTGCCTG	cttaatcacccccact	ccccqqtccqqqq	tcctcgaattaca	AGAGCCTTT	168675
Query	2470	GTGCACACA	.aaaaaaaa TATATAGA 	AAAAATCACTTCA	CAGTTTGAATCGC	A 2521	
Sbjct	168674	ĠŦĠĊĀĊĀĊĀ	AAAAAAAA-ATATAGA	AAAAAtcActtcA	ĊĀĠŦŦŦĠĀĀŦĊĠĊ	À 168624	

Range 5: 173970 to 174104

Score		Expect	Identities		Gaps	Strand	Frame	
250 bits	s(135)	1e-61()	135/135(10	0%)	0/135(0%)	Plus/Minus		_
Feature	s:							
Query	460	ATTGGGAC	CTAGGGATGC	GAATAAAAA	GATTTCTGG'	TAGGTTGTGACT	ATTATAGCCGGC	519
Sbjct	174104	ATTGGGAC	ctagggatgc	GAATAAAAA	.GATTTCTGG	raggttgtgactz	Attatadccddc	174045
Query	520	GACTTGTG	CTTGCAAGAC	AATGCCTTT	GGTAAGTTT(GTTGAGGATTTCC	GCCGCCTCAAT	579
Sbjct	174044	GACTTGTG	cttgcaagac	AATGCCTTT	'GGTAAGTTT	gttgaggatttc	gccccctcaat	173985
Query	580	GGACCAGG	TGCCACC 59	94				
Sbjct	173984	ĠĠĀĊĊĀĠĠ	rtgccacc 1	73970				

Drosophila melanogaster X BAC RP98-18K5 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence Sequence ID: **gb|AC104604.7|** Length: 167902 Number of Matches: 5 Range 1: 78812 to 80002

Score		Expect	Identities	Gaps	Strand	Frame	
2194 bit	s(1188)	0.0()	1190/1191(99%)	0/1191(0%)	Plus/Minus		
Features	s:						
Query	981	TCAGTTGTAG.	ATTGTAGAGGCTTTC	GGTCGAAAGAGGAAC	TATGGTCTGGGG	AAGCGCAA	1040
Sbjct	80002	TCACTTGTAG	AttGtAGAGGCtttC	GGTCGAAAGAGGAAC	tateeteteee	AAGCGCAA	79943
Query	1041	AGTGGATGCG'	TTGCATGGTGAAGTT(CGGATAGCGCTTGGC	CGGCAAACGTTGA	ACGGATCA	1100
Sbjct	79942	AGTGGATGCG	ttgcatggtgaagtt	CGGATAGCGCTTGGC	CGGCAAACGTTGA	ACGGATCA	79883
Query	1101	TGGCCAGGGC	GGCATCAATCTCGCT(CTCCGTTCCCTCAAT	GGTACAGATGCG(CACCTTGC	1160
Sbjct	79882	TGGCCAGGGC	ggcatcaatctcgct	ctcccttcaat	ggtacagatgcgo	caccttgc	79823
Query	1161	CCGAGTAGGG.	ATTCTTGCCTACAGA(CACGCTGGCCAGGGT	CTTGGCCTTGAT	TTGGTTAA	1220
Sbjct	79822	cceye4yqeq	AttcttgcctAcAGAG	cacecteeccaeeet	cttggccttgat	rtggttaa	79763
Query	1221	TAAACGCCCG	CTTGCGGCCGTACAG(GTGACCAATCAAGCT	GATCGGGAAGAG 	GAACTCGT	1280
Sbjct	79762	TAAACGCCCG	cttgcggccgtacag	GTGACCAATCAAGCT	GATCGGGAAGAG	SAACTCGT	79703
Query	1281	AGGTGGTTTT	CACGCGTGTCGCCTC	CGAGCGCGGCAAGCT	GGATCCCTTGCC	AGAATCGC	1340
Sbjct	79702	AGGTGGTTTT	cyceceteres	cgagcgcgcaagct	ĠĠĂŦĊĊĊŦŦĠĊĊ	AGAATCGC	79643
Query	1341	CCGATTGCAC	ACTGCAAATGCTCAG(CGATGGACTGGCCGC	ATCCACATTGCG(CTTCTGAT	1400
Sbjct	79642	CCGATTGCAC	Actecadatectcae	cgatggactggccgc.	Atccacattgcgc	cttctcat	79583

Query	1401	TACCATTGCTATCCACCACTTCCTCCTTCAGCACCGTCTGCTCCTGATCCTGCTCGAGCT	1460
Sbjct	79582	taccattgctatccaccacttccttccttcagcaccgtctgctcctgatcctgctcgagct	79523
Query	1461	CCTCCTGATCGGCCTCCTTCTTGGAGGGCTCCTCCTTGGGCTCACAGTTGTTCTGCT	1520
Sbjct	79522	cctcctgatcggcctccttcttggagggctcctccttgggctcacagttgttctgct	79463
Query	1521	CGCACTCCTTGTTGGTGTAGTTGGTATCCAGGAAGGAGTTCTCTGGCGATATTTTGGGTG	1580
Sbjct	79462	cccactccttcttcttcctacctactacttccaccaccac	79403
Query	1581	TGCGCGTGGCCTTAATCACCACCGGTTCCACCGTCTTTTTGGGTAGCCTTACGATTGTAGA	1640
Sbjct	79402	tgcgcgtggccttaatcaccaccggttcaccgtcttttgggtagccttaccattga	79343
Query	1641	AGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGAAAT	1700
Sbjct	79342	AĠĠĀŦĀĊĠĊĠŦĠŦĀŦŦŦĀĊĊĠĀĀŦĊĠĠĠŦĀĀĀŦĊĀĊĠŦĠĠĊĠĀĊĠĀŦĀĠĀŦŦĊŦĊĠĀĀĀŦ	79283
Query	1701	CCTCGTCTATGGAGCAGAGTGTCTTGTGTTTCGGCATCCTGTATCTTTGACTTCAGTATTT	1760
Sbjct	79282	ĊĊŦĊĠŦĊŦĂŦĠĠĀĠĊĀĠĀĠŦĠŦĊŦŦĠŦĠŦŦĊĠĠĊĀŦĊĊŦĠŦĀŦĊŦŦŦĠĀĊŦŦĊĀĠŦĀŦŦŦ	79223
Query	1761	CGGAATCGATCTGCTGATGCTTGCCATTTGAAGTGCGTCCATTGCTCTGGATTTTGA	1820
Sbjct	79222	ĊĠĠĂĂŦĊĠĂŦĊŦĠĊŦĠĊŦĠĂŦĠĊŦŦĠĊĊĂŦŦŦĠĂĂĠŦĠĊĠŦĊĊĂŦŦĠĊŦĊŦĠĠĂŦŦŦŦĠĀ	79163
Query	1821	TTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTACTTC	1880
Sbjct	79162	†††GGTGCTGATTTACCATACAACATGGTAGTGGGGGCTGTCCTTCTCATCACTGCTACTTC	79103
Query	1881	CGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTTCATCGACTTGCTGGCCG	1940
Sbjct	79102	ĊĠĊŦĂĊĊĠĊŦŦĊĊĠĊŦĂĊĊĠŦŦĂĂĊŦĂĂĂĠŦŦĊĊĠŦŦĠĂŦĠŦŦĊĂŦĊĠĂĊŦŦĠĊŦĠĠĊĊĠ	79043
Query	1941	ACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTTGCGCGCCTGCACAGTTG	2000
Sbjct	79042	ACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCCTTGCGCCCTGCACAGTTG	78983
Query	2001	GTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAACAAT	2060
Sbjct	78982	ĠŤŤĊĂĂŤĊĠĂĊĠĂĠŤĊĂŤŤĠĂŤĠĠĊĊĠĂŤĠĂĠŤĊĊŤĊĠŤĊĠĠĠĠĊŤŤĠŤĊŤĂĂĂĊĂĂŤ	78923
Query	2061	TTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGA	2120
Sbjct	78922	ŤŤŤŤÁŤÁŤĊŤÁĊĠĊĊĠÁÁÁĊĊÁÁÁÁĠÁĊĠĊĊĠÁĠŤÁŤÁÁÁŤĠĊŤÁĊÁĊĊĠĠĠĊÁĠŤĠÁĠÁ	78863
Query	2121	GGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTGAAAGATCT 2171	
Sbjct	78862	ĠĠŦĀĠĀĠŦĀĠĀĠĠĀĊĠĀĊĊĠĠĀŦĀĊĊĀŦŦŦŦĊĠĊŦĠĀĀŦĀŦŦĠĀĀĀĠĀŦĊŦ 78812	

Range 2: 81147 to 81602

Score		Expect	Identities	Gaps	Strand	Frame	
843 bits	(456)	0.0()	456/456(100%)	0/456(0%)	Plus/Minus		
Feature	s:						
Query	4	gtgtgtgtg	tgtgtgtgtgtgtgt	atttggcgagtgtgt 	gttgtttgttat	gtAATGATT	63
Sbjct	81602	ĠŦĠŦĠŦĠŦĠ	tgtgtgtgtgtgtgt	Atttggcgagtgtgt	ĠŦŦĠŦŦŦĠŦŦĂŦ	GTAATGATT	81543
Query	64	AAGGGGCTC	TCTCTGGGCTCAGTC	GCAATCTAAACAACG	TAACAAACGTTT	CATTTTCTT	123
Sbjct	81542	AAGGGGCTC	tctctgggctcagtc	gcaatctaaacaacg	taacaaacGttt	cattttctt	81483
Query	124	TGTTTTGAG	GCCTCTGCACTTGCC	AGTTCTTTTGGAATC	GGGCAATTGCTA'	TTTGCTGTG	183
Sbjct	81482	TGTTTTGAG	dcctctdcacttdcc.	AGTTCTTTTGGAATC	ĠĠĠĊĀĀŦŦĠĊŦĀ'	rttgctgtg	81423
Query	184	TGCTACATG	CTACATGCTAACTGC	AAAAGCTGCTAACGA	AATCCTTAATCC	GAATCCGCA	243
Sbjct	81422	TGCTACATG	ctacatgctaactgc	AAAAGCTGCTAACGA	AA†¢¢††AA†¢¢	GAATCCGCA	81363
Query	244	TCTTGGAGC	CTGTTGCGCAATACT	CAAGCATTCCTTTTT 	TGTTGCACCGCC	AAGTTGCTT	303
Sbjct	81362	tcttggagc	ctgttgcgcaatact	caagcattccttttt	tgttgcycecc;	AAGTTGCTT	81303
Query	304	GATTTGGGT	TTGAGTGATTGTTGT'	TTAAGTTTGCTTTTA 	AGTTTTCATATA	GTTCTTGGT	363
Sbjct	81302	ĠĀŢŢŢĠĠĠŢ	rttgagtgattgttgt	ተተልልĠተተተĠĊተተተተል	AGTTTTCATATA	ቌተተ ዸተተ ៤ ៤ተ	81243
Query	364	TGCTAGTTG	AGTTGTTCACTAAGG	CTGTTAGTCACTCAT	CTCCACCCATTT(GGCGAGCTT	423
Sbjct	81242	TGCTAGTTG	adttdttcactaadd	ctgttagtcactcat	ctccacccattt	GGCGAGCTT	81183
Query	424	TCTGCCGAC	CAGCTCCTTATTGAT.	AAAGATTACATT 4	59		
Sbjct	81182	tctcccdac	cagctccttattgat.	AAAGATTACATT 8	1147		

Range 3: 80270 to 80663

Score		Expect	Identities	Gaps	Strand	Frame	
728 bits	(394)	0.0()	394/394(100%)	0/394(0%)	Plus/Minus		
Feature	s:						
Query	591	CACCGATGG	GCTCAATGTTGGACAG	GATGCATTCGGTGG	ACTGGAAGGGCAC	ATTCATGA	650
Sbjct	80663	caccdatdd	gctcaatgttggacad	sgatgcattcggtgg	actegaadedeac	AttcAtcA	80604
Query	651	AATCGGTGC	GAATCTGTCGCAGTGT	GTTGAAGCCGACAT	TCATGTAGCCACC	AAAGTCAA	710
Sbjct	80603	AATCGGTGC	GAATCTGTCGCAGTG1	rGTTGAAGCCGACAT	TCATGTAGCCACC	AAAGTCAA	80544
Query	711	GAAACTTGA	TTACGCAACGCTCCTC	CGTCCTCGGGATCTG	TGTCGACAATCTG	GACGCGAT	770
Sbjct	80543	GAAACTTGA	ttacccaaccctctd	cetecteeeeatete	tgtcgycyytctg	GACGCGAT	80484
Query	771	ACCACACAT	CATTGATGGGTATCAC	CGCACACGGCACTAA	GCTCCAAACTGGG	CAGCAATG	830
Sbjct	80483	ACCACACAT	cattgatgggtatcac	cgcacacggcactaa	.gctccaaactggg	CAGCAATG	80424
Query	831	GCGCCTCCA	TGGTGGAGTAGCTATC	CGTACAGCTGCTTCT	GCAGCAAAGGCAA	CGATGGAT	890
Sbjct	80423	GCGCCTCCA	TGGTGGAGTAGCTATC	cgtacagctgcttct	GCAGCAAAGGCAA	CGATGGAT	80364
Query	891	GCGAGGGAT	GCAGCGGGTGCTGGAT	GAAAATATGCGACC	CAGATAGCACCGC	ACTCACTA	950
Sbjct	80363	GCGAGGGAT	gcygcgggtgctggy	rgaaaatatgcgacc	cydytydcycedc	ActcActA	80304
Query	951	CCACATCGT	TGTTGATGCCCTCAAT	CAGTTTCAG 984			
Sbjct	80303	CCACATCGT	tgttgatgccctcaa1	CAGTTTCAG 802	70		

