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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CNA5HNN4014

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Blast report description

Nucleotide Sequence (641 letters)

RID <u>CNA5HNN4014</u> (Expires on 02-23 13:20 pm)

Query ID lcl|Query_118187 Database Name nr

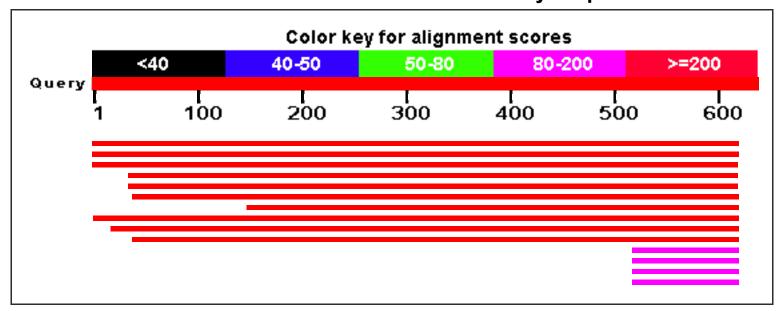
Description None **Description** Nucleotide collection (nt)

Molecule type nucleic acid **Program** BLASTN 2.3.1+

Query Length 641

□ Graphic Summary

Distribution of 14 Blast Hits on the Query Sequence



□ <u>Descriptions</u>

Sequences producing significant alignments:

Description	Max	Total	Query	E _.	Ident	Accession
	score	score	cover	value		
Drosophila melanogaster luna, transcript variant C (luna), mRNA	1144	1144	97%	0.0	99%	NM_001273950.1
Drosophila melanogaster luna, transcript variant B (luna), mRNA	1144	1144	97%	0.0	99%	NM_206089.2
Drosophila melanogaster RE40136 full insert cDNA	1136	1136	96%	0.0	99%	BT126377.1
Drosophila melanogaster chromosome 2R	1077	1077	91%	0.0	99%	AE013599.5
Drosophila melanogaster, chromosome 2R, region 47D-47E, BAC clone BACR13D20, complete sequence	1077	1077	91%	0.0	99%	AC008187.6
Drosophila melanogaster luna, transcript variant D (luna), mRNA	1074	1074	91%	0.0	99%	NM_001299374.1
Drosophila melanogaster HL07808 full insert cDNA	869	869	73%	0.0	99%	<u>AY122143.1</u>
Drosophila yakuba uncharacterized protein, transcript variant B (Dyak\GE13058), mRNA	706	706	96%	0.0	88%	XM_015196803.1
Drosophila yakuba uncharacterized protein, transcript variant A (Dyak\GE13058), mRNA	676	676	94%	0.0	88%	XM_002090305.2
Drosophila erecta uncharacterized protein (Dere\GG22702), mRNA	556	556	91%	1e-154	85%	XM_001976107.2
Synthetic construct Drosophila melanogaster clone BO17282 encodes luna-RB	191	191	16%	2e-44	100%	FJ634070.1
Drosophila melanogaster transcription factor DKLF mRNA, complete cds	191	191	16%	2e-44	100%	<u>AF461497.1</u>
Drosophila sechellia GM20477 (Dsec\GM20477), mRNA	185	185	16%	8e-43	99%	XM_002033285.1
Drosophila simulans GD25946 (Dsim\GD25946), mRNA	180	180	16%	4e-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: 1

Range 1: 873 to 1494

Score		Expect	Identities	Gaps	Strand	Frame	
1144 bit	ts(619)	0.0()	621/622(99%)	0/622(0%)	Plus/Plus		
Feature	s:						
Query	1	AGCAGCAGCAG	caacaacaacaaca	aaGTTAGCCAGAAA	CCAACACGCAA	AGGCCAC	60
Sbjct	873	AGCAGCAGCAGC	CAACAACAACAAC	AAGTTAGCCAGAAA	CCAACACGCAA	GAGGCCAC	932
Query	61	AAAATAATTGO	SAATGTAACAAATCTG	AATGAAAGTGCTGA	AGTTAAATAAAT	TTTTAAG	120
Sbjct	933	AAAAATAATTG	SAATGTAACAAATCTG		AGTTAAATAAA	rtttaag	992

