Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CNA4GDXM014

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Blast report description

Nucleotide Sequence (2097 letters)

RID <u>CNA4GDXM014</u> (Expires on 02-23 13:20 pm)

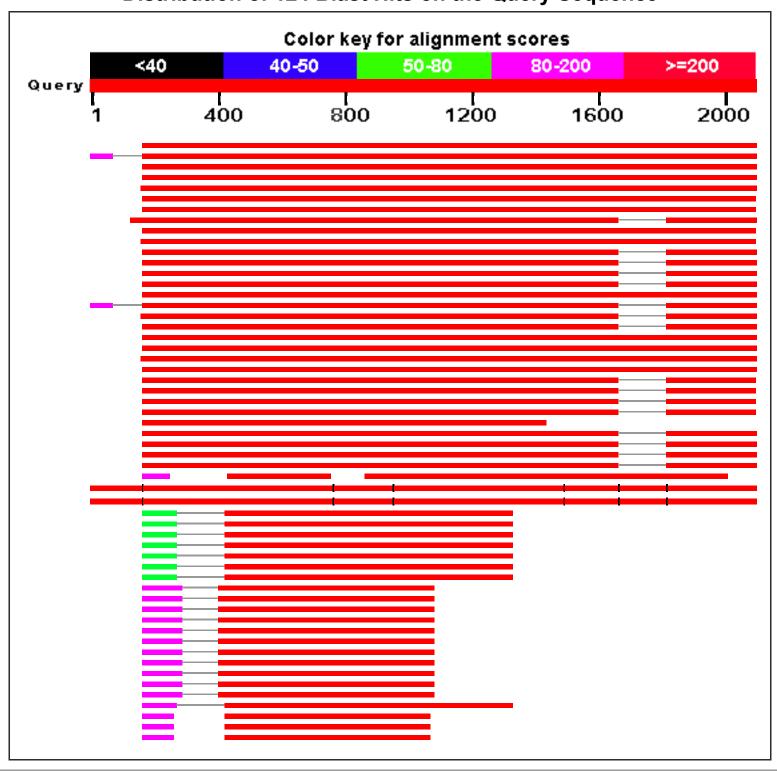
Description None **Description** Nucleotide collection (nt)

Molecule type nucleic acid Program BLASTN 2.3.1+

Query Length 2097

□ Graphic Summary

Distribution of 124 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 C3G ortholog, transcript variant F (C3G), mRNA	3483	3483	92%	0.0	99%	NM_001144696.3
Drosophila melanogaster C3G ortholog, transcript variant D (C3G), mRNA	3482	3612	95%	0.0	99%	NM_001144694.2
Drosophila melanogaster C3G ortholog, transcript variant H (C3G), mRNA	3480	3480	92%	0.0	99%	NM_132122.5
Drosophila melanogaster RE10624 full insert cDNA	3474	3474	92%	0.0	99%	BT010019.1
Drosophila melanogaster C3G ortholog, transcript variant I (C3G), mRNA	3397	3397	92%	0.0	98%	NM_001272362.1
Drosophila erecta uncharacterized protein, transcript variant B (Dere\GG17655), mRNA	2813	2813	91%	0.0	93%	XM_015155122.1
Drosophila erecta uncharacterized protein, transcript variant A (Dere\GG17655), mRNA	2813	2813	91%	0.0	93%	XM_001978447.2
Drosophila melanogaster C3G ortholog, transcript variant J (C3G), mRNA	2758	3268	86%	0.0	99%	NM_001272363.1
Drosophila erecta uncharacterized protein, transcript variant E (Dere\GG17655), mRNA	2730	2730	91%	0.0	92%	XM_015155125.1
Drosophila erecta uncharacterized protein, transcript variant C (Dere\GG17655), mRNA	2730	2730	92%	0.0	92%	XM_015155123.1
Drosophila melanogaster guanine nucleotide exchange factor DC3G (DC3G) mRNA, complete cds	2728	3256	84%	0.0	99%	<u>AF053358.1</u>
Drosophila melanogaster C3G ortholog, transcript variant K (C3G), mRNA	2693	3204	84%	0.0	99%	NM_001272364.1
Drosophila melanogaster C3G ortholog, transcript variant E (C3G), mRNA	2693	3204	84%	0.0	99%	NM_001144695.3
Drosophila melanogaster IP03271 full insert cDNA	2693	3204	84%	0.0	99%	BT025818.1
Drosophila yakuba C3G, transcript variant I (Dyak\C3G), mRNA	2691	2691	92%	0.0	92%	XM_015190007.1
Drosophila melanogaster C3G ortholog, transcript variant G (C3G), mRNA	2691	3332	88%	0.0	99%	NM_001144697.2
Drosophila melanogaster C3G ortholog, transcript variant L (C3G), mRNA	2689	3200	85%	0.0	99%	NM_001298037.1
Drosophila melanogaster C3G ortholog, transcript variant C (C3G), mRNA	2689	3200	84%	0.0	99%	NM_176694.3
Drosophila yakuba C3G, transcript variant A (Dyak\C3G), mRNA	2687	2687	92%	0.0	92%	XM_002099904.2
Drosophila yakuba C3G, transcript variant H (Dyak\C3G), mRNA	2608	2608	92%	0.0	91%	XM_015190006.1
Drosophila yakuba C3G, transcript variant E (Dyak\C3G), mRNA	2606	2606	92%	0.0	91%	XM_015190003.1
Drosophila yakuba C3G, transcript variant C (Dyak\C3G), mRNA	2604	2604	92%	0.0	91%	XM_015190001.1

Drosophila erecta uncharacterized protein, transcript variant H (Dere\GG17655), mRNA	2252	2633	84%	0.0	94%	XM_015155128.1
Drosophila erecta uncharacterized protein, transcript variant G (Dere\GG17655), mRNA	2252	2633	84%	0.0	94%	XM_015155127.1
Drosophila erecta uncharacterized protein, transcript variant F (Dere\GG17655), mRNA	2252	2633	84%	0.0	94%	XM_015155126.1
Drosophila erecta uncharacterized protein, transcript variant D (Dere\GG17655), mRNA	2252	2633	84%	0.0	94%	XM_015155124.1
Drosophila sechellia GM12551 (Dsec\GM12551), mRNA	2135	2135	60%	0.0	97%	XM_002036688.1
Drosophila yakuba C3G, transcript variant G (Dyak\C3G), mRNA	2063	2495	84%	0.0	92%	XM_015190005.1
Drosophila yakuba C3G, transcript variant D (Dyak\C3G), mRNA	2063	2495	84%	0.0	92%	XM_015190002.1
Drosophila yakuba C3G, transcript variant B (Dyak\C3G), mRNA	2063	2495	84%	0.0	92%	XM_015190000.1
Drosophila yakuba C3G, transcript variant F (Dyak\C3G), mRNA	2060	2491	84%	0.0	92%	XM_015190004.1
Drosophila simulans GD16179 (Dsim\GD16179), mRNA	1936	1936	54%	0.0	97%	XM_002106294.1
Drosophila melanogaster chromosome X	1059	3802	99%	0.0	99%	AE014298.5
Drosophila melanogaster X BAC RP98- 48O24 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence	1059	3802	99%	0.0	99%	AC023722.4
Drosophila mojavensis uncharacterized protein, transcript variant H (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_015161045.1
Drosophila mojavensis uncharacterized protein, transcript variant G (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_015161044.1
Drosophila mojavensis uncharacterized protein, transcript variant F (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_015161043.1
Drosophila mojavensis uncharacterized protein, transcript variant D (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_015161042.1
Drosophila mojavensis uncharacterized protein, transcript variant C (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_015161041.1
Drosophila mojavensis uncharacterized protein, transcript variant B (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_015161040.1
Drosophila mojavensis uncharacterized protein, transcript variant E (Dmoj\Gl21607), mRNA	761	840	48%	0.0	82%	XM_002010591.2
Drosophila ananassae uncharacterized protein, transcript variant C (Dana\GF20837), mRNA	710	835	38%	0.0	86%	XM_014905493.1
Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905492.1
Drosophila ananassae uncharacterized protein, transcript variant A (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_001964172.2

Drosophila ananassae uncharacterized protein, transcript variant D (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905491.1
Drosophila ananassae uncharacterized protein, transcript variant K (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905490.1
Drosophila ananassae uncharacterized protein, transcript variant J (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905489.1
Drosophila ananassae uncharacterized protein, transcript variant I (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905488.1
Drosophila ananassae uncharacterized protein, transcript variant H (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905487.1
Drosophila ananassae uncharacterized protein, transcript variant G (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905486.1
Drosophila ananassae uncharacterized protein, transcript variant F (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905485.1
Drosophila ananassae uncharacterized protein, transcript variant E (Dana\GF20837), mRNA	710	833	38%	0.0	86%	XM_014905484.1
Drosophila grimshawi GH24527 (Dgri\GH24527), mRNA	667	766	48%	0.0	80%	XM_001991970.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant L (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185781.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant K (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185780.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant J (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185779.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant I (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185778.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant H (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185777.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant G (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185776.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant F (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185775.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant E (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185774.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant D (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185773.1

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_015185772.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant C (Dpse\GA16131), mRNA	621	621	30%	2e-173	84%	XM_001355540.3
Drosophila persimilis GL26876 (Dper\GL26876), mRNA	616	616	30%	8e-172	84%	XM_002025088.1
Drosophila busckii chromosome X sequence	278	278	15%	4e-70	82%	CP012528.1
Drosophila simulans GD16178 (Dsim\GD16178), mRNA	128	128	4%	5e-25	93%	XM_002106295.1
Drosophila virilis uncharacterized protein, transcript variant E (Dvir\GJ16545), mRNA	87.9	87.9	4%	8e-13	83%	XM_015169995.1
Drosophila virilis uncharacterized protein, transcript variant D (Dvir\GJ16545), mRNA	87.9	87.9	4%	8e-13	83%	XM_015169994.1
Drosophila virilis uncharacterized protein, transcript variant C (Dvir\GJ16545), mRNA	87.9	87.9	4%	8e-13	83%	XM_015169993.1
Drosophila virilis uncharacterized protein, transcript variant B (Dvir\GJ16545), mRNA	87.9	87.9	4%	8e-13	83%	XM_015169992.1
Drosophila virilis uncharacterized protein, transcript variant G (Dvir\GJ16545), mRNA	87.9	87.9	4%	8e-13	83%	XM_015169991.1
Drosophila virilis uncharacterized protein, transcript variant F (Dvir\GJ16545), mRNA	87.9	87.9	4%	8e-13	83%	XM_002057044.2
Drosophila willistoni uncharacterized protein, transcript variant B (Dwil\GK25837), partial mRNA	58.4	58.4	1%	6e-04	100%	XM_015177223.1
Drosophila willistoni uncharacterized protein, transcript variant C (Dwil\GK25837), partial mRNA	58.4	58.4	1%	6e-04	100%	XM_002071466.2

□<u>Alignments</u>

Drosophila melanogaster C3G ortholog, transcript variant F (C3G), mRNA Sequence ID: **ref|NM_001144696.3|** Length: 5804 Number of Matches: 1 Range 1: 660 to 2587

Score		Expect	Identities	Gaps	Strand	Frame	
3483 bit	s(1886)	0.0()	1919/1934(99%)	6/1934(0%)	Plus/Plus		
Features	S :						
Query	163	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG	AGTGGG	222
Sbjct	660	GAACGGCAGCAT	cagttctccatccac	GCCCGGCACCTGTTCC	AGTGGCATCGG	AGTGGG	719
Query	223	CGGTGGCGGCTG	CAGCAGCAGCAGCAA	CAATAGCATCAACAGC	GGCAGCTACTC	CACCGC	282
Sbjct	720	çeeteeçeeçte	cydcydcydcydcyd	.caatagcatcaacagc	GGCAGCTACTC	caccec	779
Query	283	CTGCACTCCGCC	ACCACCCACGCATCA	GCATCACTCGCAGCAC	CAGCAGCTGCA	GGGCAC	342
Sbjct	780	ctcckctcccc	qccqccqcqcqqqq	.dcatcactcdcadcac	cagcagctgca	ręęęcyc	839
Query	343	GCCGGGAGGATC	TAGTCGGGTCGGGGG	AGCAGGAGCAGGAGCA	GGCGGAGGTGG	TGGTGT	402
Sbjct	840	ĠĊĊĠĠĠĠĠĠĠ	taktckkktakk	-dddadcaddadca	ĠĠĊĠĠĀĠĠŦĠĠ	tggtgt	893

Query	403	ACCACCGGCACCACCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAA	462
Sbjct Query	894 463	ACCACCGGCACCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAA GCTAGCGCGCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCG	953 522
Sbjct	954	GCTAGCGCGCGGGCGCTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCG	1013
Query	523	А АССАССААСААТАСАСТӨӨӨТСӨСТСССАСТСӨССӨСАСАССАССАССАССАССАССАССАССАССАССАС	582
Sbjct	1014	AACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGG	1073
Query	583	CACAAAGGCACCGCCCACCACGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCA	642
Sbjct	1074	cacaaaggcaccgccaccaccgaggaggtgctacggtccacccaaaccctggagacgca	1133
Query	643	CGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCT	702
Sbjct	1134	ĊĠŦĊĀĀĠĠĀĊĀŤŦŤĊĠĀĀŤĠĊĊĊŤĠĀĀĠĊĀĊŤŤĊĊĠĠĠĀŤĠŤŤĀŤĀĊŤĊĀĀĠĀĀĠĀĀĠĊŤ	1193
Query Sbjct	703 1194	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	762 1253
Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822
Sbjct	1254		1313
Query	823	ТТАССАGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Sbjct	1314	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	1373
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	1374	ĊĠĠĊĠĀĠŦĠĊĠĊĊŦĊĊĊŦĠĀĠĊĀĀĊĠĀĠĀĀŦĠŦĠĊĠĠĠĀĀĠŦĊĀŦŦĠĀŦĊŦŦĊŦĊĠĀĠĠĀ	1433
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002 1493
Sbjct Query	1434 1003	TĠĊŦĠŦĠĊĠĠAĂŦĊŦĊĠŦŦĂĊĠĊŦĠĠĊĠĊĀĠĠĠĊĀĀĠĊŦĠĀĀĠĠĀĠĊĀĠĠĀŦĊĀĠŦĠĊĠĊ CTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1493
Sbjct	1494	CTTTCGCTACAGTGGATCTGGCCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1553
Query	1063	ĢĢŢÇĄÇÇĢÇÇŢÇĢÇÇĢĢĀĢÇĢĄĢŢĢŢŢÇÇÇĢĢŢĄÇŢĢĢĄĢŢÇĄŢĢÇĢÇĢŢŢŢÇĢĢÇÇĢÇ	1122
Sbjct	1554	GGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGC	1613
Query	1123	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1182
Sbjct	1614	cgaatcagctgccagcgtacttcgttgccggacatagcgctcacgccaaaggagcgcga	1673
Query	1183	CATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1242
Sbjct Query	1674 1243	ĊĂTĂĊŢĠĠĀĠĊĀĠĊĀĊĀĀŢĠŢĠĀĀĊĊĊĠĀŢĠĊĠĊĠĊŢĊĊĊĀĊĀĠĊĀĊĊĠĀĀĀĠŢĀŢĊĊŢ GCGCGACACGAGŢCCACCGCCGAAGCCACCGCŢACCCAAŢAGGGCCAGŢAĀŢCCGCCGCC	1733 1302
Sbjct	1734	GCGCGACACGAGTCCACCGCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1793
Query	1303	ĢŢŢĢÇÇĄÇÇĄĄĄĢÇĢĄĢÇÇĄĢÇÇĢĄĢÇĢÇĄŢÇĄĢÇŢĢĢŢĄÇĄĢŢĢĢĢÇĢŢĄĢĢÇŢĢ	1362
Sbjct	1794	GTTGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1853
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1854	ctcatcgtcgacatccacctccaatcaggccagtccactgccctacgcccagtccataa	1913
Query	1423	TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1482
Sbjct Query	1914 1483	TÁTTÁGTCTGÁÁCTCGGÁCCTGGÁCTGCÁGTTCCÁÁTÁTCTCGCTGCTGÁÁTTÁTGGCGT GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1973 1542
Sbjct	1974	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	2033
Query	1543	ĢĢÇĢŢŢĢĄĄŢÇĄÇŢÇĄÇĢĢĢĢĢĢĢĢĢĢĢÇĄĢÇĄĄÇĄĢÇĄĄÇĄŢÇĄĢÇĄCÇŢĢĄĢĢŢÇ	1602
Sbjct	2034	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACACATCAGCATCTGAGGTC	2093
Query	1603	GTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAGCGC	1662
Sbjct	2094	atttccaaagttgcctgcgatgatgacgaagacatggacaagatggtcagctacagcgc	2153
Query	1663	CGCAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTGGTATAGCTGGTGTTGC	1722
Sbjct	2154	ĊĠĊĂĂŢĊĠĂĊĠĂĊĂĂĂĂĊĠĊĂĠĂĊĂĊĊĂĊŢŢŢĊĠĂĊŢĠĠŢĠŢĠŢĠŢ	2213
Query Sbjct	1723 2214	TGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAAC	1782 2273
Query	1783	TAAÇAGÇAATÇGÇÇAÇTÇAAAÇGAATÇGGGTTTÇGTGTÇGATGÇGTGAGTTTÇGÇAÇTTÇ	1842
Sbjct	2274	TAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTC	2333

Query	1843	TACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGA	1902
Sbjct	2334	CACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGA	2393
Query	1903	GATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGAT	1962
Sbjct	2394	GATTGCGTTCAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGAT	2453
Query	1963	TAGCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCAC	2022
Sbjct	2454	tagccagttggtgtcgcacagccagcgtcatatatcctcgagcagtagcagctgcaccac	2513
Query	2023	CACGACCACcagcagcagcaccaccggctatggcagcagcgaagtggagcagcagca	2082
Sbjct	2514	CACGACCACCAGCAGCACCACCACCGGCTATGGCAGCAGCGAAGTGGAGCAGCTGCA	2573
Query	2083	gcagcagcagc 2096	
Sbjct	2574	GCAGCAGCAGC 2587	

Drosophila melanogaster C3G ortholog, transcript variant D (C3G), mRNA Sequence ID: **ref|NM_001144694.2|** Length: 5397 Number of Matches: 2 Range 1: 254 to 2180

Score		Expect	Identities	Gaps	Strand	Frame	
3482 bi	ts(1885)	0.0()	1918/1933(99%)	6/1933(0%)	Plus/Plus		
Feature	s:						
Query	164	AACGGCAGCATC	AGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGGA	GTGGGC 22	23
Sbjct	254	AACGGCAGCATC	AGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGGA	GTGGGC 3	13
Query	224	GGTGGCGGCTGC	AGCAGCAGCAA	CAATAGCATCAACAGC(GGCAGCTACTCC	ACCGCC 28	83
Sbjct	314	ĠĠŦĠĠĊĠĠĊŦĠĊ	:AĠĊAĠĊAĠĊAĠĊAA	caatagcatcaacagc	ĠĠĊĀĠĊŦĀĊŦĊĊ	zaccccc 37	73
Query	284			GCATCACTCGCAGCAC(43
Sbjct	374			ĠĊĂŢĊĂĊŢĊĠĊĂĠĊĂĊ			33
Query	344			AGCAGGAGCAGGAGCA(03
Sbjct	434 404			-GGGAGCAGGAGCA(CTCGGGCCACAAGAAC			87 63
Query Sbjct	488		CCCAGTGCCGGATC	111111111111111	AGTCTCAAGGGC AGTCTCAAGGGC		47
Query	464			GGACGACCTCATCGAG.			23
Sbjct	548						07
Query	524	АССАССААСААТ	[,] ,	, ССАСТСВССВСАСАВТО ССАСТЕВЕТОВ В СОВТЕВЕТОВ В СОВТЕВЕТОВ В СОВТЕВЕТОВ В СОВТЕВЕТОВ В СОВТЕВЕТОВ В СОВТЕВЕТОВ В ССАСТЕВЕТОВ В СОВТЕВЕТОВ В СОВТЕВЕТ	ÇÇĞÇĞÇAÇÇAAĞ	ÇĄÇĢĢÇ 58	83
Sbjct	608	ACCACCAACAAT	ACACTGGGTCGCTC			 CACGGC 66	67
Query	584	ACAAAGGCACCG	CCCACCACCGAGGA	GGTGCTACGGTCCACC	CAAACCCTGGAG	ACGCAC 64	43
Sbjct	668	Acadaddcaccd	cccaccaccacca	ggtgctacggtccacc	CAAACCCTGGAG	acccac 72	27
Query	644	GTCAAGGACATT	TCGAATGCCCTGAA	GCACTTCCGGGATGTT	ATACTCAAGAAG	SAAGCTG 70	03
Sbjct	728			ĠĊĀĊŦŦĊĊĠĠĠĀŦĠŦŦ			87
Query	704			CATTCTGGAAACCATA(63
Sbjct	788			CATTCTGGAAACCATA(47
Query	764 848			CAGTGCCATCATGAGC 			23 07
Sbjct Query	824			GCTCTGCGACGAGGTG			83
Sbjct	908			GCTCTGCGACGAGGTG			67
Query	884			ĢĄĄŢĢŢĢÇĢĢĢĄĄĢŢÇ.			43
Sbjct	968	GGCGAGTGCGCC	 !TCCCTGAGCAACGA		 ATTGATCTTCTC	 !GAGGAT 1(027
Query	944	GCTGTGCGGAAT	CTCGTTACGCTGGC	GCAGGGCAAGCTGAAG	GAGCAGGATCAG	TGCGCC 10	003
Sbjct	1028	GCTGTGCGGAAT	ctcdttacdctddc	GCAGGGCAAGCTGAAG		rtgcgcc 10	087
Query	1004	TTTCGCTACAGT	GGATCTGGCTTGGG	CGGCATTGGAGCGGCG	GCGGAGATCATG	GGTGCG 10	063
Sbjct	1088	TTTCGCTACAGT	ŀĠĠĀŦĊŦĠĠĊŦŦĠĠĠ	ceecatteeaeceece	gcggagatcate	sddfddd 11	147
Query	1064	GTCACCGCCTCG	CCGGGAGCGAGTGT	TCCCGGTACTGGAGTC	ATGCGCGTTTCG	GCCGCC 1	123

Sbjct	1148	GTCACCGCCTCGCCGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGCC	1207
Query	1124	GAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGAC	1183
Sbjct	1208	GAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGAC	1267
Query	1184	ATACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTG	1243
Sbjct	1268	ATACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTG	1327
Query	1244	CGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCG	1303
Sbjct	1328	CGCGACACGAGTCCACCGCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCG	1387
Query	1304	TTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGC	1363
Sbjct	1388	TTGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGC	1447
Query	1364	TCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAAT	1423
Sbjct	1448	tcatcgtcgacatccacctccaatcaggccagtccactgccctacgcccagtcccataat	1507
Query	1424	ATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTG	1483
Sbjct	1508	Attagtetgaaeteggaetggaetgeagtteeaatatetegetgetgaattategeegtg	1567
Query	1484	GATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCG	1543
Sbjct	1568	ĠAŦĊĠĊĊŦAŦĊĊĠŦĠĊĠŦŦĊAĊĠĠŦĊAĊĊĠĠAŦĠAĠAAŦAĠŦĊAĠŦĠĊŦĊĊŦŦŦĠAĊŦĊĠ	1627
Query	1544	GCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGGTCG	1603
Sbjct	1628	ĠĊĠŦŦĠĀĀŦĊĀĊŦĊĀĊĠĊĠĀĠĠĀĠĠĀĠĠĀĊĊĀĠĊĀĀĊĀĠĊĀĀĊĀĠĊĀŦĊŦĠĀĠĠŦĊĀ	1687
Query	1604	TTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAGCGCC	1663
Sbjct	1688	trtccaaagtrggctgcatgatgatgacgaagacatggacaagatggtcagctacagcgcc	1747
Query	1664	GCAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTGGTATAGCTGGTGTTGCT	1723
Sbjct	1748	ĠĊĀĀŢĊĠĀĊĠĀĊĀĀĀĀĊĠĊĀĠĀĊĀĊĊĀĊŢŢŢĊĠĀĊŢĠĠŢĠĠŢĠŢĀŢĀĠĊŢĠĠŢĠŢŢĠĊŢ	1807
Query	1724	GGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAACT	1783
Sbjct	1808	ĠĠŦĠĠĂĀĊŦĠĠĀĠĠĀĠĊĀĠĠĊĠĀĀĠĠŦĠŦĀĠĊŦĠĊĀĠĊĠŦĊŦĠĠŦĠĀĊĠĠĠĠĀĀĀĊŦ	1867
Query	1784	AACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTCT	1843
Sbjct	1868	AACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTCC	1927
Query	1844	ACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGAG	1903
Sbjct	1928	ACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGAG	1987
Query	1904	ATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATT	1963
Sbjct	1988	ATTGCGTTCAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATT	2047
Query	1964	AGCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACC	2023
Sbjct	2048	AGCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACC	2107
Query	2024	ACGACCACcagcagcaccaccaccggctatggcagcagcgaagtggagcagcagcag	2083
Sbjct	2108	ACGACCACCAGCAGCACCACCACCGGCTATGGCAGCAGCGAAGTGGAGCAGCTGCAG	2167
Query	2084	cagcagcagc 2096	
Sbjct	2168	ĊAĠĊAĠĊAĠĊAĠĊ	

Range 2: 64 to 133

Score		Expect	Identities	Gaps	Strand	Frame	
130 bits	(70)	1e-25()	70/70(100%)	0/70(0%)	Plus/Plus		
Features	S :						
Query	1	AAAAAGAGGAA	atatatatatata c	AAGAATAAGTATC	GAAACTCAAGTGO	GCCACATA	60
Sbjct	64	AAAAAGAGGAA	Atatatatatatatatac	AAGAATAAGTATC	GAAACTCAAGTGG	CCACATA	123
Query	61	TATTTAGGTG	70				
Sbjct	124	TATTTAGGTG	133				