Range 4: 75386 to 75736

Score		Expect	Identities	Gaps	Strand	Frame	
643 bits	(348)	4e-180()	351/352(99%)	1/352(0%)	Plus/Minus		
Feature	s:						
Query	2170	CTTTGTGAAC	CGCTTGGGTAACTTA	TTTTGCTCACTATC	TTTGGGTGCTTTC	AAAGCTAT	2229
Sbjct	75736	CTTTGTGAAC	CGCTTGGGTAACTTA	ttttgctcactatc	4446664664446	AAAGCTAT	75677
Query	2230	CTACTGCACA	.CGCGAGTTGTGTATT	GTTTTTGCTTATTT	GCTGGCGATTTAC	TGTCGTTT	2289
Sbjct	75676	ctactgcaca	.cdcdadttdtdtatt	ĠϮϮϮϮϮĠĊϮϮĂϮϮϮ	GCTGGCGATTTAC	tgtcgttt	75617
Query	2290	TCTCAACGCT	AAAGTGCTGCACGAA	TTAAACACGTGTCT	ACGTTCCACCTTT	TACAAATC	2349
Sbjct	75616	TCTCAACGCT	AAAGTGCTGCACGAA	ttaaacacgtgtct	AcGttccAccttt	TACAAATC	75557
Query	2350	ACAATAACAT	GGCCGGCGTGCGGCA	GTGTTGCCATGCAT	CCGCAAAACTCTG	GCAATCGG	2409
Sbjct	75556	ACAATAACAT	.eecceecete	ĠŦĠŦŦĠĊĊĂŦĠĊĂŦ	ccccaaaaactctc	GCAATCGG	75497
Query	2410	AGCTGCCTGC	TTAATCACCCGCACT	CGCGATGGCCAAAT	CCTCGAATTACAA	GAGCCTTT	2469
Sbjct	75496	AGCTGCCTGC	ttaatcacccccacac	ceceateece	cctcgaattacaa	.gagccttt	75437
Query	2470	GTGCACACaa	aaaaaaaTATATAGA	AAAAATCACTTCAC	AGTTTGAATCGCA	2521	
Sbjct	75436	ĠŦĠĊĀĊĀĊĀĀ	AAAAAAA-ATATAGA	aaaaatcacttcac	AGTTTGAATCGCA	75386	

Range 5: 80732 to 80866

Score		Expect	Identitie	es	Gaps		Strand	Frame	
250 bits(135)		1e-61()	135/135	5(100%)	0/135(0	1%)	Plus/Minus		
Features	S :								
Query	460	ATTGGGACC	TAGGGATO	GCGAATAAA	AAGATTTCT	GGTAGG'	TTGTGACTAT	TATAGCCGGC	519
Sbjct	80866	ATTGGGACC	TAGGGATO	SCGAATAAA	AAGATTTCT	GTAGG'	rtgtgactat	TATAGCCGGC	80807
Query	520	GACTTGTGC	TTGCAAGA	ACAATGCCT	TTGGTAAGT'	TTGTTG	AGGATTTCGG	CCGCCTCAAT	579
Sbjct	80806	GACTTGTGC	TTGCAAG	ACAATGCCT	TTGGTAAGT'	TTGTTG	AGGATTTCGG	CCGCCTCAAT	80747
Query	580	GGACCAGGT	GCCACC	594					
Sbjct	80746	GGACCAGGT	GCCACC	80732					

Drosophila sechellia GM12645 (Dsec\GM12645), mRNA

Sequence ID: **ref|XM_002036881.1|** Length: 1722 Number of Matches: 3 Range 1: 838 to 1722

Score		Expect	Identities	Gaps	Strand	Frame	
1530 bit	s(828)	0.0()	866/885(98%)	0/885(0%)	Plus/Minus		
Feature	s:						
Query	391	TTAGTCACTCA	rctccacccatttgg(CGAGCTTTCTGCCG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	'TGATAAA	450
Sbjct	1722	TTAGTCACTCA	rctccacccaatttg	CGAGCTTTCTGCCG	SACCAGCTCCTTAT	 'TGATAAA	1663
Query	451	GATTACATTAT	rgggacctagggatg(CGAATAAAAAGATT	TCTGGTAGGTTGT	GACTATT	510
Sbjct	1662	GATTACATTAT	rgggacctagggatgo	cgaataaaaadatt	rtctggtargttgt	GACTATT	1603
Query	511	ATAGCCGGCGA(CTTGTGCTTGCAAGA(CAATGCCTTTGGTA	AGTTTGTTGAGGA	TTTCGGC	570
Sbjct	1602	Atadccddcdao	cttgtgcttgcaagac	caardcctttggta	Adttgdttdadda	tttcggc	1543
Query	571	CGCCTCAATGGA	ACCAGGTGCCACCGAT	FGGGCTCAATGTTG 	GACAGGATGCATT 	CGGTGGA	630
Sbjct	1542	ĊĠĊĊŤĊĠĂŤĠĠź	\ccaccion \delta	rĠĠĠĊϮĊAAϮĠϮϮĠ	GĠĀĊĀĠĠĀŦĠĊĀŦŦ	ĊĠĠĠĠĠĀ	1483
Query	631		CATTCATGAAATCGG: 				690
Sbjct	1482		CATTCATGAAATCGG:				1423
Query	691		CAAAGTCAAGAAACT'				750
Sbjct	1422 751		CAAAATCGAGAAACT: GGACGCGATACCACA(1363 810
Query Sbjct	1362		GACGCGATACCACAC 				1303
Query	811		GCAGCAATGGCGCCT(870
Sbjct	1302	CTCCAAACTGG			CTATCGTACAGCT	GCTTCTG	1243
Query	871	ÇĄĢÇĄĄĄĢĢÇĄ	, ÇĢĄŢĢĢĄŢĢÇĢĄĢĢ	Ģ Ā ŢĢÇĀĢÇĢĢĢŢĢÇ	СТĢĢĄТĢĄĄĄĄТĄТ	ĠĊĠŖĊĊĊ	930
Sbjct	1242	 CAGCAAAGGCAZ		 GATGCAGCGGGTGC	 CTGGATGAAAATAT	 GCGACCC	1183
Query	931	А ĢАŢĀĢÇĀÇÇĢO	САСТСАСТАССАСАТО	С ӨТТӨТТӨАТӨССО	СТСААТСАСТТТСА	.ĢТТĢТАĢ	990
Sbjct	1182	AGATAGCACCG	CACTCACCACCACATO	CGTTGTTGATGCCC	ctcgatcagtttca	GTTGTAG	1123
Query	991	ATTGTAGAGGC	TTTCGGTCGAAAGAG(GAACTATGGTCTGG	GGAAGCGCAAAGT	'GGATGCG	1050
Sbjct	1122	ATTGTAGAGGC	rttcggtcgaaagag	GAACTATGGTCTGG	GGAAGCGCAAAGT	GGATGCG	1063
Query	1051	TTGCATGGTGA	AGTTCGGATAGCGCT	rggccggcaaacg1	TGACGGATCATGG	CCAGGGC	1110
Sbjct	1062	TTGCATGGTGAZ	AGTTCGGATAGCGCT	rggccggcaaacg1	rtdacddatcatdd	CCAGGGC	1003
Query	1111	GGCATCAATCT(CGCTCTCCGTTCCCT(CAATGGTACAGATG	GCGCACCTTGCCCG	AGTAGGG	1170
Sbjct	1002	ggcytcyytch	cectetecentecent	caatggtacagatd	ceptyceptyce	adtaddd	943
Query	1171	ATTCTTGCCTAC	CAGACACGCTGGCCA(GGTCTTGGCCTTG	ATTTGGTTAATAA 	ACGCCCG	1230
Sbjct	942	Attcttgcctac	eggycycgctgccyc	ĠĠĠŦĊŦŦĠĠĊĊŦŦĊ	satttggttaataa	YÇÇÇÇÇ	883
Query	1231	CTTGCGGCCGT	ACAGGTGACCAATCAA	AGCTGATCGGGAAG	GAGGAA 1275 		
Sbjct	882	ĊŢŢĠĊĠĠĊĊĠŢ	Acaddtdaccaatca	GAĊŦĠĀŦĊĠĠĠĀĀĠ	SAGGAA 838		

Range 2: 1 to 685

Score		Expect	Identities	Gaps	Strand	Frame	
1110 bits(601) 0.0()		662/691(96%)	6/691(0%)	Plus/Minus			
Feature	s:						
Query	1458	GCTCCTCCTGA'	TCGGCCTCCTTCTTG	GAGGGCTCCTC	GGGCTCACAGTT	GTTGTTCT	1517
Sbjct	685	\$\delta \delta \	cceectpctate	sceeetteete	reegetteacaett	gttgttct	626
Query	1518	GCTCGCACTCC	TTGTTGGTGTAGTTG	GTATCCAGGAAGGA	GTTCTCTGGCGA	TATTTTGG	1577
Sbjct	625	dctcdcactcc	rtgttggtgtagttg	GTATCCAGGAAGGA	dttctctggcga	TATTTTGG	566
Query	1578	GTGTGCGCGTG	GCCTTAATCACCACC	GGTTCCACCGTCTT	TTGGGTAGCCTT	ACGATTGT	1637
Sbjct	565	g4g4gcgcg4g	gccttaatcaccacc	ĠĠŦŦĊĊĂĊĊĠŦĊŦſ	rttggctagtctt.	AcGATTGT	506

Query	1638	AGAAGGATACGCGTGTATTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGA	1697
Sbjct	505	AGAACGAGATGCGTGTTTTACCGAATCGGGTAAATCACGTGGCGACGATAGATTCTCGA	446
Query	1698	AATCCTCGTCTATGGAGCAGAGTGTCTTGTGTTCGGCATCCTGTATCTTTGACTTCAGTA	1757
Sbjct	445	AATCCTCGTCTATGGAGCAGAGTGTCTTGTGCTCGGCGTCCTGTATCTTTGACTTCAGTA	386
Query	1758	TTTCGGAATCGATCTGCTGATGCTTGCCATTTGAAGTGCGTCCATTGCTCTGGATTT	1817
Sbjct	385	tttcggaatcgatctgctgatgcttgccatttgaagagcgtccattgctttgattt	326
Query	1818	TGATTGGTGCTGATTTACCATACAACATGGTAGTGGGGCTGTCCTTCTCATCACTGCTAC	1877
Sbjct	325	TGATGGGTGCTGATTTACCATACAACATGGTAGTGGGACTGTCCTTCTCATCACTGCTAC	266
Query	1878	TTCCGCTACCGCTTCCGCTACCGTTAACTAAAGTTCCGTTGATGTTCATCGACTTGCTGG	1937
Sbjct	265	atccctacccttcccttaactaaacttccctccatcttcatccacttccc	212
Query	1938	CCGACTGCTGTGGCAGCTTGCCATTCTGCAGGACTCCGTTGGCCTTGCGCGCCTGCACAG	1997
Sbjct	211	ccccctcctctccccctcccccccccccccccccccccc	152
Query	1998	TTGGTTCAATCGACGAGTCATTGATGGCCGATGAGTCCTCGTCGTCGGGCTTGTCTAAAC	2057
Sbjct	151	tcggttcaatcgacgagtcattgatggtcgatgagtcctcgtcgtcgagcttgtctaaac	92
Query	2058	AATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTG	2117
Sbjct	91	AATTTTTATATCTACGCCGAAAACCAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTG	32
Query	2118	AGAGGTAGAGTAGAGGACCGGATACCAT 2148	
Sbjct	31	AGAGGTAGAGTAGAGGACGACCGGATACCAT 1	

Range 3: 689 to 837

Score		Expect	Identities	Gaps	Strand	Frame	
254 bits	(137)	9e-63()	145/149(97%)	0/149(0%)	Plus/Minus		
Features	S :						
Query	1351	ACTGCAAATG(CTCAGCGATGGACTG	GCCGCATCCACATT	GCGCTTCTGATTA	CCATTGCT	1410
Sbjct	837	ACTGCAAATG	ctcacccatccactc	screcatccacatt	gcgcttctgattg	ccattgrt	778
Query	1411	ATCCACCACT	rcctccttcagcacc	TCTGCTCCTGATC	CTGCTCGAGCTCC	TCCTGATC	1470
Sbjct	777	AtcGAccAct	tcctccttcagcacc	stetgeteetgate	ctgctcgygctcc	tcctgatc	718
Query	1471	GGCCTCCTTC	TTGGAGGGCTCCTCC	TTGG 1499			
Sbjct	717	ddcctccttc:	rtggagggctcctcc:	rTGG 689			

Drosophila ananassae uncharacterized protein, transcript variant C (Dana\GF20944), mRNA Sequence ID: **ref|XM_014905514.1|** Length: 3679 Number of Matches: 2 Range 1: 867 to 1907

Score		Expect	Identities	Gaps	Strand	Frame	
1081 bits	s(585)	0.0()	892/1044(85%)	6/1044(0%)	Plus/Minus		
Features	S:						
Query	358	CTTGGTTGCTA	GTTGAGTTGTTCAC	PAAGGCTGTTAGTCA(CTCATCTCCACCC	ATTTGGC	417
Sbjct	1907	CTTGATTGCTA	dttgagttgttcac	GAAGGCTGTTAGTCAG	CGAATCTCCACCC	Acttggc	1848
Query	418	GAGCTTTCTGC	CGACCAGCTCCTTA	TTGATAAAGATTACAT	TTATTGGGACCTA	GGGATGC	477
Sbjct	1847	GAGATTTCGGG	CGACCAGTTCCTTA:	rtgataaagataaca:	TTATTGGGACCTA	GGGAAGC	1788
Query	478	GAATAAAAAGA	TTTCTGGTAGGTTG	rgactattatagccg(GCGACTTGTGCTT	GCAAGAC	537
Sbjct	1787	GAATAAATAGA	cttctggtargttg	rgactattatagccg	bedaettdtett	'GCAAGAC	1728
Query	538	AATGCCTTTGG	TAAGTTTGTTGAGG	ATTTCGGCCGCCTCA	ATGGACCAGGTGC	CACCGAT	597
Sbjct	1727	AATGCCTTTGG	rtaagttggttgagg	Ytctçeeççeççte	Atggaccagttai	caccgat	1668
Query	598	GGGCTCAATGT	TGGACAGGATGCAT	rcggtggactggaag(GCACATTCATGA	AATCGGT	657
Sbjct	1667	CGGCTCCACGT	dGACAGTATACAC	rcggrggccrggaag	GCACGGACATGA	AGTCGGC	1608
Query	658	GCGAATCTGTC	GCAGTGTGTTGAAG(CCGACATTCATGTAGO	CCACCAAAGTCAA	GAAACTT	717

