BLAST®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CN9M9GN8014

- ► Formatting options
- ▶ Download

Blast report description

Nucleotide Sequence (1189 letters)

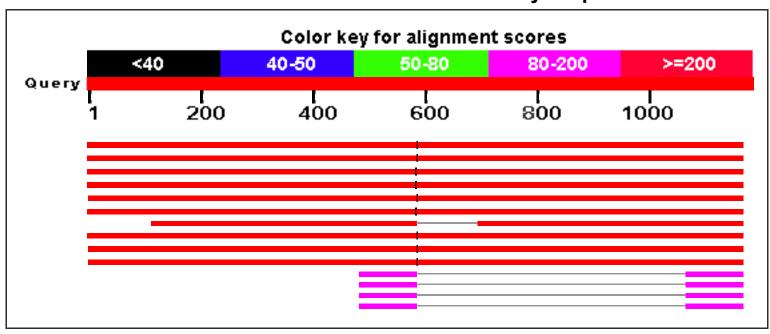
RID <u>CN9M9GN8014</u> (Expires on 02-23 13:11 pm)

Description None Description Nucleotide collection (nt)

Molecule type nucleic acid Program BLASTN 2.3.1+ Query Length 1189

Graphic Summary

Distribution of 28 Blast Hits on the Query Sequence



□ <u>Descriptions</u>

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila melanogaster luna, transcript variant C (luna), mRNA	1079	2159	98%	0.0	99%	NM_001273950.1
Drosophila melanogaster luna, transcript variant B (luna), mRNA	1079	2159	98%	0.0	99%	NM_206089.2
Drosophila melanogaster chromosome 2R	1077	2155	98%	0.0	99%	AE013599.5
Drosophila melanogaster, chromosome 2R, region 47D-47E, BAC clone BACR13D20, complete sequence	1077	2155	98%	0.0	99%	AC008187.6
Drosophila melanogaster luna, transcript variant D (luna), mRNA	1074	2148	98%	0.0	99%	NM_001299374.1
Drosophila melanogaster RE40136 full insert cDNA	1072	2144	98%	0.0	99%	BT126377.1
Drosophila melanogaster HL07808 full insert cDNA	869	1738	79%	0.0	99%	<u>AY122143.1</u>
Drosophila yakuba uncharacterized protein, transcript variant B (Dyak\GE13058), mRNA	671	1342	98%	0.0	88%	XM_015196803.1
Drosophila yakuba uncharacterized protein, transcript variant A (Dyak\GE13058), mRNA	665	1331	98%	0.0	88%	XM_002090305.2
Drosophila erecta uncharacterized protein (Dere\GG22702), mRNA	556	1113	98%	3e-154	85%	XM_001976107.2
Synthetic construct Drosophila melanogaster clone BO17282 encodes luna-RB	191	382	17%	3e-44	100%	FJ634070.1
Drosophila melanogaster transcription factor DKLF mRNA, complete cds	191	382	17%	3e-44	100%	AF461497.1
Drosophila sechellia GM20477 (Dsec\GM20477), mRNA	185	371	17%	2e-42	99%	XM_002033285.1
Drosophila simulans GD25946 (Dsim\GD25946), mRNA	180	360	17%	7e-41	98%	XM_002080935.1

□<u>Alignments</u>

Drosophila melanogaster luna, transcript variant C (luna), mRNA

Sequence ID: ref|NM_001273950.1| Length: 8446 Number of Matches: 2

Range 1: 908 to 1494

Score		Expect	Identities	Gaps	Strand	Frame	
1079 bit	ts(584)	0.0()	586/587(99%)	0/587(0%)	Plus/Plus		
Feature	s:						
Query	1	CAGAAACCAACA	.CGCAAGAGGCCACAA <i>I</i>	AATAATTGGAATG	TAACAAATCTGA	ATGAAAG	60
Sbjct	908	CAGAAACCAACA	.CGCAAGAGGCCACAA	AAATAATTGGAATG	TAACAAATCTGA	ATGAAAG	967
Query	61	TGCTGAAGTTAA	ATAAATTTTTAAGTGA	AATAAGAAACCGAA	AAATACCACACA	TAAATGA	120
Sbjct	968	tgctgaagttaa	ATAAATTTTTAAGTGA	Ataagaaaccgaa	AAATACCACACA	TAAATGA	1027

Query	121	CGAGCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCA	180
Sbjct	1028	CGAGCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCA	1087
Query	181	ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCA	240
Sbjct	1088	ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCA	1147
Query	241	GAAATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	300
Sbjct	1148	GAAATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	1207
Query	301	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	360
Sbjct	1208	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	1267
Query	361	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	420
Sbjct	1268	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	1327
Query	421	ATTCAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	480
Sbjct	1328	ATTCAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	1387
Query	481	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	540
Sbjct	1388	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	1447
Query	541	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA 587	
Sbjct	1448	cgctactactcgtcgcagccgtcgattgaggatcaatggcaacaga 1494	

Range 2: 908 to 1494

Score		Expect	Identities	Gaps	Strand	Frame	
1079 bit	s(584)	0.0()	586/587(99%)	0/587(0%)	Plus/Plus		
Features	S :						
Query	584	CAGAAACCAACAG	CGCAAGAGGCCACAA	AAATAATTGGAATG	TAACAAATCTGA	ATGAAAG	643
Sbjct	908	cadaaaccaaca	cgcaagaggccacaa	AAATAATTGGAATG	taacaaatctga	ATGAAAG	967
Query	644	TGCTGAAGTTAA	ATAAATTTTTAAGTG	AATAAGAAACCGAA	AAATACCACACA 	TAAATGA	703
Sbjct	968	tgctgaagttaaz	Ataaatttttaagtd	ahtaadaaadccdaa	yyy4yccycycy	taaatga	1027
Query	704	CGAGCGTTTGCAC	GAGTGTAGATAATTA	CATATTAGTTGTAT	CTTATTCATATA	TAGGGCA	763
Sbjct	1028	cdadcdtttdcad	SAGTGTAGATAATTA	catattagttgtat	cttattcatata	TAGGGCA	1087
Query	764	ATATTCAATCGCC	GAGTGCTAAAATGCT	GTCCTCCGCAGCAT	CGCTCATCGTCG	GGATGCA	823
Sbjct	1088	AtAttcAAtcGcc	sagtgetaaaatget	retectece	çççtçytççtç	ddatdda	1147
Query	824	GAAATCGATCTGA	AATCAAAATTAAGA	AAAGAAATCAAAAT	ATATATATTTGT	CGCTCTA	883
Sbjct	1148	gaaatcgatctga	AAATCAAAAATTAAGA	AAAGAAATCAAAAT	<mark>ልተልተልተልተተ</mark> ታ <mark></mark> ታ	ccctcta	1207
Query	884	AGTAATCAATCGT	CGTAGCCAATCAAA	TCAAAATTGCATCA	AAAGCCAACTCA 	AATTGTT	943
Sbjct	1208	Agtaatcaatcg	rcgtagccaatcaaa	\rcanadattgcatca	aaadccaactca	AATTGTT	1267
Query	944	GCCCCACCAACAC	GTTTGAGTGCACATT	CATTTCGGCCCCA	CTGTTCCTGTTC	GTGAAAC	1003
Sbjct	1268	ĠĊĊĊĊĀĊĊĀĀĊĀ	strtgagtgcacatt	rcatttccccca	ĊŦĠŦŦĊĊŦĠŦŦĊ	ĠŦĠĂĂĂĊ	1327
Query	1004	ATTCAAAAACGGC	CCTCAAAACGGATTC	CCTAGAGTTTCTGC	GTTGCGAGGAAG	AGGATAT	1063
Sbjct	1328	AttcAAAAAcccc	cctcaaaacccaactc	ccctagagtttctgc	ĠŦŦĠĊĠĀĠĠĀĀĠ	AĠĠĀŦĀŦ	1387
Query	1064	CAAGATGGATATO	CTACCGAGTGGCAA	CATCTTCAGCGAGC	TGGAGCGGATCT	GCACCAC	1123
Sbjct	1388	caadatddatatd	cctaccdadtddcaa	ckatcttckgcgkgc	tĠĠĀĠĊĠĠĀtĊt	GCACCAC	1447
Query	1124	CGGCTACTACTCC	GTCGCAGCCGTCGAT	TGAGGATCAATGGC	AACAGA 1170		
Sbjct	1448	cectactactc	stcgcagccgtcgat	rtgaggatcaatggc	AACAGA 1494		

Drosophila melanogaster luna, transcript variant B (luna), mRNA Sequence ID: **ref|NM_206089.2|** Length: 3608 Number of Matches: 2 Range 1: 908 to 1494

Score	Expect	Identities	Gaps	Strand	Frame
1079 bits(584)	0.0()	586/587(99%)	0/587(0%)	Plus/Plus	