Range 1: 1325 to 3250

Buery 165 ACGGCAGCATCAGTTCTCCATCCAGCCCGGCACCTGTTCCAGTGGCAGTGGGCG 21 Biglet 1325 ACGGCAGCATCAGTTCTCCATCCAGCCCGGCACCTGTTCCAGTGGCAGTGGCGC 21 Buery 225 GTGGCGGCTGCAGCAACAGCAACAATAGCATCAACAGCGGCACCTACTCCACCGCCT 21 Buery 285 GCACTCGGCACCCACCCAGCATCAGCAATAGCATCAACAGCGGCACCTACTCCACCGCCT 21 Biglet 1445 CCACTCGCCACCCACCCAGCATCAGCATCACTGGCAGCACCAGCAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	Score		Expect	Identities	Gaps	Strand	Frame
Buery 165 ACGGCAGCATCAGTTCTCCATCCAGCCCGGCACCTGTTCCAGTGGCAGTGGGCG 21 Biglet 1325 ACGGCAGCATCAGTTCTCCATCCAGCCCGGCACCTGTTCCAGTGGCAGTGGCGC 21 Buery 225 GTGGCGGCTGCAGCAACAGCAACAATAGCATCAACAGCGGCACCTACTCCACCGCCT 21 Buery 285 GCACTCGGCACCCACCCAGCATCAGCAATAGCATCAACAGCGGCACCTACTCCACCGCCT 21 Biglet 1445 CCACTCGCCACCCACCCAGCATCAGCATCACTGGCAGCACCAGCAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	3480 bits	s(1884)	0.0()	1917/1932(99%)	6/1932(0%)	Plus/Plus	
pjet 1325 ACGGCAGCATCAGTTCTCATCCAGCCCGGCACTTTCCAGTGCATTGGGAGTGGGGG 1325 GTGGCGGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCGGGCGG	Features	:					
bjet 1385 craccacacacacacacacacacacacacacacacacac	Query			111111111111111			
point 1385 GTGGGGGCTCCAGCACCACGAGAACAATAGCATCAACGGGGCACCTTACTCCACCGCT 14 point 1445 CCACTCCGCCACCACCCACCCACCACCACCACCACCACCACCACC	Sbjct						
bjet 1445 ccacacacaccaccaccaccaccaccaccaccaccacca	Sbjct			111111111111111			
bjet 1505 coccacactactactactactactactactactactactact	Query						
bjet 1505 CGGGGGGATCTACTCGGTAGC-G-GGACCAGGGCGAGGTGGTGGTGTAC 19 Mary 405 CACCGGCACCACCAGTGCCGGATCCTCGGGCCACAAGACAGGCCAGGGCACAAGC 46 bjet 1559 CACCGGCACCACCCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCACAGC 46 bjet 1559 CACCGGCACCACCCAGTGCCGGATCCTTCGGGCCACAAGAACAGTTTCCCTGATGCGAA 51 bjet 1619 TACCGCCCCGGGGGGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAA 52 bjet 1679 CCACCAACAATACACTGGGTGCTCCCACTCGCGCACAGTCCGGCACCACACACA	Sbjct	1445	GCACTCCGCCAC	CACCCACGCATCAGCA	TCACTCGCAGCACCA		GCACGC 15
The property of the control of the property of	Query		CGGGAGGATCTA	GTCGGGTCGGGGAGC	AGGAGCAGGAGCAGG	CGGAGGTGGTG(
bjet 1559 CACCGGCACCACCCGGATCCTTTAAGGACCACAAGAACAAGTCTCAAGGGCACAACC 16 Bury 465 TAGGGCGCGGGGGGTTCCTTTAAGGACGACTCATCGAGAAGATTTCCCTGATGCGAA bjet 1619 TAGCGCCCGGGGGGGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAA bjet 1619 TAGCGCCCCGGGGGGGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAA bjet 1679 CCACCAACAATACACTGGGTTGGTTCGCTGCCGCACAAGCCCGGCACCAAGCACGGCA bjet 1739 CAAAGGCACCGCCCACCACCGAGGGGGTGTTCACGTCGGCCACAAGCCCTGGAGACCCACG bjet 1739 CAAAGGCACTTTCGAATGCCCTGAAGCACTTCGGGGATGTTTATACTCAAGAAGAACACTGG bjet 1799 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAACACTGG bjet 1799 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAACACTGG bjet 1859 AGGTGTTGCCGGGCAACGGAAGGGTCATTCTGGGAATCATTACTCAAGAAGAACACTGG bjet 1859 AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACCTCGTGA bjet 1919 TCAAACCTACACCCTGAACCACTTCGGGATGTTATACTCAAGAAGAAACCTGG bjet 1919 TCAAACCTACACCCTGAATGAAACACTTGCCATCATAGACCACGCCACGCTGCAGGTTT bjet 1919 TCAAACCTACACCCTGAATGAAACACTTGCGCATCATTAGACCACGCCACGCTGCAGGTTT bjet 1919 TCAAACCTACACCCTGAATGAAACACTTGCAGAGAGGTGATGCTCTCCGAGGACGTTT bjet 1919 ACCAGAGCCTGGGCAAGGTCATTCAGACTCATCAGACGACGCCACGCTGCAGGTTT bjet 1919 ACCAGAGCCTTGCCTGAACCAACGACTTTTCGAGAGAGGACGCCACGCTGCAGGTTT bjet 1919 ACCAGAGCCTTGCCTGAACCAACGACTTTGCAGCAGGGTGATGCTTCTCCGAGGACAGC bjet 1979 ACCAGAGCCTTGCCTGAGCAACGAATTTGCGGGGAAGTCATTGATCTTCTCGAGGACGC bjet 1979 ACCAGAGCCTTGCCTGAGCAACGAATTTGCGGGGAAGTCATTGATCTTCTCGAGGACGC bjet 2039 GGAATGCGCCTCCCTGAGCAACGAACTATTGAGCGGAAGTCATTGACTTCCAGGATC bjet 2039 CTGTGCGGAAACTACTGTTACGCTGGCGCAAGCTTAAGGACCAGGAACTCATTGACTGGCTCCCC bjet 2159 TCCCTCACAGCACGAACGAACTATTGACCTGAGAGCAAGGAATCATTGACCTGAGCAGCCCCCCCC	Sbjct						
TAGGEGGCCGGGGGGGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAA bjet 1619 TAGCGCCGGGGCGGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAA lucry 525 CCACCAACAATACACTGGGTCGCTCCCACTGCGCGCACATCCGGGCACCAAGCACGGCA bjet 1679 CCACCAACAATACACTGGGTCGCTCCCACTGCGCGCACCAAGCCCGGCACCAAGCACGGCA lucry 585 CAAAGGCACCGCCCACCCACGAGGAGGTGCTACCGTCACCCAAACCCTGGAGACGCAC bjet 1739 CAAAGCACTCCCCACCAGGAGGTGCTACCGTCACCCAAACCCTGGAGACGACGC bjet 1739 CAAAGCATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAACCTG bjet 1799 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAACCTG bjet 1859 AGGTGTTGCCGGGAACGGAACGGTCATTCTGGAAACCATACCCAGGATGTTATACTCAAGAAGAACCTG bjet 1859 AGGTGTTGCCGGGAACGGAACGGTCATTCTGGAAACCATAGCCAGCACGTTACTCCGTGA lucry 705 AGGTGTTGCCGGGAACGGAACGGTCATTCTGGAAACCATAGCCAGCATCTACTCCGTGA lucry 705 AGGTGTTGCCGGGAACGGAACGGTCATTCTGGAAAACCATAGCCAGCATCTACTCCGTGA lucry 705 AGGTGTTGCCGGGAACGGAACGGTCATTCTGGAAAACCATAGCCAGCACGTTACTCCGTGA lucry 705 AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCGCACGCTGCAGGTTT lucry 705 ACCAAACCTACACCCTGAATGAAAACACTGCCCATCATGAGCAGCGCCACGCTGCAGGTTT lucry 825 ACCAAACCTACACCCTGAATGAAAACACTGCCCATCATGAGCAGCCCCACGCTGCAGGTTT lucry 826 ACCAGGCCTCGCGGCAACGTCATCAAGCTCTCCGAGGAACGAAC	_			111111111111111			
Digit 1799 CAAGGACATTCGATCGCTGAGGACAGTCCGCGCACCAAGCAGGCA 17 Digit 1679 CAACAACAATACACTGGGTCGCTCCCACTCGCCGCACAAGCCCGAAGCACGGCA 17 Digit 1739 CAAAGGCACCGCCCCACCACCGAGGAGGTCCTACCGCAACCCTGGAGACCACGCA 17 Digit 1739 CAAAGCCACCCCCCCCCCCCCCCCCCACCGAGGAGGTCCTACCGTCCACCCAAACCCTGGAGACCACGC 17 Digit 1739 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGACCTG 76 Digit 1739 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGACCTG 76 Digit 1739 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGACCTG 76 Digit 1739 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGACCTG 18 Digit 1859 AGGTGTTGCCGGGCAACGGAACCGTATTCTGGAAACCATAGCCAGCATGTACTCCGTGA 77 Digit 1859 AGGTGTTGCCGGGCAACGGAACCGTATTCTGGAAACCATAGCCAGCAATGACCAGCAGCTT 18 Digit 1919 TCCAAACCTACACCCTGAATGAAAACAGTGCCACTATGAGCAGGCCCACCCTGCAGGTT 18 Digit 1919 TCCAAACCTATACCCTGAATGAAAACAGTGCCAACTATGAGCAGGCCCACCCTGCAGGTT 18 Digit 1979 ACCAGACCTGGGCAAGCTCATCAAGCTCTGCGAGAGGTGATGCTCTCCCAGGACCAGG 19 Digit 1979 ACCAGACCTGGGCAAGCTCATCAAGCTCTGCGAGAGGTGATGCTCTCCCAGGACCAGG 19 Digit 1979 ACCAGACCTGGGCAAGCTCATCAAGCTCTGCGAGAGTGATGCTCTCCCAGGACCAGG 19 Digit 2039 GCGAGTCCCCCTCCCTGAGCAACGACAATGTGCCGGGAAGTCATTCAT	Query						
bjet 1679 CAACAACAATACACTGGGTCGCTCCCACTCGCGCACAACTCCGCGACCAAGCCCGGCCAAGCCAGGCACAACACTGGGTCGCCCACCACACCGACGAGGAGGTCCTCACCCCAAACCCTGGAGACGCCACACCGCGACGAGGAGGTCCTCACCCCAAACCCTGGAGACGCACGC	Sbjct	1619	TAGCGCGCCGGG	CGCGTTCCTTTAAGGA	CGACCTCATCGAGAA		TGCGAA 16
Treetace and control of the control	Query			111111111111111			
bjet 1739 CAAAGGCACCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Sbjct						
TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGG bjet 1799 TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGAGCTGG lucry 705 AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA 70 bjet 1859 AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA 71 bjet 1919 TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCCCCAGCGTGCAGGTTT 19 bjet 1919 TCCAAACCTATACCCTGAATGAAAACAGTGCCATCATGAGCAGCCCCAGCTGCAGGTTT 19 bjet 1979 ACCAGACCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCCAGAGACAGCG bjet 1979 ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCCAGAGACAGCG bjet 2039 GCGAGTGCCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCCAGAGATG bjet 2039 GCGAGTGCCCTCCCTGAGCAAACGAGAATGTGCGGGAAGTCATTGATCTTCTCCAGAGATG bjet 2099 CTGTGCGGAATCTCGTTACGCTGGCCAGGGCAAGCTGAAGAGACAGGAGTCATTGATCTTCTCCAGGATG bjet 2159 TTCGCTACAGTGGATCTGGTTGGGCGCAGGCAAGCTGAAGGACAGGAGTCAGTGCGCCT bjet 2159 TCGCTACAGTGGATCTGGTTGGGCGGCAAGCTGAAGGAGCAGGATCAGTGCGCCT bjet 2219 TCACCGCCTCGCGGGAGCGAGTGTTCCCGGGACACTCAGGAGCAGGATCATGGGTCCGC bjet 2219 TCACCGCCTCGCGGGAGCGAGTGTTCCCGGTACTGGGCGCGCGGAGATCATGGGTCCGCC bjet 2219 TCACCGCCTCGCGGGAGCGAGTGTTCCCGGTACTGGGTCAGGCCCCAAGGAGCCGCAACTTTCGGCCGCCG bjet 2219 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGGTCCACCCCAAGGAGCCGCACA bjet 2219 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGGCTCCACAGGACCCCAAGGAGCCGCACA bjet 2219 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGGCTCCACAGGACCCCAAGGAGCCGCACA bjet 2339 TACTGGAGCAGCAATGTGAACCCCATTGCGCGCGCGCTCCCACAGGACCCCAAAGGACCCGAAAGTATCCTGC bjet 2339 TACTGGAGCAGCACAATGTGAACCCGATCCCCAATAGGGCCCAAAGGACCCGAAAGTATCCTGC bjet 2349 TCCGCCACAGAGCCACCCGAAGCCACCCGATCCCCAAAGGACCCGAAAGTATCCTGC bjet 2359 GCGCCACAGAGCCACCCGAAGCCACCCGATCCCCAAAGGGCCAGCCGATACCCCCATAGGGCCAGCCGATACCCCCATAGCGCCTAGCCCCAGGCCCGCTTCCTCCCCGTTACCCCCATAATGCGCCTAGCCCCATAATGCGCCTAGCCTAGCCCCAGGCCCAGCCCAAAGCCACCCGATCCCCAAAGCCCCCAAAGCCACCCGATCCCCAAAGCCCCCCCC	_		CAAAGGCACCGC	CCACCACCGAGGAGGT 	GCTACGGTCCACCCA GCTACGGTCCACCCA	AACCCTGGAGAC 	
bjet 1799 TCAAGGACATTTCGAATGCCCTGAACCATTCCGGGATGTTATACTCAAGAAGAAGAGTGG 18 Burry 705 AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA 76 Bjet 1859 AGGTGTTGCCGGGCAACGGAACGGTCATTCTTGGAAACCATAGCCAGCATGTACTCCGTGA 76 Burry 765 TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTT 86 Burry 825 ACCAGAGCCTGGGCAAGGTCCATCATAGACCATCATCAGCAGCCCCAGCTTCCCGAGGACAGC 1979 ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGTATTCTCCGAGGACAGC 20 Burry 885 GCGAGTGCGCCTCCCTGAGCAACGAAACTTGCGCAGGATGTATTCTCCCAGGACACC 20 Burry 945 CTGTGCGGAATCTCGTTACGCTGGCAGGAGGTGAAGCAGAGTCATTCAGGATGAGCAGC 20 Burry 945 CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGACAGGC 20 Burry 1005 TCGCTACAGTGGATCTGGTTGGCCGCAGGGCAGAGCTGAGGAGATCAGTGCCCC 20 Burry 1005 TCGCTACAGTGGATCTGGTTGGCCGCGCAGGGCAGAGCTAGAGCAGGATCAGTGCCCC 20 Burry 1005 TCGCCTACAGTGGATCTGGTTTGGCCGGCGCAGGGCAGAGCTAGAGCAGGATCAGTGCCCC 20 Burry 1005 TCACCGCCTCGCGGGAGCGAGTGTTCCCGGGAAGCTCAGGGCCGAGAAGTATGGGTCCGC 20 Burry 1005 TCACCGCCTCGCGGGGAGCGAGTGTTCCCGGGAAGCTCAGGGCCGAGAAGTATGGGTCCGC 20 Burry 1005 TCACCGCCTCGCGGGGAGCGAGTGTTCCCGGTACTGAGCGCGCGAGAAGTATCGGCGCCC 20 Burry 1005 TCACCGCCTCGCGGGGAGCGAGTGTTCCCGGTACTGAGCGCGCGAGAAGTATCGGCCCC 20 Burry 1005 TCACCGCCTCGCCGGGAGCGAGTGTTCCGGGTACTGAGCGCCGCAAGGAGCCGACA 20 Burry 1005 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGAGCCCCCAAGGAGCCGCCC 20 Burry 1005 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGAGCCCCCAAGGAGCCGCCC 20 Burry 1005 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGAGCCCCCAAGGAGCCGCCC 20 Burry 1125 AATCAGCTGCCCAGCGTACTTCGTTGCCGGGACATAGCGCTCACGCCCAAGGAGCCGCCC 20 Burry 1125 AATCAGCTGCCCAGCGTACTTCGTTGCCGGGCTTCCACAGGACCCCAAAGTATCCTGC 20 Burry 1125 AATCAGCTGCCCAGCGTACTTCGTTGCCGGGCTTCCACAGGACCCCAAAGTATCCTGC 20 Burry 1125 AATCAGCTGCCCAGCGCAAAGCCACCCGAACCAAAGGACCCCAAAGGACCCCCAAAGGACCCCCAAAGGACCCCCAAAGCAACCAAATGTGAACCCCAAAGCACCCCAAAGGACCCCCAAAGCAACCAAATGTGAACCCCAAAGCAACCCAAAGCAACCAAATGTGAACCCCAAAGCAACCAAATGTGAACCCCAAAGCAACCAAC	Query		TÇAAĞĞAÇATTT	с <i>споспосо</i> носност ССААТСССТСААССА	CTTCCGGGATGTTAT.	лиссетсологк АСТСААСААСА	
bjet 1859 AGGTGTTGCCGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA 19 buery 765 TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGTGCAGGTTT 88 bjet 1919 TCCAAACCTATACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGTGCAGGTTT 19 buery 825 ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG 88 bjet 1979 ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG 88 bjet 2039 GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGCAAGTCATTGATCTTCTCGAGGATG 99 bjet 2039 GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGGAAGTCATTGATCTTTCTCGAGGATG 99 bjet 2099 CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCC 10 bjet 2099 CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCC 11 bjet 2159 TCGCTACAGTGGATCTGGTTGGGCGAGGGCAAGCTGAAGGAGCAGGATCAGTGGGCC 12 bjet 2159 TCGCTACAGTGGATCTGGTTGGGCGGCAGGCAGGCGGGGGGGG	Sbjct	1799	TCAAGGACATTT	 CGAATGCCCTGAAGCA		 ACTCAAGAAGAA	 AGCTGG 18
thery 765 TCCAAACCTACACCTGAATGAAAACAGTGCCATCATGAGGCGCCACGCTGCAGGTTT 8. bjet 1919 TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGGCCCACGCTGCAGGTTT 1919 TCCAAACCTATACCCTGAATGAAAACAGTGCCATCATGAGCAGGCCACGCTGCAGGTTT 1919 TCCAAACCTATACCCTGAATGAAAACAGTGCCATCATGAGCACGCCCAGGCCAGGCTGCAGGTTT 1919 ACCAGAGCCTGGCCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG 20 bjet 1979 ACCAGAGCCTGGCCAACCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG 20 bjet 2039 GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATG 20 bjet 2049 CTGTGCGGAATCTCGTTACGCTGGCGCAGGCAAGCTGAAGGAGCAGGATCAGTGCGCCT 10 bjet 2059 CTGTGCGGAATCTCGTTACGCTGGCGCAGGCAAGCTGAAGGAGCAGGATCAGTGGGCCCT 20 bjet 2159 TTCGCTACAGTGGATCTGGCTTGGGCGGCAAGCTGAAGGAGCAGGATCATGGGTCCG 10 bjet 2159 TCACCGCCTGGCAGGAGCGAGCTGTTCCAGGAGTCATGGGTGCGC 20 bjet 2159 TCACCGCCTGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGCTGGCGCGCGAATCATGGGTCCG 20 bjet 2150 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCCGCGGGACATCATGGGTCCG 20 bjet 2150 TCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCCGTTTCGGCCGCC 20 bjet 2150 TCACCGCCTCGCCGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCCGTTTCGGCCGCC 20 bjet 2150 TCACCGCCTGCCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCCGTTTCGGCCGCC 20 bjet 2150 TCACCGCCTCGCCGGAGCGAGCTGTTCCCGGTACTGCGCCTAAGGAGCCGCACA 11 bjet 2150 TACTGGAGCAGCCAATGTGAACCCGATAGCGCTCCACAGCACCGAAAGTATCCTGC 21 bjet 2150 TACTGGAGCAGCCAAATGTGAACCCGATGCGCCCAAGGAACCGAAAGTATCCTGC 21 bjet 2150 TACTGGAGCAGCCACCGCTACCCCAATAGGGCCCAAGAAGTATCCTGC 21 bjet 2150 TACTGGAGCACCAATGTGAACCCGATGCGCCCAATAGGGCCCAAGAAGTATCCTGC 21 bjet 2150 TACTGGAGCACCAATGTGAACCCGATGCGCCCAATAGGGCCAAGAAGTATCCTGC 21 bjet 2150 TACTGGAGCACCAATGTGAACCCGATGCGCCCAATAGGGCCAAGAAGTATCCTGC 21 bjet 2150 TACTGGAGCACCAATGTGAACCCGATCCCAATAGGGCCAAGTAACCCGATAGCTGGCCGAGCCAAGCCAAGCCAACCGATCACCTAACACTGGGCCGAGCCAGCC	Query	705	AGGTGTTGCCGG	GCAACGGAACGGTCAT	TCTGGAAACCATAGC	CAGCATGTACT(CCGTGA 76
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bjet 2219 TCACCGCCTGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGCCG 22 query 1125 AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA 1: bjet 2279 AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA 2: query 1185 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTTCCCACAGCACCGAAAGTATCCTGC 1: bjet 2339 TACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 2: query 1245 GCGACACGAGTCCACCGCCGAAGCCACCGATAATCCGCCGCCGT 1: bjet 2399 GCGACACGAGTCCACCGCCGAAGCCACCGAATAGGGCCAGTAATCCGCCGCCGT 1: query 1305 TGCCACCAAAGCGACCCAGCCGAGCGCATCCCAATAGGGCCAGTACGCTGCT 1: bjet 2459 TGCCACCAAAGCGACCCAGCCGAGCCCATCAGCTGGTACAGTGGGCCGTAGCTGCT 2: puery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 1: bjet 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTTCCACTGCCCTACGCCCAGTCCCATAATA 2: puery 1425 TTAGTCTGAACTCCGGACCTGCACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 1: puery 1425 TTAGTCTGAACTCCGGACCTGCACTGCAGTTCCAATATCTCCGCTGCTGAACTATGGCGTGG 1: puery 1425 TTAGTCTGAACTCGGACCTGCACTGCAGTTCCAATATCTCCGCTGCCCTACGCCCAGTCCCATAATA 2: puery 1425 TTAGTCTGAACTCGGACCTGCACTGCAGTTCCAATATCTCCGCTGCCTAGACTATGGCGTGG 1: puery 1425 TTAGTCTGAACTCGGACCTGCACTGCAGTTCCAATATCTCCGCTGCCTACGCCCAGTCCCATAATA 2: puery 1425 TTAGTCTGAACTCGGACCTGCACTGCAGTTCCAATATCTCCGCTGCCTAGACTATATGGCGTGG 1:	Sbjct			111111111111111			
nuery 1125 AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA 1: bjct 2279 AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA 2: nuery 1185 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 1: bjct 2339 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 2: nuery 1245 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 1: bjct 2399 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 2: nuery 1305 TGCCACCAAAGCGACGCAGCCGAGCCGAGCGCTACGCTGGTACAGTGGGCGTAGGCTGCT 1: bjct 2459 TGCCACCAAAGCGACGCAGCCGAGCCGAGCGATCAGCTGGTACAGTGGGCGTAGGCTGCT 2: nuery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 1: bjct 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCCATACGCCCAGTCCCATAATA 2: nuery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 1: nuery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 1: nuery 1425 TTAGTCTGAACTCGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 1: nuery 1425 TTAGTCTGAACTCGGACCTGCACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 1: nuery 1425 TTAGTCTGAACTCGGACCTGCAGTTCCAATATCTCGCTGCCTAAACTATGGCGTGG	Query	1065	TCACCGCCTCGC	CGGGAGCGAGTGTTCC	CGGTACTGGAGTCAT	GCGCGTTTCGG(CCGCCG 11
bjct 2279 AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA query 1185 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 12 bjct 2339 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 23 cuery 1245 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 13 bjct 2399 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 24 cuery 1305 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 13 bjct 2459 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 25 cuery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTACGCCCAGTCCCATAATA 14 bjct 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTACGCCCAGTCCCATAATA 25 cuery 1425 TTAGTCTGAACTCGGACCTGCACTGCAGTTCCAATATCCGCTGCCTAGACCTAGGCGTGG 14	Sbjct	2219	tcaccdcctcdc	çççeyççeyçtettçç	ceetacteeaetcat	ĠĊĠĊĠŦŦŦĊĠĠŒ	
nuery 1185 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 126bjct 2339 TACTGGAGCACCACATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 236uery 1245 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 136bjct 2399 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 24cuery 1305 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 136bjct 2459 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 25cuery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 14cuery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 14cuery 1425 TTAGTCTGACATCCACCTCCAATCAGGCCAGTTCCAATATCCGCCCAGTCCCATAATA 25cuery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTCGGACCTGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTCGGACCTGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTCGGACCTGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTGGACCTGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTGGACCTGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTGGACTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14cuery 1425 TTAGTCTGAACTGGACTGCACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGGACTGAATATCTCGCTGCTGAACTATGGCGTGGAACTATGAGACTAGAGACTGAACTATGAGACTAGAGACTGAACTATGAGACTGAACTATGAGACTGAACTAGAGACTGAACTATGAGACTGAACTAGAGACTGAACTATGAGACTGAACTAGAGACTGAACTATGAGACTAGAGACTAGAGACTAGAATATCTCGCTGAACTAGAGACTAGAGACTAGAGACTAGAGACTAGAGACTAGAATATCTCGCTGAACTAGAGAACTAGAGAACTAGAGAACTAGAGAACTAGAGAACTAGAGAACTAGAACTAGAGAACTAGAGAACTAGAGAACTAGAAAAAAAA	Query						
bjct 2339 TACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC 23 puery 1245 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 13 bjct 2399 GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 24 puery 1305 TGCCACCAAAGCGACGCCAGCCGAGCCGAGCCATCAGCTGGTACAGTGGGCGTAGGCTGCT 13 bjct 2459 TGCCACCAAAGCGACGCAGCCAGCCGAGCCATCAGCTGGTACAGTGGGCGTAGGCTGCT 25 puery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 14 bjct 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAATA 25 puery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14	•						
bjct 2399 GCGACACGACTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT 24 puery 1305 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 13 bjct 2459 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 25 puery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 14 bjct 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAATA 25 puery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14	Sbjct			111111111111111			
puery 1305 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 1305	Query	1245	GCGACACGAGTC	CACCGCCGAAGCCACC	GCTACCCAATAGGGC	CAGTAATCCGC	CGCCGT 13
bjct 2459 TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT 25 uery 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 14 bjct 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAATA 25 uery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCAACTATGGCGTGG 14	Sbjct	2399	GCGACACGAGTC	çycçeceyyeç	gctacccaataggc	cadtaatcccc	CGCCGT 24
query 1365 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA 14 bjct 2519 CATCGTCGACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAATA 25 query 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14	Query						
	•						
uery 1425 TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG 14	Sbjct						
bjet 2579 tragtergaacteggacetggactgcagtrecaatatetegetgctgaartatggegtgg 20	Query						
	Sbjct	2579	TTAGTCTGAACT	cgacctgactgcag	ttccaatatctccct	GCTGAATTATG(GCGTGG 26

Query	1485	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	1544
Sbjct	2639	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	2698
Query	1545	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGGTCGT	1604
Sbjct	2699	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACATCAGCATCTGAGGTCAT	2758
Query	1605	TTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAGCGCCG	1664
Sbjct	2759	ttccaaagttggctgcgatgatggacgaagacatggacaagatggtcagctacagcgccg	2818
Query	1665	CAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTGGTATAGCTGGTGTTGCTG	1724
Sbjct	2819	CAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTGGTATAGCTGGTGTTGCTG	2878
Query	1725	GTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAACTA	1784
Sbjct	2879	GTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAACTA	2938
Query	1785	ACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTCTA	1844
Sbjct	2939	Acadcaatcdccactcaaacdaatcdddtttcdtdtcdatdcdtdadttcdcacttcca	2998
Query	1845	CACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGAGA	1904
Sbjct	2999	cacagacgacgactacagtgtccagtcctccacgaagtcgtccagcagcaattcggaga	3058
Query	1905	TTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATTA	1964
Sbjct	3059	ttgcgttcagcatcagtgagtcgacggcggtcggcagcagtagcgagtaccagcagatta	3118
Query	1965	GCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACCA	2024
Sbjct	3119	GCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACCA	3178
Query	2025	CGACCACcagcagcaccaccaccggctatggcagcagcgaagtggagcagcagcagc	2084
Sbjct	3179	cgaccaccagcagcaccaccaccagctatggcagcagcgaagtggagcagctgcagc	3238
Query	2085	agcagcagcagc 2096	
Sbjct	3239	AGCAGCAGC 3250	

Drosophila melanogaster RE10624 full insert cDNA

Sequence ID: **gb|BT010019.1|** Length: 7043 Number of Matches: 1 Range 1: 1886 to 3811

Score		Expect	Identities	Gaps	Strand	Frame	
3474 bits	s(1881)	0.0()	1916/1932(99%)	6/1932(0%)	Plus/Plus		
Features	S:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGC	CCGGCACCTGTTCCAG	TGGCATCGGAG	TGGGCG	224
Sbjct	1886	ACGCAGCATCA	GTTCTCCATCCACGC	CCGGCACCTGTTCCAG	TGGCATCGGAG	TGGGCG	1945
Query	225	GTGGCGGCTGCA	GCAGCAGCAGCAACA	ATAGCATCAACAGCGG	CAGCTACTCCA	CCGCCT	284
Sbjct	1946	gtggcggctgca	recycly	Atagcatcaacagcgg	CAGCTACTCCA	ÇÇÇÇŢ	2005
Query	285	GCACTCCGCCAC	CACCCACGCATCAGC	ATCACTCGCAGCACCA	GCAGCTGCAGG	GCACGC	344
Sbjct	2006	gcyctccgccyc	cyccycycyty	atcactcccaccacca	GCAGCTGCAGG	GCACGC	2065
Query	345	CGGGAGGATCTA	GTCGGGTCGGGGAG	CAGGAGCAGGAGCAGG	CGGAGGTGGTG	GTGTAC	404
Sbjct	2066	ccccaccaccaccaccaccaccaccaccaccaccaccac	.gtcgggtagg-g	GGAGCAGGAGCAGG	CGGAGGTGGTG	GTGTAC	2119
Query	405	CACCGGCACCAC	CCAGTGCCGGATCCT	CGGGCCACAAGAACAG	TCTCAAGGGCA	CCAAGC	464
Sbjct	2120	cycedecycyc	ccqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	.ceeeccycycy	tctcaagggc _G	ccaagc	2179
Query	465	TAGCGCGCCGGG	GCGCGTTCCTTTAAGG	ACGACCTCATCGAGAA	GATTTCCCTGA	TGCGAA	524
Sbjct	2180	4yqqqqqqqqq	cccctttcctttaacc	acgacctcatcgagaa	ĠĀŦŦŦĊĊĊŦĠĀ	tgcgaa	2239
Query	525	CCACCAACAATA	CACTGGGTCGCTCCC	ACTCGCCGCACAGTCC	GCGCACCAAGC.	ACGGCA	584
Sbjct	2240	ccaccaacaata	cyctegen	actcgccgcacagtcc	GCGCACCAAGC.	ACGGCA	2299
Query	585	CAAAGGCACCGC	CCACCACCGAGGAGG	TGCTACGGTCCACCCA	AACCCTGGAGA	CGCACG	644
Sbjct	2300	caaaggcaccgc	ccaccaccaagaaga	tgctycggtccyccy	AACCCTGGAGA	cccacc	2359
Query	645	TCAAGGACATTT	CGAATGCCCTGAAGC	ACTTCCGGGATGTTAT	ACTCAAGAAGA.	AGCTGG	704
Sbjct	2360	tcaaggacattt	ccgaatgccctgaagc	acttcccccatttat	ACTCAAGAAGA	AGCTGG	2419
Query	705	AGGTGTTGCCGG	GCAACGGAACGGTCA	TTCTGGAAACCATAGC	CAGCATGTACT	CCGTGA	764

Sbjct	2420	AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA	2479
Query Sbjct	765 2480	TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTT	824 2539
Query	825 2540	ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG	884 2599
Sbjct Query	885	GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATG	944
Sbjct	2600	gcgagtgcgcctccctgagcaacgagaatgtgcgggaagtcattgatcttctcgaggatg	2659
Query Sbjct	945 2660	CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCT	1004 2719
Query	1005	TTCGCTACAGTGGATCTGGCTTGGGCGCGCATTGGAGCGGCGGCGGAGATCATGGGTGCGG	1064
Sbjct	2720 1065	TTĊĠĊŦĀĊĀĠŦĠĠĀŦĊŦĠĠĊŦŦĠĠĠĊĠĠĊĀŦŦĠĠĀĠĊĠĠĊĠĠĊĠĠĀĠĀŦĊĀŦĠĠĠŦĠĊĠĠ	2779 1124
Query Sbjct	2780	TCACCGCCTCGCCGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTTCGGCCGCCG	2839
Query	1125	AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA	1184
Sbjct Query	2840 1185	AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA TACTGGAGCACACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCTGC	2899 1244
Sbjct	2900	TACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCTGC	2959
Query	1245	GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT	1304
Sbjct Query	2960 1305	GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT	3019 1364
Sbjct	3020	TGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT	3079
Query	1365	CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA	1424
Sbjct	3080	categtegaeatecaetecaateaggeeagtecaetgeeetaegeeeagteeataata	3139
Query Sbjct	1425 3140	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG	1484 3199
Query	1485	AŢĊĠĊĊŢŖŢĊĊĠŢĠĊĠŢŢĊŖĊĠĠŢĊŖĊĊĠĠŖŢĠŖĠŖŖŢŖĠŢĊŖĠŢĠĊŢĊĊŢŢŢĠŖĊŢĊĠĠ	1544
Sbjct	3200	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	3259
Query	1545	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGGTCGT	1604
Sbjct Query	3260 1605	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCATCTGAGGTCAT TTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAGCGCCG	3319 1664
Sbjct	3320	TTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAGCGCCG	3379
Query	1665	CAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTGGTATAGCTGGTGTTGCTG	1724
Sbjct	3380 1725	ĊĂĂŢĊĠĂĊĠĂĊĂĂĂĂĊĠĊĂĠĂĊĂĊĊĂĊŢŢŢĊĠĂĊŢĠĠŢĠĠŢĠŢŢŢŢĠĊŢĠĠŢĠŢŢŢĠĊŢĠ	3439 1784
Query Sbjct	3440	GTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAACTA	3499
Query	1785	ACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTCTA	1844
Sbjct	3500	AcAGCAA+CGCCAC+CAAACGAA+CGGG+++CG+G+CGA+GCG+GAG+++CGCAC++CCA	3559
Query Sbjct	1845 3560	CACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGAGA	1904 3619
Query	1905	TTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATTA	1964
Sbjct	3620	TTGCGTTCAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATTA	3679
Query	1965	GCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACCA	2024
Sbjct Query	3680 2025	ĠĊĊĂĠŤŤĠĠŤĠŤĊĠĊĂĊĂĠĊĊĂĠĊĠŤĊĂŤĂŤĂŤĊĊŤĊĠĂĠĊĂĠŤĂĠĊĂĠĊŤĠĊĂĊĊĂĊĊĂ ÇĢĄÇÇĄÇċągċągċącċąċċċącċggċţaţgcągċągċgaagţggagċagċagċagċ	3739 2084
Sbjct	3740	CGACCACCAGCAGCACCACCACCGCTATGCCAGCGAAGTGGAGCAGCTGCAGC	3799
Query	2085	agcagcagcagc 2096	
Sbjct	3800	AĠĊAĠĊAĠĊAĠĊ 3811	

Drosophila melanogaster C3G ortholog, transcript variant I (C3G), mRNA Sequence ID: **ref|NM_001272362.1|** Length: 5648 Number of Matches: 1 Range 1: 485 to 2431

Score		Expect	Identities	Gaps	Strand	Frame	
3397 bits	s(1839)	0.0()	1920/1954(98%)	25/1954(1%)	Plus/Plus		
Features	3:						
Query	161	TCGAACGGCAGC	CATCAGTTCTCCATCC	CACGCCCGGCACCTGTT	CCAGTGGCATC	GGAGTG	220
Sbjct	485	TCG-ACGGCAGO	CATCAGTTCTCCATCC	cacecceecaccteri	CCAGTGGCATC	GGAGTG	543
Query	221	GGCGGTGGCGG(CTGCAGCAGCAGCAGC	CAACAATAGCATCAACA	GCGGCAGCTAC'	TCCACC	280
Sbjct	544			CAACAATAGCATCAACA			603
Query	281			CAGCATCACTCGCAGC			340
Sbjct	604 341	ACCCCCCCACCA		'CAGCATCACTCGCAGO GGAGCAGGAGCAGGAG			663 400
Query Sbjct	664			GGGAGCAGGAGCAGGAG 			717
Query	401			ATCCTCGGGCCACAAG <i>I</i>			460
Sbjct	718						777
Query	461	ААССТАСССС	, ССФФССССТТТ	⁻ , РААGGACGACCTCATCG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	СТĢАТĢ	520
Sbjct	778	AAGCTAGCGCGC	ccggcgcgttccttt	PAAGGACGACCTCATC	SAGAAGATTTCC		837
Query	521	CGAACCACCAAC	CAATACACTGGGTCGC	CTCCCACTCGCCGCACA	AGTCCGCGCACC.	AAGCAC	580
Sbjct	838	cgaaccaccaac	caatacactgggtcgc	ctcccactcgcccccaca	AGTCCGCGCACC.	AAGCAC	897
Query	581			GAGGTGCTACGGTCC <i>F</i>	ACCCAAACCCTG		640
Sbjct	898	ĠĠĊAĊAAAĠĠĊ		GAGGTGCTACGGTCC <i>F</i>			957
Query Sbjct	641 958	CACGTCAAGGAC		GAAGCACTTCCGGGATG			700 1017
Query	701	CTGGAGGTGTT	GCCGGGCAACGGAACG	GTCATTCTGGAAACCA	TAGCCAGCATG		760
Sbjct	1018						1077
Query	761	ĢŢĢĄŢÇÇĄĄĄÇ	, СТАСАСССТ Ģ ААТĢАА	\AAÇAGTGÇÇATÇATG <i>A</i>	\GÇAGÇGÇÇAÇG	СТССАС	820
Sbjct	1078	GTGATCCAAAC	CTATACCCTGAATGAA	AACAGTGCCATCATGA	AGCAGCGCCACG		1137
Query	821	GTTTACCAGAGO	CCTGGGCAAGCTCATC	CAAGCTCTGCGACGAGG	TGATGCTCTCC	GAGGAC	880
Sbjct	1138	GTTTACCAGAGO	ccteeecrater	cyyddagaegaegaegaegaegaegaegaegaegaegaegaegae	stdatdctctcc	GAGGAC	1197
Query	881	AGCGGCGAGTGC	CGCCTCCCTGAGCAAC	GAGAATGTGCGGGAAG	GTCATTGATCTT		940
Sbjct	1198			CGÁGÁÁTGTGCGGGÁÁG			1257
Query Sbjct	941 1258			GCGCAGGGCAAGCTG <i>P</i> 			10001317
Query	1001			GGCGCAGGGCAAGC1GA			1060
Sbjct	1318			GGCGGCATTGGAGCG			1377
Query	1061	ĢÇĢĢŢÇ <u>Ā</u> ÇÇĢÇ	СТСФССФФФФФСФА	҅҇ҾҭҭҪҪҪҪҪҭ҄ҲҪҭҪҪѧҁ	ТСАТССССТТ ВТСАТСССТТТ	ŢÇĢĢÇÇ	1120
Sbjct	1378	GCGGTCACCGC		GTTCCCGGTACTGGAC		 TCGGCC	1437
Query	1121	GCCGAATCAGCT	rgcccagcgtacttc	TTGCCGGACATAGCGC	CTCACGCCCAAG	GAGCGC	1180
Sbjct	1438	gccgaatcagc	recceaecetactic	strecceeacataecec	ctcacgcccaag	GAGCGC	1497
Query	1181		GCAGCACAATGTGAAC	CCGATGCGCGGCTCCC			1240
Sbjct	1498		ĠĊĀĠĊĀĊĀĀŦĠŦĠĀĀĊ		CÁCAGCACCGÁA.		1557
Query	1241			GCCACCGCTACCCAATA 			1300
Sbjct Query	1558 1301			GCCACCGCTACCCAATA GCCGAGCGCATCAGCTG			16171360
Sbjct	1618			GCCGAGCGCATCAGCTG 			1677
Query	1361			ŗĊġĠĠĊĊġĠŢĊĊĠĊŢĠĊ			1420
Sbjct	1678	TGCTCATCGTC	JACATCCACCTCCAAT	 CAGGCCAGTCCACTGC	CCTACGCCCAG	TCCCAT	1737

Query	1421	AATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGC	1480
Sbjct	1738	AATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAATTATGGC	1797
Query	1481	GTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGAC	1540
Sbjct	1798	GTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGAC	1857
Query	1541	TCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACACACATCAGCACCTGAGG	1600
Sbjct	1858	tcgccgttgaatcactcacgcgaggaggaggaccagcaacaacaacatcagcatctgagg	1917
Query	1601	TCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACA	1658
Sbjct	1918	TCATTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAAA	1977
Query	1659	GCGCCGCAATCGACGACAAAACGCAGACACCACTTTCGACTGGT	1702
Sbjct	1978	TCCACCGGTTACGCAGGCGCCGCAATCGACGACAAAACGCAGACACCACTTTCGACTGGT	2037
Query	1703	GGTGGTATAGCTGGTGTTGCTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCA	1762
Sbjct	2038	GGTGGTATAGCTGGTGTTGCTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCA	2097
Query	1763	GCGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCG	1822
Sbjct	2098	GCGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCG	2157
Query	1823	ATGCGTGAGTTTCGCACTTCTACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAG	1882
Sbjct	2158	AtGCGTGAGTTTCGCACTCCACACAGACGACGGACTACAGTGTCCAGTCCTCCACGAAG	2217
Query	1883	TCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGC	1942
Sbjct	2218	tcgtcagcagcaattcggagattcagcatcagcatcagtcag	2277
Query	1943	AGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	2002
Sbjct	2278	AGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	2337
Query	2003	AGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccggctatggcagc	2062
Sbjct	2338	AGCAGTAGCAGCTGCACCACCACCACCAGCAGCAGCACCAACCA	2397
Query	2063	agcgaagtggagcagcagcagcagcagc 2096	
Sbjct	2398	AGCGAAGTGGAGCAGCAGCAGCAGCAGC	

Drosophila erecta uncharacterized protein, transcript variant B (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155122.1|** Length: 5858 Number of Matches: 1 Range 1: 615 to 2566

Score		Expect	Identities	Gaps	Strand	Frame	
2813 bits	s(1523)	0.0()	1815/1954(93%)	28/1954(1%)	Plus/Plus		
Features	3 :						
Query	165	ACGGCAGCATCA	AGTTCTCCATCCACG	CCCGGCACCTGTTCCAG	rggcatcggag1	rgggcg	224
Sbjct	615	ACGGCAGCATCA	Yetteteevee	cccccccctcttccac	rggcatcggag	regeçe	674
Query	225	GTGGCGGCTGC	AGCAGCAGCAAC	AATAGCATCAACAGCGG(CAGCTACTCCAC	CCGCCT	284
Sbjct	675	dtddddddtdd	AGCAGCAGCAAC	AACAGCATCAACAGCGGG	CAGCTACTCCAC	ccect	734
Query	285	GCACTCCGCCAC	CCACCCACGCATCAG	CATCACTCGCAGCACCA(GCAGCTGCAGGO	GCACGC	344
Sbjct	735	GCACTCCGCCAC	CACCACGCACCAC	CATCACTCGCAGCACCAG	GCAGCTGCAGG(GCACGC	794
Query	345	CGGGAGGATCTA	AGTCGGGTCGGGGGA	GCAGGAGCAGGAGCAGG	CGGAGGTGGT	Ģ	398
Sbjct	795	CTGGAGCATCTA	AGTCGGGTTGGCGGA	GCAGGGGGGAGGAGGTGT:	rggaggtggtgc	GAGGCG	854
Query	399	GTGTACCACCGG	GCACCACCCAGTGCC	GGATCCTCGGGCCACAA	GAACAGTCTCAA	AGGGCA	458
Sbjct	855	GAGTGCCACCGC	scaccaccadtgcc	GGATCCTCGGGCCACAA	GAACAGTCTAAZ	AGGGCA	914
Query	459	CCAAGCTAGCGC	CGCCGGGCGCGTTCC	TTTAAGGACGACCTCAT	CGAGAAGATTTC	CCTGA	518
Sbjct	915	CCAAGCTAGCAC	cecceeecectcc	TTCAAGGACGACCTCAT	CGAGAAGATTTC	CCTAA	974
Query	519	TGCGAACCACCA	AACAATACACTGGGT	CGCTCCCACTCGCCGCA	CAGTCCGCGCAC	CCAAGC	578
Sbjct	975	TGCGTACCACCA	AACAATACACTGGGT	cecteccacteececa	CAGTCCGCGCAC	CAAGC	1034
Query	579	ACGGCACAAAGG	GCACCGCCCACCACC	GAGGAGGTGCTACGGTC	CACCCAAACCC	rggaga	638
Sbjct	1035	ACGGCTCCAAGG	PCGCCGCCACCACC	GAGGAGGTGCAGCGCTC	CACCCAAACTC	rggaga	1094
Query	639	CGCACGTCAAG	GACATTTCGAATGCC	CTGAAGCACTTCCGGGA	rgttatactca <i>i</i>	AGAAGA	698