Sbjct	1607	GCGTATCTGGCGCAGAAGACTGAAGCCGACGTTCATGTAGCCGCCAAAGTCAAGGAACCT	1548
Query	718	GATTACGCAACGCTCCTCGTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACAC	777
Sbjct	1547	GACCACACAGCGCTCCTCGTCCTCGGGATCAACGTCAACGATCTGGACGCGATACCATAC	1488
Query	778	ATCATTGATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTC	837
Sbjct	1487	TCCGTTGATGGGGATCACGCACACGGCGCTGATCTCAAGGCTGGGCAACGGGGGGCCTC	1428
Query	838	CATGGTGGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	897
Sbjct	1427	CATCGTGGAGTAGCTATCGTACAGCTGCTTCTGCAGCATGGGCAGCGATGGGTGCGAGGG	1368
Query	898	ATGCAGCGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	957
Sbjct	1367	GTGGAGCGGGTGCTGGACGAAGAAGTGCGACCCGGACAGTACCGCACTCACCACCACGTC	1308
Query	958	GTTGTTGATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGG	1017
Sbjct	1307	GTTGTTGATGCCCTCGATCAGTTTCAGTTGTAGGTTGTTGAGGCTTTCTGTCGAAAGAGG	1248
Query	1018	AACTATGGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTT	1077
Sbjct	1247	AACTATGGTCTGCGGCAGGGCAAAGTGGATGCGTTGCATCGTAAAGTTTGGATACCGCTT	1188
Query	1078	GGCCGGCAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTC	1137
Sbjct	1187	dgagggcaggcgctggcgatcatcgccaggcggcgtcgatctcgctgtcgctctc	1128
Query	1138	AATGGTACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAG-A-CACGCTGGCC	1195
Sbjct	1127	GATGGTGCAGATGCGCACCTTGGCCGAGTACGGATTCTTGC-TG-AGCACCACATTGGCC	1070
Query	1196	AGGGTCTTGGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATC	1255
Sbjct	1069	AGGGTCTTCGACTTGATCTGGTTGATGAACATGCGCTTCCGGCCGTACAGCTGGCCGATC	1010
Query	1256	AAGCTGATCGGGAAGAGGAACTCGTAGGTGGT-TTTCACGCGTGTCGCCTCCGAGCGCGG	1314
Sbjct	1009	AGACTGTTGGGGAAGAGGAACTCGTAGCTGGTCTTTGCC-CGTGTCGCCTCCGATCGCGG	951
Query	1315	CAAGCTGGATCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACT	1374
Sbjct	950	caggctggatcccttgccggagtcgcccgactggacgctgcagatgctaagcgagggct	891
Query	1375	GGCCGCATCCACATTGCGCTTCTG 1398	
Sbjct	890	ddccdcdtccacattdcdcttctd 867	

Range 2: 19 to 681

Score		Expect	Identities	Gaps	Strand	Frame
444 bits	(240)	5e-120()	531/668(79%)	34/668(5%)	Plus/Minus	
Features	S :					
Query	1533	TGGTGTAGTTG	GTATCCAGGAAGGA	GTTCTCTGGCGATAT	TTTGGGTGTGCGC	GTGGCCT 1592
Sbjct	681	†ddfdfadftd	gtgtccagaaacga	gttctccggcgatat	tttggggtgcg	GTGGCCT 622
Query	1593	TAATCACCACC	GGTTCCACCGTCTT	TTGGGTAGCCTTACG.	ATTGTAGAAGGAT	ACGCGTG 1652
Sbjct	621	tgatcaccacc	dectedacedtett	gcrdrtgdrcttgcd	cttgtggaaggag	ACCCGGT 562
Query	1653	TATTTACCGAA	TCGGGTAAATCACG'	TGGCGACGATAGATT	CTCGAAATCCTCG	TCTATGG 1712
Sbjct	561	TGTTCACCGAG	tcggggaggtcgcg	CGGCGAGGACAGGTT	ctcgaagtcctcg	trcgatgg 502
Query	1713	AGCAGAGTGTC	TTGTGTTCGGCATC	CTGTATCTTTGACTT	CAGTATTTCGGAA	TCGATCT 1772
Sbjct	501	AGCAGAGCTTC	:ttgtgtttcggcgtc	ctggatcttcgactt	gagcatctcggag	rtcgatct 442
Query	1773	GCTGCTGATGC	TTGCCATTTGAAGT	GCGTCCATTGCTCTG	GATTTTGATTGGT	GCTGATT 1832
Sbjct	441	gctgctgctgc	:44gcceeeceeeq	ĠĊĠŦĊĊĠŦŦĠĊŦĊŦĠ	gatettgatggge	dccdAct 382
Query	1833	TACCATACAAC	ATGGTAGTGGGGCT	GTCCTTCTCATCACT	GCTACT-	T 1879
Sbjct	381	tgccgtacagc	:Atcdtgttgdddct	ctccccttcctcact	gccctacccctc	CCGCTGC 322
Query	1880	C-C-GCTACCG	CTT-CCGCTACC	GTTAACTAAAGTTCC	GTTGATGTTCATC	GACTTGC 1934
Sbjct	321	CACTGCCACCG	ctgctgatgctccc	gttggctatagtccc	gttgatgttcatc	GATTTGG 262
Query	1935	TGGCCGACTGC	TGTGGCAGCTTGCC	ATTCTGCAGGACTCC	GTTGGCCTTGCGC	G-C-CTG 1992
Sbjct	261	тффсффф	tggggcygcttgcc	gttctgaaggacgcc	ĠŦŦĠĠĊĊŦŦĠĊĠĊ	ded de
Query	1993	C-ACAGTTGGT	TCAATCGAC-G-	AGTCAT-TGATG-	GCCGATGAGTCCT	CGTCGTC 2043
Sbjct	204	cgaccgtctcc	tcyycedegedege	ctggggtagggtgt	<u> </u>	cdtcatc 147

Query	2044	GGGCTTGTCTAA	ACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	2103
Sbjct	146	GGGCTTGTCTAA	ACGATTTTTATTTCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC	87
Query	2104	TACACCGGGCAG'	TGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	2163
Sbjct	86	TACACCGGGCAG	TGACAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG	27
Query	2164	AAAGATCT 21	71	
Sbjct	26	AAGGATCT 19		

Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF20944), mRNA Sequence ID: **ref|XM_014905513.1|** Length: 3980 Number of Matches: 2 Range 1: 1168 to 2208

Score		Expect	Identities	Gaps	Strand	Frame
1081 bit	s(585)	0.0()	892/1044(85%)	6/1044(0%)	Plus/Minus	
Features	s:					
Query	358	CTTGGTTGCTA	GTTGAGTTGTTCACT	AAGGCTGTTAGTCAG	CTCATCTCCACCCA	ATTTGGC 417
Sbjct	2208	CTTGATTGCTA	.gttgagttgttcacg	AAGGCTGTTAGTCA	cgaatctccaccc	ACTTGGC 2149
Query	418	GAGCTTTCTGC	CGACCAGCTCCTTATT	FGATAAAGATTACA' 	TTATTGGGACCTAG	GGATGC 477
Sbjct	2148	ĠĀĠĀŤŤŤĊĠĠĠ	ccaccacacticas	rĠATAAAĠATAAĊA:	ŗtattĠĠĠāĊĊtād	
Query	478		Γ TTTCTGGTAGGTTGT Γ			
Sbjct	2088		CTTCTGGTATGTTGT(
Query Sbjct	538 2028		;TAAGTTTGTTGAGGA; ;TAAGTTGGTTGAGGA;			
Query	598		TGGACAGGATGCATT			
Sbjct	1968		TOMONO TO THE STATE OF THE STAT			
Query	658		ĠĊŖĠŦĠŦĠŦŢĠŖŖĠĊ(
Sbjct	1908		 !GCAGAAGACTGAAGC(
Query	718	GATTACGCAAC	: ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	ĢĄŢÇTGTĢŢÇGĄÇA <i>Ž</i>	ATCTGGACGCGAT <i>A</i>	ACCACAC 777
Sbjct	1848	GACCACACAGO	cctcctcctcctccc	GATCAACGTCAACG	ATCTGGACGCGATA	ACCATAC 1789
Query	778	ATCATTGATGG	GTATCACGCACACGG	CACTAAGCTCCAAA	CTGGGCAGCAATGG	GCGCCTC 837
Sbjct	1788	TCCGTTGATGG	GGATCACGCACACGG	CGCTGATCTCAAGG	ctgggcaacgggd	GGCCTC 1729
Query	838	CATGGTGGAGT	'AGCTATCGTACAGCT(GCTTCTGCAGCAAA(GGCAACGATGGATG 	CGAGGG 897
Sbjct	1728		'AĠĊŦAŦĊĠŦAĊAĠĊŦ(
Query	898		'GCTGGATGAAAATAT(
Sbjct	1668		ĠĊŦĠĠĂĊĠĂĂĠĂĀĠŎ			
Query	958 1608		CCTCAATCAGTTTCAC 			
Sbjct Query	1008		GGGGAAGCGCAAAGT(
Sbjct	1548		GCGGCAGGGCAAAGT			
Query	1078		ĠŢŢĠĸĊĠĠĸŢĊĸŢĠĠ			
Sbjct	1488	GGAGGGCAGGC				GCCCTC 1429
Query	1138	AATGGTAÇAGA	TGCGCACCTTGCCCG	ЧСТАСССАТТСТТСС	CCTACAG-A-CACG	GCTGGCC 119
Sbjct	1428	GATGGTGCAGA	TGCGCACCTTGGCCG	AGTACGGATTCTTG	C-TG-AGCACCAC	ATTGGCC 137
Query	1196	AGGGTCTTGGC	CTTGATTTGGTTAATA	AAACGCCCGCTTGC	GGCCGTACAGGTG <i>I</i>	ACCAATC 125
Sbjct	1370	AGGGTCTTCGA	cttgatctggttgato	SAACATGCGCTTCC	gecegtacaecte	SCCGATC 131
Query	1256	AAGCTGATCGG	GAAGAGGAACTCGTA(GGTGGT-TTTCACG	CGTGTCGCCTCCG <i>F</i>	AGCGCGG 131
Sbjct	1310	AGACTGTTGGG	cdaadaddaactcdtac	sctggtctttgcc-	ċĠŦĠŦĊĠĊĊŦĊĊĠŹ	
Query	1315		CCTTGCCAGAATCGCC			
Sbjct	1251	ĊĀĠĠĊŢĠĠĀŢĊ	:ĊĊϮϮĠĊĊĠĠĀĠϮĊĠĊŒ	ĊĊĠĂĊŦĠĠĂĊĠĊŦĠŧ	ĊĀĠĀŦĠĊŦĀĀĠĊĠŹ	AGĠĠĠĊϮ 1192

Query	1375	GGCCGCATCCACATTGCGCTTCTG	1398
Sbjct	1191	GCCGCGTCCACGTTGCGCTTCTG	1168

Range 2: 290 to 982

Score		Expect	Identities	Gaps	Strand	Frame	
477 bits	(258)	5e-130()	557/698(80%)	34/698(4%)	Plus/Minus		
Features	s:						
Query	1533	TGGTGTAGTT	GGTATCCAGGAAGGA	GTTCTCTGGCGATAT	тттееететесес	GTGGCCT	1592
Sbjct	982	TGGTGTAGTT	GGTGTCCAGAAACGA	gttctccggcgatai	rtttgggggtgcg	gtggcct	923
Query	1593	TAATCACCAC	CGGTTCCACCGTCTT	TTGGGTAGCCTTACG	GATTGTAGAAGGAT	ACGCGTG	1652
Sbjct	922	tgatcaccaco	cedetecaced	gcrdrtgdrcttgcd	scttgtggaaggag	ACCCGGT	863
Query	1653	TATTTACCGA	ATCGGGTAAATCACG	TGGCGACGATAGATT	CTCGAAATCCTCG	TCTATGG	1712
Sbjct	862	tgttcaccgac	etceeeeeeeeeeee	cddddagdacaddt	rctcgaagtcctcg	rtcgatgg	803
Query	1713	AGCAGAGTGTC	CTTGTGTTCGGCATC	CTGTATCTTTGACT7	CAGTATTTCGGAA	TCGATCT	1772
Sbjct	802	AGCAGAGCTTC	cttetettete	ctggatcttcgactt	rgagcatctcggag	rtcgatct	743
Query	1773	GCTGCTGATGC	CTTGCCATTTGAAGT(GCGTCCATTGCTCTC	GATTTTGATTGGT	GCTGATT	1832
Sbjct	742	¢¢†¢¢†¢g†¢¢	cttgcceeecee	ĠĊĠŦĊĊĠŦŦĠĊŦĊŦĊ	sgatcttgatgggc	dccdact:	683
Query	1833	TACCATACAA(CATGGTAGTGGGGCT(GTCCTTCTCATCACT	TGCTACT- 	T	1879
Sbjct	682	†G¢¢G†A¢AG¢	catceterteeect	ctccccttcctckc1	rdccgctAccgctg	cccctcc	623
Query	1880	C-C-GCTACCO	GCTT-CCGCTACC(GTTAACTAAAGTTCC 	CGTTGATGTTCATC	GACTTGC	1934
Sbjct	622	ĊAĊŦĠĊĊĀĊĊ	sctgctgatgctccc	ĠϮϮĠĠĊϮĂŦĂĠϮĊĊĊ	cĠttĠAtĠttcAtc	:ĠATŤŤĠG	563
Query	1935	TGGCCGACTGC	CTGTGGCAGCTTGCC. 	$egin{array}{cccc} ext{ATTCTGCAGGACTCC} \ & & & & & & \ & & & $	GTTGGCCTTGCGC	G-C-CTG	1992
Sbjct	562	rddddd ddd ddddddddddddddddddddddddddd	ĊŦĠĠĠĠĊĀĠĊŦŦĠĊĊ	GŤŤĊŤĠAÁĠĠÁĊGĊĊ	cĠŦŦĠĠĊĊŦŦĠĊĠĊ	:ĠGĊTĊCC	506
Query	1993		TTCAATCGAC-G- 				2043
Sbjct	505	ĊĠĂĊĊĠŤĊŦĊ	ctcaacgggggggc	CTGĠGĊGŤAGĠGŤĠī	rĠĊĊĠ_Ť_TĠŤĊĊŤ	ccctcatc	448
Query	2044	GGGCTTGTCTA	\AACAATTTTTATAT(CTACGCCGAAACCA <i>F</i> 	AAGACGCCGAGTA 	TAAATGC	2103
Sbjct	447	ĠĠĠĊŢŢĠŢĊŢŹ	\AACGATTTTATTT(ĊŦĂĊĠĊĊĠĂĂĂĊĊĂŹ	AAAGACGCCGAGTA	taaatgc	388
Query	2104	TACACCGGGCA	AGTGAGAGGTAGAGT. 	AGAGGACGACCGGAT 	PACCATTTTCGCTG	AATATTG	2163
Sbjct	387		ÁĠŦĠĀCĀĠĠŦĀĠĀĠŦ.			SAATATTĠ	328
Query	2164		GTGAACCGCTTGGGT.		2201		
Sbjct	327	AAGĠATĊTTT	rgĠAAĊĊĠĊϮϮͲĠĠϮ	AACTTATTATGCT	290		