Query	121	TGAATAAGAAACCGAAAAATACCACACATAAATGACGAGCGTTTGCAGAGTGTAGATAAT	180
Sbjct	993	tgaataagaaaccgaaaaataccacacataaatgacgagcgtttgcagagtgtagataat	1052
Query	181	TACATATTAGTTGTATCTTATTCATATATAGGGCAATATTCAATCGCGAGTGCTAAAATG	240
Sbjct	1053	tacatattagttgtatcttattcatatatagggcaatattcaatcgcgagtgctaaaatg	1112
Query	241	CTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAAATCGATCTGAAATCAAAATTAA	300
Sbjct	1113	CTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAAATCGATCTGAAATCAAAATTAA	1172
Query	301	GAAAAGAAATCAAAATATATATTTGTCGCTCTAAGTAATCAATC	360
Sbjct	1173	GAAAAGAAATCAAAATATATATTTGTCGCTCTAAGTAATCAATC	1232
Query	361	AATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCCCCACCAACAGTTTGAGTGCACA	420
Sbjct	1233	AATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCCCCACCAACAGTTTGAGTGCACA	1292
Query	421	TTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAACATTCAAAAACGGCCTCAAAACGGAT	480
Sbjct	1293	TTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAACATTCAAAAACGGCCTCAAAACGGAG	1352
Query	481	TCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGGATATCAAGATGGATATCCTACCGAGTGGC	540
Sbjct	1353	tccctagagtttctgcgttgcgaggaagaggatatcaagatggatatcctaccgagtggc	1412
Query	541	AACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGGCTACTACTCGTCGCAGCCGTCG	600
Sbjct	1413	AACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGGCTACTACTCGTCGCAGCCGTCG	1472
Query	601	ATTGAGGATCAATGGCAACAGA 622	
Sbjct	1473	ATTGAGGATCAATGGCAACAGA 1494	

Drosophila melanogaster luna, transcript variant B (luna), mRNA Sequence ID: **ref|NM_206089.2|** Length: 3608 Number of Matches: 1 Range 1: 873 to 1494

Score		Expect	Identities	Gaps	Strand	Frame	
1144 bit	s(619)	0.0()	621/622(99%)	0/622(0%)	Plus/Plus		
Features	s:						
Query	1	AGCAGCAGCAGC	aacaacaacaacaa	acaaGTTAGCCAGAAA	ACCAACACGCAAG	GAGGCCAC	60
Sbjct	873	AGCAGCAGCAGC	yycyycyycyy y	Acaagttagccagaaa	rççyyçyçgçyyç	SAGGCCAC	932
Query	61	AAAAATAATTGG	AATGTAACAAATC	rgaatgaaagtgctg <i>a</i> 	AGTTAAATAAAT 	TTTTAAG	120
Sbjct	933	AAAAATAATTGG.	AATGTAACAAATC:	tgaatgaaagtgctga	AGTTAAATAAAT	rtttaag	992
Query	121	TGAATAAGAAAC	CGAAAAATACCACA 	\CATAAATGACGAGCG 	TTTGCAGAGTGT	AGATAAT	180
Sbjct	993	TĠAATAAĠAAAĊ	ĊĠĂĂĂĂĂĂŤĂĊĊĂĊ	\cataaatgacgagcd	strtgcagagtgt	'AĠATAAT	10
Query	181			\TATAGGGCAATATTC 			24
Sbjct	1053	TACATATTAGTT	ĠϮ₳ϮĊϮϮ₳ϮϮĊ₳Ϯ <i>ĭ</i>	ÀTÀTÀĠĠĠĠÀÀTÀTTĊ	CAATĊĠĊĠAĠŦĠĊ		11
Query	241	CTGTCCTCCGCA	GCATCGCTCATCGT	PCGGGATGCAGAAATC 	GATCTGAAATCA 		30
Sbjct	1113	ĊŦĠŦĊĊŦĊĊĠĊĀ	ĠĊĂŦĊĠĊŦĊĂŦĊĠŢ	rcĠĠĠàtĠĊàĠàààtc	ĊĠĀŢĊŢĠĀĀĀŢĊĀ		11
Query	301	GAAAAGAAATCA					36
Sbjct	1173	GAAAAGAAATCA		rĠŦĊĠĊŦĊŦĂĂĠŦĂĂſ			12
Query	361						42
Sbjct	1233			rcaaattgttgccc <i>t</i>			12
Query	421			FTCGTGAAACATTCA <i>F</i> 			48
Sbjct	1293	TTCATTTCGGCC			AAACGGCCTCAA		13!
Query	481			AAGAGGATATCAAGAT 			54
Sbjct	1353			\AGAGGATATCAAGA1 			14
Query	541			FCTGCACCACCGGCTA			600
Sbjct	1413			rctgcaccaccgct <i>i</i>	ACTACTCGTCGCA	AGCCGTCG	14
Query	601	ATTGAGGATCAA		22			
Sbjct	1473	ÁTTGÁGGÁTCÁÁ	TGGCAACAGA 14	194			

Drosophila melanogaster RE40136 full insert cDNA

Sequence ID: **gb|BT126377.1|** Length: 4490 Number of Matches: 1 Range 1: 873 to 1493