Sbjct	1095	CGCACGTCAAGGACATCTCGAACGCCCTGAAGCACTTCCGGGATGTCATACTGAAGAAGA	1154
Query Sbjct	699 1155	AGCTGGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACT	758 1214
Query	759	CCGTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGC	818
Sbjct	1215	CCGTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCTGCGCCACGCAGC	1274
Query	819	AGGTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGG	878
Sbjct Query	1275 879	AGGTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGG ACAGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCG	1334 938
Sbjct	1335	ACAGCGGCGAGTGCCCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTGG	1394
Query	939	AGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGT	998
Sbjct	1395	AGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGACCAGT	1454
Query	999	GCGCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGG	1058
Sbjct	1455 1059	GCGCCTTTCGCTACAGTGGATCTGGTTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGG GTGCGGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGG	1514 1118
Query Sbjct	1515	GTGCGGTCACCGCCTCGCCGGGAGTGATCCCGGTACTGGAGTCATGCGCGTTTCGG GTGCGGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCGCTGGAATCATGCGCGTCTCAG	1574
Query	1119	СССССВАТСАССТСССАССТАСТТССТТССССССВАСАТАССССТСАССССАССССАССССССВАСССССССВАССССССВАСССССС	1178
Sbjct	1575	CCGCCGAATCAGCTGCCCAGCGCACTTCGTTGCCGGACATAGCACTAACGCCCAAGGAGC	1634
Query	1179	GCGACATACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTA	1238
Sbjct	1635	ĠĊĠĂĊĂŦĂĊŦĠĠĀĠĊĀĠĊĀĊĀĀŦĠŦĠĀĀĊĊĊCĀŦĠĊĠĊĠĠĊŦĊĊĊĀĊĀĠĊĀĊĊĠĀĀĀĠĊĀ	1694
Query Sbjct	1239 1695	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGC	1298 1754
Query	1299	CGCCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTAC-AG-TGGGCG-	1355
Sbjct	1755		1814
Query	1356	TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT	1415
Sbjct	1815	tcggctgctcatcgtcgacatccacctccaatcaggccagtcccctgccctacgccagt	1874
Query	1416	CCCATAATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACT	1475
Sbjct Query	1875 1476	ĊĊĊÁŢÁĂŢĂŢĊĂĠŢĊŢĠĂĂĊŢĊĠĠĂĊĊŢĠĠĂĊŢĠĊĀĠŢŢĊĊĂĂŢĂŢŢŢĊĠĊŢĠĊŢĠĂĀĊŢ ATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCT	1934 1535
Sbjct	1935	ATGGCGTGGATCGTCTCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCT	1994
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	1995	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCACCACCATCAGCAACAGCAGC	2054
Query	1593	A-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGA	1646
Sbjct Query	2055 1647	ÁGCAGCAGCTGÁGGTCGTTTCCÁÁÁGATGCCAGCGÁTGÁTGÁCGÁCGÁGACÁTGGÁCÁÁGT TGGTCAGCTACAGCGCCGCAATCGACGACAAAACGCAGACACCACTTTCGACTGGTG	2114 1706
Sbjct	2115	TGGTCAGCTACAGCGCCGCAATCGAGGACAAAATGCAGACACCACTTTCGACTGGTGGTG	2174
Query	1707	GTA-TAGCTGGTGTTGCTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCT	1759
Sbjct	2175	TTGGCGGTGGTGGC-GGTGTTGTTGGTGGAACTGGAGGAGCAGTCGAAGGTGCAGCTGCT	2233
Query	1760	GCAGCGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTG	1819
Sbjct	2234	ĠĊĀĠĊĠĀĊŦĠĠŦĠĠĊĠĠĠĠĀĀĀĊŦĀĀĊĀĠĊĀĀŦĊĠĊĊŦĊŦĊĀĀĀĊĠĀĀŦĊĠĠĠŦŦŦĊĠŦĠ	2293
Query Sbjct	1820 2294	TCGATGCGTGAGTTTCGCACTTCTACACAGACGACGGACTACAGTGTCCAGTCCTCCACG	1879 2353
Query	1880	AAGTCGTCCAGCAGTTTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGC	1939
Sbjct	2354	AAGTCGTCCAGCAGCAATTCGGACATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGA	2413
Query	1940	AGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1999
Sbjct	2414	AGCAGCGGCGAGTACCAGCAGATCAGCCAGTCGGTGTTGCACAGCCAGC	2473
Query	2000	TCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccggctatggc	2059
Sbjct	2474	TĊĠĀĠĊĀĠĊĀĠĊĀĠĊŦĠĊĀĊĊĀĊĀĊĀĊĀĊĊĀĠĊĀĠĊĀĠĊĀĊĊĀĊĠĠĠĊŦĀĊĠĠĊ	2533
Query	2060	agcagc-gaagtggagcagcagcagcag 2092	

Drosophila erecta uncharacterized protein, transcript variant A (Dere\GG17655), mRNA Sequence ID: **ref|XM_001978447.2|** Length: 5941 Number of Matches: 1 Range 1: 698 to 2649

Score		Expect	Identities	Gaps	Strand	Frame
2813 bit	s(1523)	0.0()	1815/1954(93%)	28/1954(1%)	Plus/Plus	
Features	S :					
Query	165	ACGGCAGCATCA	AGTTCTCCATCCACGCC	CGGCACCTGTTCCAG	TGGCATCGGAGT	GGGCG 224
Sbjct	698	ACGGCAGCATCA	AGTTCTCCATCCACGCC	cccccctcttccac	TGGCATCGGAGT	GGGCG 757
Query	225	GTGGCGGCTGC	AGCAGCAGCAGCAACAA	TAGCATCAACAGCGG	CAGCTACTCCAC	CCGCCT 284
Sbjct	758	ĠŦĠĠĊĠĠĊŦĠĊ <i>ŧ</i>	AGCAGCAGCAGCAACAA	cagcatcaacagcgg	ckśctactckac	cccct 817
Query	285		CCACCCACGCATCAGCA			
Sbjct	818		CCACCACGCACCA			
Query	345		AGTCGGGTCGGGGGAGC			G 398
Sbjct	878		ÁĞTCĞĞĞTTĞĞCĞĞÂĞC			
Query Sbjct	399 938		GCACCACCAGTGCCGG 			
Query	459		GCCGGGCGCGTTCCTT			
Sbjct	998		CGCCGGGCGCGCTCCTT			
Query	519		AAÇAATAÇAÇTGGGTÇG			
Sbjct	1058	TGCGTACCACC			 \CAGTCCGCGCAC	 CAAGC 1117
Query	579	АССЕСТАТАТО	GÇAÇÇĞÇÇÇAÇÇAÇÇĞ <i>A</i>	ѵ҄ҫҫѧҫҫҭҫҫҭѧҫҫҫҭҫ	ӷ҅ҘӬҘ҄ҳ҃ӎҁ҅ҘӬҲҘ	GGAGA 638
Sbjct	1118	ACGGCTCCAAGG	GCGCCGCCACCGA	GGAGGTGCAGCGCTC	CACCAAACTC1	 GGAGA 1177
Query	639	CGCACGTCAAGO	GACATTTCGAATGCCCT	GAAGCACTTCCGGGA	TGTTATACTCAA	GAAGA 698
Sbjct	1178	cccacctcaacc	sacatetegaaegeeet	rgyygraphtar	rtgtcatactgaa	GAAGA 1237
Query	699	AGCTGGAGGTGT	TTGCCGGGCAACGGAAC	GGTCATTCTGGAAAC	CATAGCCAGCAT	GTACT 758
Sbjct	1238	AGCTGGAGGTGT	rtéccéééckákcéécké	cggtcattctggaaac	ccatroccaocat	dract 1297
Query	759	CCGTGATCCAA?	ACCTACACCCTGAATGA	AAACAGTGCCATCAT	GAGCAGCGCCAC	
Sbjct	1298		ACCTACACCCTGAATGA			
Query	819		AGCCTGGGCAAGCTCAT			
Sbjct	1358 879		AGCCTGGGCAAGCTCAT FGCGCCTCCCTGAGCAA			
Query Sbjct	1418	ACAGCGGCGAG		CGAGAATGTGCGGGA CGAGAATGTGCGGGA		
Query	939		CGGAATCTCGTTACGCT			
Sbjct	1478		CGGAATCTCGTTACGCT			
Query	999	ĢÇĢÇÇŢŢŢÇĢÇŢ	ГАСАĞТĞĞATÇTĞĞCTT	[,] РĢĢĢÇĢĢÇ <u>Ā</u> ŢŢĢĢĀĢÇ	ӷҳ҄ҕҳҕҘҘҘҘҘ	ССАТСС 1058
Sbjct	1538	GCGCCTTTCGCT		GGGCGGCATTGGAGC	 	 CATGG 1597
Query	1059	GTGCGGTCACC	GCCTCGCCGGGAGCGAG	TGTTCCCGGTACTGG	SAGTCATGCGCGT	TTCGG 1118
Sbjct	1598	GTGCGGTCACC	GCTCGCCGGGAGTGAG	rtgttcccggcgctgg	SAATCATGCGCG1	CTCAG 1657
Query	1119	CCGCCGAATCAC	GCTGCCCAGCGTACTTC	GTTGCCGGACATAGC	GCTCACGCCCAA	AGGAGC 1178
Sbjct	1658	cccccaatcac	ecteccedececacttc	:ĠttĠċċĠĠĀċĀtĀĠċ	cactaacdcccaa	AGGAGC 1717
Query	1179	GCGACATACTGO	GAGCAGCACAATGTGAA	CCCGATGCGCGGCTC	CCACAGCACCGA	AAGTA 1238
Sbjct	1718		sadcadcacaatgtgaa			AAGCA 1777
Query	1239		ACGAGTCCACCGCCGAA			
Sbjct	1778		ACGAGTCCACCGCCGAA			
Query	1299		CCAAAGCGACGCAGCCA			
Sbjct	1838	CGCCGTTGCCG	CCAAGCGACGCAGCCA	AGCCGGGCGCATCTĞC	TGGTGCGGGATC	CĠĠGĠA 1897

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Query	1356	TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT	1415
Sbjct	1898	tcĠĠĊtĠĊtĊAtĊĠtĊĠAĊAtĊĊAĊĊtĊĊAAtĊAĠĠĊĊAĠtĊĊĊĊtĠĊĊĊtAĊĠĊĊĊAĠt	1957
Query	1416	CCCATAATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACT	1475
Sbjct	1958	cccataatatcagtctgaactcggacctggactgcagttccaatatrtcgctgctgaact	2017
Query	1476	ATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCT	1535
Sbjct	2018	ATGGCGTGGATCGTCTCTCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCT	2077
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	2078	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCACCACCATCAGCAACAGCAGC	2137
Query	1593	A-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGA	1646
Sbjct	2138	AGCAGCAGCTGAGGTCGTTTCCAAAGATGCCAGCGATGATGGACGAGGACATGGACAAGT	2197
Query	1647	TGGTCAGCTACAGCGCCGCAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTG	1706
Sbjct	2198	TGGTCAGCTACAGCGCCGCAATCGAGGACAAAATGCAGACACCACTTCCGACTGGTGGTG	2257
Query	1707	GTA-TAGCTGGTGTTGCTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCT	1759
Sbjct	2258	TTGGCGGTGGTGGC-GGTGTTGTTGGTGGAACTGGAGGAGCAGTCGAAGGTGCAGCTGCT	2316
Query	1760	GCAGCGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTG	1819
Sbjct	2317	GCAGCGACTGGTGGCGGGAAACTAACAGCAATCGCCTCTCAAACGAATCGGGTTTCGTG	2376
Query	1820	TCGATGCGTGAGTTTCGCACTTCTACACAGACGACGGACTACAGTGTCCAGTCCTCCACG	1879
Sbjct	2377	TCGATGCGCGAGTTTCGCACTTCCACACAGACGACGGACTACAGCATCCAGTCATCCACG	2436
Query	1880	AAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGC	1939
Sbjct	2437	AAGTCGTCCAGCAGCAATTCGGACATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGA	2496
Query	1940	AGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1999
Sbjct	2497	AGCAGCGGCGAGTACCAGCAGATCAGCCAGTCGGTGTTGCACAGCCAGC	2556
Query	2000	TCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccggctatggc	2059
Sbjct	2557	TCGAGCAGCAGCACCACCACCACCACCAGCAGCACCACCAC	2616
Query	2060	agcagc-gaagtggagcagcagcagcagcag 2092	
Sbjct	2617	AGCAGCAGCGAA-CTGGAGCAGCAGCAG 2649	

Drosophila melanogaster C3G ortholog, transcript variant J (C3G), mRNA Sequence ID: **ref|NM_001272363.1|** Length: 5027 Number of Matches: 2 Range 1: 1 to 1526

Score		Expect	Identities	Gaps	Strand	Frame	
2758 bits	s(1493)	0.0()	1520/1532(99%)	6/1532(0%)	Plus/Plus		
Features	S :						
Query	128	GGCTGGAAATAA	AAAAGGGCGAAGCG	GACAATTCTCGAACGGC	AGCATCAGTTCT	CCATCC	187
Sbjct	1	GGCTGGAAATAA	AAAAGGGCGAAGCG	ACAATTCTCGAACGGC	AGCATCAGTTCT	CCATCC	60
Query	188	ACGCCCGGCACC	TGTTCCAGTGGCAT	CGGAGTGGGCGGTGGC	GGCTGCAGCAGC	AGCAGC	247
Sbjct	61	Acccccccccccc	tgttccagtggcat	cedadtedecedtede	ggctgcagcagc	AGCAGC	120
Query	248	AACAATAGCATC	AACAGCGGCAGCTA	CTCCACCGCCTGCACT	CCGCCACCACCC	ACGCAT	307
Sbjct	121	AACAATAGCATC	AACAGCGGCAGCTA	ctccaccccctcacact	ppedpedppedppedppedppedppedppedppedpped	ACGCAT	180
Query	308	CAGCATCACTCG	CAGCACCAGCAGCT	GCAGGGCACGCCGGGA	GGATCTAGTCGG	GTCGGG	367
Sbjct	181	CAGCATCACTCG	cadcaccadcadci	'GCAGGGCACGCCGGGA	GGATCTAGTCGG	GTA	237
Query	368	GGAGCAGGAGCA	GGAGCAGGCGGAGG	TGGTGGTGTACCACCG	GCACCACCCAGT	GCCGGA	427
Sbjct	238	dd-dddadda	.ddadcadddddadd	;tddtddtdtaccaccd	gcaccacccagt	GCCGGA	294
Query	428	TCCTCGGGCCAC	AAGAACAGTCTCAA	GGGCACCAAGCTAGCG	CGCCGGGCGCGT	TCCTTT	487
Sbjct	295	tcctcgggccac	aadaacadtctcaa	regecyccyyectyece	ҁ҇ҿҁҁҿ҇ҿ҇ҿҁҿҁҿҭ	\pm cc \pm t \pm	354
Query	488	AAGGACGACCTC	ATCGAGAAGATTTC	CCTGATGCGAACCACC	AACAATACACTG	GGTCGC	547
Sbjct	355	AAGGACGACCTC	AtcGAGAAGATTC	cctgatgcgaaccacc	AACAATACACTG	gg4çgç	414

Query	548	TCCCACTCGCCGCACAGTCCGCGCACCAAGCACGGCACAAAGGCACCGCCCACCACCGAG	607
Sbjct	415	TCCACTCGCCGCACAGCCCACGCACAAGGCACGCCCCACCACGAG	474
Query	608	GAGGTGCTACGGTCCACCCAAACCCTGGAGACGCACGTCAAGGACATTTCGAATGCCCTG	667
Sbjct	475	ĠAĠĠŦĠĊŦAĊĠĠŦĊĊAĊĊĊAAAĊĊĊŦĠĠAĠAĊĠĊAĊĠŦĊAAĠĠAĊAŦŦŦĊĠAAŦĠĊĊĊŦĠ	534
Query	668	AAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGGAGGTGTTGCCGGGCAACGGAACG	727
Sbjct	535	AAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGGAGGTGTTGCCGGGCAACGGAACG	594
Query	728	GTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGATCCAAACCTACACCCTGAATGAA	787
Sbjct	595	ĠŤĊĂŤŤĊŤĠĠĂĂĂĊĊĂŤĂĠĊĊĂĠĊĂŤĠŤĂĊŤĊĊĠŤĠĂŤĊĊĂĂĂĊĊŤĂŦĂĊĊĊŤĠĂĂŤĠĂĂ	654
Query	788	AACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTTACCAGAGCCTGGGCAAGCTCATC	847
Sbjct	655	AACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTTACCAGAGCCTGGGCAAGCTCATC	714
Query	848 715	AAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCGGCGAGTGCGCCTCCCTGAGCAAC	907 774
Sbjct Query	908	GAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGGAATCTCGTTACGCTG	967
Sbjct	775	GAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGGAATCTCGTTACGCTG	834
Query	968	GCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCTTTCGCTACAGTGGATCTGGCTTG	1027
Sbjct	835		894
Query	1028	ĢĢÇĢĢÇĀŢŢĢĢĀĢÇĢĢÇĢĢĀĢĀŢÇĀŢĢĢĢŢĢÇĢĢŢÇĀÇÇĢÇÇŢÇĢÇÇĢĢĀĢÇĢĀĢŢ	1087
Sbjct	895	GGCGGCATTGGAGCGGCGGAGATCATGGGTGCGGTCACCGCCTCGCCGGAGCGAGT	954
Query	1088	GTTCCCGGTACTGGAGTCATGCGCGTTTTCGGCCGCCGAATCAGCTGCCCAGCGTACTTCG	1147
Sbjct	955	GTTCCCGGTACTGGAGTCATGCGCCGTTTCGGCCGCAATCAGCTGCCCAGCGTACTTCG	1014
Query	1148	TTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACATACTGGAGCAGCACAATGTGAAC	1207
Sbjct	1015	tréccégacatadécéctcacécccaageagecécéacatactégaecaecacatetésaac	1074
Query	1208	CCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGCGCGACACGAGTCCACCGCCGAAG	1267
Sbjct	1075	ĊĊĠĂŦĠĊĠĊĠĠĊŦĊĊĊĂĊĂĠĊĂĊĊĠĂĂĂĠŦĂŦĊĊŦĠĊĠĊĠĂĊĂĊĠĂĠŦĊĊĂĊĊĠĊĊĠĂĀĠ	1134
Query	1268	CCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGTTGCCACCAAAGCGACGCAGCCAG	1327
Sbjct	1135 1328	CCÁCCGCTÁCCCÁÁTÁGGGCCÁGTÁÁTCCGCCGCCGTTGCCÁCCÁÁÁGCGÁCGCÁGCCÁG CCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCTCATCGTCGACATCCACCTCCAAT	1194 1387
Query Sbjct	1195	CCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCTCATCGTCGACATCCACCTCCAAT	1254
Query	1388	CAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATATTAGTCTGAACTCGGACCTGGAC	1447
Sbjct	1255	CAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAATATTAGTCTGAACTCGGACCTGGAC	1314
Query	1448	TĢÇĀĢTTÇÇĀĀTĀTÇTÇĢÇTĢÇTĢĀĀCTĀTĢĢÇĢTĢĢĀTÇĢÇÇTĀTÇÇGTĢÇĢTTÇĀÇĢĢ	1507
Sbjct	1315	TGCAGTTCCAATATCTCGCTGCTGAATTATGGCGTGGATCGCCTATCCGTGCGTTCACGG	1374
Query	1508	ŢĊĄĊĊĠĠĄŢĠĄĠĄĄŢĄĠŢĊĄĠŢĠĊŢĊĊŢŢŢĠĄĊŢĊĠĠĊĠŢŢĠĄĄŢĊĄĊŢĊĄĊ	1567
Sbjct	1375	TCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGGCGTTGAATCACTCAC	1434
Query	1568	GAGGACCAGCAACACATCAGCACCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATG	1627
Sbjct	1435	GAGGACCAGCAACACCATCAGCATCTGAGGTCATTTCCAAAGTTGGCTGCGATGATG	1494
Query	1628	GACGAAGACATGGACAAGATGGTCAGCTACAG 1659	
Sbjct	1495	GACGAAGACATGGACAAGATGGTCAGCTACAG 1526	

Range 2: 1526 to 1810

Score		Expect	Identities	Gaps	Strand	Frame	
510 bits	(276)	4e-140()	282/285(99%)	0/285(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA(CTTCTACACAGACG	ACGGACTACAG'	TGTCCAGT	1871
Sbjct	1526	GTTTCGTGTCG	ATGCGTGAGTTTCGCAG	CTTCCACACAGACG	ACGGACTACAG'	rgtccagt	1585
Query	1872	CCTCCACGAAGT	rcgrccagcagcaarr(CGGAGATTGCGTTT	'AGCATCAGTGAG	GTCGACGG	1931
Sbjct	1586	CCTCCACGAAG	rcgtccagcagcaatt	CGGAGATTGCGTTC	AGCATCAGTGA	GTCGACGG	1645
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGCA	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991

Sbjct	1646	CGGTCGGCAGCAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1705
Query	1992	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaccaccg	2051
Sbjct	1706	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACCACCACCAGCAGCAGCACCACCACCA	1765
Query	2052	gctatggcagcagcgaagtggagcagcagcagcagcagcagc 2096	
Sbjct	1766	GCTATGGCAGCAGCGAAGTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	

Drosophila erecta uncharacterized protein, transcript variant E (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155125.1|** Length: 5477 Number of Matches: 1 Range 1: 216 to 2185

O	0.0		1.1. 44	•	C 4	-
Score	- (4 470)	Expect	Identities	Gaps	Strand	Frame
2730 bits		0.0()	1815/1972(92%)	46/1972(2%)	Plus/Plus	
Features						
Query Sbjct	165 216			CCCGGCACCTGTTCCAG 		
Query	225			AATAGCATCAACAGCGG		
Sbjct	276					CCGCCT 33
Query	285	ĢÇĄÇŢÇÇĢÇÇĄ(, ССАСССАСССАТСАС	САТСАСТСССАССАССА	ĢÇĄĢÇŢĢÇĄĢĢ	ĢÇĄÇĢÇ 34
Sbjct	336	GCACTCCGCCA	CCACCCACGCACCAC	CATCACTCGCAGCACCA	GCAGCTGCAGG	GCACGC 39
Query	345	CGGGAGGATCT	AGTCGGGTCGGGGGA	GCAGGAGCAGGAGCAGG	CGGAGGTGGT-	G 39
Sbjct	396	ctggagcatct.	agtcgggtrggcgga	gcygegegygygerei	rddaddddddt	GAGGCG 45
Query	399	GTGTACCACCG(GCACCACCCAGTGCC 	GGATCCTCGGGCCACAA 	GAACAGTCTCA	
Sbjct	456			ĠĠĀŢĊĊŢĊĠĠĠĊĊĀĊĀĀ		
Query	459			TTTAAGGACGACCTCAT		
Sbjct Query	516 519		ĊĠĊĊĠĠĠĠĊĠĊĠĊŦĊĊ a a c a a m a c a c m c c c m	TTCAAGGACGACCTCAT CGCTCCCACTCGCCGCA	CAGTCCGCGCA	
Sbjct	576		11111111111111	CGCTCCCACTCGCCGCA		
Query	579			ĢĄĢĢĢĢŢĢÇTAÇĢGŢÇ		
Sbjct	636	ACGGCTCCAAG	 GCGCCGCCACCACC	 GAGGAGGTGCAGCGCTC	 CACCCAAACTC	 TGGAGA 69
Query	639	CGCACGTCAAG	GACATTTCGAATGCC	CTGAAGCACTTCCGGGA	TGTTATACTCA	AGAAGA 69
Sbjct	696	CGCACGTCAAG	GACATCTCGAACGCC	ctgaagcacttccggga	tgtcatactga	AGAAGA 75
Query	699	AGCTGGAGGTG	TTGCCGGGCAACGGA	ACGGTCATTCTGGAAAC	CATAGCCAGCA	TGTACT 75
Sbjct	756	AĠĊŢĠĠAĠĠŢĠ'	trĠċċĠĠĠċAAċĠĠc.	AĊĠĠϮĊAϮϮĊϮĠĠAAAĊ	ckatroccaoca	
Query	759			GAAAACAGTGCCATCAT 		
Sbjct	816			ĠĂĂĂĂĊĂĠŤĠĊĊĂŤĊĂŤ		
Query Sbjct	819 876			ATCAAGCTCTGCGACGA 		
Query	879			AACGAGAATGTGCGGGA		
Sbjct	936					
Query	939	А ĢĢ А ŢĢÇŢĢŢĢ	СĠĠ₳₳ŢĊŢĊĠŢŢ₳ĊĠ	СТGGCGCAGGGCAAGCT	'GAAGGAGCAGG	АТСАСТ 99
Sbjct	996	AGGATGCTGTG				 ACCAGT 10
Query	999	GCGCCTTTCGC	TACAGTGGATCTGGC	TTGGGCGGCATTGGAGC	GGCGGCGGAGA	TCATGG 10
Sbjct	1056	gcgcc+++cgc	tacactccatctcct	ttgggcggcyttggygc	:qqqqqqqq	TCATGG 11
Query	1059	GTGCGGTCACC	GCCTCGCCGGGAGCG.	AGTGTTCCCGGTACTGG	AGTCATGCGCG	
Sbjct	1116			AGTGTTCCCGGCGCTGG		
Query	1119			TCGTTGCCGGACATAGC 		
Sbjct	1176			ŤĊĠŤŤĠĊĊĠĠĂĊĂŤĂĠĊ		
Query	1179			AACCCGATGCGCGGCTC		
Sbjct	1236	GCGACATACTG	GAGCAGCACAATGTG.	ÄÄĊĊĊĊĀŦĠĊĠĊĠĠĊŦĊ	CCACAGCACCG	AAAGCA 12

Query	1239	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGC	1298
Sbjct	1296	TCCTGCGCGACACGAGTCCACCGCGAAGCCACCGCTACCCAATAGGGCCAGTAACCCGC	1355
Query	1299	ÇĞÇÇĞTTĞÇÇAÇÇAAAĞÇĞAÇĞÇAĞÇÇAĞÇÇĞAĞÇĞÇATÇAĞÇTĞĞTAÇ–AĞ–TĞĞĞCĞ–	1355
Sbjct	1356	CGCCGTTGCCGCCCAAGCGACGCAGCCAGCCGGGCGCATCTGCTGGTGCGGGATCGGGGA	1415
Query	1356	TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT	1415
Sbjct	1416	TCGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTGCCCTACGCCCAGT	1475
Query	1416	CCCATAATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACT	1475
Sbjct	1476	CCCATAATATCAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATTTCGCTGCAACT	1535
Query	1476	ATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCT	1535
Sbjct	1536	ATGGCGTGGATCGTCTCTCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCT	1595
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	1596	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCACCACCATCAGCAACAGCAGC	1655
Query	1593	A-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGA	1646
Sbjct	1656	AGCAGCAGCTGAGGTCGTTTCCAAAGATGCCAGCGATGATGGACGAGGACATGGACAAGT	1715
Query	1647	TGGTCAGCTACAGCGCCGCAATCGACGACAAAACGCAGACAC	1688
Sbjct	1716	TGGTCAGCTACAAATCCACCGGTTACGCAGGCGCCGCAATCGAGGACAAAATGCAGACAC	1775
Query	1689	CACTTTCGACTGGTGGTGGTA-TAGCTGGTGTTGCTGGTGGAACTGGAGGAGCA	1741
Sbjct	1776	CACTTCCGACTGGTGGTGTTGGCGGTGGTGGC-GGTGTTGTTGGTGGAACTGGAGGAGCA	1834
Query	1742	GGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCA	1801
Sbjct	1835	GTCGAAGGTGCAGCTGCAGCGACTGGTGGCGGGGAAACTAACAGCAATCGCCTCTCA	1894
Query	1802	AACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTCTACACAGACGACGACTAC	1861
Sbjct	1895	AACGAATCGGGTTTCGTGTCGATGCGCGAGTTTCGCACTTCCACACAGACGACGGACTAC	1954
Query	1862	AGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGT	1921
Sbjct	1955	AGCATCCAGTCATCCACGAAGTCGTCCAGCAGCAATTCGGACATTGCGTTTAGCATCAGT	2014
Query	1922	GAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCAC	1981
Sbjct	2015	GAGTCGACGGCGGTCGGAAGCAGCGGCGAGTACCAGCAGATCAGCCAGTCGGTGTTGCAC	2074
Query	1982	AGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagc	2041
Sbjct	2075	AGCCAGCGTCAAATATCCTCGAGCAGCAGCAGCTGCACCACCACCACCAGCAGCAGCAGC	2134
Query	2042	acaaccaccggctatggcagcagc-gaagtggagcagcagcagcagcagcag 2092	
Sbjct	2135	ACCACCACGGCTACGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	

Drosophila erecta uncharacterized protein, transcript variant C (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155123.1|** Length: 5736 Number of Matches: 1 Range 1: 472 to 2444

Score		Expect	Identities	Gaps	Strand	Frame	
2730 bit	s(1478)	0.0()	1818/1976(92%)	47/1976(2%)	Plus/Plus		
Features	s:						
Query	161	TCGAACGGCAG	CATCAGTTCTCCATCC	ACGCCCGGCACCTGTT	CCAGTGGCATC	GGAGTG	220
Sbjct	472	tcg-Acgccac	catcagttctccatcc	үсөссеесест	ccactcccatc	GGAGTG	530
Query	221	GGCGGTGGCGG	CTGCAGCAGCAGCAGCA	AACAATAGCATCAACA	GCGGCAGCTAC'	TCCACC	280
Sbjct	531	ęęçęę _t ęęç _ę	ctgcagcagcagcagc	AACAACAGCATCAACA	GCGGCAGCTAC'	tccacc	590
Query	281	GCCTGCACTCC	GCCACCACCCACGCAT(CAGCATCACTCGCAGC	ACCAGCAGCTG(CAGGGC	340
Sbjct	591	qqqqqqqqqqqqqqqqqqqqqqqqq	gccyccyccycqqqqqq	caccatcactcccacc	Accadcadctd	çydddq	650
Query	341	ACGCCGGGAGG	ATCTAGTCGGGTCGGGC	GAGCAGGAGCAGGAG	CAGGCGGAGGT(GGT	397
Sbjct	651	Acccc Tech	AtctActcccctrcccc	ggygggggggggggg	GTGTTGGAGGT	ĠĠĠGA	710
Query	398	GGTGTACC	ACCGGCACCACCCAGT(GCCGGATCCTCGGGCC	ACAAGAACAGT(CTCAAG 	454
Sbjct	711	GGCĠĠAĠŦGĊĊ	acceecaccaccact	eccee a technique de la constant de La constant de la constant de	ACAAGAACAGT(ĊϮAÅÅĠ	770

Query	455	GGCACCAAGCTAGCGCGCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCC	514
Sbjct	771	ĠĠĊĀĊĊĀĀĠĊŦĀĠĊĀĊĠĊĊĠĠĠĊĠĊĠĊĠĊŢĊĊŢŢĊĀĀĠĠĀĊĠĀĊĊŢĊĀŢĊĠĀĠĀĀĠĀŢŢŢĊĊ	830
Query	515 831	CTGATGCGAACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACC	574 890
Sbjct Query	575	CTAATGCGTACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACC AAGCACGGCACAAAGGCACCGCCCACCACCGAGGAGGTGCTACGGTCCACCCAAACCCTG	634
Sbjct	891	AAGCACGGCTCCAAGGCGCCCCACCACCGAGGAGGTGCAGCGCTCCACCCAAACTCTG	950
Query	635	GAGACGCACGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAG	694
Sbjct	951	GAGACGCACGTCAAGGACATCTCGAACGCCCTGAAGCACTTCCGGGATGTCATACTGAAG	1010
Query	695	AAGAAGCTGGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATG	754
Sbjct	1011	AAĠAAĠĊŢĠĠAĠĠŢĠŢŢĠĊĊĠĠĠĊĀAĊĠĠĊĀĊĠĠŢĊĀŢŢĊŢĠĠĀĀĀĊĊĀŢŢĠĊĊĀĠĊĀŢĠ	1070
Query Sbjct	755 1071	TACTCCGTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACG	814 1130
Query	815	CTGCAGGTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCC	874
Sbjct	1131		1190
Query	875	GAGGACAGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTT	934
Sbjct	1191	GAGGACAGCGGCGAGTGCCCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTT	1250
Query	935	CTCGAGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGAT	994
Sbjct	1251	ĊŢĠĠĀĠĠĀŢĠĊŢĠŢĠĊĠĠĀĀŢĊŢĊĠŢŢĀĊĠĊŢĠĠĊĠĊĀĠĠĠĊĀĀĠĊŢĠĀĀĠĠĀĠĊĀĠĠĀĊ	1310
Query Sbjct	995 1311	CAGTGCGCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATC	1054 1370
Query	1055	ATGGGTGCGGTCACCGCCTCGCCGGGAGCGAGTGTTCCCCGGTACTGGAGTCATGCGCGTT	1114
Sbjct	1371	ATGGGTGCGGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCGCTGGAATCATGCGCGTC	1430
Query	1115	TCGGCCGCCGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAG	1174
Sbjct	1431	tcagccgcaatcagctgcccagcgcacttcgttgccggacatagcactaacgcccaag	1490
Query	1175	GAGCGCGACATACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAA	1234
Sbjct	1491	ĠĂĠĊĠĊĠĂĊĂŤĂĊŤĠĠĂĠĊĂĠĊĂĊĂĂŤĠŤĠĂĂĊĊĊĊĂŤĠĊĠĊĠĠĊŤĊĊĊĂĊĂĠĊĂĊĊĠĂĂ	1550
Query Sbjct	1235 1551	AGTATCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAAT	1294 1610
Query	1295	CCGCCGCCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTAC-AG-TGG	1352
Sbjct	1611	CCGCCGCCGTTGCCGCCCAAGCGACGCAGCCAGCCGGGCGCATCTGCTGGTGCGGGATCG	1670
Query	1353	GCG-TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCC	1411
Sbjct	1671	GGGATCGGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTGCCCTACGCC	1730
Query	1412	CAGTCCCATAATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTG	1471
Sbjct	1731	ĊAĠŦĊĊĊAŦAĀŦĀŦĊĀĠŦĊŦĠĀĀĊŦĊĠĠĀĊĊŦĠĠĀĊŦĠĊĀĠŦŦĊĊĀĀŦĀŦŦŦĊĠĊŦĠĊŦĠ	1790 1531
Query Sbjct	1472 1791	AACTATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGC	1850
Query	1532	ŢĊĊŢŢŢĠĄĊŢĊĠĠĊĠŢŢĠĄĄŢĊĄĊŢĊĄĊĠĊĠĄĠĠĄĠĠĄĠĠĄĊĊĄĠĊĄĄ-ĊĄĠĊĄĄĊĄŢ	1588
Sbjct	1851	TCCTTTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCACCACCATCAGCAACAG	1910
Query	1589	CAGCA-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGAC	1642
Sbjct	1911	cagcagcagctgaggtcgtttccaaagatgccagcgatgatgatggacgagacatggac	1970
Query	1643	AAGATGGTCAGCTACAGCGCCGCAATCGACGACAAAACGCAG	1684
Sbjct	1971	AAGTTGGTCAGCTACAAATCCACCGGTTACGCAGGCGCGCAATCGAGGACAAAATGCAG	2030
Query Sbjct	1685 2031	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1737 2089
Query	1738	ĄĠÇĄĠĠÇĠĄĄĠĠŢĠŢĄĠĊŢĠĊŢĠĊĄĠĊĠŢĊŢĠĠŢĠĄĊĠĠĠĠĄĄĄĊŢĄĄĊĄĠĊĄĄŢĊĠĊĊĄ	1797
Sbjct	2090	AGCAGTCGAAGGTGCAGCTGCAGCGACTGGTGGCGGGGAAACTAACAGCAATCGCCT	2149
Query	1798	CTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTTCTACACAGACGACGGA	1857
Sbjct	2150	ctcaaacgaatcgggtttcgatgcgaggtttcgactcgactttccacacaca	2209
Query	1858	CTACAGTGTCCAGCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCAT	1917