Features	S:		
Query	1	CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAATGTAACAAATCTGAATGAA	60
Sbjct	908	CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAATGTAACAAATCTGAATGAA	967
Query	61	TGCTGAAGTTAAATAAATTTTTAAGTGAATAAGAAACCGAAAAATACCACACATAAATGA	120
Sbjct	968	tgctgaagttaaataaatttttaagtgaataagaaaccgaaaaataccacacataaatga	1027
Query	121	CGAGCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCA	180
Sbjct	1028	cgagcgtttgcagagtgtagataattacatattagttgtatcttattcatatatagggca	1087
Query	181	ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCA	240
Sbjct	1088	ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCA	1147
Query	241	GAAATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	300
Sbjct	1148	ĠAAATĊĠATĊTĠAAATĊAAAATTAAĠAAAAĠAAATĊAAAATATATAT	1207
Query	301	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	360
Sbjct	1208	AĠTAATĊAATĊĠTĊĠTAĠĊĊAATĊAAATĊAAAATTĠĊATĊAAAAĠĊĊAAĊTĊAAATTĠTT	1267
Query	361	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	420
Sbjct	1268	ĠĊĊĊĊAĊĊAAĊAĠŦŦŦĠAĠŦĠĊAĊAŦŦĊAŦŦŦĊĠĠĊĊĊĊĊAĊŦĠŦŦĊĊŦĠŦŦĊĠŦĠAAAĊ	1327
Query	421	ATTCAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	480
Sbjct	1328	ATTCAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	1387
Query	481	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	540
Sbjct	1388	ĊAAĠAŦĠĠAŦAŦĊĊŦAĊĊĠAĠŦĠĠĊAAĊAŦĊŦŦĊAĠĊĠAĠĊŦĠĠAĠĊĠĠAŦĊŦĠĊAĊĊAĊ	1447
Query	541	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA 587	
Sbjct	1448	ĊĠĠĊŦĂĊŦĂĊŦĊĠŦĊĠĊĂĠĊĊĠŦĊĠĂŤŦĠĂĠĠĂŤĊĂĂŤĠĠĊĂĂĊĂĠĂ 1494	

Range 2: 908 to 1494

Score		Expect	Identities	Gaps	Strand	Frame	
1079 bit	s(584)	0.0()	586/587(99%)	0/587(0%)	Plus/Plus		
Features	S :						
Query	584	CAGAAACCAACA	CGCAAGAGGCCAC <i>A</i>	AAAATAATTGGAATG	TAACAAATCTGA	AATGAAAG	643
Sbjct	908	cagaaaccaaca	paga a a a a a a a a a a a a a a a a a a	AAAATAATTGGAATG	taacaaatctg	AATGAAAG	967
Query	644	TGCTGAAGTTAAZ	ATAAATTTTTAAGT	GAATAAGAAACCGAA	AAATACCACAC <i>I</i>	ATAAATGA 	703
Sbjct	968	tĠĊtĠAAĠttAA	Ataaatttttaagt	rgaataagaaaccgaa	AAATACCACAC	Ataaatga	1027
Query	704	CGAGCGTTTGCAC	GAGTGTAGATAATT 	'ACATATTAGTTGTAT 	CTTATTCATATA	ATAGGGCA	763
Sbjct	1028	cgagcgtttgcac	sagtgtagataatt	racatattagttgtat	cttattcatat	Atagggca	1087
Query	764	ATATTCAATCGCC	GAGTGCTAAAATGC 	TGTCCTCCGCAGCAT	CGCTCATCGTCC	GGATGCA	823
Sbjct	1088	ATATTCAATCGC	ĠĀĠŦĠĊŦĀĀĀĀĀŦĠĊ	ctgtcttccccacacat	ĊĠĊŦĊĂŦĊĠŦĊŒ	ĠĠĠĀŢĠĊĀ	1147
Query	824	GAAATCGATCTGA	\AATCAAAATTAAG 	SAAAAGAAATCAAAAT 	ATATATATTTGT	CGCTCTA	883
Sbjct	1148	ĠĀĀĀŤĊĠĀŤĊŤĠĀ	ÄÄÄTĊÄÄÄÄTTÄÄĊ	;AAAAĠAAATĊAAAAT	ÀTÀTÀTÀTTTĠ	rĊĠĊŦĊŦÄ	1207
Query	884			ATCAAAATTGCATCA 	AAAGCCAACTC <i>I</i> 	\AATTGTT 	943
Sbjct	1208	AGTAATCAATCG:	rcgtagccaatcaa	ATCAAAATTGCATCA	AAAĠĊĊAAĊŦĊŹ	ÄÄÄTTGTT	1267
Query	944			TCATTTCGGCCCCA!	.CTGTTCCTGTT(CGTGAAAC 	1003
Sbjct	1268		ĠŦŦŦĠĀĠŦĠĊĀĊĀŦ			CGTGAAAC	1327
Query	1004			CCCTAGAGTTTCTGC	GTTGCGAGGAAC	GAGGATAT 	1063
Sbjct	1328	ÁTTCÁÁÁÁÁÁCGG(GŤŤGČĠĂĠĠĂĂĊ	GÁGGÁTÁT	1387
Query	1064			ACATCTTCAGCGAGC			1123
Sbjct	1388			ACATCTTCAGCGAGC			1447
Query	1124			ATTGAGGATCAATGGC			
Sbjct	1448	CGGCTACTACTC	JTCGCAGCCGTCG <i>P</i>	ATTGÁGGÁTCÁÁTGGC	AACAGA 1494	ł	

Drosophila melanogaster chromosome 2R

Sequence ID: **gb|AE013599.5|** Length: 25286936 Number of Matches: 2 Range 1: 11099532 to 11100117

Score	Expect	Identities	Gaps	Strand	Frame	
1077 bits(583)	0.0()	585/586(99%)	0/586(0%)	Plus/Minus		
Features: luna, isoform Bluna	, isoform C					
Query 584	CAGAAACO	CAACACGCAAGAGGCC	CACAAAAATAATTG	GAATGTAACAAA'	ICTGAATGAAAG	643
Sbjct 11100117	cagaaacc	cyycyceg	cacaaaaaataattg	gaatgtaacaaa	rctgaatgaaag	11100058
Query 644	TGCTGAA(GTTAAATAAATTTTT <i>P</i>	AAGTGAATAAGAAA 	CCGAAAAATACC	ACACATAAATGA	703
Sbjct 11100057	tĠĊtĠAA	ያተተልልልተልልልተተተተ <i>ት</i>	AAGTGAATAAGAAA	ccdaaaaaatacc	Acacataaatga	11099998
Query 704	CGAGCGTT	PTGCAGAGTGTAGATA	\ATTACATATTAGT' 	TGTATCTTATTC/ 	ATATATAGGGCA	763
Sbjct 11099997		ŗŦĠĊĀĠĀĠŦĠŦĀĠĀŦ <i>Ŕ</i>				11099938
Query 764		ATCGCGAGTGCTAAA <i>I</i> 				823
Sbjct 11099937		\tccccaccaccaccaccaccaccaccaccaccaccaccac				11099878
Query 824		ATCTGAAATCAAAATT				883
Sbjct 11099877 Query 884		\TCTGAAATCAAAAT1 \ATCGTCGTAGCCAA1				11099818 943
Query 884 Sbjct 11099817		AATCGTCGTAGCCAAT				11099758
Query 944		CAACAGTTTGAGTGC <i>A</i>				1003
Sbjct 11099757		[11099698
Query 1004		AACGGCCTCAAAACGG				1063
Sbjct 11099697	 ATTCAAAZ				 GGAAGAGGATAT	11099638
Query 1064	Ҫ҅҅҄҅҄҄Ӓ҅҄Ӓ҅Ҿ҇ӒҬҪҀ	ЗАТАТССТАССБАСТС		ҪҪѦҪҪҬҪҪѦҪҪҪ	Ģ ĄŢĊŢĠĊĄĊĊĄĊ	1123
Sbjct 11099637	 CAAGATGO		GCAACATCTTCAG		GATCTGCAC	11099578
Query 1124	CGGCTACT	PACTCGTCGCAGCCGT	TCGATTGAGGATCA	ATGGCAACAG	1169	
Sbjct 11099577	CGGCTACT	rACTCGTCGCAGCCG1	rcgattgaggatca	ATGGCAACAG	11099532	