Score		Expect	Identities	Gaps	Strand	Frame	
1136 bit	s(615)	0.0()	619/621(99%)	0/621(0%)	Plus/Plus		
Features	s:						
Query	1	AGCAGCAGCAGCA	aacaacaaca	acaaGTTAGCCAGAAA	CCAACACGCAAG	AGGCCAC	60
Sbjct	873	AGCAGCAGCAGCA	aycaycaycaycy	Acaagttagccagaaa	ccaacacgcaag	AGGCCAC	932
Query	61	AAAAATAATTGG	AATGTAACAAATC	TGAATGAAAGTGCTGA 	AGTTAAATAAAT 	TTTTAAG	120
Sbjct	933	AAAAATAATTGG	AATGTAACAAATC	tgaatgaaagtgctga	AGTTAAATAAAT	rttttååg	992
Query	121	TGAATAAGAAAC	CGAAAAATACCAC.	ACATAAATGACGAGCG	TTTGCAGAGTGT	AGATAAT	180
Sbjct	993	tgaataagaaac	cgaaaaataccac	acataaatgacgagcg	tttgcagagtgt	'AGATAAT	1052
Query	181	TACATATTAGTT(GTATCTTATTCAT	ATATAGGGCAATATTC	AATCGCGAGTGC	TAAAATG	240
Sbjct	1053	tacatattactt	gtatettatteat.	AtAtAGGGCAATATTC	AATCGCGAGTGC	taaaatg	1112
Query	241	CTGTCCTCCGCA	GCATCGCTCATCG	TCGGGATGCAGAAATC	GATCTGAAATCA	AAATTAA	300
Sbjct	1113	ctdtcctcccc	gcatcgctcatcg	tcgggatgcagaaatc	gatctgaaatca	AAATTAA	1172
Query	301	GAAAAGAAATCA	AAATATATATATT	TGTCGCTCTAAGTAAT	CAATCGTCGTAG	CCAATCA	360
Sbjct	1173	GAAAAGAAATCA	AAATATATATATA	tgtcgctctaagtaat	CAATCGTCGTAG	ccaatca	1232
Query	361	AATCAAAATTGC	ATCAAAAGCCAAC	TCAAATTGTTGCCCCA	CCAACAGTTTGA	GTGCACA	420
Sbjct	1233	AATCAAAATTGC	atcaaaagccaac	tcaaattgttgcccca	ccaacagtttga	GTGCACA	1292
Query	421	TTCATTTCGGCC	CCCACTGTTCCTG	TTCGTGAAACATTCAA	AAACGGCCTCAA	AACGGAT	480
Sbjct	1293	ttcatttcccc	cccectettccte	ttcgtgaaacattcaa	AAACGGCCTCAA	AACGGAG	1352
Query	481	TCCCTAGAGTTT	CTGCGTTGCGAGG.	AAGAGGATATCAAGAT	GGATATCCTACC	GAGTGGC	540
Sbjct	1353	tccctagagttt	ctgcgttgcgagg.	 AAGAGGATATCAAGAT	ddatatcctacc	GAGTGGC	1412
Query	541	AACATCTTCAGC	GAGCTGGAGCGGA	TCTGCACCACCGGCTA	CTACTCGTCGCA	GCCGTCG	600
Sbjct	1413	AACATCTTCAGC	GAGCTGGAGCGGA	tctgcaccaccgcta	ctactcgtcgca	'eccetce	1472
Query	601	ATTGAGGATCAA	rggcaacag 62	1			
Sbjct	1473	AttGAGGATCAA	rggcaacag 14	93			

Drosophila melanogaster chromosome 2R

Sequence ID: **gb|AE013599.5|** Length: 25286936 Number of Matches: 1 Range 1: 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, isc	s: oform Bluna,	isoform C				
Query	36	CAGAAAC	CAACACGCAAGAGGCC	ACAAAAATAATTG	GAATGTAACAAAT	CTGAATGAAAG
Sbjct	11100117	CAGAAAC	caacacgcaagaggcc	acaaaaataattg	GAATGTAACAAA1	ctgaatgaaag
Query	96	TGCTGAA	GTTAAATAAATTTTTA	AGTGAATAAGAAA	CCGAAAAATACCA	CACATAAATGA
Sbjct	11100057	TGCTGAA	GTTAAATAAATTTTTA	AGTGAATAAGAAA	CCGAAAAATACCA	CACATAAATGA
Query	156	CGAGCGT	TTGCAGAGTGTAGATA	ATTACATATTAGT	TGTATCTTATTCA	TATATAGGGCA
Sbjct	11099997	CGAGCGT'	rtgcagagtgtagata	AttAcAtAttAGt	ተĠተልተረተተልተተረፉ	tatatagggca
Query	216	ATATTCA	ATCGCGAGTGCTAAAA	TGCTGTCCTCCGC	AGCATCGCTCATC	GTCGGGATGCA
Sbjct	11099937	AtAttcAz	Atccccactctaaaa	ŢĠĊŢĠŢĊĊŢĊĊĠĊ	AGCATCGCTCATC	dtcgggatgca
Query	276	GAAATCG	ATCTGAAATCAAAATT	'AAGAAAAGAAATC	AAAATATATATATA 	TTGTCGCTCTA
Sbjct	11099877	GAAATCG	ATCTGAAATCAAAATT	'AAGAAAAGAAATC	AAAATATATATAT	TTGTCGCTCTA