Sbjct	2210	CTACAGCATCCAGCAGCAGTCGTCCAGCAGCAATTCGGACATTGCGTTTAGCAT	2269
Query	1918	CAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTC	1977
Sbjct	2270	CAGTGAGTCGACGGCGGAGAGCAGCGGCGGGGGTACCAGCAGATCAGCCAGTCGGTGTT	2329
Query	1978	GCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	2037
Sbjct	2330	GCACAGCCAGCGTCAAATATCCTCGAGCAGCAGCAGCTGCACCACCACCACCAGCAG	2389
Query	2038	cagcacaaccaccggctatggcagcagc-gaagtggagcagcagcagcagcagcag 209	2
Sbjct	2390	CAGCACCACCACGGGCTACGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	4

Drosophila melanogaster guanine nucleotide exchange factor DC3G (DC3G) mRNA, complete cds Sequence ID: **gb|AF053358.1|AF053358** Length: 6305 Number of Matches: 2 Range 1: 1318 to 2812

Score		Expect	Identities	Gaps	Strand	Frame	
2728 bit	ts(1477)	0.0()	1489/1495(99%)	0/1495(0%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGC	CCGGCACCTGTTCCAC	GTGGCATCGGAG'	TGGGCG	224
Sbjct	1318	Acgccaccatca	dttctccatccaccc	ccgcacctgttccac	stggcatcggag:	reeece	1377
Query	225	GTGGCGGCTGCA	GCAGCAGCAGCAACA	ATAGCATCAACAGCGC	GCAGCTACTCCA(CCGCCT	284
Sbjct	1378	ĠŦĠĠĊĠĠĊŦĠĊĀ	.ĠĊĀĠĊĀĠĊĀĠĊĀĀĊĀ.	ATAGCACCAACAGCGC	scadctactcca	cccct	1437
Query	285		CACCCACGCATCAGC:	1 1 1 1 1 1 1 1 1 1			344
Sbjct	1438	GCÁCTCCGCCÁC		ÁTCÁCTCGCÁGCÁCC <i>I</i>			1497
Query	345		AGTCGGGTCGGGGGAG	1 1 1 1 1 1 1 1 1 1			404
Sbjct Query	1498 405		\ĠŤĊĠĠĠŤĊĠĠĠĠĠĀĠ‹ !CCAGTGCCGGATCCT(1557 464
Sbjct	1558		CCAGTGCCGGATCCT(1617
Query	465		CGCGTTCCTTTAAGG				524
Sbjct	1618	TAGCGCGCCGGG		 ACGACCTCATCGAGAZ			1677
Query	525	CCACCAACAATA	CACTGGGTCGCTCCC	ACTCGCCGCACAGTCC	CGCGCACCAAGC	ĄÇĢĢÇĄ	584
Sbjct	1678	CCACCAACAATA	CACTGGGTCGCTCCC	ACTCGCCGCACAGTC	CGCGCACCAAGC	ACGGCA	1737
Query	585	CAAAGGCACCGC	CCACCACCGAGGAGG'	TGCTACGGTCCACCC <i>I</i>	AACCCTGGAGA(CGCACG	644
Sbjct	1738	caaaggcaccgc	:ċċaċċaċċĠaĠĠaĠĠ	rĠĊŦĀĊĠĠŦĊĊĀĊĊĊ <i>ī</i>	AAACCCTGGAGAG	çççyçç	1797
Query	645		CGAATGCCCTGAAGC!				704
Sbjct	1798		ĊĠĂĂŤĠĊĊĊŤĠĂĂĠĊ				1857
Query	705 1858		GCAACGGAACGGTCA' GCAACGGAACGGTCA'				764 1917
Sbjct Query	765		CCCTGAATGAAAACA				824
Sbjct	1918			1 1 1 1 1 1 1 1 1 1			1977
Query	825	АССАБАБССТББ	; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	ГСТĢСĢАСĢАĢĢТĢА	ГĢСТСТССĢАĢĢ	ĄÇĄĢÇĢ	884
Sbjct	1978	ACCAGAGCCTGG				 ACAGCG	2037
Query	885	GCGAGTGCGCCT	CCCTGAGCAACGAGA	ATGTGCGGGAAGTCA7	TTGATCTTCTCG	AGGATG	944
Sbjct	2038	dcdadtdcdcct	ccctgagcaacgaga.	Atgtgcggdaagtca	rtgatetteteg	AGGATG	2097
Query	945	CTGTGCGGAATC	TCGTTACGCTGGCGC	AGGGCAAGCTGAAGG <i>I</i>	AGCAGGATCAGT(GCGCCT	1004
Sbjct	2098	ctgtgcggyytc	ttcgttacgctgccc	AĠĠĠĊAAĠĊŦĠAAĠĠ <i>I</i>	AGCAGGATCAGT	gcgcct	2157
Query	1005		GATCTGGCTTGGGCGG				1064
Sbjct	2158		ĠĂŦĊŦĠĠĊŦŦĠĠĠĊĠ				2217
Query	1065		CGGGAGCGAGTGTTC	1 1 1 1 1 1 1 1 1 1			1124
Sbjct	2218 1125		'ĊĠĠĠĀĠĊĠĀĠŤĀŤŤĊ('AGCGTĀCTTCGTTGC(2277 1184
Query	1123						1104

Sbjct	2278	AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA	2337
Query	1185	TACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC	1244
Sbjct	2338	tactggagcagcacaatgtgaacccgatgcgcgctcccacagcaccgaaagtatcctgc	2397
Query	1245	GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT	1304
Sbjct	2398	GCGACACGAGTCCACCGCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT	2457
Query	1305	TGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT	1364
Sbjct	2458	tgccaccaaagcgacgcagccagccgagcgcatcagctggtacagtgggcgtaggctgct	2517
Query	1365	CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA	1424
Sbjct	2518	categtegaeatecaectecaateaggeeagteegetgeegtaegeeeagteeeataata	2577
Query	1425	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG	1484
Sbjct	2578	ttagtctgaactcggacctggactgcagttccaatatctcgctgctgaactatggcgtgg	2637
Query	1485	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	1544
Sbjct	2638	AtcGcctAtccGtGcGttcAcGGtcAccGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	2697
Query	1545	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACACACATCAGCACCTGAGGTCGT	1604
Sbjct	2698	cgttgaatcactcacgcgaggaggaggaccagcaacaacatcagcacctgaggtcgt	2757
Query	1605	TTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 1659	
Sbjct	2758	ttccaaagttggctgcgatgatgdcgaagacatggacaagatggtcagctacag 2812	

Range 2: 2812 to 3096

Score		Expect	Identities	Gaps	Strand	Frame	
527 bits(285)		4e-145()	285/285(100%)	0/285(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCAC	CTTCTACACAGACG	ACGGACTACAGT	GTCCAGT	1871
Sbjct	2812	GTTTCGTGTCG	ATGCGTGAGTTTCGCAC	cttctacacagacg.	ACGGACTACAG1	rGTCCAGT	2871
Query	1872	CCTCCACGAAG	TCGTCCAGCAGCAATTC	GGAGATTGCGTTT.	AGCATCAGTGAG	TCGACGG	1931
Sbjct	2872	CCTCCACGAAG	TCGTCCAGCAGCAATTC	cggagattgcgttt.	AGCATCAGTGAG	rtcgacgg	2931
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAGC	CAGCGTC	1991
Sbjct	2932	çeetçeeçyeç	AGTAGCGAGTACCAGCA	rgytyddagan	gtgtcgcacagc	ccaccctc	2991
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCAC	CACCACGACCACC	agcagcagcaca	accaccg	2051
Sbjct	2992	AtAtAtcctcc	agcagtagcagctgcac	ccyccyceyccycc	y g c y g c y c y c y	ryccycce	3051
Query	2052	gctatggcagc	agcgaagtggagcagca	ngcagcagcagcag	cagc 2096		
Sbjct	3052	ĠĊŦĀŦĠĠĊĀĠĊ	AGCGAAGTGGAGCAGC	ĸĠĊĀĠĊĀĠĊĀĠĊĀĠ	CAGC 3096		

Drosophila melanogaster C3G ortholog, transcript variant K (C3G), mRNA Sequence ID: **ref|NM_001272364.1|** Length: 5804 Number of Matches: 2 Range 1: 660 to 2150

Score		Expect	Identities	Gaps	Strand	Frame	
2693 bit	s(1458)	0.0()	1485/1497(99%)	6/1497(0%)	Plus/Plus		
Features	S :						
Query	163	GAACGGCAGCAT	CAGTTCTCCATCCACG	CCCGGCACCTGTTCC	AGTGGCATCGG	SAGTGGG	222
Sbjct	660	GAACGGCAGCA1	ckagttctccktckcg	cccddcacctdttcc	AGTGGCATCGG	AGTGGG	719
Query	223	CGGTGGCGGCTG	CAGCAGCAGCAGCAAC	AATAGCATCAACAGC	GGCAGCTACTC	CACCGC	282
Sbjct	720	çeeteeçeeç	cadcadcadcadcaac	AATAGCATCAACAGC	de de la company	ccacccc	779
Query	283	CTGCACTCCGCC	CACCACCCACGCATCAG	CATCACTCGCAGCAC	CAGCAGCTGCA	GGGCAC	342
Sbjct	780	ctgcyctcccc	caccaccaccacatcac	ĊATĊAĊTĊĠĊAĠĊAĊ	ckackacktck	ręęęçyç	839
Query	343	GCCGGGAGGATC	CTAGTCGGGTCGGGGGA	GCAGGAGCAGGAGCA	GGCGGAGGTGG.	TGGTGT	402
Sbjct	840	ĠĊĊĠĠĠĠĠĠĠ	ĊŢŖĠŢĊĠĠĠŢ——AĠĠ—	Ġ––ĠĠÀĠĊÀĠĠÀĠĊÀ	ĠĠĊĠĠĀĠĠŦĠĠ	ĠĠĠĠĠĠĠ	893

Query	403	ACCACCGGCACCACCCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAA	462
Sbjct	894	Accaccaccaccaccactaccacattccaccacacacaca	953
Query	463	GCTAGCGCGCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCG	522
Sbjct	954	ĠĊŦĂĠĊĠĊĠĊĠĠĠĠĠĠĠĠŦŦĊĊŦŦŦĂĂĠĠĂĊĠĂĊĊŦĊĂŦĊĠĂĠĂĂĠĂŦŦŦĊĊĊŦĠĂŦĠĊĠ	1013
Query	523	AACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGG	582
Sbjct	1014	AACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGG	1073
Query	583	CACAAAGGCACCGCCCACCACGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCA	642
Sbjct	1074	ĊAĊAAAĠĠĊAĊĊĠĊĊĊAĊĊAĊĊĠAĠĠAĠĠŦĠĊŦAĊĠĠŦĊĊAĊĊĊAAAĊĊĊŦĠĠAĠAĊĠĊA	1133
Query	643	CGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCT	702
Sbjct	1134	ĊĠŦĊĂĂĠĠĂĊĂŤŦŤĊĠĂĂŦĠĊĊĊŤĠĂĂĠĊĂĊŤŤĊĊĠĠĠĂŦĠŦŤĂŤĂĊŤĊĂĂĠĂĂĠĂĂĠĊŤ	1193
Query	703	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	762
Sbjct	1194	ĠĠĂĠĠŤĠŤĠĊĊĠĠĠĊĂĂĊĠĠĂĂĊĠĠŤĊĂŤŤĊŤĠĠĂĂĂĊĊĂŤĂĠĊĊĂĠĊĂŤĠŤĂĊŤĊĊĠŤ	1253
Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822
Sbjct	1254	GATCCAAACCTATACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	1313
Query	823	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Sbjct	1314 883	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	1373 942
Query Sbjct	1374	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	1433
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002
Sbjct	1434	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1493
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1494	CTTTCGCTACAGTGGATCTGGCCTTGGGCCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1553
Query	1063	ĢĢŢÇĄÇÇĢÇÇŢÇĢÇÇĢĢĄĢÇĢĄĢTĢTŢÇÇÇĢĢŢĄÇŢĢĢĄĢŢÇĄŢĢÇĢÇĢTŢTŢÇĢĢÇÇĢÇ	1122
Sbjct	1554	GGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGC	1613
Query	1123	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1182
Sbjct	1614	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1673
Query	1183	CATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1242
Sbjct	1674	catactggagcagcacaatgtgaacccgatgcgcgctcccacagcaccgaaagtatcct	1733
Query	1243	GCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1302
Sbjct	1734	ĠĊĠĊĠĀĊĀĊĠĀĠŦĊĊĀĊĊĠĊĊĠĀĀĠĊĊĀĊĊĠĊŦĀĊĊĊĀĀŦĀĠĠĠĊĊĀĠŦĀĀŦĊĊĠĊĊĠĊĊ	1793
Query	1303	GTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1362
Sbjct	1794	ĠŦŦĠĊĊĂĊĊĂĂĂĠĊĠĂĊĠĊĀĠĊĊĀĠĊĊĠĀĠĊĠĊĀŦĊĀĠĊŦĠĠŦĀĊĀĠŦĠĠĠĊĠŦĀĠĠĊŦĠ	1853
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1854	ĊŢĊĀŢĊĠŢĊĠĀĊĀŢĊĊĀĊĊŢĊĊĀĀŢĊĀĠĠĊĊĀĠŢĊĊAĊŢĠĊĊĊŢĀĊĠĊĊĊĀĠŢĊĊĊĀŢĀĀ	1913
Query	1423	TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1482
Sbjct	1914	TÁTTÁGTCTGÁÁCTCGGÁCCTGGÁCTGCÁGTTCCÁÁTÁTCTCGCTGÁÁTTÁTÁTGGCGT	1973
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1974	GĠĂŢĊĠĊĊŢĂŢĊĊĠŢĠĊĠŢŢĊĂĊĠĠŢĊĂĊĊĠĠĂŢĠĂĠĂĂŢĂĠŢĊĂĠŢĠĊŢĊĊŢŢŢĠĂĊŢĊ	2033
Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACACACATCAGCACCTGAGGTC	1602
Sbjct	2034	GGCGŤŤĠĂĂŤĊĂĊŤĊĂĊĠĊĠĂĠĠĂĠĠĂĠĠĂĊĊĂĠĊĂĂĊĂĠĊĂĂĊĂŤĊĂĠĊĂŦĊŤĠĂĠĠŤĊ	2093
Query	1603	GTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 16	
Sbjct	2094	ATTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 21	50

Range 2: 2150 to 2434

Score		Expect	Identities	Gaps	Strand	Frame	
510 bits	(276)	4e-140()	282/285(99%)	0/285(0%)	Plus/Plus		
Features	s:						
Query 1812 GTTTCGTGTCGATGCGTGAGTTTCGCACTTCTACACAGACGACGACTACAGTGTCCAC				GTCCAGT	1871		

Sbjct	2150	GTTTCGTGTCGATGCGTGAGTTTCGCACTTCCACACAGACGACGACTACAGTGTCCAGT	2209
Query	1872	CCTCCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGG	1931
Sbjct	2210	CCTCCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTCAGCATCAGTGAGTCGACGG	2269
Query	1932	CGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1991
Sbjct	2270	CGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	2329
Query	1992	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccg	2051
Sbjct	2330	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACGACCACCAGCAGCAGCACAACCACCG	2389
Query	2052	gctatggcagcagcgaagtggagcagcagcagcagcagcagc 2096	
Sbjct	2390	GCTATGGCAGCAGCGAAGTGGAGCAGCAGCAGCAGCAGC 2434	

Drosophila melanogaster C3G ortholog, transcript variant E (C3G), mRNA Sequence ID: **ref|NM_001144695.3|** Length: 5651 Number of Matches: 2 Range 1: 660 to 2150

Score		Expect	Identities	Gaps	Strand	Frame	
2693 bit	s(1458)	0.0()	1485/1497(99%)	6/1497(0%)	Plus/Plus		
Feature	s:						
Query	163	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCGGCACCTGTTC	CAGTGGCATCGG	AGTGGG	222
Sbjct	660	gaacgcacat	cagatacaccatccacc	ecceecy	CAGTGGCATCGG	AGTGGG	719
Query	223	CGGTGGCGGCTG	CAGCAGCAGCAAC	CAATAGCATCAACAGO	CGGCAGCTACTC	CACCGC	282
Sbjct	720		;ĊAĠĊAĠĊAĠĊAĠĊAA(779
Query	283		CACCACCCACGCATCAC				342
Sbjct	780	ĊŢĠĊĀĊŢĊĊĠĊĊ	:ACCACCCACGCATCA(:TAGTCGGGTCGGGGG	GCATCACTCGCAGCAC			839 402
Query Sbjct	343 840	GCCGGGAGGATC					893
Query	403		ACCCAGTGCCGGATC				462
Sbjct	894						953
Query	463	Ģ ÇŢ <u>Ā</u> ĢÇĢÇĢÇĢ	: GGCGCGTTCCTTTAAC	- БĢĀÇĢĀÇÇŢÇĀŢÇĢĀÇ	G AAGATTTÇÇÇT	Ģ ŢĢÇĢ	522
Sbjct	954	GCTAGCGCGCCG	GGCGCGTTCCTTTAAC	GACGACCTCATCGAC	JAAGATTTCCCT		1013
Query	523	AACCACCAACAA	TACACTGGGTCGCTC	CCACTCGCCGCACAG7	TCCGCGCACCAA	GCACGG	582
Sbjct	1014	YYCCYCCYYCYY	rtycyctegetcectc	ccactcccccccacac	rccccccaa	GCACGG	1073
Query	583	CACAAAGGCACC	GCCCACCACCGAGGAC	GTGCTACGGTCCAC	CCAAACCCTGGA	GACGCA	642
Sbjct	1074		:ĠĊĊĊÀĊĊĀĊĊĠĀĠĠĀĊ				1133
Query	643		'TTCGAATGCCCTGAA(702
Sbjct	1134		'TTĊĠĂĂTĠĊĊĊŦĠĂĂĊ				1193
Query Sbjct	703 1194		GGGCAACGGAACGGT(762 1253
Query	763		.CACCCTGAATGAAAA				822
Sbjct	1254		TACCCTGAATGAAAA				1313
Query	823	ТТАССАБАБССТ	'GGGÇAAGÇTÇATÇAA(, GCTCTGCGACGAGGTC	Б АТĢСТСТССĢА	ĢĢĄÇĄĢ	882
Sbjct	1314	TTACCAGAGCCT		GCTCTGCGACGAGGTC		GGACAG	1373
Query	883	CGGCGAGTGCGC	CTCCCTGAGCAACGAC	GAATGTGCGGGAAGTC	CATTGATCTTCT	CGAGGA	942
Sbjct	1374	ceeceaetecec	ctcctgagcaacga	SAATGTGCGGGAAGTC	CATTGATCTTCT	CGAGGA	1433
Query	943	TGCTGTGCGGAA	TCTCGTTACGCTGGC(GCAGGGCAAGCTGAAC	GGAGCAGGATCA	GTGCGC	1002
Sbjct	1434	tĠĊtĠtĠĊĠĠAA	tctcgttacgctgcc	scadddcaadctdaad	GAGCAGGATCA	ĠţĠĊĠĊ	1493
Query	1003		TGGATCTGGCTTGGG(1062
Sbjct	1494		rdgatctgcttgcc				1553
Query	1063	GGTCACCGCCTC	GCCGGGAGCGAGTGTT	rcccggtactggagt(CATGCGCGTTTC	GGCCGC	1122

Sbjct	1554	GGTCACCGCCTCGCCGGGAGCGAGTGTTCCCCGGTACTGGAGTCATGCGCGTTTCGGCCGC	1613
Query	1123	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1182
Sbjct	1614	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1673
Query	1183	CATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1242
Sbjct	1674	CATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1733
Query	1243	GCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1302
Sbjct	1734	GCGCGACACGAGTCCACCGCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1793
Query	1303	GTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1362
Sbjct	1794	GTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1853
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1854	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAA	1913
Query	1423	TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1482
Sbjct	1914	tattagtetgaaeteggaetggaetgeagtteeaatatetegetgetgaattatggegt	1973
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1974	dGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	2033
Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGGTC	1602
Sbjct	2034	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCATCTGAGGTC	2093
Query	1603	GTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 16	59
Sbjct	2094	atttccaaagttgcctgccatgatgatgacgaagacatgcacaagatgctacctac	50

Range 2: 2150 to 2434

Score		Expect	Identities	Gaps	Strand	Frame	
510 bits(276)		4e-140()	282/285(99%)	0/285(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	SACGGACTACAGT	TGTCCAGT	1871
Sbjct	2150	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCCACACAGACG	ACGGACTACAG1	TGTCCAGT	2209
Query	1872	CCTCCACGAAG'	TCGTCCAGCAGCAATT	CGGAGATTGCGTTI	AGCATCAGTGAG	GTCGACGG	1931
Sbjct	2210	cctccacgaag	rcgrccagcagcaarr	cggagattgcgttc	cadcatcadtdad	STCGACGG	2269
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAGO	CCAGCGTC	1991
Sbjct	2270	cedtcedcadc	AGTAGCGAGTACCAGC.	AGATTAGCCAGTTG	gtgtcgcacago	ccadcdtc	2329
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcaca	accaccg	2051
Sbjct	2330	ATATATCCTCG	AGCAGTAGCAGCTGCA	ccaccacgaccacc	:AGCAGCAGCACA	AACCACCG	2389
Query	2052	gctatggcagca	agcgaagtggagcagc	agcagcagcagcag	cage 2096		
Sbjct	2390	dctatddcadc	AGCGAAGTGGAGCAGC	rdcadcadcadcad	CAGC 2434		

Drosophila melanogaster IP03271 full insert cDNA

Sequence ID: **gb|BT025818.1|** Length: 5673 Number of Matches: 2 Range 1: 638 to 2128

Score		Expect	Identities	Gaps	Strand	Frame	
2693 bits(1458)		0.0()	1485/1497(99%)	6/1497(0%)	Plus/Plus		
Features	3 :						
Query	163	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG	SAGTGGG	222
Sbjct	638	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG	SAGTGGG	697
Query	223	CGGTGGCGGCTG	CAGCAGCAGCAAC	CAATAGCATCAACAGC	GGCAGCTACTO	CACCGC	282
Sbjct	698	çeeteeçeeçte	cagcagcagcagcaac	caatagcatcaacagc	GGCAGCTACTC	ccaccec	757
Query	283	CTGCACTCCGCC	ACCACCCACGCATCAC	GCATCACTCGCAGCAC	CAGCAGCTGC <i>A</i>	AGGGCAC	342
Sbjct	758	ctcckctccccc	yccyccycqcytcyc	scatcactcscascac	cagcagctgc <i>i</i>	rgggcyc	817

Query	343 818	GCCGGGAGGATCTAGTCGGGTCGGGGGAGCAGGAGCAGGAGCAGGCGGAGGTGGTGT 	402 871
Sbjct Query	403	ACCACCGCACCACCCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAA	462
Sbjct	872	ACCACCGCACCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAA	931
Query	463	GCTAGCGCGCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCG	522
Sbjct	932		991
Query	523	ААССАССААСААТАСАСТОООТООТООТООТООТООТООТООТООТООТООТООТО	582
Sbjct	992	AACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGG	1051
Query	583	CACAAAGGCACCGCCCACCACGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCA	642
Sbjct	1052	cacaaaggcaccgccaccaccgaggaggtgctacggtccacccaaaccctggagacgca	1111
Query	643	CGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCT	702
Sbjct	1112	ĊĠŦĊĀĀĠĠĀĊĀŦŦŦĊĠĀĀŦĠĊĊĊŦĠĀĀĠĊĀĊŦŦĊĊĠĠĠĀŦĠŦŦĀŦĀĊŦĊĀĀĠĀĀĠĀĀĠĊŦ	1171
Query	703	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	762
Sbjct	1172	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	1231
Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822 1291
Sbjct	1232 823	ĠĂŦĊĊĂĂĂĊĊŦĂŦĂĊĊĊŦĠĂĂŦĠĂĂĂĂĊĂĠŦĠĊĊĂŦĊĂŦĠĂĠĊĀĠĊĠĊĊĂĊĠĊŦĠĊĀĠĠŦ TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Query Sbjct	1292	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	1351
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	1352	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	1411
Query	943	ТĢСТĢТĢСĢĢAATCTCĢTTACĢСTĢĢСĢСAĢĢĢСAAĢСТĢAAĢĢAĢCAĢĢATCAĢTĢCĢC	1002
Sbjct	1412	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1471
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1472	ĊŦŦŦĊĠĊŦĂĊĀĠŦĠĠĀŦĊŦĠĠĊŦŦĠĠĠĊĠĠĊĀŦŦĠĠĀĠĊĠĠĊĠĠĠĠĠĀĠĀŦĊĀŦĠĠĠŦĠĊ	1531
Query Sbjct	1063 1532	GGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGC	1122 1591
Query	1123	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1182
Sbjct	1592	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1651
Query	1183	САТАСТGGAGCAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1242
Sbjct	1652	CATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1711
Query	1243	GCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1302
Sbjct	1712	GCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1771
Query	1303	GTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1362
Sbjct	1772	ĠŦŦĠĊĊĂĊĊĂĂĂĠĊĠĂĊĠĊĀĠĊĊĀĠĊĊĠĂĠĊĠĊĂŦĊĂĠĊŦĠĠŦĀĊĀĠŦĠĠĠĊĠŦĀĠĠĊŦĠ	1831
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1832 1423	ĊŤĊĂŤĊĠŤĊĠĂĊĂŤĊĊĂĊĊŤĊĊĂĂŤĊĂĠĠĊĊĂĠŤĊĊAĊŤĠĊĊĊŤĂĊĠĊĊĊĂĠŤĊĊĊĂŤĂĂ TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1891 1482
Query Sbjct	1892	TATTAGTCTGAACTCGGACCTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAATTATGGCGT	1951
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1952	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	2011
Query	1543	ĢĢÇĢŢŢĢĄĄŢÇĄÇŢÇĄÇĢÇĢĄĢĢĄĢĢĄĢÇĄĢÇĄĄÇĄĢÇĄĄÇĄŢÇĄĢÇĄCÇŢĢĄĢĢŢÇ	1602
Sbjct	2012	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCATCTGAGGTC	2071
Query	1603	GTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 16	59
Sbjct	2072	ATTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 21	28

Range 2: 2128 to 2412

Score	Expect	Identities	Gaps	Strand	Frame
510 bits(276)	4e-140()	282/285(99%)	0/285(0%)	Plus/Plus	_

Features	s:		
Query	1812	GTTTCGTGTCGATGCGTGAGTTTCGCACTTCTACACAGACGACGGACTACAGTGTCCAGT	1871
Sbjct	2128	GTTTCGTGTCGATGCGTGAGTTTCGCACTTCCACACAGACGACGACTACAGTGTCCAGT	2187
Query	1872	CCTCCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGG	1931
Sbjct	2188	CCTCCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTCAGCATCAGTGAGTCGACGG	2247
Query	1932	CGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1991
Sbjct	2248	CGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	2307
Query	1992	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccg	2051
Sbjct	2308	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACCACCACCAGCAGCAGCACCACCG	2367
Query	2052	gctatggcagcagcgaagtggagcagcagcagcagcagcagc 2096	
Sbjct	2368	GCTATGGCAGCAGCGAGCAGCAGCAGCAGCAGCAGC 2412	

Drosophila yakuba C3G, transcript variant I (Dyak\C3G), mRNA Sequence ID: **ref|XM_015190007.1**| Length: 5737 Number of Matches: 1 Range 1: 217 to 2134

Score		Expect	Identities	Gaps	Strand	Frame
2691 bit	ts(1457)	0.0()	1786/1942(92%)	33/1942(1%)	Plus/Plus	
Feature	s:					
Query	163	GAACGGCAGCA'	TCAGTTCTCCATCCAC	CCCGGCACCTGTTCC	CAGTGGCATCGGAG	TGGG 222
Sbjct	217	GAACGGCAGCA'	rcagttctccatccacd	ecceececeter	cagtggcatcggag	rggg 276
Query	223	CGGTGGCGGCT	GCAGCAGCAGCAAC	CAATAGCATCAACAGC	CGGCAGCTACTCCA	CCGC 282
Sbjct	277		ĠĊĀĠĊĀĠĊĀĠĊĀĠĊĀĀĊ			cccc 336
Query	283		CACCACCCACGCATCAC			
Sbjct	337		CÁCCÁCCCÁCGCÁCCÁC			
Query	343		CTAGTCGGGTCGGGGG 			
Sbjct Query	397 403		ĊŤĀĠŤĊĠĠĠŤĠĠĠĀĠĠ <i>Ĕ</i> CACCCAGTGCCGGATCO		AĞĞTĞĞTĞĞAAĞTĞ SACTCTCAACCCCA	
Sbjct	454	GCCACCGGCAC			ZAGTCTCAAGGGCA CAGTCTGAAGGGCA	
Query	463		GGGCGCGTTCCTTTAAG			
Sbjct	514					
Query	523	ААССАССААСА	 АТАСАСТGGGTCGCTCC	ССАСТСБССБСАСАБТ	г СССССТ ССТСТВ	А СССС 582
Sbjct	574	CACCACCAACA			CCGCGGACCAAGC	 ACGG 633
Query	583	CACAAAGGCAC	CGCCCACCACCGAGGAC	GTGCTACGGTCCAC	CCAAACCCTGGAGA	CGCA 642
Sbjct	634	CTCCAAGGCAC	CGCCCACCACCGAGGAG	GTGCAGCGATCCACC	CAAACTCTGGAGA	CGCA 693
Query	643	CGTCAAGGACA'	TTTCGAATGCCCTGAAG	GCACTTCCGGGATGTT	TATACTCAAGAAGA	AGCT 702
Sbjct	694	¢q4¢qqqqq	tctcgaacgcgctcaad	scarttccccccatct	catactaaadaada	AGCT 753
Query	703	GGAGGTGTTGC	CGGGCAACGGAACGGTC 	CATTCTGGAAACCAT <i>A</i>	AGCCAGCATGTACT	CCGT 762
Sbjct	754		ĊĊĠĠĸĸĸĊĠĠĸĸĊĠĠŦĊ			
Query	763		ACACCCTGAATGAAAAC 			
Sbjct	814		ACACCCTGAATGAAAAC			
Query Sbjct	823 874		FGGGCAAGCTCATCAAG 			
Query	883		CCTCCCTGAGCAACGAG			
Sbjct	934		CTCCCTGAGCAACGAC CCTCCCTGAGCAACGAC			
Query	943		ATCTCGTTACGCTGGC0			
Sbjct	994					
Query	1003	ĊŢŢŢĊĠĊŢĄĊA¢	ĢŢĢĢĄŢĊŢĢĢĊŢŢĢĢĢÇ	СĢĢÇĄŢŢĢĢĄĢÇĢĢÇĢ		Ģ ŢĢÇ 1062
Sbjct	1054	CTTTCGCTATG		CGGCATTGGAGCGGCG	GCGGAGATCATGG	

Query	1063	GGTCACCGCCTCGCCGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGC	1122
Sbjct	1114	GGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCACTGGCATCATGCGCGTTTCAGCCGC	1173
Query	1123	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1182
Sbjct	1174	CGAATCAGCTGCCAGCGAACTTCGTTGCCGGACATTGCACTCACGCCCAAGGAACGCGA	1233
Query	1183	ҪӒҭӒҪҬ҅҅҅҅҄҅Ҫ҄Ӓ҅҅Ҫ҄Ӓ҅ҪӒҪӒҪӒ҅Ӑ҅Ҭ҅Ѳ҃Ҭ҅Ѳ҄Ӓ҅҅҅҅ҪҪҪѲ҃ӒҬ҅Ѳ҄ҪѲ҄ҪҪ҄҅ҪҪҪӒҪӒҪӒҪҪҪӒӒӒ҅҅Ѳ҄҅Ҁ҅҅҅҅҅҅҅҅ҪҬ	1242
Sbjct	1234	CATACTGGAGCACAATGTGAATCCCATGCGCGCTCGCACAGCACCGAAAGCATCCT	1293
Query	1243	Ģ ÇĢÇĢĀÇĀÇĢĀĢŢÇÇĀÇÇĢÇĢĀĀĢÇÇĀÇÇĢÇŢĀÇÇÇĀĀŢĀĢĢĢÇÇĀĢŢĀĀŢÇÇĢÇÇĢÇÇ	1302
Sbjct	1294	GCGCGACACGAGTCCACCGCCAAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1353
Query	1303	GTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1362
Sbjct	1354	GTTGCCACCCAAGAGACGCAGCCAGCCGGCGCACCTGCTGGCGCTGCGGTGGTCGGCTG	1413
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1414	CTCATCGTTGACATCCGCCTCC-T-AC-G-CC-CA-GCCCCATAA	1452
Query	1423	TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1482
Sbjct	1453	TATCAGCCTGAACTTGGACCTGGACTGCAGTTCCAACATCTCGCTGCTGAACTATGGCGT	1512
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1513	GGATCGCCTATCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1572
Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAG	1599
Sbjct	1573	GGCGTTGAATCACTCACGCGAGGAGGAGGACCACCAACAGCAACAGCAGCAGCA	1632
Query	1600	GTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG	1659
Sbjct	1633	GtcGctctcgAAGAtGccAAcGAtGAtGAcGAGGACAtGGACAAGAtGGtcAGctACAG	1692
Query	1660	CGCCGCAATCGACGACAAAACGCAGACACCACTTTCGACTGGTGGTGGTATAGCTGGTGT	1719
Sbjct	1693	cececaetes control cont	1752
Query	1720	TGCTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGA	1779
Sbjct	1753	tertegegegeketegegegeketegegegegeketegegegeg	1812
Query	1780	AACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCAC	1839
Sbjct	1813	AACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGCGAGTTTCGCAC	1872
Query	1840	TTCTACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTC	1899
Sbjct	1873	trcacacacacacaccaccaccaccaccaccaccaccacca	1932
Query	1900	GGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCA	1959
Sbjct	1933	ĠĠĀĠĀŢŢĠĊĠŢŢŢĀĠĊĀŢĊĀĠŢĠĀĠŢĊĠĀĊĠĠĊĠĠŢĊĠĠĊĀĠĊĀĠĊĀĠĊĀĠŢĀĊĊĀĠĊĀ	1992
Query	1960	GATTAGCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCAC	2019
Sbjct	1993	ĠĂŢŢŖĠĊĊŖĠŢĠŢĠŢĠĊŖĊŖĠĊŖĠĊŖŢĊŖŢŖŢŢŢŢŢŢŢŢŢŢ	2052
Query	2020	CACCACGACCACcagcagcagcacaaccaccggctatggcagcagcgaagtgga	2073
Sbjct	2053	caccaccaccaccaccaccaccaccaccaccaccaccac	2112
Query	2074	gcagcagcagcagcag 2095	
Sbjct	2113	ĠĊĀĠĊĀĠĊĀĠĊĀĠĊĀĠĊĀĠ 2134	

Drosophila melanogaster C3G ortholog, transcript variant G (C3G), mRNA Sequence ID: **ref|NM_001144697.2|** Length: 5244 Number of Matches: 3 Range 1: 254 to 1743

Score		Expect	Identities	Gaps	Strand	Frame	
2691 bits(1457)		0.0()	1484/1496(99%)	6/1496(0%)	Plus/Plus		
Features	S :						
Query	164	AACGGCAGCATC	AGTTCTCCATCCACGC	CCGGCACCTGTTCC	AGTGGCATCGG <i>F</i>	AGTGGGC	223
Sbjct	254	AACGGCAGCATC	AGTTCTCCATCCACGC	CCGGCACCTGTTCCA	AGTGGCATCGG	AGTGGGC	313
Query	224	GGTGGCGGCTGC	AGCAGCAGCAGCAACA/	ATAGCATCAACAGCG	GCAGCTACTCC	CACCGCC	283
Sbjct	314	GGTGGCGGCTGC	AGCAGCAGCAACA	ATAGCATCAACAGC	GCAGCTACTCC	CACCGCC	373