Range 2: 11099532 to 11100117

Score		Expect	Identities	Gaps	Strand	Frame		
1077 bit	s(583)	0.0()	585/586(99%)	0/586(0%)	Plus/Minus			
Features: luna, isoform C								
Query	1	CAGAAAC	CAACACGCAAGAGGCC	ACAAAAATAATTGO	GAATGTAACAAA	CTGAATGAAAG	60	
Sbjct	11100117	CAGAAAC	CAACACGCAAGAGGCC	:Acadadataattgc	SAATGTAACAAA	rctgaatgaaag	111000	
Query	61	TGCTGAA	GTTAAATAAATTTTTA	AGTGAATAAGAAA	CCGAAAAATACC	ACACATAAATGA	120	
Sbjct	11100057	TGCTGAA	GTTAAATAAATTTTTA	AGTGAATAAGAAA	CCGAAAAATACC	ACACATAAATGA	110999	
Query	121	CGAGCGT	TTGCAGAGTGTAGATA	ATTACATATTAGT	rgtatcttattc	ATATATAGGGCA	180	
Sbjct	11099997	CGAGCGT	rtgcagagtgtagata	Attacatattagti	rgtatettatte	ATATATAGGGCA	110999	
Query	181	ATATTCAZ	ATCGCGAGTGCTAAAA	TGCTGTCCTCCGC	AGCATCGCTCAT	CGTCGGGATGCA	240	
Sbjct	11099937	ATATTCAZ	Atccccactcctaaaa	৻ ϮĠĊϮĠϮĊĊϮĊĊĠĊ₽	AGCATCGCTCATC	cgtcgggatgca	110998	
Query	241	GAAATCGA	ATCTGAAATCAAAATT	'AAGAAAAGAAATC <i>I</i>	AAATATATATA 	TTTGTCGCTCTA	300	
Sbjct	11099877	GAAATCG	ATCTGAAATCAAAATT	'AAGAAAAGAAATC <i>I</i>	AAAATATATATA	TTGTCGCTCTA	110998	
Query	301	AGTAATCA	AATCGTCGTAGCCAAT	CAAATCAAAATTGC	CATCAAAAGCCAA	ACTCAAATTGTT	360	
Sbjct	11099817	AGTAATC	AATCGTCGTAGCCAAT	chaatcaaaattgd	catcaaaadccaz	Actcaaattgtt	110997	
Query	361	GCCCCAC	CAACAGTTTGAGTGCA	CATTCATTTCGGC	CCCACTGTTCC	TGTTCGTGAAAC	420	
Sbjct	11099757	gcccac	CAACAGTTTGAGTGCA	ckattcktttcgcc	cccactettcc	rgttcgtgaaac	110996	
Query	421	ATTCAAAA 	AACGGCCTCAAAACGG	ATTCCCTAGAGTTT	CTGCGTTGCGAC	GAAGAGGATAT	480	

Sbjct	11099697	ATTCAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	11099638
Query	481	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	540
Sbjct	11099637	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	11099578
Query	541	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 586	
Shict	11099577	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 11099532	

Drosophila melanogaster, chromosome 2R, region 47D-47E, BAC clone BACR13D20, complete sequence Sequence ID: **gb|AC008187.6|AC008187** Length: 168417 Number of Matches: 2 Range 1: 88325 to 88910

Score		Expect	Identities	Gaps	Strand	Frame	
1077 bit	s(583)	0.0()	585/586(99%)	0/586(0%)	Plus/Minus		<u> </u>
Features	S:						
Query	584	CAGAAACCAAC	CACGCAAGAGGCCAG	CAAAAATAATTGGAA 	TGTAACAAATCT(GAATGAAAG	643
Sbjct	88910	cadaaaccaac	pacecaaeaeceae	caaaaataattggaa	tgtaacaaatctc	SAATGAAAG	88851
Query	644	TGCTGAAGTT	\AATAAATTTTTAA(GTGAATAAGAAACCG	AAAAATACCACA(CATAAATGA	703
Sbjct	88850	tgctgaagtt	AAATAAATTTTAA	gtgaataagaaaccg	AAAAATACCACAC	CATAAATGA	88791
Query	704	CGAGCGTTTGC	CAGAGTGTAGATAA!	TTACATATTAGTTGT	ATCTTATTCATAT	TATAGGGCA	763
Sbjct	88790	cgygcgtttgc	cadadtdtadataa	ttacatattagttgt	AtcttAttcAtA	ratagggca	88731
Query	764	ATATTCAATCO	GCGAGTGCTAAAAT(GCTGTCCTCCGCAGC	ATCGCTCATCGT(CGGGATGCA	823
Sbjct	88730	AtAttcAAtcc	scgagtgctaaaat	ĠĊŦĠŦĊĊŦĊĊĠĊĀĠĊ.	AtccctcAtcct	cgggatgca	88671
Query	824	GAAATCGATC7	rgaaarcaaaarta <i>i</i> 	AGAAAAGAAATCAAA 	ATATATATATTTC	GTCGCTCTA	883
Sbjct	88670	ĠAAA†ĊĠA†Ċ¹	rgaaatcaaaatta	AGAAAAGAAATCAAA	ATATATATATTC	stegeteta	88611
Query	884	AGTAATCAATO	CGTCGTAGCCAATC	AAATCAAAATTGCAT 	CAAAAGCCAACT(CAAATTGTT	943
Sbjct	88610	AGTAATCAATC	ceteetaece	AAATCAAAATTGCAT	caaaagccaactc	caaattgtt	88551
Query	944	GCCCCACCAAC	CAGTTTGAGTGCAC	ATTCATTTCGGCCCC	CACTGTTCCTGTT	CGTGAAAC	1003
Sbjct	88550	ĠĊĊĊĠĠĊĠĠ	cadriridadidddddddd	AttcAtttcccc	ĊĂĊŦĠŦŦĊĊŦĠŦſ	tcgtgaaac	88491
Query	1004	ATTCAAAAACC	GCCTCAAAACGGA'	TTCCCTAGAGTTTCT	GCGTTGCGAGGAZ	AGAGGATAT	1063
Sbjct	88490	AttcAAAAAcc	g c c t c a a a a c c c a a c	gtcctagagttc	ĠĊĠϮϮĠĊĠĂĠĠĂź	AGAGGATAT	88431
Query	1064	CAAGATGGATA	ATCCTACCGAGTGG(CAACATCTTCAGCGA 	GCTGGAGCGGAT(CTGCACCAC	1123
Sbjct	88430	caadatddat	Atcctaccdactcc	caacatcttcaccaa	ĠĊŦĠĠĀĠĊĠĠĀŦŒ	ctgcyccyc	88371
Query	1124	CGGCTACTACT	TCGTCGCAGCCGTC	GATTGAGGATCAATG 	GCAACAG 1169)	
Sbjct	88370	cĠĠċtĀċtĀċt	tcgtcgcygcgtc	ĠAŦŦĠAĠĠAŦĊAAŦĠ	ĠĊĀĀĊĀĠ 8832	25	

Range 2: 88325 to 88910

	Expect	Identities	Gaps	Strand	Frame	
ts(583)	0.0()	585/586(99%)	0/586(0%)	Plus/Minus		
s:						
1	CAGAAACCAA	CACGCAAGAGGCCAC	AAAATAATTGGAA	TGTAACAAATCTG	SAATGAAAG	60
88910	CAGAAACCAA	CACGCAAGAGGCCAC	AAAATAATTGGAA	tgtaacaaatctd	SAATGAAAG	88851
61	TGCTGAAGTT	AAATAAATTTTTAAG	rgaataagaaaccg 	AAAAATACCACAC	ATAAATGA	120
88850	TGCTGAAGTT	AAATAAATTTTAAG	rgyytyyg	yyyyyytyccycyc	:ATAAATGA	88791
121	CGAGCGTTTG	CAGAGTGTAGATAATT	PACATATTAGTTGT	ATCTTATTCATAT	ATAGGGCA	180
88790	¢ĠAĠ¢ĠŦŦŦĠ	cagagtgtagataatr	tacatattagttgt	AtcttAttcAtAt	ATAGGGCA	88731
181	ATATTCAATC	GCGAGTGCTAAAATG(CTGTCCTCCGCAGC	ATCGCTCATCGTC	GGGATGCA	240
88730	AtAttcAAtc	ĠĊĠĀĠŦĠĊŦĀĀĀĀŦĠŒ	ctetcctcccc	AtccctcAtcctc	:ĠĠĠĀŦĠĊĀ	88671
241	GAAATCGATC'		GAAAAGAAATCAAA 	ATATATATATTTG 	TCGCTCTA	300
88670	ĠAAA†ĊĠA†Ċ	tĠAAAtĊAAAAttAAc	SAAAAGAAATCAAA	ATATATATATTC	rccctcta	88611
	s: 1 88910 61 88850 121 88790 181 88730 241	1 CAGAAACCAAG 88910 CAGAAACCAAG 61 TGCTGAAGTT 88850 TGCTGAAGTT 121 CGAGCGTTTGG 88790 CGAGCGTTTGG 181 ATATTCAATCG 88730 ATATTCAATCG 241 GAAATCGATCG	SS(583) 0.0() 585/586(99%) SS: 1	S(583) 0.0() 585/586(99%) 0/586(0%) S: 1 CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAA 88910 CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAA 61 TGCTGAAGTTAAATAAATTTTTAAGTGAATAAGAAACCG 88850 TGCTGAAGTTAAATAAATTTTTAAGTGAATAAGAAACCG 121 CGAGCGTTTGCAGAGTGTAGATAATTACATATTAGTTGT 88790 CGAGCGTTTGCAGAGTGTAGATAATTACATATTAGTTGT 181 ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGC 88730 ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGC	SISTERIOR OF STATE OF	S(583) 0.0() 585/586(99%) 0/586(0%) Plus/Minus 1 CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAATGTAACAAATCTGAATGAA

Query	301	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	360
Sbjct	88610	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	88551
Query	361	GCCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	420
Sbjct	88550	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	88491
Query	421	ATTCAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGAGATAT	480
Sbjct	88490	ATTCAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	88431
Query	481	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	540
Sbjct	88430	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	88371
Query	541	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 586	
Sbict	88370	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 88325	

Drosophila melanogaster luna, transcript variant D (luna), mRNA

Sequence ID: **ref|NM_001299374.1|** Length: 3037 Number of Matches: 2

Range 1: 340 to 923

Score		Expect	Identities	Gaps	Strand	Frame	
1074 bit	s(581)	0.0()	583/584(99%)	0/584(0%)	Plus/Plus		
Features	3 :						
Query	4	AAACCAACACGCA	AGAGGCCACAAAA?	FAATTGGAATGTAAC	AAATCTGAATGA	AAGTGC	63
Sbjct	340	AAACCAACACGCA	AGAGGCCACAAAAA	raatteeaatetaac	AAATCTGAATGA	AAGTGC	399
Query	64	TGAAGTTAAATAA	ATTTTTAAGTGAATA	AAGAAACCGAAAAAT.	ACCACACATAAA	TGACGA	123
Sbjct	400	tgaagttaaataa	AtttttAAGtGAAtz	AAGAAACCGAAAAAT	YCCYCYCYLYYY	rtgacga	459
Query	124	GCGTTTGCAGAGT	GTAGATAATTACATA	ATTAGTTGTATCTTA	TTCATATATAGG	GCAATA	183
Sbjct	460	dcdtttdcadadto	gtagataattacatz	AttAGttGtAtCttA	ttcatatatadd	GCAATA	519
Query	184	TTCAATCGCGAGT(GCTAAAATGCTGTC(CTCCGCAGCATCGCT	CATCGTCGGGAT	GCAGAA	243
Sbjct	520	ttcaatccccact	gctaaaatgctgtc	ctccccaccatcatcct	çytçetçeeyt	dcagaa	579
Query	244	ATCGATCTGAAAT	CAAAATTAAGAAAA(GAAATCAAAATATAT 	ATATTTGTCGCT	CTAAGT	303
Sbjct	580	Atccatctcatatat	caaaattaagaaaaa	GAAATCAAAATATAT	AtAtttgtcgct	ctaagt	639
Query	304	AATCAATCGTCGT	AGCCAATCAAATCAA	AAATTGCATCAAAAG 	CCAACTCAAATT 	GTTGCC	363
Sbjct	640	AATCAATCGTCGT	AGCCAATCAAATCAA	AAATTGCATCAAAAG	ccaactcaaatt	ĠŦŦĠĊĊ	699
Query	364	CCACCAACAGTTTC	GAGTGCACATTCAT'	TTCGGCCCCCACTGT	TCCTGTTCGTGA	AACATT	423
Sbjct	700	ccaccaacacactro	ĠĀĠŦĠĊĀĊĀŦŦĊĀŦſ	trceeccccacter	tcctgttcgtgA	AACATT	759
Query	424	CAAAAACGGCCTC	AAAACGGATTCCCTA	AGAGTTTCTGCGTTG 	CGAGGAAGAGGA 	TATCAA	483
Sbjct	760	caaaaacccccccccccccccccccccccccccccccc	AAAAĊĠĠAGŦĊĊĊŦź	AGAGTTTCTGCGTTG	ĊĠĀĠĠĀĀĠĀĠĠĀ	rtatcaa	819
Query	484	GATGGATATCCTA	CCGAGTGGCAACAT(CTTCAGCGAGCTGGA	GCGGATCTGCAC	CACCGG	543
Sbjct	820	ĠAŦĠĠAŦAŦĊĊŦĀĠ	ccdadtddcaacato	cttcagcgagctgga	ĠĊĠĠĀŦĊŦĠĊĀĊ	ckkcccc	879
Query	544	CTACTACTCGTCGC	CAGCCGTCGATTGA(GGATCAATGGCAACA	GA 587		
Sbjct	880	ctactactcctc	ĊĂĠĊĊĠŦĊĠĂŦŦĠĂŒ	ggatcaatggcaaca	GA 923		

Range 2: 340 to 923

Score		Expect	Identities	Gaps	Strand	Frame	
1074 bits(581)		0.0()	583/584(99%)	0/584(0%)	Plus/Plus		
Feature	s:						
Query	587	AAACCAACACGC	AAGAGGCCACAAAA	PAATTGGAATGTAA	CAAATCTGAATG	SAAAGTGC	646
Sbjct	340	AAACCAACACGC	AAGAGGCCACAAAAA	raattggaatgtaa	CAAATCTGAATC	SAAAGTGC	399
Query	647	TGAAGTTAAATA	AATTTTTAAGTGAAT	AAGAAACCGAAAAA	TACCACACATAA	AATGACGA	706
Sbjct	400	TGAAGTTAAATA	AATTTTTAAGTGAATA	Adaaaccgaaaaa	TACCACACATAA	ATGACGA	459

Query	707	GCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCAATA	766
Sbjct	460	GCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCAATA	519
Query	767	TTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAA	826
Sbjct	520	TTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAA	579
Query	827	ATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	886
Sbjct	580	ATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	639
Query	887	AATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCC	946
Sbjct	640	AATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCC	699
Query	947	CCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAACATT	1006
Sbjct	700	ccaccaacagtttgagtgcacattcatttcggcccccactgttcctgttcgtgaaacatt	759
Query	1007	CAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGAGATATCAA	1066
Sbjct	760	CAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGGATATCAA	819
Query	1067	GATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGG	1126
Sbjct	820	GATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGG	879
Query	1127	CTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA 1170	
Sbjct	880	CTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA 923	

Drosophila melanogaster RE40136 full insert cDNA

Sequence ID: **gb|BT126377.1**| Length: 4490 Number of Matches: 2 Range 1: 908 to 1493

Score		Expect	Identities	Gaps	Strand	Frame	
1072 bit	s(580)	0.0()	584/586(99%)	0/586(0%)	Plus/Plus		
Features	S :						
Query	1	CAGAAACCAACA	CGCAAGAGGCCACA	AAAATAATTGGAATG	TAACAAATCTGA	AATGAAAG	60
Sbjct	908	cagaaaccaaca	cgcaagaggccaca	AAAATAATTGGAATG	taacaaatctg	AATGAAAG	967
Query	61	TGCTGAAGTTAA	ATAAATTTTTAAGT	GAATAAGAAACCGAA	AAATACCACAC <i>I</i>	ATAAATGA	120
Sbjct	968	tdctdaadttaa	ATAAATTTTTAAGT	gaataagaaaccgaa	aaataccacacz	Ataaatga	1027
Query	121	CGAGCGTTTGCA	GAGTGTAGATAATT	ACATATTAGTTGTAT	CTTATTCATATA	ATAGGGCA	180
Sbjct	1028	cgagcgtttgca	GAGTGTAGATAATT	Acatattagttgtat	cttattcatatz	Atagggca	1087
Query	181	ATATTCAATCGC	GAGTGCTAAAATGC	TGTCCTCCGCAGCAT	CGCTCATCGTC	GGATGCA	240
Sbjct	1088	ATATTCAATCGC	GAGTGCTAAAATGC	tgtcctccgcagcat	cectcatcetc	GGATGCA	1147
Query	241	GAAATCGATCTG	AAATCAAAATTAAG	AAAAGAAATCAAAAT	ATATATATTTGT	CGCTCTA	300
Sbjct	1148	GAAATCGATCTG.	AAATCAAAATTAAG	AAAAGAAATCAAAAT	AtAtAtAttdd	rccctcta	1207
Query	301	AGTAATCAATCG	TCGTAGCCAATCAA	ATCAAAATTGCATCA	AAAGCCAACTC <i>I</i>	AATTGTT	360
Sbjct	1208	AGTAATCAATCG	tcgtagccaatcaa	AtcAAAAttGcAtcA	aaagccaactc <i>i</i>	AAATTGTT	1267
Query	361	GCCCCACCAACA	GTTTGAGTGCACAT	TCATTTCGGCCCCCA	CTGTTCCTGTT(CGTGAAAC	420
Sbjct	1268	GCCCCACCAACA	GTTTGAGTGCACAT	tcatttcgccccc	ctdttcctdtt	CGTGAAAC	1327
Query	421	ATTCAAAAACGG	CCTCAAAACGGATT	CCCTAGAGTTTCTGC	GTTGCGAGGAA(GAGGATAT	480
Sbjct	1328	AttcAAAAAccc	cctcaaaacggagt	ccctagagtttctgc	gttgcgyggyy	SAGGATAT	1387
Query	481	CAAGATGGATAT	CCTACCGAGTGGCA	ACATCTTCAGCGAGC	TGGAGCGGATCT	TGCACCAC	540
Sbjct	1388	caagatggatat	cctaccgagtggca	acatetteagegage	TGGAGCGGATC	rdcaccac	1447
Query	541	CGGCTACTACTC	GTCGCAGCCGTCGA	TTGAGGATCAATGGC	AACAG 586		
Sbjct	1448	cgctactactc	g4cgcygccg4cgy	ttgaggatcaatggc	AACAG 1493		