Query	336	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	395
Sbjct	11099817	AGTAATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTT	11099758
Query	396	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	455
Sbjct	11099757	GCCCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAAC	11099698
Query	456	ATTCAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGAGATAT	515
Sbjct	11099697	ATTCAAAAACGGCCTCAAAACGGAGTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGATAT	11099638
Query	516	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	575
Sbjct	11099637	CAAGATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCAC	11099578
Query	576	CGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAG 621	
Sbjct	11099577	cgctactactcgtcgcaccgtcgattgaggatcaatggcaacag 11099532	

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

Score		Expect	Identities	Gaps	Strand	Frame	
1077 bit	ts(583)	0.0()	585/586(99%)	0/586(0%)	Plus/Minus		
Feature	s:						
Query	36	CAGAAACCAAG	CACGCAAGAGGCCAC	AAAAATAATTGGAA 	TGTAACAAATCTO	GAATGAAAG	95
Sbjct	88910	cagaaaccaa	cacccaadaddccac	AAAAATAATTGGAA	tgtaacaaatctd	GAATGAAAG	88851
Query	96	TGCTGAAGTTA	AAATAAATTTTTAAG	TGAATAAGAAACCG	AAAAATACCACAC	CATAAATGA	155
Sbjct	88850	†gc†gyygt	AAATAAATTTTAAG	tgyytyygy tgyytyy	AAAAATACCACAC	CATAAATGA	88791
Query	156	CGAGCGTTTG(CAGAGTGTAGATAAT	TACATATTAGTTGT	ATCTTATTCATAT	TATAGGGCA	215
Sbjct	88790	cgygcgtttqc	cadadtdtadataat	tacatattagttgt	Atcttattcatat	ratagggca	88731
Query	216	ATATTCAATCO	GCGAGTGCTAAAATG	CTGTCCTCCGCAGC	ATCGCTCATCGTC	CGGGATGCA	275
Sbjct	88730	AtAttcAAtc	scgagtgctaaaatg	ctgtcctccgcycc	AtccctcAtcct	cgggatgca	88671
Query	276	GAAATCGATC	rgaaatcaaaattaa 	GAAAAGAAATCAAA 	ATATATATATTTC	GTCGCTCTA	335
Sbjct	88670	daaatcdatc:	tgaaatcaaaattaa	GAAAAGAAATCAAA	ልተልተልተልተልተተተረ	stegeteta	88611
Query	336	AGTAATCAAT(CGTCGTAGCCAATCA	AATCAAAATTGCAT	CAAAAGCCAACTO	CAAATTGTT	395
Sbjct	88610	AGTAATCAATC	cetcetaeccaatca	AATCAAAATTGCAT	caaaadccaactc	caaattgtt	88551
Query	396	GCCCCACCAAC	CAGTTTGAGTGCACA	TTCATTTCGGCCCC	CACTGTTCCTGTT	CGTGAAAC	455
Sbjct	88550	¢¢¢¢¢a¢¢aa	cagtttgagtgcaca	ttcatttcgcccc	cactettcctet	rcgtgaaac	88491
Query	456	ATTCAAAAAC(GCCTCAAAACGGAT	TCCCTAGAGTTTCT	GCGTTGCGAGGAZ	AGAGGATAT	515
Sbjct	88490	AttcAAAAAcc	gcctcaaaacccac	tccctagagtttct	ĠĊĠŦŦĠĊĠĀĠĠĀŹ	Adaddatat	88431
Query	516	CAAGATGGATA	ATCCTACCGAGTGGC	AACATCTTCAGCGA	GCTGGAGCGGATC	CTGCACCAC	575
Sbjct	88430	caadatddata	łtcctacceaetec	AACATCTTCAGCGA	.gc4ggygqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	ctgcyccyc	88371
Query	576	CGGCTACTACT	TCGTCGCAGCCGTCG	ATTGAGGATCAATG	GCAACAG 621		
Sbjct	88370	ĊĠĠĊŦĀĊŦĀĊŢ	rcgtcgcagccgtcg	ATTGAGGATCAATG	dcaacad 8832	25	

Drosophila melanogaster luna, transcript variant D (luna), mRNA Sequence ID: **ref|NM_001299374.1|** Length: 3037 Number of Matches: 1 Range 1: 340 to 923