Query	284	TGCACTCCGCCACCCACGCATCAGCATCACTCGCAGCACCAGCAGCTGCAGGGCACG	343
Sbjct	374	TGCACTCCGCCACCACCACGCATCAGCATCACTCGCAGCACCAGCAGCTGCAGGGCACG	433
Query	344	CCGGGAGGATCTAGTCGGGTCGGGGGGGGGGGGGGGGGG	403
Sbjct	434	ccdddaddatctadtcdddtadd-d-ddadcaddaddadddddddddd	487
Query	404	CCACCGGCACCACCCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAAG	463
Sbjct	488 464	CCACCGGCACCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAAG CTAGCGCGCCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGA	547 523
Query Sbjct	548	CTAGCGCGCCGGGCGCTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGA	607
Query	524	ACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGGC	583
Sbjct	608	ACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGGC	667
Query	584	ACAAAGGCACCGCCCACCACGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCAC	643
Sbjct	668	AcAAAGGCACCGCCACCACCGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCAC	727
Query	644	GTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTG	703
Sbjct	728	ĠŤĊĂĂĠĠĂĊĂŤŤŤĊĠĂĂŤĠĊĊĊŤĠĂĂĠĊĂĊŤŤĊĊĠĠĠĂŤĠŤŤĂŤĂĊŤĊĂĂĠĂĂĠĂĀĠĊŤĠ	787
Query Sbjct	704 788	GAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTG	763 847
Query	764	ATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTT	823
Sbjct	848	Atccadacctataccctgadtgadadcactgccdtcatcdtgaccaccctgctgcdcdct	907
Query Sbjct	824 908	TACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGC	883 967
Query	884	GGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGAT	943
Sbjct	968	GGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGAT	1027
Query	944	GCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCC	1003
Sbjct	1028	ĠĊŦĠŦĠĊĠĠĀĀŦĊŦĊĠŦŦĀĊĠĊŦĠĠĊĠĊĀĠĠĠĊĀĀĠĊŦĠĀĀĠĠĀĠĊĀĠĠĀŦĊĀĠŦĠĊĠĊĊ	1087
Query Sbjct	1004 1088	TTTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGAGATCATGGGTGCG	1063 1147
Query	1064	GTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGCC	1123
Sbjct	1148	GTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGCC	1207
Query	1124	ĢĄĄŢĊĄĢĊŢĢĊĊĊĄĢĊĠŢĄĊŢŢĊĠŢŢĢĊĊĠĠĄĊĄŢĄĠĊĠĊŢĊĄĊĠĊĊĊĄĄĠĠĄĠĊĠĊĠĄĊ	1183
Sbjct	1208	GAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGAC	1267
Query	1184	ATACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTG	1243
Sbjct	1268	ATACTGGAGCAGCAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCTG	1327
Query	1244 1328	CGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCG	1303 1387
Sbjct Query	1304	TTGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGC	1363
Sbjct	1388	TTGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGC	1447
Query	1364	ŢĊĄŢĊĠŢĊĠĄĊĄŢĊĊĄĊĊŢĊĊĄĄŢĊĄĠĠĊĊĄĠŢĊĊĠĊŢĠĊĊĊŢĄĊĠĊĊĊĄĠŢĊĊĊĄŢĄĄŢ	1423
Sbjct	1448	TCATCGTCGACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAAT	1507
Query	1424	ATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTG	1483
Sbjct	1508	Attagtetgaaeteggaetggaetgeagtteeaatatetegetgetgaattategeegtg	1567
Query	1484	GATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCG	1543
Sbjct	1568	ĠĂŢĊĠĊĊŢĂŢĊĊĠŢĠĊĠŢŢĊĂĊĠĠŢĊĂĊĊĠĠĂŢĠĂĠĂĂŢĂĠŢĊĂĠŢĠĊŢĊĊŢŢŢĠĂĊŢĊĠ	1627
Query Sbjct	1544 1628	GCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGGTCG	1603 1687
Query	1604	TTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 165	
Sbjct	1688	TTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 174	

Score		Expect	Identities	Gaps	Strand	Frame	
510 bits	(276)	4e-140()	282/285(99%)	0/285(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG <i>I</i>	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	ACGGACTACAGT	GTCCAGT	1871
Sbjct	1743	GTTTCGTGTCGZ	ATGCGTGAGTTTCGCA	cttccacacagacg	AcGGACTACAG1	rGTCCAGT	1802
Query	1872	CCTCCACGAAGT	CGTCCAGCAGCAATT	CGGAGATTGCGTTT	AGCATCAGTGAG	GTCGACGG	1931
Sbjct	1803	CCTCCACGAAG	rcgtccagcagcaatt	cggagattgcgttc	AGCATCAGTGAG	STCGACGG	1862
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAGC	CCAGCGTC	1991
Sbjct	1863	ceetceecaeca	AGTAGCGAGTACCAGC.	AGATTAGCCAGTTG	gtgtcgcacago	ccadcdtc	1922
Query	1992	ATATATCCTCGA	AGCAGTAGCAGCTGCA	CCACCACGACCACC	agcagcagcaca	accaccg	2051
Sbjct	1923	AtAtAtcctccz	AGCAGTAGCAGCTGCA	ççyççyçèyççyçç	y g c y g c y c y c y	AACCACCG	1982
Query	2052	gctatggcagca	agcgaagtggagcagc	agcagcagcagcag	cagc 2096		
Shict	1983	GCTATGGCAGCA	AGCGAAGTGGAGCAGC	TGCAGCAGCAGCAG	CAGC 2027		

Range 3: 64 to 133

Score		Expect	Identities	Gaps	Strand	Frame	
130 bits	(70)	1e-25()	70/70(100%)	0/70(0%)	Plus/Plus		
Features	s:						
Query	1	AAAAAGAGGAA	atatatatatata c	AAGAATAAGTATC	GAAACTCAAGTGG	GCCACATA	60
Sbjct	64	AAAAAGAGGAA	ATATATATATATATAC	AAGAATAAGTATC	GAAACTCAAGTG	3CCACATA	123
Query	61	TATTTAGGTG	70				
Sbjct	124	TATTTAGGTG	133				

Drosophila melanogaster C3G ortholog, transcript variant L (C3G), mRNA Sequence ID: **ref|NM_001298037.1|** Length: 6103 Number of Matches: 2 Range 1: 485 to 1976

Score		Expect	Identities	Gaps	Strand	Frame	
2689 bit	s(1456)	0.0()	1486/1499(99%)	7/1499(0%)	Plus/Plus		
Features	3:						
Query	161	TCGAACGGCAGC	ATCAGTTCTCCATCCA	CGCCCGGCACCTGTT	CCAGTGGCATC	GGAGTG	220
Sbjct	485	TCG-ACGGCAGC	Atcagttctccatcca	cdccdddadctat	CCAGTGGCATC	GGAGTG	543
Query	221	GGCGGTGGCGGC	TGCAGCAGCAGCAGCA	ACAATAGCATCAACA	GCGGCAGCTAC	TCCACC	280
Sbjct	544	ggcggtggcggc	tgcygcygcygcygcy	rycyddiaeth ar	dcddcadctac	4ccacc	603
Query	281	GCCTGCACTCCG	CCACCACCCACGCATC	AGCATCACTCGCAGC	ACCAGCAGCTG	CAGGGC	340
Sbjct	604	gcctgcyctccg	ççyççyçççyççç	agcatcactcgcagc	caccadcadctd	cagggc	663
Query	341	ACGCCGGGAGGA	TCTAGTCGGGTCGGGG	GAGCAGGAGCAGGAG	GCAGGCGGAGGT	GGTGGT	400
Sbjct	664	aceceeeagaeea	tctagtcgggtag	g-gggygcygyg	GCAGGCGGAGGT	ĠĠŦĠĠŦ	717
Query	401	GTACCACCGGCA	CCACCCAGTGCCGGAT	CCTCGGGCCACAAGA	ACAGTCTCAAG	GGCACC	460
Sbjct	718	dtaccaccddca	ccaccadadteccedat	rcctcgggccacaaga	Acagtctcaag	g g g g g g	777
Query	461	AAGCTAGCGCGC	CGGGCGCGTTCCTTTA 	AGGACGACCTCATCG	AGAAGATTTCC	CTGATG	520
Sbjct	778	AAGCTAGCGCGC	ĊĠĠĠĊĠĊĠĦŦĊĊĦĦĦĀ	Addacdacctcatcd	sagaagatttcc	ctgatg	837
Query	521	CGAACCACCAAC	AATACACTGGGTCGCT	CCCACTCGCCGCACA	GTCCGCGCACC	AAGCAC	580
Sbjct	838	ĊĠĀĀĊĊĀĊĊĀĀĊ.	aatacactgggtcgct	rcccactccccccaca	kgtccgcgcacc	AAGCAC	897
Query	581	GGCACAAAGGCA	CCGCCCACCACCGAGG	AGGTGCTACGGTCCA	CCCAAACCCTG	GAGACG	640
Sbjct	898	ddcacaaaddca	cceccyccyccyce	addaddaddaddaddaddaddaddaddaddaddaddadd	rcccyyyycccte	ĠĀĠĀĊĠ	957
Query	641	CACGTCAAGGAC	ATTTCGAATGCCCTGA	AGCACTTCCGGGATG	TTATACTCAAG	AAGAAG	700
Sbjct	958	cacetcaaedac	AtttcckAttccctdA	Adcacttcccccatch	sttatactcaac	AAGAAG	1017

Query	701	CTGGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCC	760
Sbjct	1018	ctggaggtgttgccgggcaacggaacggtcattctggaaaccatagccagcatgtactcc	1077
Query	761	GTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAG	820
Sbjct	1078	gtgatccaaacctataccctgaatgaaaacagtgccatcatgagcagcgccacgctgcag	1137
Query	821	GTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGAC	880
Sbjct	1138	GTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGAC	1197
Query	881	AGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAG	940
Sbjct	1198	AGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAG	1257
Query	941	GATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGC	1000
Sbjct	1258	GATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGC	1317
Query	1001	GCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGT	1060
Sbjct	1318	gcctttcgctacagtggatctggctttggcgcatttggaccgccgcgcgagatcatgggt	1377
Query	1061	GCGGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCC	1120
Sbjct	1378	gcggtcaccgcctcgccggagcgagcgagtgttcccggtactggagtcatgcgcgtttcgcc	1437
Query	1121	GCCGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGC	1180
Sbjct	1438	dccdaatcadctdccadcdtacttcdttdccddacatadcdctcacdccaaddadcdc	1497
Query	1181	GACATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATC	1240
Sbjct	1498	GACATACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATC	1557
Query	1241	CTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCG	1300
Sbjct	1558	ctgcgcgacacacgacgtccaccgccgaagccaccgctacccaatacgccacgtaatccgccg	1617
Query	1301	CCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGC	1360
Sbjct	1618	cccttcccaccaaacccaccaccacccacccacccaccc	1677
Query	1361	TGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCAT	1420
Sbjct	1678	† de ten de la compara de la c	1737
Query	1421	AATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGC	1480
Sbjct	1738	AATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGAATTATGGC	1797
Query	1481	GTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGAC	1540
Sbjct	1798	ĠŦĠĠĂŦĊĠĊĊŦĂŦĊĊĠŦĠĊĠŦŦĊĂĊĠĠŦĊĂĊĊĠĠĂŦĠĂĠĂĀŦĀĠŦĊĀĠŦĠĊŦĊĊŦŦŦĠĀĊ	1857
Query	1541	TCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGG	1600
Sbjct	1858	tcgcccttgaatcactcacccaccaccaccaccaccaccaccaccacca	1917
Query	1601	TCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG	1659
Sbjct	1918	tcatttccaaagttgcctgcgatgatgatggacgaagacatggacaagatggtcagctacag	1976

Range 2: 1976 to 2260

Score		Expect	Identities	Gaps	Strand	Frame	
510 bits	(276)	4e-140()	282/285(99%)	0/285(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG <i>I</i>	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	ACGGACTACAGT	GTCCAGT	1871
Sbjct	1976	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCCACACAGACG	ACGGACTACAG1	GTCCAGT	2035
Query	1872	CCTCCACGAAG	rcgtccagcagcaatt	CGGAGATTGCGTTT	'AGCATCAGTGAG	TCGACGG	1931
Sbjct	2036	cctccacgaag	rcgrccagcagcaarr	cggagattgcgttc	AGCATCAGTGAC	atcgacgg	2095
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAGO	CAGCGTC	1991
Sbjct	2096	ceetceecaeca	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	gtgtcgcacago	ccadcdtc	2155
Query	1992	ATATATCCTCGA	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcaca	accaccg	2051
Sbjct	2156	ATATATCCTCGA	AGCAGTAGCAGCTGCA	ccaccacgaccacc	AGCAGCAGCACA	ACCACCG	2215
Query	2052	gctatggcagca	agcgaagtggagcagc	agcagcagcagcag	cagc 2096		
Sbjct	2216	dctatddcadca	AGCGAAGTGGAGCAGC	rdcadcadcadcad	CAGC 2260		

Drosophila melanogaster C3G ortholog, transcript variant C (C3G), mRNA Sequence ID: **ref|NM_176694.3|** Length: 7553 Number of Matches: 2 Range 1: 1938 to 3426

Score		Expect	Identities	Gaps	Strand	Frame
2689 bit	s(1456)	0.0()	1483/1495(99%)	6/1495(0%)	Plus/Plus	
Features	S :					
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGCC	CGGCACCTGTTCCAG	TGGCATCGGAG	TGGGCG 224
Sbjct	1938		ĠŦŦĊŦĊĊĂŦĊĊĂĊĠĊĊ			
Query	225		GCAGCAGCAGCAACAA 			
Sbjct Query	1998 285		ĠĊĀĠĊĀĠĊĀĠĊĀĀĊĀĀ CACCCACGCATCAGCĀ			
Sbjct	2058	GCACTCCGCCAC			GCAGCTGCAGG	
Query	345	ССССВОТЕ	ĢŢÇĢĢĢŢCGGGĢĢAĢC	ĿAGGAGCAGGAGCAGG	ҾҪҪҪѦҪҪҬҪҪҬҪ	- СТСТАС 404
Sbjct	2118	CGGGAGGATCTA	GTCGGGTAGG-G-	GGAGCAGGAGCAGG	CGGAGGTGGTG	GTGTAC 2171
Query	405	CACCGGCACCAC	CCAGTGCCGGATCCTC	GGGCCACAAGAACAG	TCTCAAGGGCA	CCAAGC 464
Sbjct	2172		ccactecccccatcccccccccccccccccccccccccc		rtctcaagggca	.ccaage 2231
Query	465		CGCGTTCCTTTAAGGA			
Sbjct Query	2232525		ĊĠĊĠŤŤĊĊŤŤŤĂĂĠĠ <i>Ŕ</i> CACTGGGTCGCTCCC <i>R</i>			
Sbjct	2292	CCACCAACAATA	111111111111111		GCGCACCAAGC	
Query	585	САААСССАСССС	ССАССАССВАВОВ ССОВО СО	: ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	҄҅҄҄҄҄҄҄҄҄҄҄҄ӒҲҀҪҀҬҪ҄Ҫ҄ӐҪӒ	.ÇĢÇĄÇĢ 644
Sbjct	2352	CAAAGGCACCGC	CCACCACCGAGGAGGT	rgctacggtccaccca	AACCCTGGAGA	CGCACG 2411
Query	645	TCAAGGACATTT	CGAATGCCCTGAAGC <i>A</i>	CTTCCGGGATGTTAT	ACTCAAGAAGA	AGCTGG 704
Sbjct	2412	tcaaggacatt			AĊŢĊĀĀĠĀĀĠĀ	
Query	705 2472		GCAACGGAACGGTCAT			
Sbjct Query	765		GCAACGGAACGGTCAT CCCTGAATGAAAACAG			
Sbjct	2532	TCCAAACCTATA		TGCCATCATGAGCAG	CGCCACGCTGC	
Query	825	ACCAGAGCCTGG	GCAAGCTCATCAAGCT	'CTGCGACGAGGTGAT	GCTCTCCGAGG	ACAGCG 884
Sbjct	2592	ACCAGAGCCTGG	GCAAGCTCATCAAGCT	CTGCGACGAGGTGAT	GCTCTCCGAGG	ACAGCG 2651
Query	885	GCGAGTGCGCCT	CCCTGAGCAACGAGAA 			
Sbjct	2652	GCGAGTGCGCCT		rgtgcgggaagtcat		
Query Sbjct	945 2712		TCGTTACGCTGGCGC <i>A</i> 	111111111111111		
Query	1005		GATCTGGCTTGGGCGG			
Sbjct	2772	 TTCGCTACAGTG			 GGAGATCATGG	 GTGCGG 2831
Query	1065	TCACCGCCTCGC	CGGGAGCGAGTGTTCC	CGGTACTGGAGTCAT	GCGCGTTTCGG	CCGCCG 1124
Sbjct	2832	tcacccctccc	çqqqqqqqqqqqqqqqqqqqqqqqq	ccectactectect	ĠĊĠĊĠŦŦŦĊĠĠ	
Query	1125		AGCGTACTTCGTTGCC	111111111111111		
Sbjct	2892 1185		AGCGTACTTCGTTGCC			
Query Sbjct	2952		ACAATGTGAACCCGAT 	111111111111111		
Query	1245		ÇĄÇÇĢÇĢĄĄĢÇÇĄÇÇ			
Sbjct	3012	GCGACACGAGTC		:GCTACCCAATAGGGC	CAGTAATCCGC	CGCCGT 3071
Query	1305	TGCCACCAAAGC	GACGCAGCCAGCCGAG	GCGCATCAGCTGGTAC	AGTGGGCGTAG	GCTGCT 1364
Sbjct	3072		gycecyecyecegye			
Query	1365		CCACCTCCAATCAGGC			
Sbjct	3132	CATCGTCGACAT	ĊĊĂĊĊŤĊĊĂĂŤĊĂĠĠĊ	CAGTCCACTGCCCTÁ	.CGCCCAGTCCC	ÀTÀÀTÀ 3191

Query	1425	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG	1484
Sbjct	3192	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAATTATGGCGTGG	3251
Query	1485	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	1544
Sbjct	3252	AtcGcctAtccGtGcGttcAcGGtcAccGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	3311
Query	1545	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCACCTGAGGTCGT	1604
Sbjct	3312	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACATCAGCATCTGAGGTCAT	3371
Query	1605	TTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 1659	
Sbjct	3372	TTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 3426	

Range 2: 3426 to 3710

Score		Expect	Identities	Gaps	Strand	Frame	
510 bits(276) 4e-140()		282/285(99%)	0/285(0%)	Plus/Plus			
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	GACGGACTACAGT	TGTCCAGT	1871
Sbjct	3426	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCCACACAGACG	ACGGACTACAG1	rGTCCAGT	3485
Query	1872	CCTCCACGAAG	rcgtccagcagcaatt	CGGAGATTGCGTTI	'AGCATCAGTGAC	GTCGACGG	1931
Sbjct	3486	cctccacdaad	rcgrccagcagcaarr	cggygyttgcgttc	adcatcagtgad	stcdacdd	3545
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAGO	CCAGCGTC	1991
Sbjct	3546	çççtççççyçç	y de la compara	AGATTAGCCAGTTG	gtgtcgcycyc	ccaccetc	3605
Query	1992	ATATATCCTCGA	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcaca	accaccg	2051
Sbjct	3606	AtAtAtcctcc	AGCAGTAGCAGCTGCA	ccyccyceyccyc	agcagcagcac	AACCACCG	3665
Query	2052	gctatggcagca	agcgaagtggagcagc	agcagcagcagcag	cage 2096		
Sbjct	3666	ĠĊŦĀŦĠĠĊĀĠĊ	AGCGAAGTGGAGCAGC	тĠĊѦĠĊѦĠĊѦĠĊѦĠ	scadc 3710		

Drosophila yakuba C3G, transcript variant A (Dyak\C3G), mRNA Sequence ID: **ref|XM_002099904.2|** Length: 6902 Number of Matches: 1 Range 1: 1384 to 3299

Score		Expect	Identities	Gaps	Strand	Frame	
2687 bits(1	1455)	0.0()	1784/1940(92%)	33/1940(1%)	Plus/Plus		
Features:							
Query 1	.65	ACGGCAGCATCA	AGTTCTCCATCCACGC	CCGCCACCTGTTCCAG	TGGCATCGGAGT	'GGGCG	224
Sbjct 1	384	ACGCAGCATCA	AGTTCTCCATCCACGCC	ccgcccctcttccac	tggcatcggag	reeece	144
Query 2	25	GTGGCGGCTGC	AGCAGCAGCAGCAACA?	ATAGCATCAACAGCGG	CAGCTACTCCAC	CGCCT	284
Sbjct 1	444	gtggcggctgcz	AGCAGCAGCAACAZ	Acadcatcaacadcdd	cadctactccad	:ççççt	150
Query 2	85	GCACTCCGCCA	CCACCCACGCATCAGC	ATCACTCGCAGCACCA	GCAGCTGCAGG	CACGC	344
Sbjct 1	504	gcactccccc	ccacccacccaccacca	Atcacacdcadcacca	gcagctgcaggd	3CACGC	156
Query 3	45	CGGGAGGATCT	AGTCGGGTCGGGGAG(CAGGAGCAGGAGCAGG	CGGAGGTGGTG	FTGTAC	404
Sbjct 1	564	CCGCAGGATCT	AGTCGGGTGGGAGGAG	CA-G-G-TGGAGCAGG	TGGTGGAAGTGC	AGTGC	162
Query 4	05	CACCGGCACCAC	CCCAGTGCCGGATCCT	CGGGCCACAAGAACAG	TCTCAAGGGCAC	CAAGC	464
Sbjct 1	621	caccadcacca	ccadtdccddatcctd	cgggccacaagaacag	tctgaadddcad	caage	168
Query 4	65	TAGCGCGCCGG	GCGCGTTCCTTTAAGG	ACGACCTCATCGAGAA	GATTTCCCTGA7	rgcgaa	524
Sbjct 1	681	TAGCACGCCGAG	GCGCGCTCCTTTAAGG	Acgacctcatcgagaa	ĠĀŦŦŦĊĊĊŦĠĀſ	rdddca	174
Query 5	25	CCACCAACAATA	ACACTGGGTCGCTCCC	ACTCGCCGCACAGTCC	GCGCACCAAGC	ACGGCA	584
Sbjct 1	741	CCACCAACAATA	ACACTGGGTCGCTCCC	ATTCGCCGCACAGTCC	GCGGACCAAGC	4CGGCT	180
Query 5	85	CAAAGGCACCG	CCACCACCGAGGAGG'	TGCTACGGTCCACCCA	AACCCTGGAGAC	CGCACG	644
Sbjct 1	801	ccaaggcaccg	CCACCACCGAGGAGG	rgcagcgatccaccca	AACTCTGGAGAC	GCACG	186

Query	645	TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGG	704
Sbjct	1861	TCAAGGACATCTCGAACGCGCTCAAGCATTTCCGGGATGTCATACTAAAGAAGAAGCTGG	1920
Query	705	AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA	764
Sbjct	1921	AĠĠŦĠŦŦĠĊĊĊĠĠAAAĊĠĠAAĊĠĠŦĊAŦŦĊŦĠĠAAAĊĊAŦAĠĊĊAĠĊAŦĠŦAŦŦĊĊĠŦĠA	1980
Query	765	TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTT	824
Sbjct	1981 825	†CCAAACGTACACCCTGAATGAAAACAGTGCCATCATGAGCTGCGCGCCACACAGCAGGTTT ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG	2040 884
Query Sbjct	2041	ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG	2100
Query	885	ĢÇĢĀĢŢĢÇĢÇÇŢÇÇÇŢĢĀĢÇĀĀÇĢĀĢĀĀŢĢŢĢÇĢGĢĀAĢŢÇĀŢŢĢĀŢÇŢŢÇŢCĢĀĢĢĀŢĢ	944
Sbjct	2101	GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGAGAGGTCATTGATCTTCTGGAGGATG	2160
Query	945	CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCT	1004
Sbjct	2161	ctgtgcggaatctcgttacgctgcgcaggcaaactgaaggagcagcagatcagtgcgcct	2220
Query	1005	TTCGCTACAGTGGATCTGGCTTGGGCGCGCATTGGAGCGGCGGGGGGAGATCATGGGTGCGG	1064
Sbjct	2221 1065	TTCGCTATGGTGGATCTGGTTTTGGGCGCATTGGAGCGGCGGCGGAGATCATGGGCTGCGGGCGG	2280 1124
Query Sbjct	2281	TCACCGCCTCGCCGGAGTGATTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGCCG	2340
Query	1125	ĄĄŢĊĄĢĊŢĢĊĊĊĄĢĊĢTĄĊŢŢĊĠŢŢĢĊĊĢĢĄĊĄŢĄĢĊĠĊŢĊĄĊĢĊĊĊĄĄĢĢĄĠĊĢĊĢĄĊĄ	1184
Sbjct	2341	AATCAGCTGCCCAGCGAACTTCGTTGCCGGACATTGCACTCACGCCCAAGGAACGCGACA	2400
Query	1185	TACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCTGC	1244
Sbjct	2401	tactggagcagcacaatgtgaatcccatgcgcgctcgcacagcaccgaaagcatcctgc	2460
Query	1245	GCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT	1304
Sbjct	2461	GCGACACGAGTCCACCGCCAAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT	2520
Query Sbjct	1305 2521	TGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT	1364 2580
Query	1365	CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA	1424
Sbjct	2581	CATCGTTGACATCCGCCTCC-T-A-C-G-CC-CA-GCCCCATAATA	2619
Query	1425	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG	1484
Sbjct	2620	tcagcctgaactregacctggactgcagttccaacatctcgctgctgaactatggcgtgg	2679
Query	1485	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	1544
Sbjct	2680	ATCGCCTATCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	2739
Query Sbjct	1545 2740	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAGGT	1601 2799
Query	1602	CGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAGCG	1661
Sbjct	2800	CGCTCTCGAAGATGCCAACGATGATGGACGAGGACATGGACAAGATGGTCAGCTACAGCG	2859
Query	1662	ССССААТССАССАСААААСССАСАССАСТТТССАСТСССТССТ	1721
Sbjct	2860	CCGCAGTCGAGGACAAAATGCAGACACCACTTGCGACTGGTGGTGGTGGTGGTGGTG	2919
Query	1722	CTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAGCGTCTGGTGACGGGGAAA	1781
Sbjct	2920	TŤĠĠĊĠĠĂĂĊŤĠĠĂĠĠĂĠĊĂĠĊĊĠĂĂĠĠŤĠĊĂĠĊŤĠĊŤĠĊĂĠĊĠĂĊŤĠĠŤĠĠĊĠĠĠĠĂĀĀ	2979
Query Sbjct	1782 2980	CTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGATGCGTGAGTTTCGCACTT	1841 3039
Query	1842	CTACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGG	1901
Sbjct	3040	CCACACAGACGACGACTACAGCATCCAGTCCTCCACGAAGTCGTCCAGCAGCAATTCGG	3099
Query	1902	AGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGTAGCGAGTACCAGCAGA	1961
Sbjct	3100	AGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCAGCAGCAGCAGCAGA	3159
Query	1962	TTAGCCAGTTGGTGTCGCACAGCCAGCGTCATATATCCTCGAGCAGTAGCAGCTGCACCA	2021
Sbjct	3160	††AĠĊĊĀĠŢĊĠĠŢĠŢĊĠĊĀĊĀĠĊĊĀĠĊĠŢĊĀŢĀŢĊŢŢĊĠĀĠĊĀĠŢĀĠŢĀĠĊŢĠĊĀĊĊĀ	3219
Query	2022	CCACGACCACCACCACCACCACCACCACCACCACCACCAC	2075
Sbjct Query	3220 2076	ccacaaccaccaccaccaccaccaccaccaccaccacca	3279
Zuci	2070	49049049049049 20 73	

Drosophila yakuba C3G, transcript variant H (Dyak\C3G), mRNA

Sequence ID: **ref|XM_015190006.1|** Length: 5755 Number of Matches: 1 Range 1: 217 to 2152

Score		Expect	Identities	Gaps	Strand	Frame
2608 bit	s(1412)	0.0()	1786/1960(91%)	51/1960(2%)	Plus/Plus	
Features	s:					
Query	163	GAACGGCAGCA!	rcagttctccatccac(GCCCGGCACCTGTTCC	CAGTGGCATCGG	AGTGGG 22
Sbjct	217	GAACGGCAGCA:	rcagttctccatccac	GCCCGGCGCCTGTTCC	AGTGGCATCGG	AGTGGG 27
Query	223	CGGTGGCGGCTG	GCAGCAGCAGCAA(CAATAGCATCAACAGC	GGCAGCTACTC	CACCGC 282
Sbjct	277	¢ĠĠŧĠĠċĠĠċŧċ	scadcadcadcadcaa	caacagcatcaacagc	cdddaddaddddddddddddddddddddddddddddddd	cacccc 33
Query	283		CACCACCCACGCATCA(
Sbjct	337		ČÁCCÁCCCÁCGCÁCCÁ.			
Query	343		CTAGTCGGGTCGGGGG.			
Sbjct	397 403		CTAGTCGGGTGGGAGG. CACCCAGTGCCGGATC		GGTGGTGGAAG	
Query Sbjct	454		CACCCAGTGCCGGATC CACCCAGTGCCGGATC			
Query	463		GGCGCGTTCCTTTAA			
Sbjct	514		GAGCGCGCTCCTTAA	111111111111111		GATGCG 57:
Query	523	AĄÇÇĄÇÇĄĄÇĄ <i>I</i>	ATAÇAÇTGGGTÇGÇTÇ	ÇÇACTÇĞÇÇĞÇAÇAĞT	'ÇÇĞÇĞCAÇÇAA	ĢÇĀÇĢĢ 582
Sbjct	574	CACCACCAACA			CCGCGGACCAA	GCACGG 63
Query	583	ÇAÇAAAGGÇAÇ	CGCCCACCACCGAGGA	GGTGCTACGGTCCACC	CAAACCCTGGA	GACGCA 64
Sbjct	634	CTCCAAGGCAC	CGCCCACCACCGAGGA	GGTGCAGCGATCCACC	CAAACTCTGGA	GACGCA 69
Query	643	CGTCAAGGACA	TTTCGAATGCCCTGAA(GCACTTCCGGGATGTI	ATACTCAAGAA	GAAGCT 702
Sbjct	694	cgtcaaggaca:	tctcgaacgcgctcaa	gcarttccgggatgtc	CATACTAAAGAA	GAAGCT 75
Query	703	GGAGGTGTTGC	CGGGCAACGGAACGGT(CATTCTGGAAACCATA 	GCCAGCATGTA	
Sbjct	754		ĊĊĠĠAĂĂĊĠĠĂĂĊĠĠŤ(
Query	763		ACACCCTGAATGAAAA(111111111111111		
Sbjct	814 823		\CACCCTGAATGAAAA rgggcaagctcatcaa			
Query Sbjct	874		rggcaagereareaa 	111111111111111		
Query	883		CCTCCCTGAGCAACGA			
Sbjct	934	CGGCGAGTGCG		 GAATGTGCGAGAGGTC	 ATTGATCTTCT	 GGAGGA 99:
Query	943	Т ĢСТĢТĢСĢĢĀ	<u> </u> ЧТСТСĞТТАСĞСТĞĞС	Ģ Ç Ā ĢĢĢÇ Ā ĀGÇŢĢ Ā ĀĢ	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	.ĢŢĢÇĢÇ 10
Sbjct	994	TGCTGTGCGGAZ	ATCTCGTTACGCTGGC	GCAGGGCAAACTGAAG	GAGCAGGATCA	 GTGCGC 10!
Query	1003	CTTTCGCTACAC	GTGGATCTGGCTTGGG	CGGCATTGGAGCGGCG	GCGGAGATCAT	GGGTGC 10
Sbjct	1054	CTTTCGCTATG		CGGCATTGGAGCGGCG	GCGGAGATCAT	GGGTGC 11
Query	1063	GGTCACCGCCTC	CGCCGGGAGCGAGTGT'	TCCCGGTACTGGAGTC	ATGCGCGTTTC	GGCCGC 11
Sbjct	1114	ggtcycpcqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	cecceeeq	tcccgcactgcatc	atgegeette	
Query	1123		CCAGCGTACTTCGTT(
Sbjct	1174		CCAGCGAACTTCGTT			
Query	1183		AGCACAATGTGAACCC			
Sbjct	1234 1243		ÁĠĊĀĊĀĀŤĠŤĠĀĀTĊĊŒ GTCCACCGCCGAAGCC			
Query Sbjct	1243		FTCCACCGCCGAAGCC 	111111111111111		
Query	1303		AGCGACGCAGCCAGCC			
~ ~ C - 1	_000					

Sbjct	1354	GTTGCCACCCAAGAGACGCAGCCAGCCGGGCGCACCTGCTGGCGCTGCGGTGGTCGGCTG	1413
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1414	ctcatcgtrgacatccgcctcct-acg-cc-ca-gccccataa	1452
Query	1423	TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1482
Sbjct	1453	tatcagcctgaactrggacctggactgcagttccaacatctcgctgctgaactatggcgt	1512
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1513	ĠĠĂŦĊĠĊĊŦĂŦĊŦĠŦĠĊĠĠŦĊĠĊĠĠŦĊĂĊĊĠĠĂŦĠĂĠĂĂŦĂĠŦĊĂĠŦĠĊŦĊĊŦŦŦĠĂĊŦĊ	1572
Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAG	1599
Sbjct	1573	ĠĠĊĠŦŦĠĂĂŦĊĂĊŦĊĂĊĠĊĠĂĠĠĂĠĠĂĠĠĂĊĊĂĊĊĂĂĊĂĠĊĀĠĊĀĠĊĀĠĊĀĠĊŦĠĀĠ	1632
Query	1600	GTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACA-	1658
Sbjct	1633	ĠŦĊĠĊŦĊŦĊĠĂĀĠĀŦĠĊĊĀĀĊĠĀŦĠĀŦĠĠĀĊĠĀĠĠĀĊĀŦĠĠĀĊĀĠĠŦĊĀĠĊŦĀĊĀĀ	1692
Query	1659	GCGCCGCAA-TCGACGACAAAACGCAGACACCACTTTCGACTGG	1701
Sbjct	1693	ATCCACCĠGTTAĊĠĊAGGĊĠĊCGCÁGŤĊĠÁGĠÁĊÁÁÁÁŤĠĊÁĠÁĊÁĊĆÁĊŤŤGĊĠÁĊŤĠĠ	1752
Query	1702	TGGTGGTATAGCTGGTGTTGCTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGC	1761
Sbjct	1753	TĠĠŦĠŦŦĠĠŦĠĠŦĠŦŦĠŦŦĠĠĊĠĠĂĂĊŦĠĠĀĠĠĀĠĊĀĠĊĊĠĂĀĠĠŦĠĊĀĠĊŦĠĊŦĠĊ	1812
Query	1762	AGCGTCTGGTGACGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTC	1821
Sbjct	1813	AĞCĞACTĞĞTĞĞCĞĞĞAAACTAACAĞCAATCĞCCACTCAAACĞAATCĞĞĞTTTCĞTĞTC	1872
Query	1822	GATGCGTGAGTTTCGCACTTCTACACAGACGACGGACTACAGTGTCCAGTCCTCCACGAA	1881
Sbjct	1873	ĠĂŦĠĊĠĊĠĂĠŦŦŦĊĠĊĂĊŦŦĊĊĂĊĂĊĂĠĂĊĠĂĊĠĠĂĊŦĂĊĂĠĊĀŦĊĊĀĠŦĊĊŦĊĊĂĊĠĂĂ	1932
Query	1882	GTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAG	1941
Sbjct	1933	ĠŢĊĠŢĊĊĀĠĊĀĠĊĀĀŢŢĊĠĠĀĠĀŢŢĠĊĠŢŢŢĀĠĊĀŢĊĀĠŢĠĀĠŢĊĠĀĊĠĠĊĠĠŢĊĠĠĊĀĠ	1992
Query	1942	CAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	2001
Sbjct	1993	ĊĂĠĊĀĠĊĠĀĠŤĀĊĊĀĠĊĀĠĀŤŤĀĠĊĊĀĠŤĊĠĠŤĠŤĊĠĊĀĊĀĠĊĊĀĠĊ	2052
Query	2002	GAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccggctatg	2057
Sbjct	2053	GAGCAGTAGTAGCTGCACCACCACCACCACCAGCAGCAGCACCACCACCGGCTATGGGAG	2112
Query	2058	gcagcagcgaagtggagcagcagcagcagcagcag 2095	
Sbjct	2113	CAĠĊĀĠĊĀĠĊĠĀĀTŤĠĠĀĠĊĀĠĊĀĠĊĀĠĊĀĠĊĀĠĊĀĠ 2152	