Range 2: 908 to 1493

Score	Expect	Identities	Gaps	Strand	Frame
1072 bits(580)	0.0()	584/586(99%)	0/586(0%)	Plus/Plus	_

Feature	S:		
Query	584	CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAATGTAACAAATCTGAATGAA	643
Sbjct	908	CAGAAACCAACACGCAAGAGGCCACAAAAATAATTGGAATGTAACAAATCTGAATGAA	967
Query	644	TGCTGAAGTTAAATAAATTTTTAAGTGAATAAGAAACCGAAAAATACCACACATAAATGA	703
Sbjct	968	tgctgaagttaaattaatttttaagtgaataagaaaccgaaaaataccacacaca	1027
Query	704	CGAGCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCA	763
Sbjct	1028	ĊĠĀĠĊĠŦŦŦĠĊĀĠĀĠŦĠŦĀĠĀŦĀĀŦŦĀĊĀŦĀŦŦĀĠŦŦĠŦĀŦĊŦŦĀŦŦĊĀŦĀŦĀŦĀĠĠĠĊĀ	1087
Query	764	ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCA	823
Sbjct	1088	ATATTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCA	1147
Query	824	GAAATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	883
Sbjct	1148	ĠAAATĊĠATĊŢĠAAAŢĊAAAAŢŢAAĠAAAAĠAAAŢĊAAAAŢĀŢĀŢĀŢĀŢŢŢĠŢĊĠĊŢĊŢĀ	1207
Query	884	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	943
Sbjct	1208	AĞTAATCAATCĞTCĞTAĞCCAATCAAATCAAAATTĞCATCAAAAĞCCAACTCAAATTĞTT	1267
Query	944	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	1003
Sbjct	1268	ĠĊĊĊĠĊĊĠĊĠĠĊĠĠĠŢŢŢĠĠĠŢĠĊĠĊĠĊĠĠŢŢĊĊŢĠŢŢĊĠŢĠĠĠĠĊĠĊĠĠĠĊĊĊĠĠŢĠŢŢĊĠŢĠĠĠĠĠĠ	1327
Query	1004	ATTCAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	1063
Sbjct	1328	ATTCAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGAGATAT	1387 1123
Query Sbjct	1064 1388	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	1447
	1124	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 1169	144/
Query Sbjct	1448	CGGCTACTACTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 1109	
	1440	COOCINGINGICOTCOCCOTCOMITOMOCATION 1475	

Drosophila melanogaster HL07808 full insert cDNA

Sequence ID: **gb|AY122143.1**| Length: 2605 Number of Matches: 2 Range 1: 1 to 473

Score		Expect	Identities	Gaps	Strand	Frame	
869 bits	(470)	0.0()	472/473(99%)	0/473(0%)	Plus/Plus		
Feature	s:						
Query	115	AAATGACGAGCG	TTTGCAGAGTGTAGA	ATAATTACATATTAGT	TGTATCTTATT(CATATAT	174
Sbjct	1	AAATGACGAGCG	tttgcagagtgtag <i>i</i>	Ataattacatattagt	rtgtytçttyt	CATATAT	60
Query	175	AGGGCAATATTC	AATCGCGAGTGCTA <i>l</i>	AAATGCTGTCCTCCGC	AGCATCGCTCAT	CGTCGG	234
Sbjct	61	AGGGCAATATTC	aatccccactcta	AAATGCTGTCCTCCGC	agcatcgctca	rcgrcgg	120
Query	235	GATGCAGAAATC	GATCTGAAATCAAA 	ATTAAGAAAAGAAATC 	:AAAATATATATA 	ATTTGTC 	294
Sbjct	121	datdcadaaatc	GATCTGAAATCAAA	Attaagaaaagaaatc	:ልልልልተልተልተልተ <i>រ</i>	\thrace the state of the state	180
Query	295	GCTCTAAGTAAT	CAATCGTCGTAGCC	AATCAAATCAAAATTG 	CATCAAAAGCC <i>I</i>	AACTCAA 	354
Sbjct	181	ĠĊϮĊϮÅÅĠϮÅÅϮ	ĊĂĂŦĊĠŦĊĠŦĂĠĊĊ	AATCAAATCAAAATTG	ckatcaaaadcc	AAĊŦĊAA	240
Query	355	ATTGTTGCCCCA	CCAACAGTTTGAGT(GCACATTCATTTCGGC	CCCCACTGTTCC	CTGTTCG	414
Sbjct	241	ATTGTTGCCCA	ĊĊĀĀĊĀĠŢŢŢĠĀĠŢŒ	ĠĊĀĊĀŢŢĊĀŢŢŢĊĠĠĊ	ccccactctccc	ctsttcs	300
Query	415	TGAAACATTCAA 	AAACGGCCTCAAAA(CGGATTCCCTAGAGTT 	'TCTGCGTTGCG <i>I</i> 	AGGAAGA 	474
Sbjct	301	TĠAAAĊATTĊAA	AAAĊĠĠĊĊϮĊAAAA	ĊĠĠĀĠŦĊĊĊŦĀĠĀĠŦŦ	'tctgcgttgcg <i>i</i>	AĠĠĀĀĠĀ	360
Query	475	GGATATCAAGAT	GGATATCCTACCGA(GTGGCAACATCTTCAG 	CGAGCTGGAGC	GGATCTG 	534
Sbjct	361	ĠĠAϮAϮĊAAĠAϮ	ĠĠĂŦĂŦĊĊŦĂĊĊĠĂŒ	ĠŦĠĠĊĀĀĊĀŦĊŦŦĊĀĠ	ccdactrocacc	ĠĠĀŢĊŢĠ	420
Query	535	CACCACCGGCTA	CTACTCGTCGCAGC(CGTCGATTGAGGATCA 	ATGGCAACAGA	587	
Sbjct	421	ĊAĊĊAĊĊĠĠĊϮĀ	ĊŦĀĊŦĊĠŦĊĠĊĀĠĊŒ	ĊĠϮĊĠÀϮϮĠÀĠĠÀϮĊÀ	ATĠĠĊĀĀĊĀĠĀ	473	

Score Expect	Identities	Gaps	Strand	Frame	
--------------	------------	------	--------	-------	--

869 bits((470)	0.0()	472/473(99%)	0/473(0%)	Plus/Plus	
Features	s:					
Query	698	AAATGACGAG	CGTTTGCAGAGTGTAGA	TAATTACATATTAG'	TTGTATCTTATTCATATAT	757
Sbjct	1	AAATGACGAG	CGTTTGCAGAGTGTAGA	.TAATTACATATTAG	TTGTATCTTATTCATATAT	60
Query	758	AGGGCAATAT	TCAATCGCGAGTGCTAA	AATGCTGTCCTCCG	CAGCATCGCTCATCGTCGG	817
Sbjct	61	AGGGCAATAT	tcaatcgcgagtgctaa	AATGCTGTCCTCCG	cadcatcdctcatcdtcdd	120
Query	818	GATGCAGAAA	TCGATCTGAAATCAAAA	TTAAGAAAAGAAAT	CAAAATATATATATTTGTC	877
Sbjct	121	GATGCAGAAA	tcgatctgaaatcaaaa	ttaagaaaagaaat	caaaatatatatatatteete	180
Query	878	GCTCTAAGTA	ATCAATCGTCGTAGCCA	ATCAAATCAAAATT	GCATCAAAAGCCAACTCAA	937
Sbjct	181	GCTCTAAGTA	atcaatcgtcgtagcca	Atcaaatcaaaatt	GCATCAAAAGCCAACTCAA	240
Query	938	ATTGTTGCCC	CACCAACAGTTTGAGTG	CACATTCATTTCGG	CCCCACTGTTCCTGTTCG	997
Sbjct	241	ATTGTTGCCC	caccaacagtttgagtg	cacattcatttcgc	ccccactgttcctgttcg	300
Query	998	TGAAACATTC	AAAAACGGCCTCAAAAC	GGATTCCCTAGAGT	TTCTGCGTTGCGAGGAAGA	1057
Sbjct	301	tgaaacattc.	aaaaacggcctcaaaac	ĠĠĀĠŦĊĊĊŦĀĠĀĠŦ [,]	ttctcccttcccaccacca	360
Query	1058	GGATATCAAG.	ATGGATATCCTACCGAG	TGGCAACATCTTCA	GCGAGCTGGAGCGGATCTG	1117
Sbjct	361	GGATATCAAG.	atggatateetaeegag	tggcaacatcttca	gcgagctggagcggatctg	420
Query	1118	CACCACCGGC	TACTACTCGTCGCAGCC	GTCGATTGAGGATC	AATGGCAACAGA 1170	
Sbjct	421	caccaccacc	tactactcgtcgcagcc	ĠtĊĠĀttĠĀĠĠĀtĊ	AATGGCAACAGA 473	

Drosophila yakuba uncharacterized protein, transcript variant B (Dyak\GE13058), mRNA Sequence ID: **ref|XM_015196803.1|** Length: 3574 Number of Matches: 2 Range 1: 884 to 1448