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
1074 bit	ts(581)	0.0()	583/584(99%)	0/584(0%)	Plus/Plus		
Feature	s:						
Query	39	AAACCAACACGCA	AGAGGCCACAAAAAT <i>I</i>	AATTGGAATGTAAC	А ААТСТБААТБА	AAGTGC	98
Sbjct	340	AAACCAACACGCA	AGAGGCCACAAAAATz	AATTGGAATGTAAC	AAATCTGAATGA	AAGTGC	399
Query	99	TGAAGTTAAATAA	ATTTTTAAGTGAATA <i>I</i>	AGAAACCGAAAAAT	ACCACACATAAA'	TGACGA	158

Sbjct	400	TGAAGTTAAATAAATTTTTAAGTGAATAAGAAACCGAAAAATACCACACATAAATGACGA	459
Query	159	GCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCAATA	218
Sbjct	460	GCGTTTGCAGAGTGTAGATAATTACATATTAGTTGTATCTTATTCATATATAGGGCAATA	519
Query	219	TTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAA	278
Sbjct	520	TTCAATCGCGAGTGCTAAAATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAA	579
Query	279	ATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	338
Sbjct	580	ATCGATCTGAAATCAAAATTAAGAAAAGAAATCAAAATATATAT	639
Query	339	AATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCC	398
Sbjct	640	AATCAATCGTCGTAGCCAATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCC	699
Query	399	CCACCAACAGTTTGAGTGCACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAACATT	458
Sbjct	700	ccaccaacagtttgagtgcacattcatttcggcccccactgttcctgttcgtgaaacatt	759
Query	459	CAAAAACGGCCTCAAAACGGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGGATATCAA	518
Sbjct	760	caaaaacgcctcaaaacgcagtccctagagtttctgcgttgcgaggaagaggatatcaa	819
Query	519	GATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGG	578
Sbjct	820	GATGGATATCCTACCGAGTGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGG	879
Query	579	CTACTACTCGTCGCAGCCGTCGATTGAGGATCAATGGCAACAGA 622	
Sbjct	880	ctactactcgtcgcagccgattgaggatcaatggcaacaga 923	

Drosophila melanogaster HL07808 full insert cDNA

Sequence ID: gb|AY122143.1| Length: 2605 Number of Matches: 1

Range 1: 1 to 473

Score		Expect	Identities	Gaps	Strand	Frame	
869 bits	(470)	0.0()	472/473(99%)	0/473(0%)	Plus/Plus		
Features	s:						
Query	150	AAATGACGAGCG	TTTGCAGAGTGTAG	ATAATTACATATTAGT	TGTATCTTATT	CATATAT	209
Sbjct	1	AAATGACGAGCG	TTTGCAGAGTGTAG	ATAATTACATATTAGT	rtgtatcttatt	CATATAT	60
Query	210	AGGGCAATATTC	AATCGCGAGTGCTA	AAATGCTGTCCTCCGC	CAGCATCGCTCAT	CGTCGG	269
Sbjct	61	AGGGCAATATTC	AATCGCGAGTGCTA	AAATGCTGTCCTCCGC	cadcatcdctcat	tcgtcgg	120
Query	270	GATGCAGAAATC	GATCTGAAATCAAA	ATTAAGAAAAGAAATC	CAAAATATATATA	ATTTGTC	329
Sbjct	121	gatgcagaaatc	GATCTGAAATCAAA	AttAAGAAAAGAAAtd	cadadatatatata	Atttgtc	180
Query	330	GCTCTAAGTAAT	CAATCGTCGTAGCC	AATCAAATCAAAATTO	CATCAAAAGCC <i>I</i>	AACTCAA 	389
Sbjct	181	ĠĊŦĊŦĀĀĠŦĀĀŦ	caatcgtcgtagcc	AATCAAATCAAAATTC	scatcaaaadcc	AACTCAA	240
Query	390	ATTGTTGCCCCA	CCAACAGTTTGAGT(GCACATTCATTTCGGC	CCCCACTGTTCC	CTGTTCG	449
Sbjct	241	Attgttgccca	ccaacagtttcact	ĠĊĀĊĀŦŦĊĀŦŦŦĊĠĠĊ	ccccactettc	ctgttcg	300
Query	450	TGAAACATTCAA 	AAACGGCCTCAAAA(CGGATTCCCTAGAGTT	TCTGCGTTGCG	AGGAAGA 	509
Sbjct	301	tgaaacattcaa	AAACGGCCTCAAAA	cddagtccctadagtt	rtctdcdttdcd <i>i</i>	AGGAAGA	360
Query	510	GGATATCAAGAT	GGATATCCTACCGA	GTGGCAACATCTTCAG	GCGAGCTGGAGCC	GGATCTG	569
Sbjct	361	ĠĠÀŦÀŦĊÀĀĠĀŦ	ĠĠĀŦĀŦĊĊŦĀĊĊĠĀŒ	ĠŦĠĠĊĀĀĊĀŦĊŦŦĊĀĠ	scgagctggagc	ĠĠĀŦĊŦĠ	420
Query	570	CACCACCGGCTA	CTACTCGTCGCAGC	CGTCGATTGAGGATCA	ATGGCAACAGA	622	
Sbjct	421	caccaccacta	ctactcgtcgcagc	cgtcgattgaggatca	Atggcaacaga	473	