Drosophila yakuba C3G, transcript variant E (Dyak\C3G), mRNA Sequence ID: **ref|XM_015190003.1|** Length: 6013 Number of Matches: 1 Range 1: 474 to 2410

Score		Expect	Identities	Gaps	Strand	Frame	
2606 bit	s(1411)	0.0()	1787/1962(91%)	52/1962(2%)	Plus/Plus		
Features	s:						
Query	161	TCGAACGGCAG	CATCAGTTCTCCATC	CACGCCCGGCACCTGT	CCAGTGGCATC	GGAGTG	220
Sbjct	474	TCG-ACGGCAG	catcagttctccatd	ckaceccceecctet:	rccagtggcatc	GGAGTG	532
Query	221	GGCGGTGGCGG	CTGCAGCAGCAGCAG	CAACAATAGCATCAACA	AGCGGCAGCTAC	TCCACC	280
Sbjct	533	ęęçęętęęç	ctgcagcagcagcad	ccaacaacagcatcaac	AGCGGCAGCTAC	4ccacc	592
Query	281	GCCTGCACTCC	GCCACCACCCACGC <i>A</i>	TCAGCATCACTCGCAG(CACCAGCAGCTG	CAGGGC	340
Sbjct	593	GCCTGCACTCC	SCCACCACCCACGC	ACCACCATCACACGCAG	CACCAGCAGCTG	CAGGGC	652
Query	341	ACGCCGGGAGGA	ATCTAGTCGGGTCGG	GGGAGCAGGAGCAGGA	GCAGGCGGAGGT	GGTGGT	400
Sbjct	653	yceccecycy y y y y y y y y y y y y y y y	Atctactcccctaccc	saggagca-g-g-tgga	gcyget general ar a gan a g	AGTGGA	709
Query	401	GTACCACCGGC	ACCACCCAGTGCCGG	SATCCTCGGGCCACAAG	AACAGTCTCAAG	GGCACC	460
Sbjct	710	gtgccaccgcc	yccycccygtecee	satcctcdddccacaad	AACAGTCTGAAG	GGCACC	769
Query	461	AAGCTAGCGCG(CCGGGCGCGTTCCTT	TAAGGACGACCTCATC	GAGAAGATTTCC	CTGATG	520
Sbjct	770	AAGCTAGCACG	cceaececectcctd	rtaaggacgacctcatc	GAGAAGATTTCC	ĊŦĠĀŦĠ	829
Query	521	CGAACCACCAA	CAATACACTGGGTCG	CTCCCACTCGCCGCAC	AGTCCGCGCACC	AAGCAC 	580
Sbjct	830	cecyceycey	caatacactgggtcd	ctcccartccccccaca	AGTCCGCGGACC	yygcyc	889

Query	581	GGCACAAAGGCACCGCCCACCACCGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACG	640
Sbjct Query	890 641	ĠĠĊŦĊĊĂĂĠĠĊĂĊĊĠĊĊĊĂĊĊĂĊĊĠĂĠĠĂĠĠŤĠĊAĠĊĠAŤĊĊĂĊĊĊĂĂĂĊŦĊŤĠĠĂĠĂĊĠ CACGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAG	949 700
Sbjct	950	CACGTCAAGGACATCTCGAACGCGCTCAAGCATTTCCGGGATGTCATACTAAAGAAGAAG	1009
Query	701	СТĢĢĀĢĢŢĢŢŢĢÇÇĢĢĢCĀĀÇĢĢĀĀÇĢĢŢÇĀŢŢÇŢĢĢĀĀĀÇÇĀŢĀĢÇÇĀĢÇĀŢĢŢĀСŢÇÇ	760
Sbjct	1010	CTGGAGGTGTTGCCCGGAAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTATTCC	1069
Query	761	GTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAG	820
Sbjct	1070	ĠŦĠĂŦĊĊĀĀĀĊĠŦĀĊĀĊĊŦĠĀĀŦĠĀĀĀĀĊĀĠŦĠĊĊĀŦĠĀĠĊŦĠĊĠĊĊĀĊĀĊĀĠĊĀĠ	1129
Query Sbjct	821 1130	GTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGAC	880 1189
Query	881	АĢÇĢĢÇĢAĢŢĢÇĢÇŢŢÇÇŢĢAĢÇAAÇĢAĢAAŢĢŢĢÇĢGĢAAĢŢÇAŢŢĢAŢÇŢŢÇŢCĢAĢ	940
Sbjct	1190	AGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGAGAGGTCATTGATCTTCTGGAG	1249
Query	941	GATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGC	1000
Sbjct	1250	ĠAŦĠĊŦĠŦĠĊĠĠAAŦĊŦĊĠŦŦAĊĠĊŦĠĠĊĠĊAĠĠĠĊAAAĊŦĠAAĠĠAĠĊAĠĠAŦĊAĠŦĠĊ	1309
Query Sbjct	1001 1310	GCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGCGGAGATCATGGGT	1060 1369
Query	1061	ĢÇĢĢTÇĄÇÇĢÇÇTÇĢÇÇĢĢĀĢCĢĄĢTĢTTÇÇÇĢĢTĄÇTĢĢAGTÇATĢÇĢÇĢTTTÇGĢÇÇ	1120
Sbjct	1370	GCGGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCACTGGCATCATGCGCGTTTCAGCC	1429
Query	1121	GCCGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGC	1180
Sbjct	1430	dccdaatcadctdccadcdaacttcdttdccddacattdcactcacdccaaddaacdc	1489
Query Sbjct	1181 1490	GACATACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATC	1240 1549
Query	1241	CTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCG	1300
Sbjct	1550	CTGCGCGACACGAGTCCACCGCCAAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCG	1609
Query	1301	CCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGC	1360
Sbjct	1610	cccttcccccccccccccccccccccccccccccccccc	1669
Query Sbjct	1361 1670	TGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCAT	1420 1708
Query	1421	А АТАТТАĢТСТĢААСТСĢĢАССТĢĢАСТĢСАĢТТССААТАТСТСĢСТĢСТĢААСТАТĢĢС	1480
Sbjct	1709	AATATCAGCCTGAACTTGGACCTGGACTGCAGTTCCAACATCTCGCTGCTGAACTATGGC	1768
Query	1481	GTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGAC	1540
Sbjct	1769	ĠŢĠĠĀŢĊĠĊĊŢĀŢĊŢĠŢĠĊĠĠŢĊĠĊĠĠŢĊĀĊĊĠĠĀŢĠĀĠĀĀŢĀĠŢĊĀĠŢĠĊŢĊĊŢŢŢĠĀĊ	1828
Query Sbjct	1541 1829	TCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACACATCAGCA-CCTG	1597 1888
Query	1598	AGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGACAACAGCAACAGCAGCAGCAGCTAC	1657
Sbjct	1889	AGGTCGCTCTCGAAGATGCCAACGATGATGGACGAGGACATGGACAAGATGGTCAGCTAC	1948
Query	1658	AGCGCCGCA-A-TCGACGACAAAACGCAGACACCACTTTCGACT	1699
Sbjct	1949	AAATCCACCGGTTACGCAGGCGCCGCAGTCGAGGACAAAATGCAGACACCACTTGCGACT	2008
Query	1700	GGTGGTGGTATAGCTGGTGGTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCT	1759
Sbjct Query	2009 1760	GGTGGTGTTGGTGGTGTTGTTGGCGGAACTGGAGGAGCAGCCGAAGGTGCAGCTGCT GCAGCGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTG	2068 1819
Sbjct	2069	GCAGCGACTGGTGGCGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTG	2128
Query	1820	TCGATGCGTGAGTTTCGCACTTCTACACAGACGACGACTACAGTGTCCAGTCCTCCACG	1879
Sbjct	2129	TCGATGCGCGAGTTTCGCACTTCCACAGACGACGGACTACAGCATCCAGTCCTCCACG	2188
Query	1880	AAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGC	1939
Sbjct	2189	AAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGCGGTCGGC	2248
Query Sbjct	1940 2249	AGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1999 2308
اكارين	444	AGCAGCAGCAGATTAGCCAGTCGGTGTCGCAGCAGCAGCATATATCT	43 00

Query	2000	ТСФАССАСТАССАССТССАССАССАССАССАССАССАССАССА	caaccaccggctatg	2057
Sbjct	2309	TCGAGCAGTAGCAGCTGCACCACCACCACCACCAGCAGCAGCAGCAGCAGCAGCAG	CCACCACCGGCTATGGG	2368
Query	2058	gcaqcaqcqaagtqqaqcaqcaqcaqcaqcaq	2095	
Sbjct	2369	gcagcagcgaagtggagcagcagcagcagcagcagcagcagcagcagcagcag	2410	

Drosophila yakuba C3G, transcript variant C (Dyak\C3G), mRNA Sequence ID: **ref|XM_015190001.1|** Length: 6918 Number of Matches: 1 Range 1: 1382 to 3315

Score		Expect	Identities	Gaps	Strand	Frame
2604 bit	s(1410)	0.0()	1784/1958(91%)	51/1958(2%)	Plus/Plus	
Features	s:					
Query	165	ACGGCAGCATCA	AGTTCTCCATCCACGC	CCGGCACCTGTTCCA	GTGGCATCGGAGT	rgggcg 224
Sbjct	1382	ACGGCAGCATCA	AGTTCTCCATCCACGC	ccgcccctgttcca	GTGGCATCGGAG	rgggcg 144
Query	225	GTGGCGGCTGC	AGCAGCAGCAGCAACA	ATAGCATCAACAGCG	GCAGCTACTCCAC	CCGCCT 284
Sbjct	1442	ĠţĠĠĊĠĠĊţĠĊ	y de para de la composição	acagcatcaacagcg	gcagctactccac	ਟੇਟੇਫੇਟੇਟੇ ਸ 150
Query	285	GCACTCCGCCAC	CCACCCACGCATCAGC	ATCACTCGCAGCACC.	AGCAGCTGCAGG(GCACGC 344
Sbjct	1502		ĊĊĂĊĊĊĂĊĠĊĂĊĊĂĊĊ		AĠĊAĠĊŦĠĊAĠĠŒ	
Query	345		AGTCGGGTCGGGGGAG(
Sbjct	1562		ÁĠŤĊĠĠĠŤĠĠĠAĠĠÁĠŒ			
Query	405		CCAGTGCCGGATCCT	11111111111111		
Sbjct	1619 465		CCCAGTGCCGGATCCT(GCGCGTTCCTTTAAGG			
Query Sbjct	465 1679		GCGCGTTCCTTTAAGGA 	1 1 1 1 1 1 1 1 1 1		IGCGAA 522
Query	525		ACACTGGGTCGCTCCC			
Sbjct	1739		CACTGGGTCGCTCCC			
Query	585		CCCACCACCGAGGAGG'			
Sbjct	1799	CCAAGGCACCG	[AAACTCTGGAGA(CGCACG 185
Query	645	ТСААССАСТ	ӷҪĢĄみҭĢҪСҪҭĠĄĄĢҪӣ	 АСТТССБББАТБТТА	ӶӒҀҬСӒӒ҅ҀӒӒҀӒӒ	ĄĢÇŢĢĢ 704
Sbjct	1859	TCAAGGACATC	rcgaacgcgctcaagc	ATTTCCGGGATGTCA	TACTAAAGAAGAZ	 AGCTGG 191
Query	705	AGGTGTTGCCGC	GGCAACGGAACGGTCA!	TTCTGGAAACCATAG	CCAGCATGTACT	CCGTGA 764
Sbjct	1919	AGGTGTTGCCC	GGAAACGGAACGGTCA:	TTCTGGAAACCATAG	CCAGCATGTATT	CCGTGA 197
Query	765	TCCAAACCTACA	ACCCTGAATGAAAACA(GTGCCATCATGAGCA	GCGCCACGCTGC <i>I</i>	AGGTTT 824
Sbjct	1979	tccaaacgtaca	Accctgaatgaaaaca	ĠŦĠĊĊĂŦĊĂŦĠĀĠĊŦſ	dedecatatat de la constanta de	AGGTTT 203
Query	825	ACCAGAGCCTGC	GCAAGCTCATCAAGC' 	TCTGCGACGAGGTGA' 	TGCTCTCCGAGG <i>I</i> 	ACAGCG 884
Sbjct	2039		sdcaadctcatcaadc:			
Query	885		PCCCTGAGCAACGAGAA 			
Sbjct	2099		rĊĊĊŦĠĂĠĊĂĂĊĠĂĠĂ <i>ĭ</i>			
Query	945		CTCGTTACGCTGGCGC 			
Sbjct	2159		CTCGTTACGCTGGCGC <i>I</i> GGATCTGGCTTGGGCGC			
Query Shict	1005 2219		GGATCTGGCTTGGGCGC 	1 1 1 1 1 1 1 1 1 1		
Sbjct Query	1065		CCGGGAGCGAGTGTTC			
Sbjct	2279		CCGGGAGTGAGTGTTCC			
Query	1125		CAGCGTACTTCGTTGC			
Sbjct	2339		[
Query	1185		С <u>А</u> СААТĢТĢААСССGА!			
Sbjct	2399	TACTGGAGCAG		 TGCGCGGCTCGCACA	 GCACCGAAAGCAT	 CCTGC 245
Query	1245	GCGACACGAGTO	CCACCGCCGAAGCCAC	CGCTACCCAATAGGG	CCAGTAATCCGC	CGCCGT 130

Sbjct	2459	GCGACACGAGTCCACCGCCAAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCGT	2518
Query	1305	TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT	1364
Sbjct	2519	TGCCACCCAAGAGACGCAGCCAGCCGGCGCGCTGCTGCTGCTGCTGCTGCT	2578
Query	1365	CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA	1424
Sbjct	2579	CATCGTTGACATCCGCCTCC-T-ACG-CC-CA-GCCCCATAATA	2617
Query	1425	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG	1484
Sbjct	2618	tcagcctgaactrggactgcagttccaacatctcgctgctgaactatggcgtgg	2677
Query	1485	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	1544
Sbjct	2678	ATCGCCTATCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	2737
Query	1545	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAGGT	1601
Sbjct	2738	cgttgaatcactcacgcgaggaggaggaccaccaacagcaacagcagcagctgaggt	2797
Query	1602	CGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACA	1658
Sbjct	2798	cctctcgaagatccaaccatcatcdatcdaccaccatcdacatcdacatcdactaccaat	2857
Query	1659	GCGCCGCA-A-TCGACGACAAAACGCAGACACCACTTTCGACTGGTG	1703
Sbjct	2858	CCACCGGTTACGCAGGCGCCGCAGTCGAGGACAAAATGCAGACACCACTTGCGACTGGTG	2917
Query	1704	GTGGTATAGCTGGTGTTGCTGGTGGAACTGGAGGAGCAGGCGAAGGTGTAGCTGCTGCAG	1763
Sbjct	2918	dtdttggtggtgttgttgttgcggaactggaggagcagccgaaggtgcagctgcagctgcag	2977
Query	1764	CGTCTGGTGACGGGGAAACTAACAGCAATCGCCACTCAAACGAATCGGGTTTCGTGTCGA	1823
Sbjct	2978	cgactggtggcgggaaactaacagcaatcgccactcaaacgaatcggtttcga	3037
Query	1824	TGCGTGAGTTTCGCACTTCTACACAGACGACGACTACAGTGTCCAGTCCTCCACGAAGT	1883
Sbjct	3038	TGCGCGAGTTTCGCACTCCACACAGACGACGACTACAGCATCCAGTCCTCCACGAAGT	3097
Query	1884	CGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGGCGGTCGGCAGCA	1943
Sbjct	3098	cgtccagcagcaattcggagattgcgtttagcatcagtgagtcgacggcggtcggcagca	3157
Query	1944	GTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	2003
Sbjct	3158	gcagcgagtaccagcagattagccagtcggtgtcgcacagccagc	3217
Query	2004	GCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccggctatg	2057
Sbjct	3218	GCAGTAGTAGCTGCACCACCACCACCACCAGCAGCACCACCACCGGCTATGGGAGCA	3277
Query	2058	gcagcagcgaagtggagcagcagcagcagcag 2095	
Sbjct	3278	GCAGCAGCGAATTGGAGCAGCAGCAGCAGCAGCAG 3315	

Drosophila erecta uncharacterized protein, transcript variant H (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155128.1|** Length: 5699 Number of Matches: 2 Range 1: 615 to 2127

Score		Expect	Identities	Gaps	Strand	Frame	
2252 bits(1219)		0.0()	1418/1513(94%)	18/1513(1%)	Plus/Plus		
Features	:						
Query	165	ACGGCAGCATCA	AGTTCTCCATCCACG	CCCGGCACCTGTTCCAC	GTGGCATCGGAG	TGGGCG	224
Sbjct	615	ACGGCAGCATCA	AGTTCTCCATCCACG	CCCGGCGCCTGTTCCAC	STGGCATCGGAG	STGGGCG	674
Query	225	GTGGCGGCTGC	AGCAGCAGCAAC	AATAGCATCAACAGCG(GCAGCTACTCCA	ACCGCCT	284
Sbjct	675	gtggcggctgcz	y de propieta de la composição de la com	AACAGCATCAACAGCG	SCAGCTACTCCA	7ÇÇÇÇÇ	734
Query	285	GCACTCCGCCAC	CCACCCACGCATCAG	CATCACTCGCAGCACCA	AGCAGCTGCAGG	GCACGC	344
Sbjct	735	gcactcccccac	ccaccacdcaccac	catcactcgcagcacc <i>i</i>	AGCAGCTGCAGG	GCACGC	794
Query	345	CGGGAGGATCTA	AGTCGGGTCGGGGGA	GCAGGAGCAGGAGCAG	GCGGAGGTGGT-	G	398
Sbjct	795	CTGGAGCATCTA	AGTCGGGTTGGCGGA	GCAGGGGGGAGGTG	TTGGAGGTGGTG	GAGGCG	854
Query	399	GTGTACCACCGG	GCACCACCCAGTGCC	GGATCCTCGGGCCACA	AGAACAGTCTCA	AGGGCA	458
Sbjct	855	dadtgccaccdd	scaccaccadadcc	ggatcctcgggccaca	AGAACAGTCTAA	AGGGCA	914
Query	459	CCAAGCTAGCGC	CGCCGGGCGCGTTCC	TTTAAGGACGACCTCAT	CGAGAAGATTT	CCCTGA	518

Sbjct	915	CCAAGCTAGCACGCCGGGCGCGCTCCTTCAAGGACGACCTCATCGAGAAGATTTCCCTAA	974
Query	519	TGCGAACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGC	578
Sbjct	975	TGCGTACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGC	1034
Query	579	ACGGCACAAAGGCACCGCCCACCACCGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGA	638
Sbjct	1035	ACGGCTCCAAGGCGCCCCCCCCCCGAGGAGGTGCAGCGCTCCACCCAAACTCTGGAGA	1094
Query	639	CGCACGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGA	698
Sbjct	1095	cgcacgtcaaggacatctcgaacgccctgaagcacttccgggatgtcatactgaagaaga	1154
Query	699	AGCTGGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACT	758
Sbjct	1155	AGCTGGAGGTGTTGCCGGGCAACGGCACGGTCATTCTGGAAAACCATTGCCAGCATGTACT	1214
Query	759	CCGTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGC	818
Sbjct	1215	ĊĊĠŦĠĂŦĊĊĂĂĂĊĊŦĂĊĂĊĊĊŦĠĂĂŦĠĂĂĂĂĊĂĠŦĠĊĊĂŦĊĂŦĠĂĠĊŦĠĊĠĊĊĂĊĠĊĀĠĊ	1274
Query	819	AGGTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGG	878
Sbjct	1275	AĠĠŢŢŢĄĊĊĄĠĄĠĊĊŢĠĠĠĊĄĄĠĊŢĊĄŢĊĄĄĠĊŢĊŢĠĊĠĄĊĠĄĠĠŢĠĄŢĠĊŢĊŢĊĊĠĄĠĠ	1334
Query	879	ACAGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCG	938
Sbjct	1335	ACAGCGGCGAGTGCCCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTGG	1394
Query	939	AGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGT	998
Sbjct	1395	AĠĠĀŦĠĊŦĠŦĠĊĠĠĀĀŦĊŦĊĠŦŦĀĊĠĊŦĠĠĊĠĊĀĠĠĠĊĀĀĠĊŦĠĀĀĠĠĀĠĊĀĠĠĀĊĊĀĠŦ	1454
Query	999	GCGCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCATGG	1058
Sbjct	1455	GCGCCTTTCGCTACAGTGGATCTGGTTTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGG	1514
Query	1059 1515	GTGCGGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGG	1118 1574
Sbjct	1119	ĠŦĠĊĠĠŦĊĂĊĊĠĊĊŦĊĠĊĊĠĠĠĀĠŦĠĀĠŦĠŦĊĊĊĠĠĊĠĊŢĠĠĀĀŦĊĀŦĠĊĠĊĠŦĊŦĊĀĠ CCGCCGAĀTCĀGCTGCCCĀGCGTĀCTTCGTTGCCGGĀCĀTĀGCGCTCĀCGCCCĀĀGGĀGC	1178
Query Sbjct	1575	CCGCCGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGC	1634
Query	1179	GCGACATACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTA	1238
Sbjct	1635	GCGACATACTGGAGCACAATGTGAACCCCATGCGCGCTCCCACAGCACCGAAAGCA	1694
Query	1239	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGC	1298
Sbjct	1695	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAACCCGC	1754
Query	1299	ÇĢÇÇĢTŢĢÇÇAÇÇAĀĀĢÇĢĀÇĢÇĀĢÇÇĀĢÇÇĢĀĢÇĢÇĀŢÇAĢÇŢĢĢŢAÇ–AĢ–ŢGĢĢCĢ–	1355
Sbjct	1755		1814
Query	1356	ŢねĢĢĊŢĢĊŢĊĄŢĊĢĄĊĄŢĊĊĄĊĊŢĊĊĄĄŢĊĄĢĢĊĊĄĢŢĊĊĠĊŢĢĊĊĊŢĄĊĢĊĊĄĢŢ	1415
Sbjct	1815	TCGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTGCCCTACGCCCAGT	1874
Query	1416	СССАТААТАТТАGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACT	1475
Sbjct	1875	CCCATAATATCAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATTTCGCTGCTGAACT	1934
Query	1476	ATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCT	1535
Sbjct	1935	ATGGCGTGGATCGTCTCTCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCT	1994
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	1995	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCACCACCATCAGCAACAGCAGC	2054
Query	1593	A-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGA	1646
Sbjct	2055	AGCAGCAGCTGAGGTCGTTTCCAAAGATGCCAGCGATGATGGACGAGGACATGGACAAGT	2114
Query	1647	TGGTCAGCTACAG 1659	
Sbjct	2115	tggtcagctacag 2127	

Range 2: 2127 to 2407

Score		Expect	Identities	Gaps	Strand	Frame	
381 bits	(206)	3e-101()	257/282(91%)	2/282(0%)	Plus/Plus		
Features	s:						
Query	1812	GTTTCGTGTCG <i>F</i>	ATGCGTGAGTTTCGCA(CTTCTACACAGACG	ACGGACTACAGT	GTCCAGT	1871
Sbjct	2127	GTTTCGTGTCG	Atgegegagtttegeac	cttccacacacadacd	ACGGACTACAGC.	ATCCAGT	2186

Query	1872	CCTCCACGAAGTCGTCCAGCAGCAATTCGGAGATTGCGTTTAGCATCAGTGAGTCGACGG	1931
Sbjct	2187	CATCCACGAAGTCGTCCAGCAGCAATTCGGACATTGCGTTTAGCATCAGTGAGTCGACGG	2246
Query	1932	CGGTCGGCAGCAGTAGCGAGTACCAGCAGATTAGCCAGTTGGTGTCGCACAGCCAGC	1991
Sbjct	2247	CGGTCGGAAGCAGCGGCGAGTACCAGCAGATCAGCCAGTCGGTGTTGCACAGCCAGC	2306
Query	1992	ATATATCCTCGAGCAGTAGCAGCTGCACCACCACGACCACcagcagcagcacaaccaccg	2051
Sbjct	2307	AAATATCCTCGAGCAGCAGCAGCACCACCACCACCAGCAGCAGCACCAC	2366
Query	2052	gctatggcagcagc-gaagtggagcagcagcagcagcag 2092	
Sbjct	2367	GCTACGCAGCAGCAGCGAA-CTGGAGCAGCAGCAGCAG 2407	

Drosophila erecta uncharacterized protein, transcript variant G (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155127.1**| Length: 5436 Number of Matches: 2 Range 1: 217 to 1729

Score		Expect	Identities	Gaps	Strand	Frame	
2252 bit	s(1219)	0.0()	1418/1513(94%)	18/1513(1%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATC	AGTTCTCCATCCACGC	CCGGCACCTGTTCCAC	GTGGCATCGGAG	TGGGCG	224
Sbjct	217	ACGGCAGCATC	AGTTCTCCATCCACGC	cceccccqccqcqcddccac	stggcateggag	4gggcg	276
Query	225	GTGGCGGCTGC	AGCAGCAGCAGCAACA	ATAGCATCAACAGCGC	GCAGCTACTCCA	CCGCCT	284
Sbjct	277	ĠŦĠĠĊĠĠĊŦĠĊ.	AGCAGCAGCAGCAACA	acagcatcaacagcgc	scadctactcca	¢¢Ġ¢¢ŧ	336
Query	285		CCACCCACGCATCAGC 				344
Sbjct	337		ĊĊĂĊĊĊĂĊĠĊĂCĊĂCĊ.			ĠĊĀĊĠĊ	396
Query	345		AGTCGGGTCGGGGGAG 			G	398
Sbjct	397		AĠŦĊĠĠĠŦŦĠĠĊĠĠĀĠ				456
Query	399 457	GAGTGCCACCG	GCACCACCCAGTGCCG 	GATCCTCGGGCCACAA 		AGGGCA AGGGCA	458 516
Sbjct Query	457		GCCCGGGCGCGTTCCT				518
Sbjct	517					CCCTAA	576
Query	519		AACAATACACTGGGTC			CCAAGC	578
Sbjct	577	TGCGTACCACC	 AACAATACACTGGGTC			 CCAAGC	636
Query	579	АСССАСАРАС	ĢÇAÇÇĢÇÇAÇÇAÇÇG.	АĢĢĀĢĢŢĢÇTAÇĢGŢĢ	ССАСССАААССС	ŢĢĢĄĢĄ	638
Sbjct	637	ACGGCTCCAAG	GCGCCGCCACCACCG	 AGGAGGTGCAGCGCTC	CACCCAAACTC	 TGGAGA	696
Query	639	CGCACGTCAAG	GACATTTCGAATGCCC	TGAAGCACTTCCGGG	ATGTTATACTCA	AGAAGA	698
Sbjct	697	CGCACGTCAAG	GACATCTCGAACGCCC	tgaagcacttccggg	Atgtcatactga	AGAAGA	756
Query	699	AGCTGGAGGTG	TTGCCGGGCAACGGAA	CGGTCATTCTGGAAAC	CCATAGCCAGCA	TGTACT	758
Sbjct	757	AGCTGGAGGTG	trgccgggcaacgca	ccctcattctcccaaaac	ccatrgccagca	tgtact	816
Query	759	CCGTGATCCAA	ACCTACACCCTGAATG 	AAAACAGTGCCATCAT	TGAGCAGCGCCA 	CGCTGC 	818
Sbjct	817		ACCTACACCCTGAATG				876
Query	819		AGCCTGGGCAAGCTCA 				878
Sbjct	877		AGCCTGGGCAAGCTCA				936 938
Query Sbjct	879 937		FGCGCCTCCCTGAGCA 				996
Query	939		CGGAATCTCGTTACGC				998
Sbjct	997			11111111111111			1056
Query	999		TAÇAĞTĞĞATÇTĞĞCT				1058
Sbjct	1057	GCGCCTTTCGC	 TACAGTGGATCTGGTT	 TGGGCGGCATTGGAG(TCATGG	1116
Query	1059	ĢŢĢÇĢĢŢÇ <u></u> ĄÇÇ	Ģ ÇÇŢÇĢÇĢĢĀĢCĢĀ	Ģ ŢĢŢŢÇÇÇĢĢТАÇŢĢ(_Б АСТСАТСССС	ŢŢŢÇGĢ	1118
Sbjct	1117	GTGCGGTCACC			AATCATGCGCG	TCTCAG	1176
Query	1119	CCGCCGAATCA	GCTGCCCAGCGTACTT	CGTTGCCGGACATAGO	CGCTCACGCCCA	AGGAGC	1178

Ch ≟ c+	1177		1006
Sbjct	1177	ĊĊĠĊĊĠĂĂŦĊĂĠĊŦĠĊĊĊĂĠĊĠĊĀĊŦŦĊĠŦŦĠĊĊĠĠĂĊĂŦĂĠĊĀĊŦĀĂĊĠĊĊĊĂĂĠĠĀĠĊ	1236
Query	1179	GCGACATACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTA	1238
Sbjct	1237	dcdacatactddadcadcadtdtdadcdccatdcdcdcdc	1296
Query	1239	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGC	1298
Sbjct	1297	tcctgcgcgycycqqqqqqqqqqqqqqqqqqqqqqqqqqq	1356
Query	1299	CGCCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTAC-AG-TGGGCG-	1355
Sbjct	1357	cecepttecececeance	1416
Query	1356	TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT	1415
Sbjct	1417	TCGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTGCCCTACGCCCAGT	1476
Query	1416	CCCATAATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACT	1475
Sbjct	1477	cccataatatcagtctgaactcggacctggactgcagttccaatatttcgctgctgaact	1536
Query	1476	ATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCT	1535
Sbjct	1537	AtgccgtggAtcgtctctctgtgcggtcgcggtcAccggAtgAgAAtAgtcAgtgctcct	1596
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	1597	ttgactcggcgttgaatcactcacgcgaggaggaggaccaccaccatcagcaacagcagc	1656
Query	1593	A-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGA	1646
Sbjct	1657	AGCAGCAGCTGAGGTCGTTTCCAAAGATGCCAGCGATGATGGACGAGGACATGGACAAGT	1716
Query	1647	TGGTCAGCTACAG 1659	
Sbjct	1717	TGGTCAGCTACAG 1729	

Range 2: 1729 to 2009

Score		Expect	Identities	Gaps	Strand	Frame	
381 bits(206)		3e-101()	257/282(91%)	2/282(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	SACGGACTACAG'	TGTCCAGT	1871
Sbjct	1729	GTTTCGTGTCG	ATGCGCGAGTTTCGCA	cttccacacacadacd	ACGGACTACAG	catccagt	1788
Query	1872	CCTCCACGAAG'	rcgtccagcagcaatt	CGGAGATTGCGTTT	'AGCATCAGTGA	GTCGACGG	1931
Sbjct	1789	catccacgaag:	rcgrccagcagcaarr	cddacattdcdttt	'AGCATCAGTGA	GTCGACGG	1848
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991
Sbjct	1849	CGGTCGGAAGC	AGCGGCGAGTACCAGC	AGATCAGCCAGTCG	GTGTTGCACAG	CCAGCGTC	1908
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcac	aaccaccg	2051
Sbjct	1909	AAATATCCTCG	AGCAGCAGCAGCTGCA	ççyççyçvyççyçç	agcagcagcac	caccacgg	1968
Query	2052	gctatggcagca	agc-gaagtggagcag	cagcagcagcagca 	g 2092		
Sbjct	1969	gctacggcagc	AGCAGCAGCGAA-CTG	gagcagcagcagca	d 2009		

Drosophila erecta uncharacterized protein, transcript variant F (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155126.1|** Length: 5454 Number of Matches: 2 Range 1: 217 to 1729

Score		Expect	Identities	Gaps	Strand	Frame	
2252 bits(1219)		0.0()	1418/1513(94%)	18/1513(1%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGCC	CGGCACCTGTTCCAG	TGGCATCGGAG	TGGGCG	224
Sbjct	217	Acgccaccatca	.gttctccatccacgcc	ceecectatte	tggcatcggag	tegegee	276
Query	225	GTGGCGGCTGCA	.GCAGCAGCAGCAACAA	TAGCATCAACAGCGG	CAGCTACTCCA	CCGCCT	284
Sbjct	277	gtggcggctgcy	.dcadcadcadcaacaa	cagcatcaacagcgg	cadctactcca	rççêçç‡	336
Query	285	GCACTCCGCCAC	CACCCACGCATCAGCA	TCACTCGCAGCACCA	GCAGCTGCAGG	GCACGC	344