Drosophila ananassae uncharacterized protein, transcript variant A (Dana\GF20944), mRNA Sequence ID: **ref|XM_001963992.2|** Length: 3749 Number of Matches: 2 Range 1: 937 to 1977

Score		Expect	Identities	Gaps	Strand	Frame	
1081 bits	s(585)	0.0()	892/1044(85%)	6/1044(0%)	Plus/Minus		
Features	3 :						
Query	358	CTTGGTTGCTA	GTTGAGTTGTTCACT	TAAGGCTGTTAGTCA	CTCATCTCCACCC	ATTTGGC	417
Sbjct	1977	CTTGATTGCTA	GTTGAGTTGTTCAC	GAAGGCTGTTAGTCA	CGAATCTCCACCC	ACTTGGC	1918
Query	418	GAGCTTTCTGC	CGACCAGCTCCTTAT	TTGATAAAGATTACA'	TTATTGGGACCTA	GGGATGC	477
Sbjct	1917	GAGATTTCGGG	ccaccacttcctta	rtgataaagataaca	ttattgggaccta	GGGAAGC	1858
Query	478	GAATAAAAAGA	TTTCTGGTAGGTTGT	rgactattatagccg(GCGACTTGTGCTT	GCAAGAC	537
Sbjct	1857	GAATAAATAGA	cttctggtargttgi	rgactattatagccg	gcgacttgtgctt	'GCAAGAC	1798
Query	538	AATGCCTTTGG	TAAGTTTGTTGAGG <i>I</i>	ATTTCGGCCGCCTCA	ATGGACCAGGTGC	CACCGAT	597
Sbjct	1797	AATGCCTTTGG	staagttggttgagg <i>i</i>	Atctcggccgcctcg.	ATGGACCAGTTAT	'CACCGAT	1738
Query	598	GGGCTCAATGT	TGGACAGGATGCATT	CGGTGGACTGGAAG	GGCACATTCATGA	AATCGGT	657

Sbjct	1737	cĠĠċtċcAcĠttĠĠAċAĠtAtaċActċĠĠtĠĠcċtĠĠAAĠĠĠċAċGGAċAtĠAAGtċĠĠc	1678
Query	658	GCGAATCTGTCGCAGTGTGTTGAAGCCGACATTCATGTAGCCACCAAAGTCAAGAAACTT	717
Sbjct	1677	GCGTATCTGGCGCAGAAGACTGAAGCCGACGTTCATGTAGCCGCCAAAGTCAAGGAACCT	1618
Query	718	GATTACGCAACGCTCCTCGTCCTCGGGATCTGTGTCGACAATCTGGACGCGATACCACAC	777
Sbjct	1617	GACCACACAGCGCTCCTCGTCCTCGGGATCAACGTCAACGATCTGGACGCGATACCATAC	1558
Query	778	ATCATTGATGGGTATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTC	837
Sbjct	1557	TCCGTTGATGGGGATCACGCACACGGCGCTGATCTCAAGGCTGGGCAACGGGGGGCCCTC	1498
Query	838	CATGGTGGAGTAGCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	897
Sbjct	1497	catcgtggagtagctatcgtacagctgcttctgcagcatgggcagcgatgggtgcgaggg	1438
Query	898	ATGCAGCGGGTGCTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	957
Sbjct	1437	GtGGAGCGGGTGCTGGACGAAGAAGTGCGACCGGACAGTACCGCACTCACCACGTC	1378
Query	958	GTTGTTGATGCCCTCAATCAGTTTCAGTTGTAGATTGTAGAGGCTTTCGGTCGAAAGAGG	1017
Sbjct	1377	ĠŦŦĠŦŦĠĀŦĠĊĊĊŦĊĠĀŦĊĀĠŦŦŦĊĀĠŦŦĠŦĀĠĠŦŦĠŦŦĠĀĠĠĊŦŦŦĊŦĠŦĊĠĀĀĀĠĀĠĠ	1318
Query	1018	AACTATGGTCTGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTT	1077
Sbjct	1317	AACTATGGTCTGCGGCAGGGCAAAGTGGATGCGTTGCATCGTAAAGTTTGGATACCGCTT	1258
Query	1078	GGCCGGCAAACGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTC	1137
Sbjct	1257	ĠĠĸĠĠĠĊĸĠĠĊĠĠĊĠĠĸŢĊĸŢĊĠĊĊĸĠĠĠĠĠĠĠĠĠĠĠĠŢĊĠĸŢĊĠĊŢĠŢĠĠŢĠĊĊĊŢĊ	1198
Query	1138	AATGGTACAGATGCGCACCTTGCCCGAGTAGGGATTCTTGCCTACAG-A-CACGCTGGCC	1195
Sbjct	1197	GATGGTGCAGATGCGCACCTTGGCCGAGTACGGATTCTTGC-TG-AGCACCACATTGGCC	1140
Query	1196	AGGGTCTTGGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATC	1255
Sbjct	1139	AĠĠĠŦĊŦŦĊĠAĊŦŦĠAŦĊŦĠĠŦŦĠAŦĠĀĀĊAŦĠĊĠĊŦŦĊĊĠĠĊĊĠŦĀĊĀĠĊŦĠĠĊĊĠĀŦĊ	1080
Query	1256	AAGCTGATCGGGAAGAGGAACTCGTAGGTGGT-TTTCACGCGTGTCGCCTCCGAGCGCGG	1314
Sbjct	1079	AGACTGTTGGGGGAAGAGGAACTCGTAGCTGGTCTTTGCC-CGTGTCGCGCTCCGATCGCGG	1021
Query	1315	CAAGCTGGATCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACT	1374
Sbjct	1020	cagectegateccttegeagtegect	961
Query	1375	GGCCGCATCCACATTGCGCTTCTG 1398	
Sbjct	960	ĠĠĊĊĠĊĠŦĊĊĂĊĠŦŦĠĊĠĊŦŦĊŦĠ 937	

Range 2: 91 to 751

Score		Expect	Identities	Gaps	Strand	Frame	
440 bits	(238)	6e-119()	529/666(79%)	34/666(5%)	Plus/Minus		
Features	S:						
Query	1533	TGGTGTAGTTC	GTATCCAGGAAGGA(GTTCTCTGGCGATAT	TTTGGGTGTGCGC	GTGGCCT	1592
Sbjct	751	†gdtgtagtt	sgtgtccagaaacga	GTTCTCCGGCGATAT	tttgggggtgcg	gtggcct	692
Query	1593	TAATCACCACO	CGGTTCCACCGTCTT	TTGGGTAGCCTTACG.	ATTGTAGAAGGAT	ACGCGTG	1652
Sbjct	691	TGATCACCACC	cddctcddcddtctt	cretteetetee	CTTGTGGAAGGAG	ACCCGGT	632
Query	1653	TATTTACCGA	ATCGGGTAAATCACG	rggcgacgatagatt	CTCGAAATCCTCG	TCTATGG	1712
Sbjct	631	tgttcaccdac	stedddaagateddd	cggcgaggacaggtt	ctcgaagtcctcg	rtcgatgg	572
Query	1713	AGCAGAGTGTC	CTTGTGTTCGGCATC	CTGTATCTTTGACTT	CAGTATTTCGGAA	TCGATCT	1772
Sbjct	571	AGCAGAGCTTC	cttdtdtttdddcatc	ctggatcttcgactt	gagcatctcggag	stegatet	512
Query	1773	GCTGCTGATGC	CTTGCCATTTGAAGT(GCGTCCATTGCTCTG	GATTTTGATTGGT	GCTGATT	1832
Sbjct	511	gctgctggtgd	cttdccgggcggdt	ĠĊĠŦĊĊĠŦŦĠĊŦĊŦĠ	GATCTTGATGGGC	GCCGACT	452
Query	1833	TACCATACAAC	CATGGTAGTGGGGCT	GTCCTTCTCATCACT	GCTACT-	T	1879
Sbjct	451	tgccgtacagd	catedtgrtddddct	ctccccttcctcact	gcccctacccctc	cccctcc	392
Query	1880	C-C-GCTACCG	GCTT-CCGCTACC	GTTAACTAAAGTTCC	GTTGATGTTCATC	GACTTGC	1934
Sbjct	391	CACTGCCACCG	schgchgangcheced	gttggctatagtccc	GTTGATGTTCATC	GATTTGG	332
Query	1935	TGGCCGACTGC	TGTGGCAGCTTGCC	ATTCTGCAGGACTCC	GTTGGCCTTGCGC	G-C-CTG	1992
Sbjct	331	TGGCCGGC	CTGGGGCAGCTTGCC	GTTCTGAAGGACGCC	GTTGGCCTTGCGC	GGCTCCC	275

Query	1993	C-ACAGTTGGTTCAATCGAC-GAGTCAT-TGATG-GCCGATGAGTCCTCGTCGTC 20	043
Sbjct	274	CGACCGTCTCCTCAACGGGGGGCGTGGGCGTAGGGTGTGCCG-T-TGTCCTCGTCATC 2	17
Query	2044	GGGCTTGTCTAAACAATTTTTATATCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC 2	103
Sbjct	216	GGGCTTGTCTAAACGATTTTTATTTCTACGCCGAAACCAAAAGACGCCGAGTATAAATGC 1	57
Query	2104	TACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG 2	163
Sbjct	156	TACACCGGGCAGTGACAGGTAGAGTAGAGGACGACCGGATACCATTTTCGCTGAATATTG 9	7
Query	2164	AAAGAT 2169	
Sbjct	96	AAGGAT 91	

Drosophila persimilis GL14640 (Dper\GL14640), mRNA

Sequence ID: **ref|XM_002022623.1|** Length: 1818 Number of Matches: 1 Range 1: 802 to 1818

Score		Expect	Identities	Gaps	Strand	Frame
837 bits	(453)	0.0()	836/1024(82%)	14/1024(1%)	Plus/Minus	
Features	s:					
Query	391	TTAGTCACT	CATCTCCACCCATTT(- - - - - - - - - - - - - - - - - - -	ACCAGCTCCTTATT	GATAAA 450
Sbjct	1818	TTAGTCACG	CATCTCCACCCATTT	CGCGAGATTTCTGGCG	ACCAGTTCCTTATT	GAGAAA 1759
Query	451	GATTACATT.	ATTGGGACCTAGGGA	rgcgaataaaaagatt	TCTGGTAGGTTGTG	GACTATT 510
Sbjct	1758	GATTACATT.	AttGGGGCCtAGGGA	agcadatddddddddtt	tctggtargttgtd	sactatt 1699
Query	511	ATAGCCGGC	GACTTGTGCTTGCAA(GACAATGCCTTTGGTA	AGTTTGTTGAGGAT	TTCGGC 570
Sbjct	1698	GTAGCCGGC	gycttetectyc	GACAATGCCTTTGGTT	AGTTTGCTGAGGAC	CATCGAT 1639
Query	571	CGCCTCAAT	GGACCAGGTGCCACC	GATGGGCTCAATGTTG	GACAGGATGCATTC	CGGTGGA 630
Sbjct	1638	¢Ġ¢¢†¢cÅG.	adaccaddtaccgtt	aatgggctcaatgttg	ĠĀĊĀĠĠĀŦĠĊĀŦŦĊ	crótcóc 1579
Query	631	CTGGAAGGG	CACATTCATGAAATCO	GGTGCGAATCTGTCGC	AGTGTGTTGAAGCC	CGACATT 690
Sbjct	1578	ĊŢĠĠĀĀĠĠĠ	TÁCCACCÁTGÁÁÁTC	agtgcgaatctgacgg	AĠCACĠGAĠĀGĠŦŢ	rcAcGtt 1519
Query	691	CATGTAGCC.	ACCAAAGTCAAGAAA(CTTGATTACGCAACGC	TCC-TCGTCCTC	CGGGATC 747
Sbjct	1518	ĊATĠTAĠĊĊ.	AĊĊGAAATĊAAĠGAA:	rttaaccacacaaddcc	tcttcatcctc	CÀTC 1462
Query	748	TGTG-TCGA	CAATCTGGACGCGATA 	ACCACACATCATTGAT 	GGGTATCACGCAC <i>F</i>	ACGGCAC 806
Sbjct	1461			ÁCCÁGÁTCCCGTTGÁC		
Query	807			GCGCCTCCATGGTGGA 		
Sbjct	1402			ĠĊĠĊĊϮĊĊĂϮττCAĠĀ		AAĊŦĠĊŦ 1343
Query	867			GCGAGGGATGCAGCGG 		
Sbjct	1342			ĠĊĠĀĠĠĠĀŦĠĊĀĠĊĠĠ		
Query	927			CCACATCGTTGTTGAT		
Sbjct	1282			ĊĊĂĊĂŢĊĂŢŢĠŢŢĠĂŢ		
Query	987 1222			AAAGAGGAACTATGGT 		
Sbjct	1047			AGCGCTTGGCCGGCAA		
Query Sbjct	1162			AGCGCTTGGCCGGCAA 		
Query	1102			TTCCCTC-A-ATGGTA		
Sbjct	1107					
Query	1165			CGCTGGCCAGGGTCTT		
Sbjct	1044			CATTCGCCTGGGTCTT		
Query	1224			GACCAATCAAGCTGAT		
Sbjct	985					
Query	1284			AGCGCGGCAAGCTGGA		
Sbjct	925					
J - G						