Drosophila yakuba uncharacterized protein, transcript variant B (Dyak\GE13058), mRNA Sequence ID: **ref|XM_015196803.1|** Length: 3574 Number of Matches: 1 Range 1: 850 to 1448

Score	Expect	Identities	Gaps	Strand	Frame
706 bits(382)	0.0()	550/626(88%)	32/626(5%)	Plus/Plus	_

Features	s:		
Query	2	GCAGCAGCAGcaacaacaacaacaaGTTAGCCAGAAACCAACACGCAAGAGGCCACA	61
Sbjct	850	GCAGCAACAGCAGCAGCAACAACGAGTTAGCCAGAAACCAACACACGAGAGGCCACG	909
Query	62	AAAATAATTGGAATGT-AACAAATCTGAATGAAAGTGCTGAAGTTAAATAAATTTT	116
Sbjct	910	AAAATA-TTGGAATTTGAAGTCGGAAATCTGAATGAAAGTGCTGAAATGAAATAAA-TCT	967
Query	117	TAAGTGAATAAGAAACCGAAAAATACCACACATAAATGACGAGCGTTTGCAGAGTGTAGA	176
Sbjct	968	TAAGTGCATAAGAAACC-AAAAATTCCACTTATAAATGACGAGCGTGTGCAAAGTGTAAA	1026
Query	177	TAATTACATATTAGTTGTATCTTATTCATATATAGGGCAATATTCAATCGCGAGTGCTAA	236
Sbjct	1027	TAATTACATATTAGCTGTATATTATTCATATATATATTCAATCGCGAGTGCTAA	1080
Query	237	AATGCTGTCCTCCGCAGCATCGCTCATCGTCGGGATGCAGAAATCGATCTGAAATCAAAA	296
Sbjct	1081	AATGCTATCCATCGCAGCATCGGTCATCGTCGGGGATGCAGCAATCTGTCTG	1139
Query	297	TTAAGAAAAGAAATCAAAATATATATTTGTCGCTCTAAGTAATCAATC	356
Sbjct	1140	ttaagccaatcaa-a-atatatcggtcgctctaagtaatcaatcgtcgtagcca	1191
Query	357	ATCAAATCAAAATTGCATCAAAAGCCAACTCAAATTGTTGCCCCACCAACAGTTTGAGTG	416
Sbjct	1192	ATCAAATCAAAATTGCATCAAAAGCAACCTCAAATTGTTGCCCCACCAACAGTTTGAGTG	1251
Query	417	CACATTCATTTCGGCCCCCACTGTTCCTGTTCGTGAAACATTCAAAAACGGCCTCAAAAC	476
Sbjct	1252	CACATTTCCGTCGG-CCCCACTT-CC-TGAAACATTTAAAAACGGCCTCAAAAC	1302
Query	477	GGATTCCCTAGAGTTTCTGCGTTGCGAGGAAGAGGGATATCAAGATGGATATCCTACCGAG	536
Sbjct	1303	GGAGTCCCTAGAGTTTTTGCGGTGCGAGGAAGAGGGATATCAAGATGGATATCCTTCCGAG	1362
Query	537	TGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGGCTACTACTCGTCGCAGCC	596
Sbjct	1363	TGGCAACATCTTCAGCGAGCTGGAGCGGATCTGCACCACCGGCTACTACTCGTCGCAGCC	1422
Query	597	GTCGATTGAGGATCAATGGCAACAGA 622	
Sbjct	1423	GTCGATCGAGGATCAATGGCAACAGA 1448	

Drosophila yakuba uncharacterized protein, transcript variant A (Dyak\GE13058), mRNA Sequence ID: **ref|XM_002090305.2|** Length: 3275 Number of Matches: 1 Range 1: 585 to 1163