Sbjct	337	GCACTCCGCCACCACCACCACCACCATCACTCGCAGCACCAGCAGCTGCAGGGCACGC	396
Query	345	CGGGAGGATCTAGTCGGGTCGGGGGAGCAGGAGCAGGAGCAGGCGGAGGTGGTG	398
Sbjct	397	CTGGAGCATCTAGTCGGGGTTGGCGGAGCAGGGGGGGGGG	456
Query	399	GTGTACCACCGGCACCACCCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGGGCA	458
Sbjct	457	GAGTGCCACCGGCACCACCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTAAAGGGCA	516
Query	459	CCAAGCTAGCGCGCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGA	518
Sbjct	517	CCAAGCTAGCACGCCGGGCGCGCTCCTTCAAGGACGACCTCATCGAGAAGATTTCCCTAA	576
Query	519	ŢĢĊĢĀĄĊĢĀĊĀĀĊĀĀŢĀĊĀĊŢĢĢĢŢĊĢĊŢĊĊĢĊŢĊĢĊĢĊĀĊĀĢŢĊĊĢĊĢĊĀĊĊĀĀĢĊ	578
Sbjct	577	TGCGTACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGC	636
Query	579	АССЕСТАТЬ В В В В В В В В В В В В В В В В В В В	638
Sbjct	637	ACGGCTCCAAGGCGCCCCCCCCCCCGAGGAGGTGCAGCGCTCCACCCAAACTCTGGAGA	696
Query	639	ҪҪҪ҇҅҇҅ҪҪ҇ҾҪҾ҇҅҅ҪҾ҇҅҅҅Ҳ҇҅Ҿ҇Ҫ҅҅҅Ҿ҅҅҅Ҿ҅҅Ҿ҅҅Ҿ҅҅Ҿ҅҅҅Ҿ҅҅Ҿ҅҅Ҿ҅҅Ҿ҅҅Ҿ҅Ҿ҅҅Ҿ҅	698
Sbjct	697	CGCACGTCAAGGACATCTCGAACGCCCTGAAGCACTTCCGGGATGTCATACTGAAGAAGA	756
Query	699	ĄĢĊŢĢĢĄĢĢŢĢŢŢĢĊÇĢĢĢĊĄĄĊĢĢAĄĊĢĢŢĊĄŢŢĊŢĢĢĄĄĄĊĊĄŢAĢĊĊĄĢĊĄŢĠŢĄĊŢ	758
Sbjct	757	AGCTGGAGGTGTTGCCGGGCAACGGCACGGTCATTCTGGAAACCATTGCCAGCATGTACT	816
Query	759	ÇÇÇTÇATÇÇAAAÇÇTAÇAÇÇÇTÇAATÇAAAAÇAÇTÇÇÇATÇAT	818
Sbjct	817		876
Query	819	AGGTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGG	878
Sbjct	877		936
Query	879	ACAGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCG	938
Sbjct	937		996
Query	939	AGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGT	998
Sbjct	997		1056
Query	999	ĢÇĢÇÇTTTÇĢÇTAÇAĢTĢĢATÇTĢĢCTTĢĢĢÇĢĢÇATTĢĢAĢÇĢĢÇĢĢÇĢĀĢATÇATĢĢ	1058
Sbjct	1057	GCGCCTTTCGCTACAGTGGATCTGGTTTTGGGCGGCATTTGGAGCGGCGGCGGAGATCATGG	1116
Query	1059	ĢŢĢÇĢĢŢÇĄÇÇĢÇÇÇĢĢĢĀĢCĢĄĢŢĢŢŢÇÇÇĢĢTAÇŢĢĢĄGŢÇĄŢĢÇĢÇĢŢTŢÇGĢ	1118
Sbjct	1117	GTGCGGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCGCTGGAATCATGCGCGTCTCAG	1176
Query	1119	ҪҪҪҪҪѦ҈ѧҭҪѧ҇ҪҪҭҫҪҪҁѧ҇ҪҪ҆ҭѧҪҭҭҪҫҭҭҫҪҫҫ҄ҩѧҪѧҭѧҫҪҫҪҭҁѧҫҫҫҪҁѧѧҫҁѧҫҫ	1178
Sbjct	1177	CCGCCGAATCAGCTGCCCAGCGCACTTCGTTGCCGGACATAGCACTAACGCCCAAGGAGC	1236
Query	1179	ĢÇĢĄÇĄŢĄÇŢĢĢĄĢÇĄÇĄÇĄĄŢĢŢĢĄĄÇÇÇGĄŢĢÇĢÇĢÇŢÇÇÇĄÇĄĢÇĄÇÇĢĄĄĄĢTĄ	1238
Sbjct	1237	GCGACATACTGGAGCACAATGTGAACCCCATGCGCGCTCCCACAGCACCGAAAGCA	1296
Query	1239	ŢÇÇŢĢÇĢÇĢĀÇĀÇĢĀĢŢÇÇĀÇÇĢÇĢĀĀĢÇÇĀÇÇĢÇŢĀÇÇÇĀĀŢĀĢĢĢÇÇĀĢŢĀĀŢÇÇĢÇ	1298
Sbjct	1297	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAACCCGC	1356
Query	1299	ÇĢÇÇĢŢŢĢÇÇAÇÇAĀĀĢÇĢĀÇĢÇĀĢÇÇĀĢÇÇĢĀĢÇĢÇĀŢÇĀĢÇŢĢĢŢAÇ—AĢ—ŢĠĢĢCĢ—	1355
Sbjct	1357	CGCCGTTGCCGCCCAAGCGACGCAGCCAGCCGGGCGCATCTGCTGGTGCGGGATCGGGGA	1416
Query	1356	ŢΆĢĢĊŢĢĊŢĊĄŢĊĢĄĊĄŢĊĊĄĊĊŢĊĊĄĄŢĊĄĠĢĊĊĄĠŢĊĊĠĊŢĠĊĊĊŢĄĊĠĊĊĄĠŢ	1415
Sbjct	1417	TCGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCCCTGCCCTACGCCCAGT	1476
Query	1416	ҪҪҪ҅҇҅Ҳ҇҇҅Ҳ҇҇҅Ҳ҇҅҅҅҄҅Ҳ҇Ҡ҅҅҅҅҅҄҅Ҳ҄ҾҠҾ҅҅Ҫ҅҅҅Ҿ҅҅҅҅Ҿ҅҅Ҫ҅҅҅҅Ҁ҅҅҅Ҿ҅҅Ҿ҅҅҅Ҿ҅҅҅Ҿ҅҅҅Ҿ	1475
Sbjct	1477	CCCATAATATCAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATTTCGCTGCTGAACT	1536
Query	1476	ĄŢĢĢÇĢŢĢĢĀŢÇĢCÇŢAŢÇCĢŢĢÇĢTŢÇAÇĢĢŢÇĄÇÇĢĢĄŢĢĄĢĄĄŢĄĢŢÇĄĢŢĢÇŢÇÇŢ	1535
Sbjct	1537		1596
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	1597	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCACCATCAGCAACAGCAGC	1656
Query	1593	A-ÇÇTGAGGTÇGTTTÇÇAAAGTTGGÇTGÇGATGATGGAÇGAAGAÇATGGAÇAAGA	1646
Sbjct	1657	AGCAGCAGCTGAGGTCGTTTCCAAAGATGCCAGCGATGATGGACGAGGACATGGACAAGT	1716
Query	1647	ŢĢĢŢÇĀĢÇŢĀÇĀĢ 1659	
Sbjct	1717	 TGGTCAGCTACAG 1729	

Score		Expect	Identities	Gaps	Strand	Frame	
381 bits(206)		3e-101()	257/282(91%)	2/282(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	SACGGACTACAGT	TGTCCAGT	1871
Sbjct	1729	gtttcgtgtcg	Atgegegagtttegea	cttccacacacagaca	acggactacago	catccagt	1788
Query	1872	CCTCCACGAAG	rcgtccagcagcaatt	CGGAGATTGCGTTT	'AGCATCAGTGAG	GTCGACGG	1931
Sbjct	1789	CATCCACGAAG:	rcgrccagcagcaarr	CGGACATTGCGTTT	'AGCATCAGTGAG	STCGACGG	1848
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAGO	CCAGCGTC	1991
Sbjct	1849	ccctcccaacc	AGCGGCGAGTACCAGC	AGATCAGCCAGTCG	schchrackchch	ccadcdtc	1908
Query	1992	ATATATCCTCGA	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcaca	accaccg	2051
Sbjct	1909	AAATATCCTCG	AGCAGCAGCAGCTGCA	ccycrycayccyc	agcagcagcaco	CACCACGG	1968
Query	2052	gctatggcagca	agc-gaagtggagcag	cagcagcagcagca 	ıg 2092 T		
Sbjct	1969	dctacddcadca	AGCAGCAGCGAA-CTG	gagcagcagcagca	d 2009		

Drosophila erecta uncharacterized protein, transcript variant D (Dere\GG17655), mRNA Sequence ID: **ref|XM_015155124.1|** Length: 5782 Number of Matches: 2 Range 1: 698 to 2210

Score		Expect	Identities	Gaps	Strand	Frame	
2252 bit	s(1219)	0.0()	1418/1513(94%)	18/1513(1%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATCA	AGTTCTCCATCCACGC	CCGCACCTGTTCCAC	GTGGCATCGGAG'	rgggcg	224
Sbjct	698	AcGccaccatca	/g44c4ccq4ccqcqcq	cceecectettccy	stggcatcggag:	reeece	757
Query	225	GTGGCGGCTGC	AGCAGCAGCAGCAACA?	ATAGCATCAACAGCG(GCAGCTACTCCAG	CCGCCT	284
Sbjct	758	ĠŦĠĠĊĠĠĊŦĠĊź	AĠĊĀĠĊĀĠĊĀĠĊĀĀĊĀZ	^A CAĠĊAŦĊAAĊAĠĊĠĊ	scadctactcca	cccct	817
Query	285		CCACCCACGCATCAGCA				344
Sbjct	818		ĊĊĂĊĊĊĂĊĠĊĂĊĊĂĊĊ			ĠĊĀĊĠĊ	877
Query	345		AGTCGGGTCGGGGGAGG			G	398
Sbjct	878 399		\Ġ†ĊĠĠĠŤŦĠĠĊĠĠĂĠŒ GCACCACCCAGTGCCGŒ				937 458
Query Sbjct	938		JCACCACCCAGTGCCGC 				997
Query	459		CGCCGGGCGCGTTCCT				518
Sbjct	998						1057
Query	519	ŢĢÇĢAĄÇÇĄÇÇ	\ AÇAATAÇAÇTGGGTÇ(ĢÇTÇÇÇ <u>A</u> ÇTÇĞÇÇĞÇ <i>I</i>	\ÇAGTÇÇGÇGÇA(ÇÇĄĄĢÇ	578
Sbjct	1058	TGCGTACCACCA	ACAATACACTGGGTC	 	ACAGTCCGCGCA	CCAAGC	1117
Query	579	ACGGCACAAAG	GCACCGCCCACCACCGA	AGGAGGTGCTACGGTC	CACCCAAACCC'	rggaga	638
Sbjct	1118	ACGGCTCCAAGG	GCGCCGCCCACCACCG	AGGAGGTGCAGCGCTC	CACCCAAACTC	rggaga	1177
Query	639	CGCACGTCAAGO	GACATTTCGAATGCCC	rgaagcacttccggg <i>i</i> 	ATGTTATACTCAZ	AGAAGA 	698
Sbjct	1178	cccacctca	sacatetégaacécée:	tĠAAĠĊAĊŦŦĊĊĠĠĠ	Atgtcatactgaz	AGAAGA	1237
Query	699		rtgccgggcaacggaa(758
Sbjct	1238		rtgccggcaacgca				1297
Query	759		ACCTACACCCTGAATG <i>I</i>				818
Sbjct	1298		ÁCCTÁCÁCCCTGÁÁTG <i>I</i>				1357
Query Sbjct	819 1358		AGCCTGGGCAAGCTCA' 				878 1417
Query	879		AGCCTGGGCAAGCTCA: FGCGCCTCCCTGAGCAA				938
Sbjct	1418		rgcccctccctgagca/				1477
Query	939		CGGAATCTCGTTACGC				998

Sbjct	1478	AGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGACCAGT	1537
Query	999	GCGCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGG	1058
Sbjct	1538	GCGCCTTTCGCTACAGTGGATCTGGTTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGG	1597
Query	1059	GTGCGGTCACCGCCTCGCCGGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGG	1118
Sbjct	1598	GTGCGGTCACCGCCTCGCCGGGAGTGAGTGTTCCCCGGCGCTGGAATCATGCGCGTCTCAG	1657
Query	1119	CCGCCGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGC	1178
Sbjct	1658	ccccccaatcaccccaccacctccccccccccccccccc	1717
Query	1179	GCGACATACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTA	1238
Sbjct	1718	ĠĊĠAĊAŤAĊŤĠĠAĠĊĀĠĊĀĊĀĀŤĠŤĠĀĀĊĊĊCĀŤĠĊĠĊĠĠĊŤĊĊĊĀĊĀĠĊĀĊĊĠĀĀĀĠĊĀ	1777
Query	1239	TCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGC	1298
Sbjct	1778	†cctgcgcgacacactaccaccgccgaagccaccactacccaataggccaactaacccgc	1837
Query	1299	CGCCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTAC-AG-TGGGCG-	1355
Sbjct	1838	ĊĠĊĊĠŤŤĠĊĊĠĊĊĊĂĂĠĊĠĂĊĠĊĀĠĊĊĀĠĊĊĠĠĠĊĠĊĀŤĊŤĠĊŤĠĠŤĠĊĠĠĠĀŤĊĠĠĠĠĀ	1897
Query	1356	TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT	1415
Sbjct	1898	TCĠĠĊŦĠĊŦĊĂŦĊĠŦĊĠĂĊĂŦĊĊĂĊĊŦĊĊĂĂŦĊĂĠĠĊĊĂĠŦĊĊCĊŦĠĊĊĊŦĂĊĠĊĊĊĀĠŦ	1957
Query	1416	CCCATAATATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACT	1475
Sbjct	1958	ĊĊĊĂŦĂĂŦĂŦĊĂĠŦĊŦĠĂĂĊŦĊĠĠĂĊĊŦĠĠĂĊŦĠĊĀĠŦŦĊĊĂĂŦĂŦŦŦĊĠĊŦĠĊŦĠĂĀĊŦ	2017
Query	1476	ATGGCGTGGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCT	1535
Sbjct	2018	ATĠĠĊĠŦĠĠĀŦĊĠŦĊŤĊŦĊŦĠŦĠĊĠĠŦĊĠĊĠĠŦĊĂĊĊĠĠĀŦĠĀĠĀĀŦĀĠŦĊĀĠŦĠĊŦĊĊŦ	2077
Query	1536	TTGACTCGGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAA-CAGCAACATCAGC	1592
Sbjct	2078	TTĠĂĊŦĊĠĠĊĠŦŦĠĂĂŦĊĂĊŦĊĂĊĠĊĠĂĠĠĂĠĠĀĠĠĂĊĊĂCĊĂCĊĂTĊĂĠĊĀĀĊĀĠĊĀĠĊ	2137
Query	1593	A-CCTGAGGTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGA	1646
Sbjct	2138	ÄĠĊAĠĊĀĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ	2197
Query	1647	TGGTCAGCTACAG 1659	
Sbjct	2198	TĠĠTĊĀĠĊTĀĊĀĠ 2210	

Range 2: 2210 to 2490

Score		Expect	Identities	Gaps	Strand	Frame	
381 bits	(206)	3e-101()	257/282(91%)	2/282(0%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	ACGGACTACAG	TGTCCAGT	1871
Sbjct	2210	GTTTCGTGTCG	ATGCGCGAGTTTCGCA	CTTCCACACAGACG	ACGGACTACAG	CATCCAGT	2269
Query	1872	CCTCCACGAAG	rcgrccagcagcaarr	CGGAGATTGCGTTT	'AGCATCAGTGAG	GTCGACGG	1931
Sbjct	2270	catccacgaag	rcgtccagcagcaatt	cggacattgcgttt	'AGCATCAGTGAG	rcgacgg	2329
Query	1932	CGGTCGGCAGCA	AGTAGCGAGTACCAGC.	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991
Sbjct	2330	ccctccccaacc	AGCGGCGAGTACCAGC.	AGATCAGCCAGTCG	gtgtrgcycyc	ccaccetc	2389
Query	1992	ATATATCCTCGA	AGCAGTAGCAGCTGCA	CCACCACGACCACC	agcagcagcaca	accaccg	2051
Sbjct	2390	AAATATCCTCG	AGCAGCAGCAGCTGCA	ccaccacaaccacc	AGCAGCAGCAC	CACCACGG	2449
Query	2052	gctatggcagca	agc-gaagtggagcag	cagcagcagcagca	g 2092		
Sbjct	2450	dctacddcadca	AGCAGCAGCGAA-CTG	gagcagcagca	G 2490		

Drosophila sechellia GM12551 (Dsec\GM12551), mRNA

Sequence ID: **ref|XM_002036688.1|** Length: 1791 Number of Matches: 1 Range 1: 515 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
2135 bits(1156)	0.0()	1239/1278(97%)	10/1278(0%)	Plus/Plus	
Footuroo					

Features:

Query	165	ĄÇĢĢÇĄĢÇĄTÇĄĢTŢĊŢĊÇĄŢÇÇĄÇĢÇÇÇĢĢCĄCÇŢĢŢŢÇÇĄĢŢĢĢÇĄŢÇĢĢĄĢŢĢĢĢÇĢ	224
Sbjct	515	ACGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGTTCCAGTGGCATCGGAGTGGGCG	574
Query	225	GTGGCGGCTGCAGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGCTACTCCACCGCCT	284
Sbjct	575	GTGGCGGCTGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGCTACTCCACCGCCT	634
Query	285	GCACTCCGCCACCACCCACGCATCAGCATCACTCGCAGCACCAGCAGCTGCAGGGCACGC	344
Sbjct	635	dcactccdccaccaccatcaccatcactcdcaccaccaccaccaccaccaccaccaccaccaccacca	694
Query	345	CGGGAGGATCTAGTCGGGTCGGGGGAGCAGGAGCAGGAGCAGGCGGAGG-TGGTGG	399
Sbjct	695	ĊĊĠĠĀĠĠĀŢĊŢĀĠŢĊĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ	754
Query	400	-TG-TACCACCGGCACCACCCAGTGCCGGATCCTCGGGCCACAAGAACAGTCTCAAGG	455
Sbjct	755	GTĠĠTĠTĠĊĊĂĊĊĠĠĊĂĊĊĀĊĊĊĀĠŦĠĊĊĠĠĂŤĊĊŤĊĠĠĠĊĊĂĊĀĀĠĀĀĊĀĠŤĊŤĊĀĀĠĠ	814
Query	456	GCACCAAGCTAGCGCGCGCGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCC	515
Sbjct	815	ĠĊĂĊĊĂĂĠŦŤĂĠĊĠĊĠĠĠĠĠĠĠĠĠĊĠĊĠĊŦĊŦŤŤŤĂĂĠĠĂĊĠĂĊĊŤĊĂŤĊĠĂĠĂĂĠĂŤŤŤĊĊĊ	874
Query	516 875	TGATGCGAACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCA	575 934
Sbjct Query	576	AGCACGGCACAAAGGCACCGCCCACCACCGAGGAGGTGCTACGGTCCACCCAAACCCTGG	635
Sbjct	935	AGCACGCTCAAAGGCACCGTCCACCACGAGGAGGTGCTCCGGTCCACCCAAACGCTGG	994
Query	636	AGACGCACGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGA	695
Sbjct	995	AGACGCACGTCAAGGACATCTCGAATGCCCTGAAGCACTTCCGGGATGTCATACTCAAGA	1054
Query	696	АĢ АĀĢÇŢĢĢĀĢĢŢĢŢŢĢÇÇĢĢĢÇĀĀÇĢĢĀĀÇĢĢŢÇĀŢŢÇŢĢĢĀĀĀÇÇĀŢĀĢÇÇĀĢÇĀŢĢŢ	755
Sbjct	1055	AGAAGCTGGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGT	1114
Query	756	ACTCCGTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGC	815
Sbjct	1115	ACTCCGTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCTCCGCCACGC	1174
Query	816	TGCAGGTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCG	875
Sbjct	1175	aĠĊAĠĠŦŦŦAĊĊĀĠĀĠĊĊŦĠĠĠĊĀĀĠĊŦĊĀŦĊĀĀĠĊŦĊŦĠĊĠĀĊĠĀĠĠŦĠĀŦĠĊŦĊŦĊĊĠ	1234
Query	876	AGGACAGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTC	935
Sbjct	1235	AĞĞACAĞCĞĞCĞAĞTĞTĞCCTCCCTĞAĞCAACĞAĞAATĞTĞCĞĞĞAAĞTCATTĞATCTTC	1294
Query Sbjct	936 1295	TCGAGGATGCTGTGCGGAATCTCGTTACGCTGGCGCAGGCAAGCTGAAGGAGCAGGATC	995 1354
Query	996	AGTGCGCCTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCA	1055
Sbjct	1355	AGTGCGCCTTCGCTACAGTGGATCTGGCCTGGGCGCGCATTGGAGCGGCGGCGAGATCA	1414
Query	1056	ŢĢĢĢŢĢÇĢĢŢÇĄÇÇĢÇÇĢĢĢĀĢСĢĀĢŢĢŢŢÇÇÇĢĢŢĄÇŢĢĢĀĢŢÇĀŢĢÇĢÇĢŢŢŢ	1115
Sbjct	1415	TGGGTGCGGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGTACTGGAGTCATGCGCGTTT	1474
Query	1116	CGGCCGCCGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGG	1175
Sbjct	1475	ccccccccaatcaccccaccccccccccccccccccccc	1534
Query	1176	AGCGCGACATACTGGAGCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAA	1235
Sbjct	1535	AGCGCGACATACTGGAGCAGCACAATGTGAACCCGATGCGCGGCT-CCACAGCACCGAAA	1593
Query	1236	GTATCCTGCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATC	1295
Sbjct	1594	ĠŦÀŦĊĊŦĠĊĠĊĠÀĊÀĊĠĀĠŦĊĊÀĊĊĠĊĊĠÀĀĠĊĊĀĊĊĠĊŦĂĊĊĊĀĀŦĀĠĠĠĊĊĀĠŦĀĀCĊ	1653
Query	1296	CGCCGCCGTTGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCG	1355
Sbjct	1654	CGCCGCCGTTGCCACCCAAGCGACGCAGCCAGCCGGGCGCATCAGCTGGTGCAGTGGGCG	1713
Query	1356	TAGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT	1415
Sbjct	1714	TGGGCTGCTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGT CCCATAATATTAGTCTGA 1433	1773
Query Sbjct	1416 1774	CCCATAATATTAGTCTGA 1433	
	1114		

Score		Expect	Identities	Gaps	Strand	Frame
2063 bit	ts(1117)	0.0()	1377/1500(92%)	27/1500(1%)	Plus/Plus	
Feature	s:					
Query	163	GAACGGCAGCA'	TCAGTTCTCCATCCA(CGCCCGGCACCTGTTC	CAGTGGCATCGG	AGTGGG 222
Sbjct	217			ĊĠĊĊĊĠĠĊĠĊĊŦĠŦŦĊŒ		
Query	223 277			ACAATAGCATCAACAG(CACCGC 282 CACCGC 336
Sbjct Query	283			ACAACAGCATCAACAG(AGCATCACTCGCAGCA(
Sbjct	337					
Query	343	GCCGGGAGGAT	CTAGTCGGGTCGGGG	GAGCAGGAGCAGGAGCA	AGGCGGAGGTGG'	TGGTGT 402
Sbjct	397	GCCCGCAGGAT				TGGAGT 453
Query	403			CCTCGGGCCACAAGAA(
Sbjct	454			ĊĊŦĊĠĠĠĊĊĂĊĂĂĠĂĂŒ		
Query	463 514			AGGACGACCTCATCGA(
Sbjct Query	523			CCCACTCGCCGCACAG		
Sbjct	574					
Query	583	CACAAAGGCAC	CGCCCACCACCGAGGA	AGGTGCTACGGTCCAC	CCAAACCCTGGA	GACGCA 642
Sbjct	634	CTCCAAGGCAC	CGCCCACCACCGAGG	AGGTGCAGCGATCCAC	CCAAACTCTGGA	GACGCA 693
Query	643			AGCACTTCCGGGATGT' 		
Sbjct	694			AGCATTTCCGGGATGT		
Query Sbjct	703 754			PCATTCTGGAAACCATA 		
Query	763			AÇAĞTĞÇÇATÇATĞAĞ(
Sbjct	814	GATCCAAACGT.	ACACCCTGAATGAAAZ		 CTGCGCCACACA(GCAGGT 873
Query	823	TTACCAGAGCC'	TGGGCAAGCTCATCA	AGCTCTGCGACGAGGT(GATGCTCTCCGA(GGACAG 882
Sbjct	874	ttaccadadcc	tgggcaagctcatcaz	/decteteeeq	GATGCTCTCCGA	GGACAG 933
Query	883			AGAATGTGCGGGAAGT(
Sbjct Query	934 943			AGAATGTGCGAGAGGT(CGCAGGGCAAGCTGAA(
Sbjct	994		ATCTCGTTACGCTGG(ATCTCGTTACGCTGG(
Query	1003	СТТТСССТАСА	<mark>ĢŢĢĢ</mark> ĄŢĊŢĢĢĊŢŢĢĢĆ	, БСФФСАТТФФАФСФФС	GGCGGAGATCAT(ĢĢĢŢĢÇ 1062
Sbjct	1054	CTTTCGCTATG	GTGGATCTGGTTTGG	GCGCATTGGAGCGGC		GGGTGC 1113
Query	1063	GGTCACCGCCT(CGCCGGGAGCGAGTGT	TTCCCGGTACTGGAGT(CATGCGCGTTTC	GGCCGC 1122
Sbjct	1114			rtcccgcactgcatg		
Query Sbjct	1123 1174			FGCCGGACATAGCGCT(
Query	1174			CGATGCGCGGCTCCCA		
Sbjct	1234			CCATGCGCGGCTCGCA		
Query	1243	GCGCGACACGA	GTCCACCGCCGAAGCC	CACCGCTACCCAATAGO	GGCCAGTAATCC	GCCGCC 1302
Sbjct	1294	GCGCGACACGA	GTCCACCGCCAAAGC	CACCGCTACCCAATAG	GGCCAGTAATCC	GCCGCC 1353
Query	1303			CGAGCGCATCAGCTGG' 		
Sbjct	1354			ĊĠĠĠĊĠĊĀĊĊŦĠĊŦĠĠĠ		
Query Sbjct	1363 1414		CATCCACCTCCAATCA 	AGGCCAGTCCGCTGCC0 		CCATAA 1422 CCATAA 1452
Query	1423					
Sbjct	1453					
Query	1483	GGATCGCCTAT	CCGTGCGTTCACGGTC	CACCGGATGAGAATAG	PCAGTGCTCCTT	TGACTC 1542
Sbjct	1513	GGATCGCCTAT	cretecestcecest	CACCGGATGAGAATAG	rcagtgctcctt	TGACTC 1572

Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAG	1599
Sbjct	1573	GGCGTTGAATCACTCACGCGAGGAGGAGGACCACCAACAGCAACAGCAGCAGCA	1632
Query	1600	GTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG	1659
Sbjct	1633	GtCGCtCtCGAAGATGCCAACGATGATGGACGAGGACATGGACAAGATGGTCAGCTACAG	1692

Range 2: 1692 to 1981

Score		Expect	Identities	Gaps	Strand	Frame	
431 bits(233)		3e-116()	272/290(94%)	6/290(2%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGAC	GACGGACTACAG'	TGTCCAGT	1871
Sbjct	1692	GTTTCGTGTCG	ATGCGCGAGTTTCGCA	CTTCCACACAGAC	SACGGACTACAG	catccagt	1751
Query	1872	CCTCCACGAAG'	rcgtccagcagcaatt	CGGAGATTGCGTTT	AGCATCAGTGA	GTCGACGG	1931
Sbjct	1752	cctccacdaad	tcgtccagcagcaatt	ceeaeattece	radcatcadtdao	STCGACGG	1811
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991
Sbjct	1812	cddtcddcadc	AGCAGCGAGTACCAGC	AGATTAGCCAGTCG	GtGtCGCACAG	CCAGCGTC	1871
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcaca	aaccaccg	2051
Sbjct	1872	AtAtAtcttcc	AGCAGTAGTAGCTGCA	ccyccycyyccyc	agcagcagcac	caccaccd	1931
Query	2052	gctatg	-gcagcagcgaagtgg	agcagcagcagcag	cagcagcag :	2095	
Sbjct	1932	dctatdggagc	addaddadddaattdd	AGCAGCAGCAGCA <i>A</i>	rcycycycycycycycycycycycycycycycycycycy	1981	

Drosophila yakuba C3G, transcript variant D (Dyak\C3G), mRNA

Sequence ID: **ref|XM_015190002.1|** Length: 5721 Number of Matches: 2 Range 1: 219 to 1694

Score		Expect	Identities	Gaps	Strand	Frame	
2063 bit	s(1117)	0.0()	1377/1500(92%)	27/1500(1%)	Plus/Plus		
Feature	s:						
Query	163	GAACGGCAGCA	TCAGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG	AGTGGG	222
Sbjct	219	GAACGGCAGCA	tcagttctccatccac	gcccgcccctcttcc	AGTGGCATCGG	AGTGGG	278
Query	223	CGGTGGCGGCT	GCAGCAGCAGCAA 	CAATAGCATCAACAGC	GGCAGCTACTC	CACCGC	282
Sbjct	279	çeçteççeç	gcygcygcygcyg	caacagcatcaacagc	deckerkere	caccec	338
Query	283	CTGCACTCCGC	CACCACCCACGCATCA	GCATCACTCGCAGCAC	CAGCAGCTGCA	GGGCAC 	342
Sbjct	339	ctcckctcccc	cyccyccycqcqcq	ccatcacacccacacac	chdchdctdch	ĠĠĠĊĀĊ	398
Query	343	GCCGGGAGGAT	CTAGTCGGGTCGGGGG 	AGCAGGAGCAGGAGCA	GGCGGAGGTGG'	TGGTGT 	402
Sbjct	399	ĠĊĊĊĠĊĀĠĠĀŢ	ĊŦĀĠŦĊĠĠĠŦĠĠĠĀĠĠ	AĠĊA_Ġ_Ġ_TĠĠAĠĊA	.ĠĠŦĠĠŦĠĠAAĠ [,]	tĠĠAĠŦ	455
Query	403	ACCACCGGCAC	CACCCAGTGCCGGATC 	CTCGGGCCACAAGAAC	AGTCTCAAGGG	CACCAA 	462
Sbjct	456		ĊĂĊĊĊĀĠŦĠĊĊĠĠĀŦĊ		:AĠTĊTGAAĠĠĠ		515
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTTAA 	GGACGACCTCATCGAG 	BAAGATTTCCCT(GATGCG 	522
Sbjct	516	ĠĊŦÄĠĊĀĊĠĊĊ		ĠĠŔĊĠŔĊĊŤĊŔŤĊĠŔĠ			575
Query	523		ATACACTGGGTCGCTC 				582
Sbjct	576		ATACACTGGGTCGCTC				635
Query	583		CGCCCACCACCGAGGA 				642
Sbjct	636	CTCCAAGGCAC		ĠĠŦĠĊAĠĊĠAŦĊĊÁĊĊ			695
Query	643		${ t TTTCGAATGCCCTGAA} ig ig ig ig ig ig ig ig $				702
Sbjct	696		ŤĊŤĊĠĂĂĊĠĊĠĊŤĊĂĂ				755
Query	703		CGGGCAACGGAACGGT	111111111111111			762
Sbjct	756	GGAGGTGTTGC	CCGGAAACGGAACGGT	CATTCTGGAAACCATA	GCCAGCATGTA'	TTCCGT	815

Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822
Sbjct	816	GATCCAAACGTACACCCTGAATGAAAACAGTGCCATCATGAGCTGCGCCACACAGCAGGT	875
Query	823	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Sbjct	876	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	935
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	936	cgccgagtgcgcctccctgagcaacgagaatgtgcgagaggtcattgatcttctggagga	995
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002
Sbjct	996	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAACTGAAGGAGCAGGATCAGTGCGC	1055
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1056	CTTTCGCTATGGTGGATCTGGTTTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1115
Query	1063	GGTCACCGCCTCGCCGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTTCGGCCGC	1122
Sbjct	1116	GGTCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCACTGGCATCATGCGCGTTTCAGCCGC	1175
Query	1123	CGAATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGA	1182
Sbjct	1176	CGAATCAGCTGCCCAGCGAACTTCGTTGCCGGACATTGCACTCACGCCCAAGGAACGCGA	1235
Query	1183	CATACTGGAGCACAATGTGAACCCGATGCGCGCTCCCACAGCACCGAAAGTATCCT	1242
Sbjct	1236	catactegages	1295
Query	1243	GCGCGACACGAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1302
Sbjct	1296	GCGCGACACGAGTCCACCGCCAAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCC	1355
Query	1303	GTTGCCACCAAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTG	1362
Sbjct	1356	GTTGCCACCCAAGAGACGCAGCCAGCCGGGCGCACCTGCTGGCGCTGCGGTGGTCGGCTG	1415
Query	1363	CTCATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAA	1422
Sbjct	1416	ctcatcgttgacatccgcctcct-acg-cc-ca-gccccataa	1454
Query	1423	TATTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGT	1482
Sbjct	1455	tatcagcctgaactregacctggactgcagttccaacatctcgctgctgaactatggcgt	1514
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1515	GGATCGCCTATCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1574
Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAG	1599
Sbjct	1575	GGCGTTGAATCACTCACGCGAGGAGGAGGACCACCAACAGCAGCAGCAGCAGCA	1634
Query	1600	GTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG	1659
Sbjct	1635	GTCGCTCTCGAAGATGCCAACGATGATGGACGAGGACATGGACAAGATGGTCAGCTACAG	1694

Range 2: 1694 to 1983

Score		Expect	Identities	Gaps	Strand	Frame	
431 bits	(233)	3e-116()	272/290(94%)	6/290(2%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	GACGGACTACAG	TGTCCAGT	1871
Sbjct	1694	GTTTCGTGTCG	ATGCGCGAGTTTCGCA	CTTCCACACAGACG	SACGGACTACAG	CATCCAGT	1753
Query	1872	CCTCCACGAAG'	TCGTCCAGCAGCAATT	CGGAGATTGCGTTT	AGCATCAGTGA	GTCGACGG	1931
Sbjct	1754	cctccacdaad;	tcgtccagcagcaatt	cggagattgcgttt	adcatcagtga	GTCGACGG	1813
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991
Sbjct	1814	ceetceecaeca	agcagcgagtaccagc	AGATTAGCCAGTCG	GTGTCGCACAG	CCAGCGTC	1873
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcac	aaccaccg	2051
Sbjct	1874	AtAtAtcttcc	AGCAGTAGTAGCTGCA	ççyççyçvyççyçç	agcagcagcac	caccaccd	1933
Query	2052	gctatg	-gcagcagcgaagtgg	agcagcagcagcag	cagcagcag	2095	
Sbjct	1934	dctatdggagc	addaddadddaattdd	AGCAGCAGCAGCAA	rcygcygcyg	1983	

Sequence ID: **ref|XM_015190000.1|** Length: 5738 Number of Matches: 2 Range 1: 218 to 1693

Score		Expect	Identities	Gaps	Strand	Frame	
2063 bit	s(1117)	0.0()	1377/1500(92%)	27/1500(1%)	Plus/Plus		_
Features	s:						
Query	163			ACGCCCGGCACCTGTTC	CAGTGGCATCGG		222
Sbjct	218 223	GÁÁCGGCÁGCÁ		ACGCCCGGCGCCTGTTC AACAATAGCATCAACAG	CAGTGGCATCGG		277 282
Query Sbjct	278			AACAATAGCATCAACAG 			337
Query	283	CTGCACTCCGC	САССАСССАСССАТ	CAGCATCACTCGCAGCA	CCAGCAGCTGCA	GGGCAC 3	342
Sbjct	338	ctgcactccgc	cycyccycgcyc	caccatcacacccacca	CCAGCAGCTGCA	GGGCAC 3	397
Query	343			GGAGCAGGAGCAGGAGC			402
Sbjct Query	398 403			.ĠĠĀĠĊĀ-Ġ-Ġ-TĠĠĀĠĊ TCCTCGGGCCACAAGAA			454 462
Sbjct	455			TCCTCGGGCCACAGAA			514
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTT	AAGGACGACCTCATCGA	GAAGATTTCCCT	GATGCG 5	522
Sbjct	515			AAGGACGACCTCATCGA			574
Query Sbjct	523 575	AACCACCAACA CACCACCAACA		TCCCACTCGCCGCACAG			582 634
Query	583			GAGGTGCTACGGTCCAC			642
Sbjct	635	CTCCAAGGCAC	CGCCCACCACCGAG		CCAAACTCTGGA	GACGCA 6	694
Query	643	CGTCAAGGACA	TTTCGAATGCCCTG	AAGCACTTCCGGGATGT	TATACTCAAGAA		702
Sbjct	695			AAĠĊATŤŤĊĊĠĠĠAŤĠŤ			754
Query Sbjct	703 755			GTCATTCTGGAAACCAT 			762 814
Query	763			AACAGTGCCATCATGAG			822
Sbjct	815	GATCCAAACGT	ACACCCTGAATGAA	AACAGTGCCATCATGAG	CTGCGCCACACA	GCAGGT 8	874
Query	823			AAGCTCTGCGACGAGGT			882
Sbjct Query	875 883			AAĠĊϮĊϮĠĊĠAĊĠAĠĠϮ GAGAATGTGCGGGAAGT			934 942
Sbjct	935						994
Query	943	TGCTGTGCGGA	ATCTCGTTACGCTG	GCGCAGGGCAAGCTGAA	GGAGCAGGATCA	GTGCGC 1	1002
Sbjct	995			gcgcygggcyyyctgyy			1054
Query Sbjct	1003 1055			GGCGGCATTGGAGCGGC 			1062 1114
Query	1063			ĠŢŢĊĊĊĠĠŢŸĊŢĠĊŦĠŢ			1122
Sbjct	1115	GGTCACCGCCT				 !AGCCGC 1	1174
Query	1123	CGAATCAGCTG		TTGCCGGACATAGCGCT			1182
Sbjct	1175 1183	CAMACUCAGCTG		TTGCCGGACATTGCACT CCGATGCGCGGCTCCCA			1234 1242
Query Sbjct	1235			CCCATGCGCGGCTCCCA 			1242 1294
Query	1243	GCGCGACACGA	.GТССАССБССБААБ	ССАССССТАСССААТАС	GGCCAGTAATCC	GCCGCC 1	1302
Sbjct	1295	GCGCGACACGA	GTCCACCGCCAAAG	CCACCGCTACCCAATAG	GGCCAGTAATCC	GCCGCC 1	1354
Query	1303			CCGAGCGCATCAGCTGG			1362
Sbjct Query	1355 1363			ĊĊĠĠĠĊĠĊĀĊĊŦĠĊŦĠĠ CAGGCCAGTCCGCTGCC			1414 1422
Sbjct	1415		CATCCGCCTCCT				1453
Query	1423	TATTAGTCTGA	ACTCGGACCTGGAC	TGCAGTTCCAATATCTC	GCTGCTGAACTA	TGGCGT 1	1482