Query	1344	ATTGC	ACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTAC	1403
Sbjct	865	ACTGA		806
Query	1404	CATT	1407	
Sbjct	805	CATT	802	

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant A (Dpse\GA28855), mRNA Sequence ID: **ref|XM_002134382.2|** Length: 2252 Number of Matches: 2 Range 1: 1182 to 2199

Score		Expect	Identities	Gaps	Strand	Frame	
806 bits	(436)	0.0()	831/1025(81%)	14/1025(1%)	Plus/Minus		
Features	s:						
Query	390	GTTAGTCAC'	TCATCTCCACCCATT	TTGGCGAGCTTTCTGCC	GACCAGCTCCTTA!	TTGATAA	449
Sbjct	2199	GTTAGTCAC	GCATCTCCACCCAT	TTCGCGAGATTTCTGGC		rtgagaa	2140
Query	450	AGATTACAT	TATTGGGACCTAGG	GATGCGAATAAAAAGAT	TTCTGGTAGGTTG	rgactat	509
Sbjct	2139	AGATTACAT	tattggggcctagg	SAAGCAAATAAAAAGAT	ttctggtargttg	rgactat	2080
Query	510	TATAGCCGG	CGACTTGTGCTTGC <i>I</i>	AAGACAATGCCTTTGGT.	AAGTTTGTTGAGGA	ATTTCGG	569
Sbjct	2079	†G†AGCCGG	ċĠĂĊŦŦĠŦĠĊŦŦĠĊź	\AĠAĊAA†ĠĊĊ†††ĠĠ†	ragtttgctgagg	Acatcga	2020
Query	570	CCGCCTCAA!	TGGACCAGGTGCCAC	CCGATGGGCTCAATGTT	GGACAGGATGCAT'	rcggtgg 	629
Sbjct	2019	TTĠĊĊĊĊĊ	grĠÁĊĊÁĠĠŦAĊĊG1	ŗŦĸĸĠĠĠĠĊĠĊĸĸĸĠĠĠ	ĠĠĀĊĀĠĠĀŦĠĊĀŦ	rctgtcg	1960
Query	630	ACTGGAAGG(GCACATTCATGAAAT 	rcggtgcgaatctgtcg 	CAGTGTGTTGAAG(CCGACAT 	689
Sbjct	1959	CĊŢĠĠĀĀĠĠ	GTACCACCATAAAA1	rcagtgcgaatctgacg	GÅĠCACĠGAĠĀGĠ!	rtcåĊGŤ	1900
Query	690			\ACTTGATTACGCAACG 			746
Sbjct	1899			\ATTTAACCACACAACG			1843
Query	747			ATACCACACATCATTGA' 			805
Sbjct	1842			ÁTÁCCÁGÁTCCCGTTGÁ			1784
Query	806			rGGCGCCTCCATGGTGG.			865
Sbjct	1783			AĞĞCĞCCTCCATTTCAĞ.			1724
Query	866 1723			ATGCGAGGGATGCAGCG 			925 1664
Sbjct	926			FACCACATCGTTGTTGA			985
Query Sbjct	1663			CACCACATCGTTGTTGA 			1604
Query	986			CGAAAGAGGAACTATGG			1045
Sbjct	1603						1544
Query	1046			ATAGÇÇÇTTÇGÇÇÇÇÇA.			1105
Sbjct	1543	ATGCGTTGC				 CATGGCC	1484
Query	1106	ĄĢĢĢÇĢĢÇĄ!	ГСААТСТСБСТСТСС	СĞТТСССТС-А-АТGĞT.	ĄCĄGĄŢĢÇĢCĄCÇ'	ŗŢGCCCĢ	1163
Sbjct	1483	AGGGCGGCA					1426
Query	1164	AGTAGGGAT'	rcttgccta-cagac	CACGCTGGCCAGGGTCT'	ŢĢĢÇÇŢŢĢĄŢŢŢĢ	GTTAATA	1222
Sbjct	1425	TGCATGGGT	rcttgctgagcag-c	CACATTCGCCTGGGTCT	TGGCCTTGATCTG	GTTGATG	1367
Query	1223	AACGCCCGC'	TTGCGGCCGTACAGO	GTGACCAATCAAGCTGA'	TCGGGAAGAGGAAG	CTCGTAG	1282
Sbjct	1366	AAGGCGCGC	ttgcggccgtacago	CTGGCCAATCAGGCTGA	CGGGGAAGACAAA	ctcgtag	1307
Query	1283	GTGGTTTTC	ACGCGTGTCGCCTC	CGAGCGCGGCAAGCTGG.	ATCCCTTGCCAGA	ATCGCCC	1342
Sbjct	1306	CTGACCTTGA	ACACGTGTCGCCTC	CGAGCGGGGCAGACTAG.	AGCCCTTACCAGAG	gtcccc	1247
Query	1343	GATTGCACA(CTGCAAATGCTCAG(CGATGGACTGGCCGCAT	CCACATTGCGCTT(CTGATTA	1402
Sbjct	1246	GACTGAACG	ctdcaaatdctgad	cdagddactddccdcat	ccycytagegepte	ctdgttg	1187
Query	1403	CCATT 140	07				
Sbjct	1186	टेटेंबर्नर 118	82				

Score		Expect	Identities	Gaps	Strand	Frame	
353 bits	(191)	8e-93()	527/685(77%)	39/685(5%)	Plus/Minus		
Features	s:						
Query	1505	CAGTTGTTGT	TCTGCTCGCACTCCT	ŢGTTGĢŢĢŢĄGTŢĢ¢	ĢTAŢÇCĄĢĢĄĄGĢĄ	GTTCTCT	1564
Sbjct	1033	CAGTTGTTGT	tctgctcgcactcct	tcGtGtAtGtG	GCCTCAAGGAACGA	GTTCTCT	977
Query	1565	GGCGATAT-T	TTGGGTGTGCGCGTG	GCCTTAATCACCAC	CGGTTCC-ACCG	T-CTTTT	1619
Sbjct	976	GGCGATATCT	ttggg-gtgcgtgtg	GCCTTGATTACCAC	CGGCTCGACGACCT	tgctgtt	918
Query	1620	GGGTAGCCTT	ACGATTGTAGAAGGA	TACGCGTGTATTTA	CCGAATCGGGTAAA 	TCACGTG	1679
Sbjct	917	-ĠĠtĊtt	gcgattgtggaataa	.gactccttctctctca	cceaatcee	т çесесе	862
Query	1680	GCGACGATAG	ATTCTCGAAATCCTC	GTCTATGGAGCAGA	GTGTCTTGTGTTCG 	GCATCCT	1739
Sbjct	861	ĠĊĠĀĊĠĀĊĀĠ	Attctcaaagtcttc	ATCAATCGAGCAGAG	\$CTTTTTGTGCTCG	ĠĊĀŢĊĊŢ	802
Query	1740	GTATCTTTGA	CTTCAGTATTTCGGA	ATCGATCTGCTGCT(GATGCTTGCCATTT 	GAAGTGC 	1799
Sbjct	801	ĠŦĀŦĊŦŦŦĠĀ	ĊϮϮĠÅĠĊÅϮĊϮĊŦĠÅ	.G†ĊĠÀ†Ċ†ĠĊ†Ġ_†	†ĠĊACAĊĊCGGC	ĠĠĀĠŦĊĊ	745
Query	1800	GTCCATTGCT	CTGGATTTTGATTGG	TGCTGATTTACCATA	ACAACATGGTAGTG 	GGGCTGT 	1859
Sbjct	744	ĠŦĊĊĂŦŦĠĊŦ	ĊϮĠŦĂϮĊϮϮĠĂϮĠĠĠ	AĠĊĊĠĂĊŤŤŦĊĊĠŤ	ACAGCATTGTGTTG	ĠĠAĊŦAŦ	685
Query	1860	CCTTCTCATC	ACTGCTACTTCCGCT	ACCGCTTCCGCTAC	CGTTAACTAAAGTT 	CCGTTGA	1919
Sbjct	684	ccttttcctc	gctgccgctgcccct	CCCGTTGCCATTTT	ctgtggcatctgtg	ĊĊĠŦŦĠĂ	625
Query	1920	TGTTCATCGA	CTTG-CTGG	CC-GACTGCT-G'	r-ggcagcttgcca 	TTCTGCA	1967
Sbjct	624	†a††ca†cga	тттветтвсствств	ĊTGĊAĠĀAAĠĊŤĊĠ:	tcĠĠĠĀĠĊţţĠĊĊĀ	ттстста	565
Query	1968		GGCCTTGCGCGCCTG				2020
Sbjct	564	GCCCACCGTT	rdcagtddddddddtc	ĊAĊA-TGĠĠAGAĊG	AcgccAcccGAcGA	ctccttc	506
Query	2021	ATGGCCGATG	AGTCCTCGTCGTCGG	GCTTGTCTAAACAA'	TTTTTATATCTACG	CCGAAAC	2080
Sbjct	505	GTG-CTG-T-	retectectect	ĠĊŦŦĠŦĊŦĂĂĂĊĠĂŗ	tttttatttctacc	TĊĠĠĀĀĊ	449
Query	2081	CAAAAGACGC	CGAGTATAAATGCTA	CACCGGGCAGTGAG	AGGTAGAGTAGAGG	ACGACCG	2140
Sbjct	448	ĊAAAACAĊĠĊ	ccaggataaatgcta	.caccgggcagtgac	akagtagagtagtgg	AĊĠĀĊĊĠ	389
Query	2141	GATACCATTT	TCGCTGAATATTGAA	2165			
Sbjct	388	GATACCATTT	tcgctgaatattgaa	364			

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA28855), mRNA Sequence ID: **ref|XM_015186614.1|** Length: 2259 Number of Matches: 2 Range 1: 1189 to 2206

Score		Expect	Identities	Gaps	Strand	Frame	
806 bits((436)	0.0()	831/1025(81%)	14/1025(1%)	Plus/Minus		
Features	3 :						
Query	390	GTTAGTCAC	TCATCTCCACCCATTT	rggcgagctttctgcc	GACCAGCTCCTTA	TTGATAA	449
Sbjct	2206	GTTAGTCAC	GCATCTCCACCCATT	rcgcgagatttctggc	GACTAGTTCCTTA	TTGAGAA	2147
Query	450	AGATTACAT	TATTGGGACCTAGGG	ATGCGAATAAAAAGAT	TTCTGGTAGGTTG	TGACTAT	509
Sbjct	2146	AGATTACAT	TATTGGGGCCTAGGG	AAGCAAATAAAAAGAT	TTCTGGTATGTTG	stgactat	2087
Query	510	TATAGCCGG	CGACTTGTGCTTGCA	AGACAATGCCTTTGGT	'AAGTTTGTTGAGG	SATTTCGG	569
Sbjct	2086	TGTAGCCGG	cdacttdtdcttdcaz	AGACAATGCCTTTGGT	TAGTTTGCTGAGG	SACATCGA	2027
Query	570	CCGCCTCAA	TGGACCAGGTGCCAC	CGATGGGCTCAATGTT	GGACAGGATGCAT	TCGGTGG	629
Sbjct	2026	TTGCCTCCA	GTGACCAGGTACCGT	raatgggctcaatgtt	GGACAGGATGCAT	TCTGTCG	1967
Query	630	ACTGGAAGG	GCACATTCATGAAATO	CGGTGCGAATCTGTCG	CAGTGTGTTGAAG	CCGACAT	689
Sbjct	1966	CCTGGAAGG	GTACCACCATAAAAT	CAGTGCGAATCTGACG	GAGCACGGAGAGG	TTCACGT	1907
Query	690	TCATGTAGC	CACCAAAGTCAAGAA/	ACTTGATTACGCAACG	CTCC-TCGTCC	TCGGGAT	746
Sbjct	1906	tcatgtagc	caccgaaatcaagga	ATTTAACCACACAACG	ctcrrcatcgtcc	rtcAt	1850