Score		Expect	Identities	Gaps	Strand	Frame	
676 bits	(366)	0.0()	534/609(88%)	35/609(5%)	Plus/Plus		
Features	s:						
Query	19	aacaacaacaa	GTTAGCCAGAAACG	CAACACGCAAGAGGCC	ACAAAAATAATTG	GAATGT-	77
Sbjct	585	AACAACAACAA	Acagcca-aaacc	CAACACACGAGAGGCC	ACGAAAATA-TTG	GAATTTG	640
Query	78	AACAAAT	CTGAATGAAAGTGO	CTGAAGTTAAATAAAT!	TTTTAAGTGAATA	AGAAACC	133
Sbjct	641	AAGTCGGAAA1	rctgaatgaaagtgo	ctgaaatgaaataaa-	tcttaagtgcata	AGAAACC	699
Query	134	GAAAAATACC <i>I</i>	ACACATAAATGACGA	AGCGTTTGCAGAGTGT	AGATAATTACATA	TTAGTTG	193
Sbjct	700	-AAAAATTCC	Actrataaatgacga	Agcgtgtgcaaagtgt	AAATAATTACATA	ttagctg	758
Query	194	TATCTTATTC	ATATATAGGGCAATA	ATTCAATCGCGAGTGC'	TAAAATGCTGTCC	TCCGCAG	253
Sbjct	759	tatattattc	ATATATATA	Attcaatcgcgagtgc	raaaatgetatee	ATCGCAG	812
Query	254	CATCGCTCATC	CGTCGGGATGCAGA	AATCGATCTGAAATCA	AAATTAAGAAAAG 	AAATCAA 	313
Sbjct	813	catcggtcatc	cgtcgggatgcagca	AAtctgtctgaaatc_	AAATTAAGC	caatc	865
Query	314	AATATATATA 	TTTGTCGCTCTAAG7	TAATCAATCGTCGTAG	CCAATCAAATCAA	AATTGCA	373
Sbjct	866	AA-A-AtAtAt	tcggtcgctctaag	taatcaatcgtcgtag	ccaatcaaatcaa	AATTGCA	923
Query	374	TCAAAAGCCAA	ACTCAAATTGTTGC(CCACCAACAGTTTGA(GTGCACATTCATT	TCGGCCC	433
Sbjct	924	tcaaaagcaac	cctcaaattgttgcd	cccaccaacagtttga	gtgcacattrccg	±cdd-cc	982
Query	434	CCACTGTTCCT	rgttcgtgaaacat	rcaaaaacggcctcaa 	AACGGATTCCCTA	GAGTTTC	493
Sbjct	983	ccyc44-c-	c-tgaaacati	rtaaaaacGGcctcaa	AACGGAGTCCCTA	ĠĀĠŦŦŦŦ	1034
Query	494	TGCGTTGCGAC	GGAAGAGGATATCAZ	AGATGGATATCCTACC	GAGTGGCAACATC	TTCAGCG	553
Sbjct	1035	tgcggtgcgad	GAAGAGGATATCA	AGATGGATATCCTTCC	gagtggcaacatc	ttcagcg	1094

Query	554	AGCTGGAGCG	GATCTGCACCACCGGCTACTACTCGTCGCAGCCGTCGATTGAGGATCAAT	613
Sbjct	1095	AGCTGGAGCG	GATCTGCACCACCGGCTACTACTCGTCGCAGCCGTCGATCGA	1154
Query	614	GGCAACAGA GGCAACAGA	622	
Sbjct	1155	GGCAACAGA	1163	

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

Range 1: 1 to 576

Score		Expect	Identities	Gaps	Strand	Frame	
556 bits	(301)	1e-154()	514/607(85%)	54/607(8%)	Plus/Plus		
Feature	s:						
Query	39	AAACCAACAC	GCAAGAGGCCAC-AAA	AATAATTGGAATGTAA	ACAAATCTGAATG.	AAAGTG	97
Sbjct	1	AAACCAACACA	ACAACAGGCCACGAGTA	AAT-ATTGGAATGTAA	ACAAATCTGAATG.	AAAGTG	59
Query	98	CTGAAGTTAA-	-ATAAATTTTTAAGTGA	AATAAGAAACC(GA-AAAATACCAC	ACATAA 	151
Sbjct	60	ctdaaatgaar	raaaaaaatttaagtga	AATAAGAAACCAAAAZ	yyddyddaeth	ттатаа	119
Query	152	ATGACGAGCGT	TTGCAGAGTGTAGATA	AATTACATATTAGTTO	TATCTTATTCAT.	ATATAG 	211
Sbjct	120	atgacgagcg1	rgtgcaaagtgtacatz	AATTACATATTAGCTO	statattattcat.	ATATAG	179
Query	212	GGCAATATTCA	ATCGCGAGTGCTAAAZ	ATGCTGTCCTCCGCAC	CATCGCTCATCG	TCGGGA	271
Sbjct	180	gccaatattca	AAACGCGAGTGCTAAAA	AtGC	SĠ-tcaacc	tcggga	223
Query	272	TGCAGAAATCG	GATCTGAAATCAAAAT	TAAGAAAAG-AA	ATCAAAATATAT.	ATATTT 	326
Sbjct	224	tecaeaaatcı	rgtctgaaatc-aaatz	AAATCAAATTAAGCTA	Atcaaaatatat	СТА	279
Query	327	GTCGCTCTAAC	TAATCAATCG!	TCGTAGCCAATC <i>I</i>	AATCAAAA-TTG	CATCAA	377
Sbjct	280	-tccctctAAc	staatcgtaatcgtaa	rcgtrgtagccaatca	AAATCAAAATTTG	ĊATĊAA	338
Query	378	AAGCCAA-CTC	CAAATTGTTGCCCCAC	CAACAGTTTGAGTGC <i>I</i>	CATTCATTTCGG	CCCCCA	436
Sbjct	339	AAGCAAACCTC	caaattgttgccacac	caacagtttgagtgc	Acattttc	CTTGCA	393
Query	437	CTGTTCCTGTT	CGTGAAACA-TTCAAA	AAACGGCCTCAAAACG	GATTCCCTAGAG	TTTCTG	495
Sbjct	394	accactd	rcctcaaaacarttgaa	aaacggcctcaaaacd	ggydtccctygyg	ተተተ ተተ Ġ	449
Query	496	CGTTGCGAGG <i>A</i>	AAGAGGATATCAAGAT(GGATATCCTACCGAG7	GGCAACATCTTC	AGCGAG	555
Sbjct	450	CGTTGCGAGGA	AAGAGGATAGCAAGAT(GGATATCCTTCCGAG1	rddcaacatcttc	AGCGAG	509
Query	556	CTGGAGCGGAT	CTGCACCACCGGCTA(CTACTCGTCGCAGCC	GTCGATTGAGGAT	CAATGG	615
Sbjct	510	ctggagcggat	cctdcaccaccddcta	ctactcgtcgcagccd	stegattgaggat	caatgg	569
Query	616	CAACAGA 62	22				
Sbjct	570	CAACAGA 57	76				