Score		Expect	Identities	Gaps	Strand	Frame	
671 bits	(363)	0.0()	521/592(88%)	32/592(5%)	Plus/Plus		
Feature	s:						
Query	1	CAGAAACCAA	CACGCAAGAGGCCAC	AAAAATAATTGGAAT	GT-AACAAA	TCTGAAT	55
Sbjct	884	cagaaaccaa	CACACGAGAGGCCAC	:GAAAATA-TTGGAAT	rtgåågt¢ggååå	TCTGAAT	942
Query	56	GAAAGTGCTG	AAGTTAAATAAATTI	TTAAGTGAATAAGAA	ACCGAAAAATACC	ACACATA	115
Sbjct	943	GAAAGTGCTG	AAATGAAATAAA-TC	ttaagtgcataagaa	Acc-AAAAAtrcc	ACTTATA	1000
Query	116	AATGACGAGC	GTTTGCAGAGTGTAG	ATAATTACATATTAG'	TTGTATCTTATTC	ATATATA	175
Sbjct	1001	AATGACGAGC	stgtgcaaagtgtaa	ATAATTACATATTAG	ctdtatattattd	:AtAtAt_	1059
Query	176	GGGCAATATT	CAATCGCGAGTGCTA	AAATGCTGTCCTCCG	CAGCATCGCTCAT	CGTCGGG	235
Sbjct	1060	ATATT	CAATCGCGAGTGCTA	AAATGCTATCCATCG	cadcatcdgtcat	cq4cqqq	1114
Query	236	ATGCAGAAAT(CGATCTGAAATCAAA	ATTAAGAAAAGAAAT(CAAAATATATATA 	TTTGTCG	295
Sbjct	1115	AtGCAGCAAto	ctgtctgaaatc-aa	AttAAGccAAt	c44-4-4444	tcggtcg	1165
Query	296	CTCTAAGTAA:	rcaatcgtcgtagcc	AATCAAATCAAAATT	GCATCAAAAGCCA	ACTCAAA	355
Sbjct	1166	ctctaagtaa	rcaatcgtcgtagcc	:AATCAAATCAAAATT	gcatcaaaagcaa	cctcaaa	1225
Query	356	TTGTTGCCCC	ACCAACAGTTTGAGT	GCACATTCATTTCGG	CCCCACTGTTCC	TGTTCGT	415
Sbjct	1226	++6++6ccc	Accaacagtttgagt	dcacattrccgtcgd:	-cccactt-c	:Ċ-廿	1276
Query	416	GAAACATTCAA	AAAACGGCCTCAAAA 	CGGATTCCCTAGAGT	TTCTGCGTTGCGA	GGAAGAG	475
Sbjct	1277	GAAACATTTA	AAAACGGCCTCAAAA	cccadactccctacact	ttrtgcggtgcga	GGAAGAG	1336
Query	476	GATATCAAGA:	rggatatcctaccga	GTGGCAACATCTTCA	GCGAGCTGGAGCG	GATCTGC	535
Sbjct	1337	gatatcaaga:	rddatateetreeda	dtggcaacatcttca	gcgagctggagcg	gatctgc	1396
Query	536	ACCACCGGCTA	ACTACTCGTCGCAGC	CGTCGATTGAGGATC	AATGGCAACAGA	587	
Sbjct	1397	Accaccact	Actactcgtcgcagc	CGTCGATCGAGGATC	AATGGCAACAGA	1448	

Score		Expect	Identities	Gaps	Strand	Frame	
671 bits	(363)	0.0()	521/592(88%)	32/592(5%)	Plus/Plus		
Features	S:						
Query	584	CAGAAACCAAG	CACGCAAGAGGCCAC	AAAATAATTGGAAT(GT-AACAAA	TCTGAAT	638
Sbjct	884	CAGAAACCAA	CACACGAGAGGCCACG	saaaata-ttggaat'	rtgaagteggaaa	TCTGAAT	942
Query	639	GAAAGTGCTGA	AAGTTAAATAAATTTT	TAAGTGAATAAGAA	ACCGAAAAATACC	ACACATA	698
Sbjct	943	GAAAGTGCTGA	AAATGAAATAAA-TC1	TTAAGTGCATAAGAA	ACC-AAAAATTCC	ACTTATA	1000
Query	699	AATGACGAGC	GTTTGCAGAGTGTAG <i>A</i>	ATAATTACATATTAG'	TTGTATCTTATTC	ATATATA 	758
Sbjct	1001	AATGACGAGC	stgtgcaaagtgtaa	Ataattacatattac	ctdtatattattd	AtAtAt_	1059
Query	759	GGGCAATATT(CAATCGCGAGTGCTA <i>A</i>	AATGCTGTCCTCCG	CAGCATCGCTCAT	CGTCGGG	818
Sbjct	1060	ATATT	caarceceaetectaa	AAATĠĊŦAŦĊĊAŦĊĠ	cadcatcdgtcat	çqtçqqq	1114
Query	819	ATGCAGAAAT(CGATCTGAAATCAAAA 	ATTAAGAAAAGAAAT(CAAAATATATATA 	TTTGTCG	878
Sbjct	1115			ATTÁÁGCCÁÁT		ŤCGĠŤĊĠ	1165
Query	879			ATCAAATCAAAATT(GCATCAAAAGCCA 	ACTCAAA 	938
Sbjct	1166			AATCAAATCAAAATT			1225
Query	939		ACCAACAGTTTGAGTO 			TGTTCGT	998
Sbjct	1226	ŤŤĠŤŤĠĊĊĊĊ <i>Ĭ</i>	ACCAACAGTTTGAGTC	ĠĊĀĊĀŢŢŢĊĠĠ-	-ĊĊĊĊĂĊŤŤ-Ċ	Ċ-Ť	1276
Query	999	GAAACATTCAA	AAAACGGCCTCAAAAC 	GGATTCCCTAGAGT" 	TTCTGCGTTGCGA 	GGAAGAG 	1058
Sbjct	1277		^À ÀÀÀĊĠĠĊĊĊĊAÀÀÀĊ				1336
Query	1059	GATATCAAGAT	FGGATATCCTACCGAG	GTGGCAACATCTTCA(GCGAGCTGGAGCG 	GATCTGC	1118
Sbjct	1337		rĠĠĂŦĂŦĊĊŦŦĊĊĠĂĊ				1396
Query	1119	ACCACCGGCTA	ACTACTCGTCGCAGC(GTCGATTGAGGATC 	AATGGCAACAGA 	1170	
Sbjct	1397	ACCACCGGCT	ACTACTCGTCGCAGCC	ĊĠŦĊĠĂŦĊĠĂĠĠĂŦĊ	AATGGCAACAGA	1448	

Drosophila yakuba uncharacterized protein, transcript variant A (Dyak\GE13058), mRNA Sequence ID: **ref|XM_002090305.2|** Length: 3275 Number of Matches: 2 Range 1: 602 to 1163

Score		Expect	Identities	Gaps	Strand	Frame	
665 bits	(360)	0.0()	518/589(88%)	32/589(5%)	Plus/Plus		
Features	S :						
Query	4	AAACCAACAC	GCAAGAGGCCACAA	AAATAATTGGAATGT-A	AACAAATCT	GAATGAA	58
Sbjct	602	AAACCAACACA	vçeyeyeçeye	AAATA-TTGGAATTTGA	AAGTĊGGAAATĊT	GAATGAA	660
Query	59	AGTGCTGAAGT	TTAAATAAATTTTTT.	AAGTGAATAAGAAACC	GAAAAATACCACA	CATAAAT	118
Sbjct	661	AdtddtdAAA1	rgaaataaa-tctt	AAGTGCATAAGAAACC-	-аааааттссаст	татаааат	718
Query	119	GACGAGCGTTT	GCAGAGTGTAGATA	AATTACATATTAGTTG	PATCTTATTCATA	TATAGGG	178
Sbjct	719	gacgagcgtgt	rdcaaadtdtaaata	lattacatattagctg:	ratattattcata	TAT	774
Query	179	CAATATTCAAT	CGCGAGTGCTAAA?	ATGCTGTCCTCCGCAG(CATCGCTCATCGT	CGGGATG	238
Sbjct	775	&\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\	rcdcdadtdctaaa	Atgctatccatcgcago	catcatcatcat	ccccatch	832
Query	239	CAGAAATCGAT	CTGAAATCAAAAT7	TAAGAAAAGAAATCAA <i>I</i> 	AATATATATATTT 	GTCGCTC	298
Sbjct	833	caccaatctct	rctgaaatc-aaatt	taagccaatc <i>i</i>	AA-A-ATATATCG	ĠŦĊĠĊŦĊ	883
Query	299	TAAGTAATCAA	TCGTCGTAGCCAA7	TCAAATCAAAATTGCAT	FCAAAAGCCAACT 	CAAATTG	358
Sbjct	884	taagtaatcaa	Atcetcetaeceaa	rcaaatcaaaattgca:	tcaaaagcaacct	ĊAAATTĠ	943
Query	359	TTGCCCCACCA	ACAGTTTGAGTGC <i>I</i>	ACATTCATTTCGGCCC(CCACTGTTCCTGT 	TCGTGAA	418
Sbjct	944	††dccccacca	AACAGTTTGAGTGC <i>I</i>	Acattrccgtcgg-cc	ccactt-c	-c-tgaa	994
Query	419	ACATTCAAAAA	ACGGCCTCAAAACG(GATTCCCTAGAGTTTCT	FGCGTTGCGAGGA 	AGAGGAT	478
Sbjct	995	Acatttaaaa	\cddcctcaaaacdd	SAGTCCCTAGAGTTT	tĠĊĠĠŦĠĊĠĀĠĠĀ	AĠAĠĠAϮ	1054
Query	479	ATCAAGATGGA	ATATCCTACCGAGTO	GGCAACATCTTCAGCGA	AGCTGGAGCGGAT 	CTGCACC	538