Query	747	CTGTG-TCGACAATCTGGACGCGATACCACACATCATTGATGGGTATCACGCACACGGCA	805
Sbjct	1849	C-GAGATCGACGATTTGTACGCGATACCAGATCCCGTTGACAGGCAGCACGCAAACGGCA	1791
Query	806	CTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGTGGAGTAGCTATCGTACAGCTGC	865
Sbjct	1790	CTGATCTCAATGCCCGGAAGCAGAGGCGCCCCCATTTCAGAGTAACTGTCGAACAACTGC	1731
Query	866	TTCTGCAGCAAAGGCAACGATGGATGCGAGGGATGCAGCGGGTGCTGGATGAAAATATGC	925
Sbjct	1730	ttctgcagcattgcagtgctggatgcgagggatgcagcagatgattgacaaacagatgc	1671
Query	926	GACCCAGATAGCACCGCACTCACTACCACATCGTTGTTGATGCCCTCAATCAGTTTCAGT	985
Sbjct	1670	GATCCCGAGAGCACGGCACTGACCACCACATCATTGTTGATGCCCTCAAAGAGTTTAAGT	1611
Query	986	TGTAGATTGTAGAGGCTTTCGGTCGAAAGAGGAACTATGGTCTGGGGAAGCGCAAAGTGG	1045
Sbjct	1610	tetaeattegaeaeeettetetetetetetetetetetet	1551
Query	1046	ATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGGCAAACGTTGACGGATCATGGCC	1105
Sbjct	1550	AtGCGTTGCATTGTAAAGTTGGGATACCGCTTGACCGGCAGACGCTGACGGATCATGGCC	1491
Query	1106	AGGGCGGCATCAATCTCGCTCTCCGTTCCCTC-A-ATGGTACAGATGCGCACCTTGCCCG	1163
Sbjct	1490	AGGGCGGCATCGATCTCGCTCCGTGCCTTCGACAACGCA-A-ATGCGAAGCTTATTTG	1433
Query	1164	AGTAGGGATTCTTGCCTA-CAGACACGCTGGCCAGGGTCTTGGCCTTGATTTGGTTAATA	1222
Sbjct	1432	rgcargggttcttgctgagcag-cacartcgcctgggtcttggccttgatctggttgatg	1374
Query	1223	AACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGATCGGGAAGAGGAACTCGTAG	1282
Sbjct	1373	AAGGCGCGCTTGCGCCGTACAGCTGGCCAATCAGGCTGACGGGGAAGACAAACTCGTAG	1314
Query	1283	GTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGATCCCTTGCCAGAATCGCCC	1342
Sbjct	1313	ctgaccttgacacgtgtcgcctccgagcgggcagactagagcccttaccagagtccccg	1254
Query	1343	GATTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTA	1402
Sbjct	1253	GACTGAACGCTGCAAATGCTGAGCGAGGGACTGGCCGCATCCACATTGCGCTTCTGGTTG	1194
Query	1403	CCATT 1407	
Sbjct	1193	ccatt 1189	

Range 2: 355 to 1040

Score		Expect	Identities	Gaps	Strand	Frame	
361 bits	(195)	5e-95()	540/702(77%)	41/702(5%)	Plus/Minus		
Features	S:						
Query	1505	CAGTTGTTGT	TCTGCTCGCACTCC	TTGTTGGTGTAGTTGG	TATCCAGGAAGGA	GTTCTCT	1564
Sbjct	1040	CAGTTGTTGT	tctgctcgcactcc	rtcdrdtatgrdd	cctcaaggaacga	ĠŦŦĊŦĊŦ	984
Query	1565	GGCGATAT-T	TTGGGTGTGCGCGT	GGCCTTAATCACCACC	GGTTCC-ACCG	T-CTTTT	1619
Sbjct	983	GGCGATATCT	- -	GGCCTTGATTACCACC	:ddctcgacgacct	tgctgtt	925
Query	1620	GGGTAGCCTT	ACGATTGTAGAAGG	ATACGCGTGTATTTAC	CGAATCGGGTAAA	TCACGTG	1679
Sbjct	924	-GGTCTT	GCGATTGTGGAATA	AGACTCGTGTGCTGAC	:cdaatcdddgaaga	4cecece	869
Query	1680	GCGACGATAG	ATTCTCGAAATCCT(CGTCTATGGAGCAGAG	TGTCTTGTGTTCG	GCATCCT	1739
Sbjct	868	GCGACGACAG	AttctcaAAgtctt	catcaatcgagcagad	crtrttdtdctd	dcatcct	809
Query	1740	GTATCTTTGA	CTTCAGTATTTCGG	AATCGATCTGCTGCTG	ATGCTTGCCATTT	GAAGTGC	1799
Sbjct	808	GTATCTTTGA	.cttgagcatctctg	Agtcgatctgctg-t-	tgcacacccgc	ggygtcc	752
Query	1800	GTCCATTGCT	CTGGATTTTGATTG	GTGCTGATTTACCATA	CAACATGGTAGTG	GGGCTGT	1859
Sbjct	751	ĠŦĊĊĂŦŦĠĊŦ	ctgratcttgatgg	gagccgactttccgta	ckgcktrgtgttg	ĠĠaĊϮaϮ	692
Query	1860	CCTTCTCATC	ACTGCTACTTCCGC	TACCGCTTCCGCTACC	GTTAACTAAAGTT	CCGTTGA	1919
Sbjct	691	ccttrtcctc	·gċtĠċcgċtgċċĠċ	tcccctrtcccartrtc	rgtgg¢atctģtg	cccttca	632
Query	1920	TGTTCATCGA	CTTG-CTG0	GCC-GACTGCT-GT	-GGCAGCTTGCCA	TTCTGCA	1967
Sbjct	631	tattcatcga	rrrggttgcctgcr	śctgcagaaagctcgt	rcĠĠĠĀĠĊŦŦĠĊĊĀ	ттстста	572
Query	1968	GGACTCCGTT	GGCCTTGCGCGCCT	GCACAGTTGG-TTC-A	A-TCGACGA	GTCATTG	2020
Sbjct	571	ĠĊĊĊĀĊĊĠŦŦ	ŢĠĊAGŤĠĊĠĊĠĊĊŤ	ccaca-tgggagacga	cgccacccdacda	ctccttg.	513
Query	2021	ATGGCCGATG	AGTCCTCGTCGTCG(GGCTTGTCTAAACAAT 	TTTTATATCTACG	CCGAAAC 	2080

Sbjct	512	GTG-CTG-T-TGTCCTCGTCGGGCTTGTCTAAACGATTTTTATTTCTACGTCGGAAC	456
Query	2081	CAAAAGACGCCGAGTATAAATGCTACACCGGGCAGTGAGAGGTAGAGTAGAGGACGACCG	2140
Sbjct	455	CAAAACACGCCCAGGATAAATGCTACACCGGGCAGTGACAAGTAGAGTAGTGGACGACCG	396
Query	2141	GATACCATTTTCGCTGAATATTGAAAGATCTTT-GTGAACCG 2181	
Shict	395	GATACCATTTTCGCTGAATATTGAAGGCTCTTTTGT-AACCG 355	

Drosophila virilis uncharacterized protein (Dvir\GJ14809), mRNA

Sequence ID: **ref|XM_002059478.2|** Length: 2676 Number of Matches: 2 Range 1: 1334 to 2374

Score		Expect	Identities	Gaps	Strand	Frame	
749 bits	(405)	0.0()	844/1055(80%)	34/1055(3%)	Plus/Minus		
Features	s:						
Query	374	ĢŢŢĢŢŢÇĄC:	ГААĢĢСТĢТТАĢТСА	СТСАТСТССАСССАТТ	[,] ТĢĢÇĢĀĢСŢŢŢĊŢ	ĢCÇĢĄÇC	433
Sbjct	2374	GTTGTTCAT	GAAGGCTGTTAGTCA	CGCATCTCGACCCACT	rtggcgagatttct	GGCGACA	2315
Query	434	AGCTCCTTA!	TTGATAAAGATTACA	TTATTGGGACCTAGGG	ATGCGAATAAAAA	GATTTCT	493
Sbjct	2314	AGTTCCTTA:	rtgataaaaataaca	TTATTTGGACCTAGAG	AAGCAAATAAATA	GATTTCT	2255
Query	494	GGTAGGTTG	rgactattatagccg	GCGACTTGTGCTTGCA	AGACAATGCCTTT	GGTAAGT	553
Sbjct	2254	GGTATATTA	rdgctattgtadccd	gcgycttgtgcttgcy	Adacaatdccttt	GGTTAAT	2195
Query	554	TTGTTGAGG	ATTTCGGCCGCCTCA	ATGGACCAGGTGCCAC	CGATGGGCTCAAT	GTTGGAC 	613
Sbjct	2194	††d††dådda	Atatcacccccatcc	gcagaccaggtgtcat	cccatrcccat	gttggac	2135
Query	614	AGGATGCAT	FCGGTGGACTGGAAG 	GGCACATTCATGAAAT	'CGGTGCGAATCTG' 	TCGCAGT	673
Sbjct	2134	AGTATGCAT:	rcgctreck	ĠĠĊĀGCGŤĊĀŤĠĀĀGŤ	ccdtdddrattd.	AĊĠĊĀĠŦ	2075
Query	674	GTGTTGAAG(CCGACATTCATGTAG 	CCACCAAAGTC-AAGA	AACTTGATTACGC.	AACGCTC 	732
Sbjct	2074	TCĠCŤAÁÁĠ	ĊŢĠĀĊĀŢŢĊĀŢĠŢĀĠ	ccaccaaagtccaaga	.AT-TTGACCAGAC.	AGĊĠĊϮG	2016
Query	733			-AATCTGGACGCGATA		GATGGGT 	790
Sbjct	2015			AAATĊTĠTAĊĠĊĠAŢĀ			1958
Query	791			AAACTGGGCAGCAAT-			847
Sbjct	1957			ÀÀT-TCC-ĊGĠĊÀÀTT			1901
Query	848			TGCAGCAAAGGCAACG			904
Sbjct	1900	TAACTGTC-		TGTAGCGCATGCAAGG			1844
Query	905 1843			-CCAGATAGCACCGCA			963 1785
Sbjct Query	964			TAGATTGTAGAGGCTT			1023
Sbjct	1784			TAGGCTGTGGAGGCTT			1725
Query	1024			GCGTTGCATGGTGAAG			1083
Sbjct	1724		 AAGCGCATAGTGGAT	 TCTCTGCATTGTGAAA	 .TTTGGATAGCGTC'	 TGGCTGG	1665
Query	1084	ҪѦ҈ѦѦҪ҅Ҫ҄҅҄҄ТҬ҅Ҫ҈	AÇĞGATÇATĞĞÇÇAĞ	GGÇGGÇATÇAATÇTÇG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	СААТĢĢТ	1143
Sbjct	1664	CAAACGCTG	GCGTATCATGGCCAG	CGCGGCATCGATCTCG	CTCTCGGTGCCCT	 CGATGGT	1605
Query	1144	АСАСАТССС	ÇĄССŢŢGÇÇСĢĄ-Ģ-	-ŢĄGGĢĄŢŢÇŢŢĢÇCŢ	'AÇAGAÇAÇGÇ-TG	–ĢÇÇĀGĢ	1198
Sbjct	1604	GCAAATGCG			'-CAGTCCCACATT'	TGCCAAG	1547
Query	1199	GTCTTGGCC'	PTGATTTGGTTAATA	AACGCCCGCTTGCGGC	CGTACAGGTGACC.	AATCA-A	1257
Sbjct	1546	GTTTTGGCC'	rtgatttgattgatg	AACGAACGCTTCCGTC	CATACAGCTGGCC	GATCAGA	1487
Query	1258	GÇTGATCGG	GAAGAGGAACTCG-T	AGGTGGTTTTCACG	CGT-GTCGCCTCC	GAGCGCG	1313
Sbjct	1486	AC-ATTTGG	adagaagaaa-cgat	ACGAGGTCTTCATACG	reteeteeeter	GAACGCG	1429
Query	1314	GCAAGCTGG	ATCCCTTGCCAGAAT	CGCCCGATTGCACACT	GCAAATGCTCAGC	GATGGAC	1373
Sbjct	1428	GCAGGCTGG	AACCTTTACCAGAAT	CACCGGATTGTACACT	'GCAAATGCTGAGC	GATGGAC	1369
Query	1374	TGGCCGCAT	CCACATTGCGCTTCT	GATTACCATTG 140	8		
Sbjct	1368	†ggccgca†	ccacattacccttct	GATTGCCATTG 133	4		

Range 2: 365 to 487

Score		Ex	pect	Identities	Gaps	Strand	Frame	
183 bits(99)		1e-	41()	115/123(93%)	0/123(0%)	Plus/Minus		
Features	s:							
Query	2051	ТСТА	AACAAT	TTTTTATATCTACGO	CCGAAACCAAAAGAC	GCCGAGTATAAAT	GCTACACCG	2110
Sbjct	487	ффф	CACGA	rtttatrtctacc	CCGAAACCAAAAGAC	GCCGAGTATAAAT	GCTACACCG	428
Query	2111	GGCA	GTGAG <i>I</i>	AGGTAGAGTAGAGG	ACGACCGGATACCATT	TTTCGCTGAATAT	TGAAAGATC	2170
Sbjct	427	GGCA	GTGAC	AGATAGAGTAGAGG	ACGACCGGATACCAT	rttccctcaatat	TGGAGAATC	368
Query	2171	$\mathbf{T}\mathbf{T}\mathbf{T}$	2173					
Sbjct	367	ተተተ	365					

Drosophila grimshawi GH24358 (Dgri\GH24358), mRNA

Sequence ID: **ref|XM_001992140.1|** Length: 1884 Number of Matches: 2 Range 1: 861 to 1875