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

Score		Expect	Identities	Gaps	Strand	Frame	
191 bits	(103)	2e-44()	103/103(100%)	0/103(0%)	Plus/Plus		
Feature	s:						
Query	520	ATGGATATCCT	ACCGAGTGGCAACATCT	TCAGCGAGCTGGAG	CGGATCTGCACC	CACCGGC	579
Sbjct	17	Atggatateetz	Acceaeteecaacatct	tcagcgagctggag	cggatctgcacd	Accede	76
Query	580	TACTACTCGTCC	CAGCCGTCGATTGAGG.	ATCAATGGCAACAG.	A 622		
Sbjct	77	tactactcctc	scadccdtcdattdadd.	atcaatggcaacag.	Å 119		

Drosophila melanogaster transcription factor DKLF mRNA, complete cds

Sequence ID: gb|AF461497.1| Length: 1713 Number of Matches: 1

Range 1: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
191 bits	(103)	2e-44()	103/103(100%)	0/103(0%)	Plus/Plus		
Features	s:						
Query	520	ATGGATATCCT	ACCGAGTGGCAACATCTT	rcagegagetggag	CGGATCTGCACC	ACCGGC	579
Sbjct	1	ATGGATATCCTA	ACCGAGTGGCAACATCT:	rcagcgagctggag	CGGATCTGCACC	ACCGGC	60
Query	580	TACTACTCGTCG	GCAGCCGTCGATTGAGG	ATCAATGGCAACAG	A 622		
Sbjct	61	tactactcgtcd	CAGCCGTCGATTGAGG	Atcaatggcaacag	A 103		

Drosophila sechellia GM20477 (Dsec\GM20477), mRNA

Sequence ID: ref|XM_002033285.1| Length: 1713 Number of Matches: 1

Range 1: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
185 bits	(100)	8e-43()	102/103(99%)	0/103(0%)	Plus/Plus		
Features	S :						
Query	520	ATGGATATCCTA	CCGAGTGGCAACATCT	TTCAGCGAGCTGGAG	CGGATCTGCAC	CACCGGC	579
Sbjct	1	ATGGATATCCTA	CCGAGTGGCAACATC	rtcagcgagctggag	CGGATCTGCAC	CACCGGC	60
Query	580	TACTACTCGTCG	CAGCCGTCGATTGAGC	GATCAATGGCAACAG	A 622		
Sbjct	61	tactactcgtcg	CAGCCCTCGATTGAG	GATCAATGGCAACAG	A 103		

Drosophila simulans GD25946 (Dsim\GD25946), mRNA

Sequence ID: ref|XM_002080935.1| Length: 1710 Number of Matches: 1

Range 1: 1 to 103

Score		Expect	Identities	Gaps	Strand	Frame	
180 bits	(97)	4e-41()	101/103(98%)	0/103(0%)	Plus/Plus		
Features	S :						
Query	520	ATGGATATCCT	'ACCGAGTGGCAACATC	TTCAGCGAGCTGGA	GCGGATCTGCAC	CACCGGC	579
Sbjct	1	ATGGATATCCT	ACCGAGTGGCAACATI	TTCAGCGAGCTGGA	GCGGATCTGCAC	CACCGGC	60
Query	580	TACTACTCGTC	GCAGCCGTCGATTGAG	GATCAATGGCAACA	GA 622		
Sbjct	61	tactactcdtc	GCAGCCGTCGATAGAG	GATCAATGGCAACA	GA 103		