Sbjct	1055	ATCAAGATGGATATCCTTCCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGA	TCTGCACC	1114
Query	539	ACCGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA 5	87	
Sbjct	1115	ACCGCTACTACTCGTCGCAGCCGTCGATCGAGGATCAATGGCAACAGA 1	163	

Range 2: 602 to 1163

Score		Expect	Identities	Gaps	Strand	Frame	
665 bits	(360)	0.0()	518/589(88%)	32/589(5%)	Plus/Plus		
Features	S :						
Query	587	AAACCAACAC(GCAAGAGGCCACAAA	AATAATTGGAATGT-A	AACAAATCT	GAATGAA	641
Sbjct	602	AAACCAACACA	rcgygygggcgygyy	AATA-TTGGAATTTG	AAGTCGGAAATC1	GAATGAA	660
Query	642	AGTGCTGAAGT	TTAAATAAATTTTTA 	AGTGAATAAGAAACC	GAAAAATACCAC <i>A</i>	CATAAAT	701
Sbjct	661	AGTGCTGAAA	rgaaataaa-tctta	Agtgcataagaaacc	-yyyyyy	rahaah	718
Query	702	GACGAGCGTTT	rgcagagtgtagata 	ATTACATATTAGTTG	TATCTTATTCATA	TATAGGG	761
Sbjct	719	ĠĀĊĠĀĠĊĠŦĠ:	rdcaaadtdtaaata	AttAcAtAttAGctG	tatattattcata	\TAT	774
Query	762	CAATATTCAA	rcgcgagtgctaaaa 	TGCTGTCCTCCGCAG	CATCGCTCATCGT 	CGGGATG	821
Sbjct	775	AtAttcAAr	rcgcgagtgctaaaa	tgctatccatcgcag	catcgctcatcgt	rceeeate	832
Query	822	CAGAAATCGAT	CTGAAATCAAAATT 	AAGAAAAGAAATCAA 	AATATATATTT 	GTCGCTC	881
Sbjct	833	ĊĀĠĊĀĀŦĊŦĠŢ	rctgaaatc-aaatt	'AAĠCCAA†Ċ	AA-A-ATATATCG	sĠtĊĠĊtĊ	883
Query	882	TAAGTAATCAA	ATCGTCGTAGCCAAT 	CAAATCAAAATTGCA' 		CAAATTG	941
Sbjct	884	†AAĠ†AA†ĊAZ	ÁTCGTCGTÁGCCÁÁT	'ĊAAATĊAAAATTĠĊA'	rcaaaadcaacci	rcaaattg -	943
Query	942			.CATTCATTTCGGCCC(CCACTGTTCCTGT 	TCGTGAA	1001
Sbjct	944	ŤŤĠĊĊĊĊĂĊĊ <i>I</i>	\A¢AĠϮϮϮĠAĠϮĠĊA	ĊATTTCCGTĊĠĠ-ĊĊŒ	ĊĊĂĊTT-Ċ	Ċ-TĠAA	994
Query	1002	ACATTCAAAAA	ACGGCCTCAAAACGG 	ATTCCCTAGAGTTTC	IGCGTTGCGAGGA 	AGAGGAT	1061
Sbjct	995	AĊATTTAAAA		AGTCCCTAGAGTTTT			1054
Query	1062	ATCAAGATGGA	\TATCCTACCGAGTG 	GCAACATCTTCAGCGA	AGCTGGAGCGGAT 	CTGCACC	1121
Sbjct	1055	ÀTCÀÀGÀTGG <i>I</i>			AĠĊŦĠĠAĠĊĠĠA1		1114
Query	1122	ACCGGCTACTA	\CTCGTCGCAGCCGT 	'CGATTGAGGATCAAT(.70	
Sbjct	1115	AĊĊĠĠĊŢĀĊŢ <i>I</i>	Actcgtcgcagccgt	ĊĠĂŢĊĠĀĠĠĀŢĊĀĀŢ	ĠĠĊĀĀĊĀĠĀ 11	.63	

Drosophila erecta uncharacterized protein (Dere\GG22702), mRNA Sequence ID: **ref|XM_001976107.2|** Length: 2662 Number of Matches: 2 Range 1: 1 to 576

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
556 bits	(301)	3e-154()	514/607(85%)	54/607(8%)	Plus/Plus		
Features	s:						
Query	4	AAACCAACACGC	AAGAGGCCAC-AAAA	ATAATTGGAATGTAA	CAAATCTGAATG.	AAAGTG	62
Sbjct	1	AAACCAACACAC	AACAGGCCACGAGTA	AT-ATTGGAATGTAA	caaatctgaatg.	AAAGTG	59
Query	63	CTGAAGTTAA-A	TAAATTTTTAAGTGA	ATAAGAAACCG	A-AAAATACCAC	ACATAA	116
Sbjct	60	CTGAAATGAATA	aaaaaatttaagtga	ATAAGAAACCAAAAA	AGAAAATACCAC'	rtataa	119
Query	117	ATGACGAGCGTT	TGCAGAGTGTAGATA	ATTACATATTAGTTG	TATCTTATTCAT.	ATATAG	176
Sbjct	120	AtGACGAGCGTG	tgcaaagtgtacata	AttAcAtAttAGctG	tatattattdt.	AtAtAG	179
Query	177	GGCAATATTCAA	TCGCGAGTGCTAAAA	TGCTGTCCTCCGCAG	CATCGCTCATCG'	TCGGGA	236
Sbjct	180	GCCAATATTCAA	ACGCGAGTGCTAAAA	.TGCG	Ġ-TCAACĠ'	rcggga	223
Query	237	TGCAGAAATCGA	TCTGAAATCAAAATT	AAGAAAAG-AA	ATCAAAATATAT.	ATATTT	291
Sbjct	224	tgcagaaatctg	tctgaaatc-aaata	AATCAAATTAAGCTA	Atcaaaatatat	cta	279
Query	292	GTCGCTCTAAGT	AATCAATCGT	CGTAGCCAATCA	AATCAAAA-TTG	CATCAA	342
Sbjct	280	-tccctctaagt	AA†¢GTAA†¢GTAA†	cerretaeccaatca	AATCAAAATTTG	CATCAA	338

Query	343	AAGCCAA-CTCAAATTGTTGCCCCACCAACAGTTTGAGTGCACATTCATT	401
Sbjct	339	AAGCAAACCTCAAATTGTTGCCACACCAACAGTTTGAGTGCACATTTTCCTTGCA	393
Query	402	CTGTTCCTGTTCGTGAAACA-TTCAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTG	460
Sbjct	394	accacttcgtgaaacatttgaaaaacggcctcaaaacggagtccctagagtttttg	449
Query	461	CGTTGCGAGGAAGAGGATATCAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAG	520
Sbjct	450	CGTTGCGAGGAAGAGGATAGCAAGATGGATATCCTTCCGAGTGGCAACATCTTCAGCGAG	509
Query	521	CTGGAGCGGATCTGCACCACCGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGG	580
Sbjct	510	ctggagcggatctgcaccaccggctactactcgtcgcagccgtcgattgaggatcaatgg	569
Query	581	CAACAGA 587	
Sbjct	570	CAACAGA 576	