Score		Expect	Identities	Gaps	Strand	Frame
706 bits	(382)	0.0()	814/1024(79%)	24/1024(2%)	Plus/Minus	
Features	S :					
Query	400	CATCTCCAC	CCATTTGGCGAGCTTT	CTGCCGACCAGCTCC	TTATTGATAAAGAT	TACATT 45
Sbjct	1875	CATCTCGAC	CCATTTTGCGAGATTT	'CTAGCGACAAGTTCC'	TTATTGATAAAAAT	TATATT 18
Query	460	ATTGGGACC	TAGGGATGCGAATAAA	AAGATTTCTGGTAGG	TTGTGACTATTATA	AGCCGGC 51
Sbjct	1815	Attredace	tagagaagcaaataaa	ĸŦĀĠĀŦŦŦĊŦĠĠŦĀŦĠ	ttatggctattgta	sdeedde 17
Query	520	GACTTGTGC	TTGCAAGACAATGCCT 	TTGGTAAGTTTGTTG.	AGGATTTCGGCCGC	CTCAAT 57
Sbjct	1755	ĠĀĊŢŢĠŢĠĊ	trĠĊAAĠAĊAAtĠĊĊt	יִלילְּלֵּלִידִאֹבִלִילִילִּילִילִילִילִילָּ	AĠĠĀŦĀŦĊĀĠĊĊĠĊ	
Query	580		GCCACCGATGGGCTCA			
Sbjct	1695		ATĊĀTĊĠĀŤŦĠĠĊŤĊŒ			
Query	640		TGAAATCGGTGCGAAT			
Sbjct	1635		TAAAATCTGTCCGAAT			
Query Sbjct	699 1576		C-AAGAAACTTGATTA 			
Query	758		CGATACCACACAT0			
Sbjct	1517	ATCTGCACA		ZATTGATGGGCATCAC.		
Query	816		GCAATGGCGCCTCCAT			
Sbjct	1459	TGTTTGGCA			 GTACA-TGGCCTTC	
Query	875	AAAGGÇAAC	<mark>Ģ</mark> ĄŢĢĢĄŢĢÇĢĄGĢĢĄŢ	ŀĢÇĄGÇĢĢGŢĢÇŢĢĢĄ	ŢĢĄĄAĄTĄŢĢCĢAÇ	С-ССАБА 93
Sbjct	1400	GCATGCAGT		GCAACGGATGCTGGA	TGAACACATG-GTC	CTCCAGA 13
Query	934	TAGCACCGC.	ACTCACTACCACATCO	TTGTTGATGCCCTCA.	ATCAGTTTCAGTTC	STAGATT 99
Sbjct	1341	GAGCACAGC	GCTGACCACAACATCA	ATTGTTGATGCCTTCG.	ATCAGATTTAGTTC	STAGATT 12
Query	994	GTAGAGGCT	TTCGGTCGAAAGAGG <i>A</i>	ACTATGGTCTGGGGA	AGCGCAAAGTGGAT	GCGTTG 10
Sbjct	1281	ATAGAGGCT	ttcagtcgaaagagga	Actacggtttgcgga	adcdcataatddat	rcdttd 12
Query	1054	CATGGTGAA	GTTCGGATAGCGCTTG	GCCGGCAAACGTTGA	CGGATCATGGCCAG	GGCGGC 11
Sbjct	1221	cattgtgaa	attgggatagcgtcta	ĸĠĊŦĠĠĊAAAĊĠŦŦĠĠĸ	ĊĠŦĂŦĊĂŦŦĠĊĊĂĀ	
Query	1114		GCTCTCCGTTCCCTC <i>P</i> 			
Sbjct	1161		ATŤĊŤĊŦĠŤGĊĊĊŤĊ <i>Ŕ</i>			
Query	1171		TA-CAGACACGCTGGC 			
Sbjct	1101	TGTCTTGCT	TAGĊAC-ĊAĊATTTĠĊ	CCAAAGTTTTCGCCTT.	AA'I'CTGATTGATGA	AATĠTĊĊ 10

Query	1230	GCTTGCGGCCGTACAGGTGACCAATCAAGCTGATCGGGAA-G-AGGAACTCGTAGGTGGT	1287
Sbjct	1042	GTTTGCGTCCATACAACTGGCCAATTAGGCC-ATTGGGAAAGTAGAAACGA-TATGAGGT	985
Query	1288	TTTCACGCGTGTCGCCTCCGAGCGCGCAAGCTGGATCCCTTGCCAGAATCGCCCGA	1344
Sbjct	984	CTTCACGCGCGTTGTCGCCTCGAACGTGGCAGGCTAGAACCCTTGCCCGAATCACCCGA	925
Query	1345	TTGCACACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTGCGCTTCTGATTACC	1404
Sbjct	924	TTGTACACTGCAAATGCTCAGCGATGGACTTGCTGCATCCACATTACGCTTCTGATTGCC	865
Query	1405	ATTG 1408	
Sbjct	864	ATTG 861	

Range 2: 1 to 98

Score		Expect	Identities	Gaps	Strand	Frame	
143 bits	(77)	2e-29()	91/98(93%)	0/98(0%)	Plus/Minus		
Feature	s:						
Query	2051	TCTAAACAAT'	TTTTATATCTACGC	CGAAACCAAAAGAC	GCCGAGTATAAAT	GCTACACCG	2110
Sbjct	98	tctatacgat:	ttttatrtctaccc	CGAAACCAAAAGAC	sccgagtataaat	GCTACACCG	39
Query	2111	GGCAGTGAGA	GGTAGAGTAGAGGAG	CGACCGGATACCAT	2148		
Sbjct	38	GGCAGTGACA	J GAAAGAGTAGTGGA(CGACCGGATACCAT	1		

Drosophila willistoni uncharacterized protein (Dwil\GK25472), mRNA Sequence ID: **ref|XM_002070817.2|** Length: 1885 Number of Matches: 2 Range 1: 850 to 1848

Score		Expect	Identities	Gaps	Strand	Frame	
688 bits	(372)	0.0()	792/1001(79%)	3/1001(0%)	Plus/Minus		
Feature	s:						
Query	391	TTAGTCACTO	CATCTCCACCCATTTGG	GCGAGCTTTCTGCCG	SACCAGCTCCTTAT'	TGATAAA	450
Sbjct	1848	TTAGTCACGC	CATCTCGACCCATTTT	cGAGGTTTCTACCG	SACAAGTTCCTTAT	rgataaa	1789
Query	451	GATTACATTA	TTGGGACCTAGGGATG	CGAATAAAAAGATT	TCTGGTAGGTTGT	GACTATT	510
Sbjct	1788	AATTACATTA	tttggacctagagaad	ccaatagataaatt	rtctggtacattato	GGCTATT	1729
Query	511	ATAGCCGGCG	ACTTGTGCTTGCAAGA	CAATGCCTTTGGT <i>A</i>	AGTTTGTTGAGGA	TTTCGGC	570
Sbjct	1728	GTAGCCGGCT	akttgtgcttgcaaga	caatgeetttegt	Addttattdddadi	tttcagc	1669
Query	571	CGCCTCAATG	GACCAGGTGCCACCGA	TGGGCTCAATGTTC	GACAGGATGCATT(CGGTGGA	630
Sbjct	1668	¢¢¢T†¢GACA	daccaagtcttatcta	rtreectes	sgacaatatgcatt	стеттес	1609
Query	631	CTGGAAGGGC	CACATTCATGAAATCGG	TGCGAATCTGTCGC	CAGTGTGTTGAAGC(CGACATT	690
Sbjct	1608	ĊŦĠĠĀĀĀĠĠī	rACCGACATAAAGTCCC	stdddrattddddd	CÁGCAAGCCAÁÁGT'	raacatt	1549
Query	691	CATGTAGCCA	CCAAAGTCAAGAAACT	TGATTACGCAACGC	CTC-CTCGTCCTCG	GGATCTG	749
Sbjct	1548	catatagcca	cccaaatctaaaaatt	rbokkobbkookorr	rtcact-gtcctcg	ĠĠĀŦĊĠĠ	1490
Query	750	TGTCGACAAT	CTGGACGCGATACCAC	CACATCATTGATGGG	TATCACGCACACG	GCACTAA 	809
Sbjct	1489	tgtcaacaat	rtgcacacgataccaa	ArctcAttGAtGG	catcacccaaacc	ĠĊĀĊŦĠĀ	1430
Query	810	GCTCCAAACT	GGGCAGCAATGGCGCC	CTCCATGGTGGAGTA	AGCTATCGTACAGC'	IGCTTCT	869
Sbjct	1429	TĊŦĊAÅTGĊŦ	rĠĠĠĊĀAAĀGŦĠĠĀĠĊĀ	\r\ccatggtgtgtat	\dctgtcataaadg@	ccċttċt	1370
Query	870	GCAGCAAAGG	GCAACGATGGATGCGAG	GGATGCAGCGGGTG	CTGGATGAAAATA' 	TGCGACC	929
Sbjct	1369	GTAGCATGGG	ckaccarteckateckac	sddgtddaatddatd	rtggacaaacaca:	rgtgaac	1310
Query	930	CAGATAGCAC	CGCACTCACTACCACA	TCGTTGTTGATGCC	CTCAATCAGTTTC	AGTTGTA 	989
Sbjct	1309	сggatagtac	caddgdtgaddaddadd	rtcattgttaatacc	cctcgatcacttcg	AGTTGCA	1250
Query	990	GATTGTAGAG	GCTTTCGGTCGAAAGA	GGAACTATGGTCTG	GGGAAGCGCAAAG'	TGGATGC	1049
Sbjct	1249	ĠĀŢŢĠŢĀĠĀĠ	scctttctctctcdataaa	dgaactatagtrtd	ccgcyddggcyyydd	rgaatgc	1190
Query	1050	GTTGCATGGT	GAAGTTCGGATAGCGC	CTTGGCCGGCAAACG	GTTGACGGATCATG(GCCAGGG	1109

Sbjct	1189	GTTGCATTGTGAAATTTGGATAACGTTTCGATGGTAAACGCTGGCGTATCATTGAGAGAG	1130
Query	1110	CGGCATCAATCTCGCTCTCCGTTCCCTCAATGGTACAGATGCGCACCTTGCCCGAGTAGG	1169
Sbjct	1129	CCGCATCTATCTCGCTTTCAGTGCCCTCAATAGTGCAAATCCGCACCTTGCCCGAATATG	1070
Query	1170	GATTCTTGCCTACAGACACGCTGGCCAGGGTCTTGGCCTTGATTTGGTTAATAAACGCCC	1229
Sbjct	1069	GATTCTTGCCAAGCGACACACTGGCCAGAGTTTTGGTTTTGATTTGATTAATAAAGGCTC	1010
Query	1230	GCTTGCGGCCGTACAGGTGACCAATCAAGCTGATCGGGAAGAGGAACTCGTAGGTGGTTT	1289
Sbjct	1009	GCTTGCGGCCATATAGCTGGCCAATCAGACTAATCGGAAATAGAAATTCATATTTGGTCT	950
Query	1290	TCACGCGTGTCGCCTCCGAGCGCGGCAAGCTGGATCCCTTGCCAGAATCGCCCGATTGCA	1349
Sbjct	949	TGATGCGTGTAGCCTCCGAACGTGGCAGGCTGGAGCCTTTGCCGGAATCACCGGACTGAA	890
Query	1350	CACTGCAAATGCTCAGCGATGGACTGGCCGCATCCACATTG 1390	
Sbjct	889	TGCTGCAAATGCTCAACGATGGACTAGCTGCATCCAC-TTG 850	

Range 2: 29 to 158

Score		Expect	Identities	Gaps	Strand	Frame	
174 bits	(94)	7e-39()	119/131(91%)	2/131(1%)	Plus/Minus		
Features	s:						
Query	2051	TCTAAACAATT	TTTATATCTACGCCGA	ААССААААGACGC	ССАСТАТАААТСС	FACACCG	2110
Sbjct	158	TCTAAACGATT	TTTATTTCTACGCCGG	AACCAAAAGACTC	CGAGTATAAATGC:	TACACCG	99
Query	2111	GGCAGTGAGAG	GTAGAGTAGAGGACGA	CCGGATACCATTT	TCGCTGAATATTG	AAAGATC	2170
Sbjct	98	GGTAGTGATAA	atagagtagaggacga	ccggataccattt	tccctcaatattc	AAGAATC	39
Query	2171	T-TTGTGAACC	2180				
Sbjct	38	tcttgt-AAcc	29				

Drosophila mojavensis uncharacterized protein, transcript variant B (Dmoj\GI11050), mRNA Sequence ID: **ref|XM_015160555.1|** Length: 2997 Number of Matches: 2 Range 1: 1142 to 2185

Score		Expect	Identities	Gaps	Strand	Frame	
684 bits	(370)	0.0()	827/1050(79%)	22/1050(2%)	Plus/Minus		
Features	S :						
Query	375	TTGTTCACT	AAGGCT-GTTAGTCAC	TCATCTCCACCCATT'	TGGCGAGCTTTCTC	SCCGACC	433
Sbjct	2185	TTGTTCATT	rgggctrgttagtcag	GCATCTCGACCCATT	TAGCGAGATTTCT	GCGACA	2126
Query	434	AGCTCCTTA	TTGATAAAGATTACAT	TATTGGGACCTAGGG.	ATGCGAATAAAAAG	SATTTCT	493
Sbjct	2125	ATTTCCTTA	ttgataaaaattatgt	tgtttggacctagag.	AAGCAAATAAATAC	SATTTCT	2066
Query	494	GGTAGGTTG	rgactattatagccgg	CGACTTGTGCTTGCA	AGACAATGCCTTT(GTAAGT	553
Sbjct	2065	GGTATATTA	rggctattatagccgg	CGACTTGTGCTTGCA	AGACAATGCCTTTC	GTTAAT	2006
Query	554	TTGTTGAGG	ATTTCGGCCGCCTCAA	TGGACCAGGTGCCAC	CGATGGGCTCAATG	TTGGAC	613
Sbjct	2005	TTGCTGAGG	AtatcggccgcatcAA	CAGACCAGGTCTCAT	cgattggctcgac <i>i</i>	ATTGGAC	1946
Query	614	AGGATGCAT	rcggtggactggaagg	GCACATTCATGAAAT(CGGTGCGAATCTG1	CGCAGT	673
Sbjct	1945	AGTATGCAT	rcggtrgcctggaaag	gcaacgtcataaaat	ĊŦĠŦĠĊĠŦĂŦĊŦĠ <i>₽</i>	ACGCAAT	1886
Query	674	GTGTTGAAG(CCGACATTCATGTAGC	CACCAAAGTC-AAGA	AACTTGATTACGC <i>I</i>	ACGCTC	732
Sbjct	1885	ACACTAAAG	ctgacattcatatagc	CGCCAAAGTCCAAGA	AT-TTGACCACGC	recect.	1827
Query	733	CTCGTCCTC	GGG-ATCTGTGTCG	ACAATCTGGACGCGA'	TACCACACATCATT	GATGGG	789
Sbjct	1826	ctcgacatc	grigggategrigtec	ACGATTTGCACGCGA'	taccaaccgccatd	rgatggg	1767
Query	790	TATCACGCA	CACGGCACTAAGCTCC	AAACTGGGCAGCAAT	GGCGCCTCCATGG7	TGGAGTA	849
Sbjct	1766	CAACACACA	gacgcccctgatctcg	ATGCTCGGCAACTTG	ggcgcctccytgc	CGAGTA	1707
Query	850	GCTATCGTA	CAGCTGCTTCTGCAGC	AAAGGCAACGATGGA'	TGCGAGGGATGCAG	CGGGTG	909

Sbjct	1706	GCTGTCGAGCATGTTCTTCTGCAGTGCGTGTAGCGATGGGTGTGACGGATGCAGCGGATG	1647
Query	910	CTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	969
Sbjct	1646	CTGCACGAACACATGATTGCCAGAGAGCACTGCGGTGACGGACACATCATTGTTGATGCC	1587
Query	970	CTCAATCAGTTTCAGTTGTA-GAT-TGTAGAGGCTTTCGGTCGAAAGAGGGAACTATGGTC	1027
Sbjct	1586	CTCGATCAGGTTTAGTTGTAAGCTATGGAGGCTTTCAGTCGACAGAGGAACTATGGAT	1529
Query	1028	TGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGGCAAA	1087
Sbjct	1528	tgcggaagcgcatagtgaattctttgcattgtgaaattgggatagcgtctggatggcaaa	1469
Query	1088	CGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGTACAG	1147
Sbjct	1468	certegeetateategeeaecetegetegateteaetegetegetegetegetegeteget	1409
Query	1148	ATGCGCACCTTGCCCGAGTAGGGATTCTTGC-CTA-CAGACACGCTGGCCAGGGTCT	1202
Sbjct	1408	ATGCGCAGCTTGCCGGATGAGTAGCGATTCTTGCTCAAGCTGACATTGGCCAGAGTCT	1351
Query	1203	TGGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGA	1262
Sbjct	1350	tcGacttGatttattGatGatGatCGttGcGtcCatAtAGctGGcCAAtCAAGCtAT	1291
Query	1263	TCGGGAAGAGGAACTCG-TAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGGCAAG	1318
Sbjct	1290	trggaaagaagaag-cgatacgagctcttcacgcgtgacgtrgcctccgatcgcgcaag	1232
Query	1319	CTGGATCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCC	1378
Sbjct	1231	CTGGAGCCTTTGCCCGAATCGCCAGATTGTACGCTGCAAATGCTCAGCGATGGACTGGCT	1172
Query	1379	GCATCCACATTGCGCTTCTGATTACCATTG 1408	
Sbjct	1171	dcatccacgttdcdcttctdattgccattd 1142	

Range 2: 98 to 212

Score		Expect	Identities	Gaps	Strand	Frame	
185 bits	(100)	3e-42()	110/115(96%)	0/115(0%)	Plus/Minus		
Features	s:						
Query	2059	ATTTTTATATO	CTACGCCGAAACCAAA	AGACGCCGAGTAT	AAATGCTACACCGG	GCAGTGA	2118
Sbjct	212	AtttttAttt	CTACGCCGAAACCAAA	AAGACGCCGAGTAT	AAATGCTACACCGG	GCAGTGA	153
Query	2119	GAGGTAGAGT	AGAGGACGACCGGAT <i>A</i>	ACCATTTTCGCTGA	ATATTGAAAGATCT	TT 2173	
Sbjct	152	GAGATAGAGT	AGAGGACGACCGGATA	Accattttccctca	AtAttGGAGAAtct	rtt 98	

Drosophila mojavensis uncharacterized protein, transcript variant A (Dmoj\GI11050), mRNA Sequence ID: **ref|XM_002011490.2|** Length: 3253 Number of Matches: 2 Range 1: 1399 to 2442

Score		Expect	Identities	Gaps	Strand	Frame	
684 bits	(370)	0.0()	827/1050(79%)	22/1050(2%)	Plus/Minus		
Features	S :						
Query	375	TTGTTCACT	AAGGCT-GTTAGTCA	CTCATCTCCACCCATT	TGGCGAGCTTTCT	GCCGACC	433
Sbjct	2442	TTGTTCATT	TGGGCTTGTTAGTCA	GGCATCTCGACCCATT	TAGCGAGATTTCT	GGCGACA	2383
Query	434	AGCTCCTTA	TTGATAAAGATTACA'	TTATTGGGACCTAGGG	ATGCGAATAAAA 	GATTTCT	493
Sbjct	2382	ATTTCCTTA	ttgataaaaattatg	rtgttrggacctagad	adcadatdaatd	GATTTCT	2323
Query	494	GGTAGGTTG	TGACTATTATAGCCG	GCGACTTGTGCTTGCA	AGACAATGCCTTT	GGTAAGT	553
Sbjct	2322	GGTATATTA	tggctattatatagccg	gcgacttgtgcttgca	Adacaatdccttt	GGTTAAT	2263
Query	554	TTGTTGAGG	ATTTCGGCCGCCTCA	ATGGACCAGGTGCCAC	CGATGGGCTCAAT	GTTGGAC	613
Sbjct	2262	TTGCTGAGG	ATATCGGCCGCATCA	ACAGACCAGGTCTCAT	ccdattggctcgac	ATTGGAC	2203
Query	614	AGGATGCAT	TCGGTGGACTGGAAG	GGCACATTCATGAAAT	CGGTGCGAATCTG	TCGCAGT	673
Sbjct	2202	AGTATGCAT	tcggttgcctggaaa	ggcaacgtcataaaat	cctctccctctctcccc	acccaat	2143
Query	674	GTGTTGAAG	CCGACATTCATGTAG	CCACCAAAGTC-AAGA	AACTTGATTACGC	AACGCTC	732
Sbjct	2142	acactadag	crgacattcatatag	ccccaaadtccaada	AT-TTGACCACGC	Agccctc	2084

Query	733	CTCGTCCTCGGG-ATCTGTGTCGACAATCTGGACGCGATACCACACATCATTGATGGG	789
Sbjct	2083	ctcgacatcgttgggatcgttgtcacgatttgcacgcgattaccaaccgccattgatggg	2024
Query	790	TATCACGCACACGGCACTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGTGGAGTA	849
Sbjct	2023	CAACACAGACGGCGCTGATCTCGATGCTCGGCAACTTGGGCGCCCTCCATGCTCGAGTA	1964
Query	850	GCTATCGTACAGCTGCTTCTGCAGCAAAGGCAACGATGGATG	909
Sbjct	1963	GCTGTCGAGCATGTTCTTCTGCAGTGCGTGTAGCGATGGGTGTGACGGATGCAGCGGATG	1904
Query	910	CTGGATGAAAATATGCGACCCAGATAGCACCGCACTCACT	969
Sbjct	1903	ctgcacgaacacatgattgccagagagcactgcggtgacggacacatcattgttgatgcc	1844
Query	970	CTCAATCAGTTTCAGTTGTA-GAT-TGTAGAGGCTTTCGGTCGAAAGAGGGAACTATGGTC	1027
Sbjct	1843	ctcgatcaggtttagttgtaagctatggaggcttttcagtcgacagaggaactatggat	1786
Query	1028	TGGGGAAGCGCAAAGTGGATGCGTTGCATGGTGAAGTTCGGATAGCGCTTGGCCGGCAAA	1087
Sbjct	1785	TGCGGAAGCGCATAGTGAATTCTTTGCATTGTGAAATTGGGATAGCGTCTGGATGGCAAA	1726
Query	1088	CGTTGACGGATCATGGCCAGGGCGGCATCAATCTCGCTCTCCGTTCCCTCAATGGTACAG	1147
Sbjct	1725	cectegeetateateeteaceeteeteateateteacteteeteeteeteeteeteeteeteeteeteeteeteet	1666
Query	1148	ATGCGCACCTTGCCCGAGTAGGGATTCTTGC-CTA-CAGACACGCTGGCCAGGGTCT	1202
Sbjct	1665	Atgcccagcttcccccataccccattcttcctcaacctcatcattcccacactct	1608
Query	1203	TGGCCTTGATTTGGTTAATAAACGCCCGCTTGCGGCCGTACAGGTGACCAATCAAGCTGA	1262
Sbjct	1607	tcGacttGatttattGatGaacGtacGcttGcGtcCatataGctGGccAatcAaGctat	1548
Query	1263	TCGGGAAGAGGAACTCG-TAGGTGGTTTTCACGCGTGTCGCCTCCGAGCGCGCAAG	1318
Sbjct	1547	trggaaagaagaag-cgatacgagctcttcacgcgtgacgtrgcctccgatcgcgcaag	1489
Query	1319	CTGGATCCCTTGCCAGAATCGCCCGATTGCACACTGCAAATGCTCAGCGATGGACTGGCC	1378
Sbjct	1488	ctggagcctttgcccgaatcgccagattgtacgctgcaaatgctcagcgatggactggct	1429
Query	1379	GCATCCACATTGCGCTTCTGATTACCATTG 1408	
Sbjct	1428	GCATCCACGTTGCGCTTCTGATTGCCATTG 1399	

Range 2: 331 to 469

Score		Expect	Identities	Gaps	s	Strand	Frame	
191 bits	(103)	7e-44()	128/140(91	%) 2/140	0(1%)	Plus/Minus		
Feature	s:							
Query	2059	ATTTTTATAT	CTACGCCGAAA	.CCAAAAGACGCC	CGAGTATAAA	TGCTACACC	GGGCAGTGA	2118
Sbjct	469	ATTTTTATTT	CTACGCCGAAA	.ccaaaagacgcc	CGAGTATAAA	TGCTACACC	GGCAGTGA	410
Query	2119	GAGGTAGAGT	AGAGGACGACC	GGATACCATTTI	CGCTGAATA	TTGAAAGAT	CTTTGTGAA	2178
Sbjct	409	GAGATAGAGT	AGAGGACGACC	ddataccattt	rCGCTGAATA	TTGGAGAAT	CTTT-TGAA	351
Query	2179	-CCGCTTGGG	TAACTTATTT	2197				
Sbjct	350	ACCAGTGGGG	taaataattt	331				

Drosophila pseudoobscura pseudoobscura uncharacterized protein (Dpse\GA28909), partial mRNA Sequence ID: **ref|XM_002134381.2|** Length: 588 Number of Matches: 1 Range 1: 19 to 535

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
401 bits	(217)	3e-107()	421/521(81%)	8/521(1%)	Plus/Minus		
Feature	s:						
Query	390	GTTAGTCACTCA	TCTCCACCCATTTGGC	CGAGCTTTCTGCCC	GACCAGCTCCTTAT	TGATAA	449
Sbjct	535	GTTAGTCACGCA	tctccacccatttccc	cdadatttctddcd	ACTAGTTCCTTAT	TGAGAA	476
Query	450	AGATTACATTAT	TGGGACCTAGGGATGC	CGAATAAAAAGATT	TCTGGTAGGTTGT	GACTAT	509
Sbjct	475	AGATTACATTAT	TGGGGCCTAGGGAAGC	CAAATAAAAAGATI	rtctggtargttgt	GACTAT	416

Query	510	ŢĂŢĄĠĊĊĠĠĊĠĄĊŢŢĠŢĠĊŢŢĠĊĄĄĠĄĊĄĄŢĠĊĊŢŢŢĠĠŢĄĄĠŢŢŢĠŦŢĠĄĠĠĄŢŢŢĊĠĠ	569
Sbjct	415	TGTAGCCGGCGACTTGTGCTTGCAAGACAATGCCTTTGGTTAGTTTGCTGAGGACATCGA	356
Query	570	CCGCCTCAATGGACCAGGTGCCACCGATGGGCTCAATGTTGGACAGGATGCATTCGGTGG	629
Sbjct	355	TTGCCTCCAGTGACCAGGTACCGTTAATGGGCTCAATGTTGGACAGGATGCATTCTGTCG	296
Query	630	АСТĞĞAAĞĞĞCACATTÇATĞAAATÇĞĞTĞÇĞAATÇTĞTÇĞCAĞTĞTĞTTĞAAĞCCĞAÇAT	689
Sbjct	295	CCTGGAAGGGTACCACCATGAAATCAGTGCGAATCTGACGGAGCACGGAGAGGTTCACGT	236
Query	690	TCATGTAGCCACCAAAGTCAAGAAACTTGATTACGCAACGCTCC-TCGTCCTCGGGAT	746
Sbjct	235	TCATGTAGCCACCGAAATCAAGGAATTTAACCACACACGCTCTTCATCGTCCTCAT	179
Query	747	CTGTG-TCGACAATCTGGACGCGATACCACACATCATTGATGGGTATCACGCACACGGCA	805
Sbjct	178	C-GAGATCGACGATTTGTACGCGATACCAGATCCCGTTGACAGGCAGCACGCAAACGGCA	120
Query	806	CTAAGCTCCAAACTGGGCAGCAATGGCGCCTCCATGGTGGAGTAGCTATCGTACAGCTGC	865
Sbjct	119	CTGATCTCAATGCCCGGAAGCAGAGGCGCCCCCATTTCAGAGTAACTGTCGAACAACTGC	60
Query	866	TTCTGCAGCAAAGGCAACGATGGATGCGAGGGATGCAGCGG 906	
Sbjct	59	TTCTGCAGCATTGGCAGTGCTGGATGCGAGGGATGCAGCGG 19	

Drosophila busckii chromosome X sequence

Sequence ID: **gb|CP012528.1|** Length: 23724088 Number of Matches: 1 Range 1: 3573944 to 3574056

Score		Expect	Identities	Gaps	Strand	Frame	
176 bits	176 bits(95)		rs(95) 2e-39() 107/113(95%) 0/113(0%) Plus/Plus			'	
Feature: spoon	s:						
Query	2051	TCTAAA	CAATTTTTATATCTAC	GCCGAAACCAAAAG <i>I</i>	ACGCCGAGTATAA	ATGCTACACCG	2110
Sbjct	3573944	TCTAAA	CGATTTTTATTTCTACC	GCCGAAACCAAAAC	ACGCCGAGTATAA	ATGCTACACCG	3574003
Query	2111	GGCAGT	GAGAGGTAGAGTAGAG	GACGACCGGATACC	ATTTTCGCTGAAT.	ATTG 2163	
Shict	3574004	GGTAGTG	HACAGATAGAGTAGAG	ACGACCGGATACC	$\frac{1}{2}$	 ATTG 357405	6