Range 2: 1 to 576

Score		Expect	Identities	Gaps	Strand	Frame	
556 bits	(301)	3e-154(514/607(85%)	54/607(8%)	Plus/Plus		
Features	S :						
Query	587	AAACCAACA	ACGCAAGAGGCCAC-AA	AAATAATTGGAATGT	AACAAATCTGAAT	GAAAGTG	645
Sbjct	1	AAACCAACA	ACACAGGCCACGAG	TAAT-ATTGGAATGT	AACAAATCTGAAT	GAAAGTG	59
Query	646	CTGAAGTTA	AA-ATAAATTTTTAAGT	'GAATAAGAAACC	-GA-AAAATACCA	CACATAA	699
Sbjct	60	ctgaaatga	ATAAAAAAATTTAAGT	'GAATAAGAAACCAAA	aaagaaaatacca	CTTATAA	119
Query	700	ATGACGAGO	CGTTTGCAGAGTGTAGA	TAATTACATATTAGT	rgtatcttattca	TATATAG	759
Sbjct	120	ATGACGAGO	cgtgtgcaaagtgtaca	taattacatattagc:	rgtatattattca	TATATAG	179
Query	760	GGCAATATT	CAATCGCGAGTGCTAA	AATGCTGTCCTCCGC	AGCATCGCTCATC	GTCGGGA	819
Sbjct	180	GCCAATAT	rcaaacgcgagtgctaa	AATGC	-dd-tcaac	GTCGGGA	223
Query	820	TGCAGAAAT	CGATCTGAAATCAAAA	TTAAGAAAAG-	AAATCAAAATATA	TATATTT	874
Sbjct	224	TGCAGAAA	ctgtctgaaatc_aaa	taaatcaaattaagc	raatcaaaatata	tcta	279
Query	875	GTCGCTCT	AGTAATCAATCG	-TCGTAGCCAAT	CAAATCAAAA-TT	GCATCAA	925
Sbjct	280	-TCGCTCT	AGTAATCGTAATCGTA	ATCGTTGTAGCCAAT	CAAATCAAAATTT	GCATCAA	338
Query	926	AAGCCAA-C	CTCAAATTGTTGCCCCA	CCAACAGTTTGAGTG	CACATTCATTTCG	GCCCCA	984
Sbjct	339	AAGCAAAC	ctcaaattgttgccaca	.ccaacagtttgagtg	CACATTTTC-	-CTTGCA	393
Query	985	CTGTTCCTC	GTTCGTGAAACA-TTCA	AAAACGGCCTCAAAA	CGGATTCCCTAGA	GTTTCTG	1043
Sbjct	394	ACCAC	cttcgtgaaacarttga	AAAACGGCCTCAAAA	cggagtccctaga	gtttttg	449
Query	1044	CGTTGCGAC	GAAGAGGATATCAAGA	TGGATATCCTACCGA	GTGGCAACATCTT	CAGCGAG	1103
Sbjct	450	CGTTGCGAC	GAAGAGGATAGCAAGA	TGGATATCCTTCCGA	GTGGCAACATCTT	CAGCGAG	509
Query	1104	CTGGAGCGG	ATCTGCACCACCGGCT	'ACTACTCGTCGCAGC	CGTCGATTGAGGA	TCAATGG	1163
Sbjct	510	CTGGAGCG	SATCTGCACCACCGGCT	ActactcGtcGcAGC	cgtcgattgagga	TCAATGG	569
Query	1164	CAACAGA	1170				
Sbjct	570	CAACAGA	576				

Synthetic construct Drosophila melanogaster clone BO17282 encodes luna-RB Sequence ID: **gb|FJ634070.1**| Length: 1744 Number of Matches: 2 Range 1: 17 to 119

Score		Expect	Identities	Gaps	Strand	Frame	
191 bits(103)		3e-44()	103/103(100%)	0/103(0%)	Plus/Plus		
Features	S :						
Query	485	ATGGATATCCTA	CCGAGTGGCAACATCT	TCAGCGAGCTGGAG	CGGATCTGCACC	ACCGGC	544
Sbjct	17	Atggatatccta	.ccgagtggcaacatct	TCAGCGAGCTGGAG	cggatctgcacc	Accede	76

Query	545	TACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA	587
~ 1			
Sbjct	77	TÁCTÁCTCGTCGCÁGCCGTCGÁTTGÁGGÁTCÁÁTGGCÁÁCÁGÁ	119

Range 2: 17 to 119

Score		Expect	Identities	Gaps	Strand	Frame	
191 bits	(103)	3e-44()	103/103(100%)	0/103(0%)	Plus/Plus		
Feature	s:						
Query	1068	ATGGATATCC	TACCGAGTGGCAACATC	TTCAGCGAGCTGGA	GCGGATCTGCAC	CACCGGC	1127
Sbjct	17	ATGGATATCC:	TACCGAGTGGCAACATC	ttcagcgagctgga	dcggatctgcac	:CACCGGC	76
Query	1128	TACTACTCGT	CGCAGCCGTCGATTGAG	GATCAATGGCAACA	.GA 1170		
Sbjct	77	TACTACTCGT	CGCAGCCGTCGATTGAG	GATCAATGGCAACA	GA 119		

Drosophila melanogaster transcription factor DKLF mRNA, complete cds Sequence ID: **gb|AF461497.1**| Length: 1713 Number of Matches: 2 Range 1: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	!
191 bits	(103)	3e-44()	103/103(100%)	0/103(0%)	Plus/Plus		
Feature	s:						
Query	485	ATGGATATCCT	ACCGAGTGGCAACATCT	TCAGCGAGCTGGAG	CGGATCTGCACC	ACCGGC	544
Sbjct	1	ATGGATATCCT	ACCGAGTGGCAACATCT	TCAGCGAGCTGGAG	CGGATCTGCACC	ACCGGC	60
Query	545	TACTACTCGTC	GCAGCCGTCGATTGAGG	ATCAATGGCAACAGA	A 587		
Sbjct	61	TACTACTCGTC	GCAGCCGTCGATTGAGG.	ATCAATGGCAACAG <i>I</i>	103		

Range 2: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
191 bits(103)		3e-44()	103/103(100%)	0/103(0%)	Plus/Plus		
Features	s:						
Query	1068	ATGGATATCC	TACCGAGTGGCAACATC	TTCAGCGAGCTGGA	GCGGATCTGCA(CCACCGGC	1127
Sbjct	1	ATGGATATCC	TACCGAGTGGCAACATC	TTCAGCGAGCTGGA	GCGGATCTGCA	CCACCGGC	60
Query	1128	TACTACTCGT	CGCAGCCGTCGATTGAG	GATCAATGGCAACA	GA 1170		
Sbjct	61	TACTACTCGT	CGCAGCCGTCGATTGAG	GATCAATGGCAACA	GA 103		

Drosophila sechellia GM20477 (Dsec\GM20477), mRNA

Sequence ID: **ref|XM_002033285.1|** Length: 1713 Number of Matches: 2 Range 1: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
185 bits	(100)	2e-42()	102/103(99%)	0/103(0%)	Plus/Plus		
Feature	s:						
Query	485	ATGGATATCCTA	ACCGAGTGGCAACATCT	TCAGCGAGCTGGAG	GCGGATCTGCACC	ACCGGC	544
Sbjct	1	ATGGATATCCTA	ACCGAGTGGCAACATC1	TCAGCGAGCTGGAG	GCGGATCTGCACC	ACCGGC	60
Query	545	TACTACTCGTCG	CAGCCGTCGATTGAGG	GATCAATGGCAACAG	GA 587		
Sbjct	61	TACTACTCGTCG	CAGCCCTCGATTGAGG	SATCAATGGCAACAG	GA 103		

Range 2: 1 to 103

Score	Expect	Identities	Gaps	Strand	Frame

185 bits(100)		2e-42()	102/103(99%)	0/103(0%)	Plus/Plus	
Features	s:					
Query	1068	ATGGATATCCT	ACCGAGTGGCAACATG	CTTCAGCGAGCTGGAG	GCGGATCTGCACCACCGGC	1127
Sbjct	1	ATGGATATCCT	ACCGAGTGGCAACAT	CTTCAGCGAGCTGGAG	GCGGATCTGCACCACCGGC	60
Query	1128	TACTACTCGTC	GCAGCCGTCGATTGAG	GGATCAATGGCAACAG	A 1170	
Sbict	61	TACTACTCGTC	GCAGCCCTCGATTGAG	GGATCAATGGCAACAG	A 103	

Drosophila simulans GD25946 (Dsim\GD25946), mRNA

Sequence ID: **ref|XM_002080935.1|** Length: 1710 Number of Matches: 2 Range 1: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
180 bits	(97)	7e-41()	101/103(98%)	0/103(0%)	Plus/Plus		
Features	S :						
Query	485	ATGGATATCCT	'ACCGAGTGGCAACATC	TTCAGCGAGCTGGA	GCGGATCTGCAC	CACCGGC	544
Sbjct	1	ATGGATATCCT	ACCGAGTGGCAACATI	TTCAGCGAGCTGGA	GCGGATCTGCAC	CACCGGC	60
Query	545	TACTACTCGTC	GCAGCCGTCGATTGAG	GATCAATGGCAACA	GA 587		
Sbjct	61	tactactcdtc	GCAGCCGTCGATAGAG	GATCAATGGCAACA	GA 103		

Range 2: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
180 bits(97)		7e-41()	101/103(98%)	0/103(0%)	Plus/Plus		
Feature	s:						
Query	1068	ATGGATATCO	CTACCGAGTGGCAACAT	CTTCAGCGAGCTGG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	CCACCGGC	1127
Sbjct	1	ATGGATATCO	CTACCGAGTGGCAACAT	TTTCAGCGAGCTGG	AGCGGATCTGCA	CCACCGGC	60
Query	1128	TACTACTCGT	CGCAGCCGTCGATTGA	GGATCAATGGCAAC	AGA 1170		
Sbjct	61	TACTACTCG	CGCAGCCGTCGATAGA	.ggatcaatggcaac	AGA 103		