Sbjct	1454	TATCAGCCTGAACTTGGACCTGGACTGCAGTTCCAACATCTCGCTGCTGAACTATGGCGT	1513
Query	1483	GGATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1542
Sbjct	1514	GGATCGCCTATCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTC	1573
Query	1543	GGCGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAG	1599
Sbjct	1574	GGCGTTGAATCACTCACGCGAGGAGGAGGACCACCAACAGCAACAGCAGCAGCA	1633
Query	1600	GTCGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG	1659
Sbict	1634	GTCGCTCTCGAAGATGCCAACGATGATGGACGAGGACATGGACAAGATGGTCAGCTACAG	1693

Range 2: 1693 to 1982

Score		Expect	Identities	Gaps	Strand	Frame	
431 bits	(233)	3e-116()	272/290(94%)	6/290(2%)	Plus/Plus		
Feature	s:						
Query	1812	GTTTCGTGTCG.	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	GACGGACTACAG	TGTCCAGT	1871
Sbjct	1693	GTTTCGTGTCG.	ATGCGCGAGTTTCGCA	CTTCCACACAGACG	SACGGACTACAG	CATCCAGT	1752
Query	1872	CCTCCACGAAG	TCGTCCAGCAGCAATT	CGGAGATTGCGTTT	AGCATCAGTGA	GTCGACGG	1931
Sbjct	1753	cctccacgaag	rcgrccagcagcaarr	cddadattdcdtt	ragcatcagtga	GTCGACGG	1812
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991
Sbjct	1813	ceetceecaec	agcagcgagtaccagc	AGATTAGCCAGTCG	GTGTCGCACAG	ccaccetc	1872
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcac	aaccaccg	2051
Sbjct	1873	AtAtAtcttcc	AGCAGTAGTAGCTGCA	ccaccacaaccacc	CAGCAGCAGCAC	CACCACCG	1932
Query	2052	gctatg	-gcagcagcgaagtgg	agcagcagcagcag	gcagcagcag	2095	
Sbjct	1933	dctatdggagc.	addaddadddaartdd	AGCAGCAGCAGCAA	rcygcygcyg	1982	

Drosophila yakuba C3G, transcript variant F (Dyak\C3G), mRNA Sequence ID: **ref|XM_015190004.1**| Length: 6749 Number of Matches: 2 Range 1: 1384 to 2857

Score		Expect	Identities	Gaps	Strand	Frame	
2060 bits	s(1115)	0.0()	1375/1498(92%)	27/1498(1%)	Plus/Plus		
Features	S :						
Query	165	ACGGCAGCATC	AGTTCTCCATCCACGC	CCGGCACCTGTTCCAG'	TGGCATCGGAGT	GGGCG	224
Sbjct	1384	ACGGCAGCATC	AGTTCTCCATCCACGC	ccgcccctcttccac	TGGCATCGGAGT	qqqqq	1443
Query	225	GTGGCGGCTGC	AGCAGCAGCAGCAACA	ATAGCATCAACAGCGG	CAGCTACTCCAC	CGCCT	284
Sbjct	1444	gtggcggctgc	AGCAGCAGCAGCAACA	Acadeateaaeadedd	cydchychccyc	ccct	1503
Query	285	GCACTCCGCCA	CCACCCACGCATCAGC	ATCACTCGCAGCACCA	GCAGCTGCAGGG	CACGC	344
Sbjct	1504	gcyctccccy	ççyççyçèçycçycç	Atcacaccacaccacca	gcygctgcyggg	caccc	1563
Query	345	CGGGAGGATCT	AGTCGGGTCGGGGAG	CAGGAGCAGGAGCAGG	CGGAGGTGGTGG	TGTAC	404
Sbjct	1564	ccccaccaccatct	AGTCGGGTGGGAGGAG	·ca-g-g-rggagcagg	rddrddaadddd	AĠŤĠĊ	1620
Query	405	CACCGGCACCA	CCCAGTGCCGGATCCT	CGGGCCACAAGAACAG'	TCTCAAGGGCAC 	CAAGC	464
Sbjct	1621	çyçççççyçy	cccactccccatcct	·¢ĠĠĠċċaċaaĠaaċaĠ	tctgaagggcac	caagc	1680
Query	465	TAGCGCGCCGG	GCGCGTTCCTTTAAGG	ACGACCTCATCGAGAA(GATTTCCCTGAT 	GCGAA	524
Sbjct	1681	†ÁĠĊAĊĠĊĊĠA	ĠĊĠĊĠĊϮĊĊϮϮϮÅÄĠĠ	·AĊĠĀĊĊŢĊĀŢĊĠĀĠĀĀ(ĠĂϮϮϮĊĊĊϮĠĂϮ	ĠĊĠĊĀ	1740
Query	525	CCACCAACAAT.	ACACTGGGTCGCTCCC	ACTCGCCGCACAGTCC	GCGCACCAAGCA 	CGGCA	584
Sbjct	1741	ĊĊAĊĊAAĊAA†.	Acacteectce	ATTCGCCGCACAGTCC	ĠĊĠĠĂĊĊĂĂĠĊĀ	ĊĠĠĊŦ	1800
Query	585	CAAAGGCACCG	CCCACCACCGAGGAGG	TGCTACGGTCCACCCA	AACCCTGGAGAC 	GCACG	644
Sbjct	1801	ccaaggcaccg	cccaccaccaagaaga	rtgcagcgarccaccca	AAĊTĊŦĠĠĀĠĀĊ	ĠĊĀĊĠ	1860
Query	645	TCAAGGACATT	TCGAATGCCCTGAAGC	ACTTCCGGGATGTTAT	ACTCAAGAAGAA 	GCTGG	704
Sbjct	1861	tcaaggacatc	†ċĠAAcĠċĠċtcAAĠċ	ATTTCCGGGATGTCAT	AĊTAAAĠAAĠAA	ĠĊŦĠĠ.	1920

Query	705	AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGA	764
Sbjct	1921	AĠĠŦĠŦŦĠĊĊĊĠĠAAAĊĠĠAAĊĠĠŦĊAŦŦĊŦĠĠAAAĊĊAŦĀĠĊĊĀĠĊĀŦĠŦĀŦŦĊĊĠŦĠĀ	1980
Query	765	TCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTT	824
Sbjct	1981	tccaaacgtacaccctgaatgaaaacagtgccatcatgagctgcgccacacagcaggttt	2040
Query	825	ACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCG	884
Sbjct	2041	accadadcctddddddddddddddddddddddddddddd	2100
Query	885	GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATG	944
Sbjct	2101	GCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGAGAGGTCATTGATCTTCTGGAGGATG	2160
Query	945	CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCT	1004
Sbjct	2161	CTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAACTGAAGGAGCAGGATCAGTGCGCCT	2220
Query	1005	TTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGTGCGG	1064
Sbjct	2221	TTCGCTATGGTGGATCTGGTTTGGGCGCGCATTGGAGCGGCGGGGGAGATCATGGGTGCGG	2280
Query	1065	TCACCGCCTCGCCGGAGCGAGTGTTCCCGGTACTGGAGTCATGCGCGTTTCGGCCGCCG	1124
Sbjct	2281	TCACCGCCTCGCCGGGAGTGAGTGTTCCCGGCACTGGCATCATGCGCGTTTCAGCCGCCG	2340
Query	1125	AATCAGCTGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCGCGACA	1184
Sbjct	2341	AATCAGCTGCCCAGCGAACTTCGTTGCCGGACATTGCACTCACGCCCAAGGAACGCGACA	2400
Query	1185	TACTGGAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATCCTGC	1244
Sbjct	2401	TACTGGAGCACAATGTGAATCCCATGCGCGGCTCGCACAGCACCGAAAGCATCCTGC	2460
Query	1245	GCGACACGAGTCCACCGCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCCGT	1304
Sbjct	2461	GCGACACGAGTCCACCGCAAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGCGT	2520
Query	1305	TGCCACCAAAGCGACGCAGCCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCT	1364
Sbjct	2521	teccaccaagagacecaeccaecegececacctectecegecectectect	2580
Query	1365	CATCGTCGACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATA	1424
Sbjct	2581	CATCGTTGACATCCGCCTCC-T-ACG-CC-CA-GCCCCATAATA	2619
Query	1425	TTAGTCTGAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGG	1484
Sbjct	2620	TCAGCCTGAACTTGGACCTGGACTGCAGTTCCAACATCTCGCTGCTGAACTATGGCGTGG	2679
Query	1485	ATCGCCTATCCGTGCGTTCACGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	1544
Sbjct	2680	ATCGCCTATCTGTGCGGTCGCGGTCACCGGATGAGAATAGTCAGTGCTCCTTTGACTCGG	2739
Query	1545	CGTTGAATCACTCACGCGAGGAGGAGGACCAGCAACAGCAACATCAGCA-CCTGAGGT	1601
Sbjct	2740	CGTTGAATCACTCACGCGAGGAGGAGCACCACCAACAGCAACAGCAGCAGCA	2799
Query	1602	CGTTTCCAAAGTTGGCTGCGATGATGGACGAAGACATGGACAAGATGGTCAGCTACAG 1	659
Sbjct	2800	CGCTCTCGAAGATGCCAACGATGATGGACGAGGACATGGACAAGATGGTCAGCTACAG 2	857

Range 2: 2857 to 3146

Score		Expect	Identities	Gaps	Strand	Frame	
431 bits	(233)	3e-116()	272/290(94%)	6/290(2%)	Plus/Plus		
Features	s:						
Query	1812	GTTTCGTGTCG.	ATGCGTGAGTTTCGCA	CTTCTACACAGACG	GACGGACTACAG	TGTCCAGT	1871
Sbjct	2857	GTTTCGTGTCG.	ATGCGCGAGTTTCGCA	CTTCCACACAGACG	GACGGACTACAG	CATCCAGT	2916
Query	1872	CCTCCACGAAG'	TCGTCCAGCAGCAATI	CGGAGATTGCGTTI	AGCATCAGTGA	GTCGACGG	1931
Sbjct	2917	cctccacgaag	tcgtccagcagcaatt	ŀĊĠĠĀĠĀŦŦĠĊĠŦŦŦ	radcatcadtda	GTCGACGG	2976
Query	1932	CGGTCGGCAGC	AGTAGCGAGTACCAGC	AGATTAGCCAGTTG	GTGTCGCACAG	CCAGCGTC	1991
Sbjct	2977	cggtcggcagc	AGCAGCGAGTACCAGC	adattadccadtcd	GTGTCGCACAG	ccaccetc	3036
Query	1992	ATATATCCTCG	AGCAGTAGCAGCTGCA	CCACCACGACCAC	agcagcagcac	aaccaccg	2051
Sbjct	3037	AtAtAtcttcc	AGCAGTAGTAGCTGCA	rccaccacraccacc	cadcadcadcad	CACCACCG	3096
Query	2052	gctatg	-gcagcagcgaagtgg	agcagcagcagcag	gcagcagcag	2095	
Sbjct	3097	dctatdggagc.	adcadcadcdaartdd	adcadcadcadcaa	rcygcygcyg	3146	

Drosophila simulans GD16179 (Dsim\GD16179), mRNA

Sequence ID: **ref|XM_002106294.1|** Length: 1476 Number of Matches: 1 Range 1: 1 to 1141

Score		Expect	Identities	Gaps	Strand	Frame	
1936 bit	ts(1048)	0.0()	1110/1141(97%)	0/1141(0%)	Plus/Plus		
Feature	s:						
Query	866	ATGCTCTCCGAG	GACAGCGGCGAGTG	CGCCTCCCTGAGCAAC	CGAGAATGTGCGG	GAAGTC 9	925
Sbjct	1	AtGCTCTCCGAG	GACAGCGGCGAGTG	rdcctccctdadcaad	CGAGAATGTGCGG	GAAGTC 6	60
Query	926	ATTGATCTTCTC	GAGGATGCTGTGCG	GAATCTCGTTACGCT(GCGCAGGGCAAG	CTGAAG 9	985
Sbjct	61			ĠĂĂŦĊŦĊĠŦŦĂĊĠĊŦĊ			120
Query	986			${f CAGTGGATCTGGCTTC}$			1045
Sbjct	121			ĊĂĠŦĠĠĂŦĊŦĠĠĊĊŦĊ			180
Query Sbjct	1046 181	GCGGAGATCATG GCGGAGATCATG		CTCGCCGGGAGCGAGT 			1105 240
Query	1106			TGCCCAGCGTACTTC			240 1165
Sbjct	241			TGCCCAGCGCACTTC			300
Query	1166	ĄÇĢÇÇĄĄGĢĄG	ÇĢÇĢĄÇĄŢĄÇŢĢĢĄ [,]	ĢÇ Ā ĢÇ Ā ÇĀĀŢĢŢĢĀĀ(ССССВАТСССССССССССССССССССССССССССССССС	СТСССАС 1	1225
Sbjct	301	ACGCCCAAGGAG			CCGATGCGCGGC	TCCCAC 3	360
Query	1226	AGCACCGAAAGT	ATCCTGCGCGACAC	GAGTCCACCGCCGAAC	GCCACCGCTACCC	CAATAGG 1	1285
Sbjct	361	AGCACCGAAAGT	ATCCTGCGCGACAC	GAGTCCACCGCCGAA	SCCACCGCTACCC	CAATAGG 4	420
Query	1286	GCCAGTAATCCG	CCGCCGTTGCCACC.	AAAGCGACGCAGCCAC	GCCGAGCGCATCA	GCTGGT 1	1345
Sbjct	421	ĠĊĊĀĠŦĀĀCĊĊĠ			sccgggcgcatca		480
Query	1346			GACATCCACCTCCAAT			1405
Sbjct	481	GĊĀĠŦĠĠĠĊĠŦĠ					540 1465
Query Sbjct	1406 541			GAACTCGGACCTGGAC 			1465 600
Query	1466			ATCCGTGCGTTCACG(1525
Sbjct	601						660
Query	1526	САСТССТТТ	<mark>Ģ</mark> ĄĊŢĊĠĠĊĠŢŢĠĄĄ	ТСАСТСАСССАСО	- GAGGAÇÇAGÇAA	ÇAÇÇAA 1	1585
Sbjct	661	CAGTGCTCCTTT	GACTCGGCGTTGAA	TCACTCACGCGAGGAC	GAGGACCACCAA	CAGCAA 7	720
Query	1586	CATCAGCACCTG	AGGTCGTTTCCAAA	GTTGGCTGCGATGAT(GACGAAGACATG	GACAAG 1	1645
Sbjct	721	cagcagcacctg	AGGTCGTTTCCAAA	gttggcagcgatgatd	GACGAAGACATG	GACAAG 7	780
Query	1646	ATGGTCAGCTAC	AGCGCCGCAATCGA	CGACAAAACGCAGAC <i>I</i> 	ACCACTTTCGACT	GGTGGT 1	1705
Sbjct	781			ĊĠĀĊĀĀĀĀĊĠĊĀĠĀĊĀ			840
Query	1706 841			TGGAGGAGCAGGCGA/ 			1765 900
Sbjct Query	1766			TGGAGGAGCAGCCGA <i>I</i> TCGCCACTCAAACGA <i>I</i>			900 1825
Sbjct	901			TCGCCTCTCAAACGAA			960
Query	1826			GACGGACTACAGTGT(1885
Sbjct	961	CGTGAGTTTCGC	 ACTTGCACACAGAC			 SAAGTCG 1	1020
Query	1886	ҭҪҪѧ҇҅҅ҪҪѧ҅Ҫҁѧҁҁѧѧҭ	ТСĞĞAĞATTĞÇĞT Т	ŢĄĢÇĄŢÇĄĢŢĢĄĢŢÇĢ	- БАСӨӨСӨӨТСӨӨС	САССАСТ 1	1945
Sbjct	1021	TCCAGCAGCAAT	TCGGAGATTGCGTT	TAGCATCAGTGAGTC	ACGGCGGTCGGC	AGCAGC 1	1080
Query	1946	AGCGAGTACCAG	CAGATTAGCCAGTT	GGTGTCGCACAGCCA(GCGTCATATATCC	TCGAGC 2	2005
Sbjct	1081	AGCGAATACCAG	cagattagccagtc	GGTGTCGCACAGCCA	Scetcatatatec	rtcgage 1	1140
Query	2006	A 2006					
Sbjct	1141	Å 1141					

Drosophila melanogaster chromosome X

Sequence ID: gb|AE014298.5| Length: 23542271 Number of Matches: 7

Range 1: 6788457 to 6789051

Score		Expect	Identities	Gaps	Strand	Frame	
1059 bit	ts(573)	0.0()	593/601(99%)	7/601(1%)	Plus/Minus		
Feature C3G ort	s: t holog, isof	orm IC3G or	tholog, isoform D				
Query	165	ACGGCAGC	ATCAGTTCTCCATCCAC	GCCCGGCACCTG'	TTCCAGTGGCATC	GGAGTGGGCG	224
Sbjct	6789051	Accccacca	Atcacttctccatcac	cęcceecycate	ttccactccatc	ddadtddddd	6788992
Query	225	GTGGCGGCT	rgcagcagcagcagca 	ACAATAGCATCAA(CAGCGGCAGCTAC	TCCACCGCCT	284
Sbjct	6788991	ĠŦĠĠĊĠĠĊ1	recyecyecyecyecyecye	vcyytydcy	cyęcecyczyczyc	tccacccct	6788932
Query	285	GCACTCCG	CCACCACCCACGCATCA	AGCATCACTCGCA(GCACCAGCAGCTG 	CAGGGCACGC	344
Sbjct	6788931	gcyct-cce.	ccaccaccaccatca	AGCATCACTCGCA	gcąccąccąctc	CAGGGCACGC	6788872
Query	345	CGGGAGGAT	CTAGTCGGGTCGGGG	GAGCAGGAGCAGG	AGCAGGCGGAGGT 	GGTGGTGTAC	404
Sbjct	6788871	¢ g g g g g g g	tctagtcgggtagggg	aggaggaggagg	ċĠĠĀĠĠŦ	ĠĠŦĠĠŦĠŦĀĊ	6788818
Query	405	CACCGGCAC	CCACCCAGTGCCGGATC	CTCGGGCCACAA(GAACAGTCTCAAG 	GGCACCAAGC	464
Sbjct	6788817	cacceccac	ccaccadadeccadade	cctcgggccycyy	ĠAAĊAĠϮĊϮĊAAĠ	ĠĠĊĀĊĊĀĀĠĊ	6788758
Query	465	TAGCGCGC	CGGGCGCGTTCCTTTA <i>A</i>	AGGACGACCTCAT(CGAGAAGATTTCC 	CTGATGCGAA	524
Sbjct	6788757	†AĠĊĠĊĠĊ	ĊĠĠĠĊĠĊĠŦŦĊĊŦŦŦĀĀ	AĠĠĀĊĠĀĊĊŦĊĀŦŒ	ĊĠĀĠĀĀĠĀŦŦŦĊĊ	ĊŦĠĀŦĠĊĠĀĀ	6788698
Query	525	CCACCAACA	AATACACTGGGTCGCTC	CCACTCGCCGCA(CAGTCCGCGCACC 	AAGCACGGCA	584
Sbjct	6788697	¢¢4¢¢44¢	AATACACTGGGTCGCTC	cccactcccccccc	ckerccececkc	AAGCACGGCA	6788638
Query	585	CAAAGGCA(CCGCCCACCACCGAGGA	AGGTGCTACGGTC(CACCCAAACCCTG 	GAGACGCACG	644
Sbjct	6788637	ĊAAAĠĠĊĀŒ	cccccaccaccidacd	\ddatactacddd a charactaeth a	cacccaaaccctd	ĠĀĠĀĊĠĊĀĊĠ	6788578
Query	645	TCAAGGAC <i>I</i>	\TTTCGAATGCCCTGA <i>A</i> 	AGCACTTCCGGGA!	TGTTATACTCAAG 	AAGAAGCTGG	704
Sbjct	6788577	ŤĊÁÁĠĠÁĊ <i>I</i>	\r\r\r\c\gamma\ar\r\r\r\r\r\r\r\r\r\r\r\r\r\r\r\r\	ĸĠĊĀĊŦŦĊĊĠĠĠĀ!	rgttatactcaag	AAGAAGCTGG	6788518
Query	705	AGGTGTTGC	CCGGGCAACGGAACGGT	CATTCTGGAAAC	CATAGCCAGCATG 	TACTCCG-TG	763
Sbjct	6788517	AĠĠŦĠŦŦĠĊ	ccececapos	rcattctggaaac	catagccagcatg	tactcccctc	6788458
Query	764	A 764					
Sbjct	6788457	Å 678845	57				

Range 2: 6787590 to 6788126

Score		Expect	Identities	Gaps	Strand	Frame	
981 bits	(531)	0.0()	535/537(99%)	0/537(0%)	Plus/Minus		
Features C3G ort	s: holog, isofo	orm IC3G o	rtholog, isoform D				
Query	952	GAATCTCC	TTACGCTGGCGCAGGG	CAAGCTGAAGGAG	CAGGATCAGTGC	GCCTTTCGCTA	1011
Sbjct	6788126	GAATCTCG	TTACGCTGGCGCAGGG	CAAGCTGAAGGAG	CAGGATCAGTGC	GCCTTTCGCTA	6788067
Query	1012	CAGTGGAT	CTGGCTTGGGCGGCAT	TGGAGCGGCGGCG	GAGATCATGGGT	GCGGTCACCGC	1071
Sbjct	6788066	cagtggat	rchggchhgggcggcah	TGGAGCGGCGGCG	GAGATCATGGGT	GCGGTCACCGC	6788007
Query	1072	CTCGCCGG	GAGCGAGTGTTCCCGG	TACTGGAGTCATG	CGCGTTTCGGCC	GCCGAATCAGC	1131
Sbjct	6788006	ÇŢĊĠĊĊĠĠ	sgygcgygtgtacccgg	tactddadtcatd	central	GCCGAATCAGC	6787947
Query	1132	TGCCCAGC	GTACTTCGTTGCCGGA	CATAGCGCTCACG	CCCAAGGAGCGC	GACATACTGGA	1191
Sbjct	6787946	TGCCCAGC	cdtacttcdttdccdda	CATAGCGCTCACG	cccaaggagcgc	GACATACTGGA	6787887
Query	1192	GCAGCACA	ATGTGAACCCGATGCG	CGGCTCCCACAGC	ACCGAAAGTATC	CTGCGCGACAC	1251
Sbjct	6787886	GCAGCACA	rateteaaccceatece	ceectcccycye	acceaaaactatc	ctdcdcdacac	6787827
Query	1252	GAGTCCAC	CGCCGAAGCCACCGCT	ACCCAATAGGGCC	AGTAATCCGCCG	CCGTTGCCACC	1311
Sbjct	6787826	GAGTCCAC	cccccaadccacccc	ACCCAATAGGGCC	agtaatccccc	ccetteccyce	6787767
Query	1312	AAAGCGAC	CGCAGCCAGCCGAGCGC	ATCAGCTGGTACA	GTGGGCGTAGGC	rgctcatcgtc 	1371

Sbjct	6787766	AAAGCGACGCAGCCGAGCGCATCAGCTGGTACAGTGGGCGTAGGCTGCTCATCGTC	6787707
Query	1372	GACATCCACCTCCAATCAGGCCAGTCCGCTGCCCTACGCCCAGTCCCATAATATTAGTCT	1431
Sbjct	6787706	GACATCCACCTCCAATCAGGCCAGTCCACTGCCCTACGCCCAGTCCCATAATATTAGTCT	6787647
Query	1432	GAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAACTATGGCGTGGATCG 14	88
Shict	6787646	GAACTCGGACCTGGACTGCAGTTCCAATATCTCGCTGCTGAATTATGGCGTGGATCG 67	87590

Range 3: 6786528 to 6786813

Score		Expect	Identities	Gaps	Strand	Frame	
512 bits(277)	1e-140()	283/286(99%)	0/286(0%)	Plus/Minus		
Features C3G orth	: holog, isof	orm IC3G or	tholog, isoform D				
Query	1811	GGTTTCGT	GTCGATGCGTGAGTT	rcgcacttctacac	CAGACGACGGACT	ACAGTGTCCAG	1870
Sbjct	6786813	GGTTTCGT	GTCGATGCGTGAGTT	rcgcacttccacac	CAGACGACGGACT	ACAGTGTCCAG	6786
Query	1871	TCCTCCAC	GAAGTCGTCCAGCAG	CAATTCGGAGATTC	GCGTTTAGCATCA	GTGAGTCGACG	1930
Sbjct	6786753	TCCTCCAC	GAAGTCGTCCAGCAGC	CAATTCGGAGATTC	scgttcagcatca	GTGAGTCGACG	6786
Query	1931	GCGGTCGG	CAGCAGTAGCGAGTAG	CCAGCAGATTAGCC	AGTTGGTGTCGC	ACAGCCAGCGT	1990
Sbjct	6786693	GCGGTCGG	CAGCAGTAGCGAGTAG	CCAGCAGATTAGCC	AGTTGGTGTCGC	ACAGCCAGCGT	6786
Query	1991	CATATATC	CTCGAGCAGTAGCAG	CTGCACCACCACGA	CCACcagcagca	gcacaaccacc	2050
Sbjct	6786633	CATATATC	CTCGAGCAGTAGCAG	CTGCACCACCACGA	CCACCAGCAGCA	GCACAACCACC	6786
Query	2051	ggctatgg	cagcagcgaagtgga	gcagcagcagcagc	agcagcagc 2	096	
Sbjct	6786573	GGCTATGG	CAGCAGCGAAGTGGAG	GCAGCTGCAGCAGC	AGCAGCAGC 6	786528	

Range 4: 6788203 to 6788394

Score		Expect	Identities	Gaps	Strand	Frame			
350 bits	(189)	9e-92()	191/192(99%	%) 0/192(0	%) Plus/Minu	S			
Features: C3G ortholog, isoform IC3G ortholog, isoform D									
Query	761	GTGATCCA	AACCTACACC	CTGAATGAAAACAG	TGCCATCATGAGCA	GCGCCACGCTGCAG	820		
Sbjct	6788394	GTGATCCA	AACCTATACC	ctgaatgaaaacag	rtgccatcatgagca	dedecacectecae	6788335		
Query	821	GTTTACCA	AGAGCCTGGGC	AAGCTCATCAAGCT	CTGCGACGAGGTGA	TGCTCTCCGAGGAC	880		
Sbjct	6788334	GTTTACCA	AGAGCCTGGGC	AAGCTCATCAAGCT	'ctgcgacgaggtga	TGCTCTCCGAGGAC	6788275		
Query	881	AGCGGCGA	AGTGCGCCTCC	CTGAGCAACGAGAA	TGTGCGGGAAGTCA	TTGATCTTCTCGAG	940		
Sbjct	6788274	AGCGGCG	/q4qqqqqqqqqq	ctgagcaacgagaa	rtgtgcgggaagtca	ttgatettetegag	6788215		
Query	941	GATGCTGT	GCGG 952						
Sbjct	6788214	GATGCTGT	rdcdd 6788:	203					

Range 5: 6787350 to 6787521

Score		Expect	Identities	Gaps	Strand	Frame	
307 bits	(166)	6e-79()	170/172(99%)	0/172(0%)	Plus/Minus		
Features: C3G ortholog, isoform IC3G ortholog, isoform D							
Query	1488	GCCTATC	CGTGCGTTCACGGTC	ACCGGATGAGAATAG	GTCAGTGCTCCTTT(GACTCGGCGT	1547
Sbjct	6787521	GCCTATC	CGTGCGTTCACGGTC	ACCGGATGAGAATAC	stcagtgctccttt	GACTCGGCGT	6787462
Query	1548	TGAATCA	CTCACGCGAGGAGGA	GGACCAGCAACAGC <i>A</i>	AACATCAGCACCTG	AGGTCGTTTC	1607
Sbjct	6787461	TGAATCA	CTCACGCGAGGAGGA	GGACCAGCAACAGCA	AACATCAGCATCTG	AGGTCATTTC	6787402
Query	1608	CAAAGTT	GGCTGCGATGATGGA	CGAAGACATGGACAA	AGATGGTCAGCTAC	AG 1659	
Sbjct	6787401	CAAAGTT	GGCTGCGATGATGGA	cgaagacatggaca <i>t</i>	AGATGGTCAGCTAC	AG 6787350	

Range 6: 6795352 to 6795515

Score		Expect	Identities	Gaps	Strand	Frame			
303 bits((164)	7e-78()	164/164(100%)	0/164(0%)	Plus/Minus				
Features: C3G ortholog, isoform IC3G ortholog, isoform F									
Query	1	AAAAAGAG	GGAAatatatatatata 	CAAGAATAAGTA	TCGAAACTCAAG	GGCCACATA	60		
Sbjct	6795515	AAAAAGAG	GAAATATATATATATATA	ACAAGAATAAGTA	TCGAAACTCAAG	GGCCACATA	6795456		
Query	61	TATTTAGO	GTGTGTGCTTCACGTTTTT	PAATTTGTTTGCG	CGGGGTGAAAAA	TTAAATAAT	120		
Sbjct	6795455	TATTTAGG	stetetecttekeettet	rAATTTGTTTGCG	cdddddaaaaad	tradataat	6795396		
Query	121	ACACGGCG	GCTGGAAATAAAAAAGGG	GCGAAGCGACAAT'	TCTCGA 164				
Sbjct	6795395	ACACGGC	GCTGGAAATAAAAAAGGG	cgaagcgacaat	TCTCGA 67953	352			

Range 7: 6787094 to 6787248

Score		Expect	Identities	Gaps	Strand	Frame	
287 bits(155)		7e-73()	155/155(100%)	0/155(0%)	Plus/Minus		
Features: C3G ortholog, isoform IC3G ortholog, isoform D							
Query	1659	GCGCCGC	AATCGACGACAAAACGO	CAGACACCACTTTC	GACTGGTGGTGGT	ATAGCTGGTG	1718
Sbjct	6787248	gcgccgc	AATCGACGACAAAACGC	CAGACACCACTTTC	GACTGGTGGTGGT	ATAGCTGGTG	6787189
Query	1719	TTGCTGG	TGGAACTGGAGGAGCAG	GGCGAAGGTGTAGC	TGCTGCAGCGTCT	GGTGACGGGG	1778
Sbjct	6787188	TTGCTGG	TGGAACTGGAGGAGCAC	GCGAAGGTGTAGC	TGCTGCAGCGTCT	GGTGACGGGG	6787129
Query	1779	AAACTAA	CAGCAATCGCCACTCA	AACGAATCGGGT	1813		
Sbjct	6787128	AAACTAA	CAGCAATCGCCACTCAZ	AACGAATCGGGT	6787094		

Drosophila melanogaster X BAC RP98-48O24 (Roswell Park Cancer Institute Drosophila BAC Library) complete sequence Sequence ID: **gb|AC023722.4|** Length: 191590 Number of Matches: 7 Range 1: 102812 to 103406

Score		Expect	Identities	Gaps	Strand	Frame	
1059 bit	s(573)	0.0()	593/601(99%)	7/601(1%)	Plus/Minus		_
Features	S :						
Query	165	ACGGCAGCAT	CAGTTCTCCATCCAC	CGCCGGCACCTGT	TCCAGTGGCATC	GGAGTGGGCG	224
Sbjct	103406	ACGGCAGCAT	cagttctccatccac	CGCCGGCACCTGT	tccagtggcatc	GGAGTGGGCG	103347
Query	225	GTGGCGGCTG	CAGCAGCAGCAGCA	ACAATAGCATCAAC	AGCGGCAGCTAC	TCCACCGCCT	284
Sbjct	103346	gtggcggctg	cygcygcygcygcyg	Acaatagcatcaac	yęceęcyectyc.	tccacccct	103287
Query	285	GCACTCCGCC	ACCACCCACGCATCA	AGCATCACTCGCAG	CACCAGCAGCTG	CAGGGCACGC	344
Sbjct	103286	gcyctccecc	caccaccaccacate	y de parte de la	çyççyêçyêçtê ç	çyeçeçyçeç	103227
Query	345	CGGGAGGATC	TAGTCGGGTCGGGGG	GAGCAGGAGCAGGA 	GCAGGCGGAGGT(GGTGGTGTAC	404
Sbjct	103226	ĊĠĠĠĠĠĠĀĊ	thagtegggtagggg	sádcáddádcádd–	ċĠĠÀĠĠŦ	ĠĠŦĠĠŦĠŦĀĊ	103173
Query	405	CACCGGCACC	CACCCAGTGCCGGATC	CCTCGGGCCACAAG.	AACAGTCTCAAG(GGCACCAAGC	464
Sbjct	103172	ĊĀĊĊĠĠĊĀĊĊ	:Acccagtgccgatc	cctcgggccacaag.	AAĊAĠTĊTĊAAĠ(ĠĠĊĀĊĊĀĀĠĊ	103113
Query	465	TAGCGCGCCG	GGCGCGTTCCTTTA <i>F</i>	AGGACGACCTCATC	GAGAAGATTTCC(CTGATGCGAA	524
Sbjct	103112	TAĠĊĠĊĠĊĊĠ	ĠĠĊĠĊĠŢŢĊĊŢŢŢ	AĠĠĀĊĠĀĊĊŦĊĀŦĊ	ĠĀĠĀĀĠĀŦŦŦĊĊ	ĊŢĠĄŢĠĊĠĄĄ	103053
Query	525	CCACCAACAA	TACACTGGGTCGCTC	CCACTCGCCGCAC.	AGTCCGCGCACC.	AAGCACGGCA	584
Sbjct	103052	ĊĊĀĊĊĀĀĊĀĀ	\rhackcrccctcdctcccrc	ĊĊĊĀĊŦĊĠĊĊĠĊĀĊ.	AĠŦĊĊĠĊĠĊĀĊĊ.	Á Á ĠĊ Á ĊĠĠĊ Á	102993
Query	585	CAAAGGCACC	GCCCACCACCGAGG <i>P</i>	AGGTGCTACGGTCC. 	ACCCAAACCCTG(GAGACGCACG	644
Sbjct	102992	ĊAAAĠĠĊAĊĊ	:ĠĊĊĊAĊĊAĊĊĠAĠĠ <i></i>	AĠĠŦĠĊŦĂĊĠĠŦĊĊ.	AĊĊĊAAAĊĊĊŢĠ(ĠĀĠĀĊĠĊĀĊĠ	102933
Query	645	TCAAGGACAT	TTCGAATGCCCTGAA	AGCACTTCCGGGAT	GTTATACTCAAG.	AAGAAGCTGG 	704

Sbjct	102932	TCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGG	102873
Query	705	AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCG-TG	763
Sbjct	102872	AGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGGTG	102813
Query	764	A 764	
Sbict	102812	A 102812	

Range 2: 101945 to 102481

Score		Expect	Identities	Gaps	Strand	Frame	
981 bits	(531)	0.0()	535/537(99%)	0/537(0%)	Plus/Minus		_
Feature	s:						
Query	952	GAATCTCG	TTACGCTGGCGCAGG	GCAAGCTGAAGGAG(CAGGATCAGTGCG	CCTTTCGCTA	1011
Sbjct	102481	GAATCTCG	ttaccctcccccccccccccccccccccccccccccccc	bcaagctgaaggago	caggatcagtgcg	cctttcccta	102422
Query	1012	CAGTGGAT	CTGGCTTGGGCGGCAT	TTGGAGCGGCGGCG	GAGATCATGGGTG(CGGTCACCGC	1071
Sbjct	102421	CAGTGGAT	ctggcttgggcgca	rtggagcggcggcg	GAGATCATGGGTG	CGGTCACCGC	102362
Query	1072	CTCGCCGG	GAGCGAGTGTTCCCG(GTACTGGAGTCATG	CGCGTTTCGGCCG	CCGAATCAGC	1131
Sbjct	102361	ÇŢĊĠĊĊĠĠ	GAGCGAGTGTTCCCGG	gtactggagtcatg	 ceceptated cecept	CCGAATCAGC	102302
Query	1132	TGCCCAGC	GTACTTCGTTGCCGG	ACATAGCGCTCACG	CCCAAGGAGCGCG	ACATACTGGA	1191
Sbjct	102301	TGCCCAGC	ĠŦĀĊŦŦĊĠŦŦĠĊĊĠĠ <i>ĭ</i>	ycytyddddd ach y chaellodd o chaellodd Caellodd o chaellodd o chae	cccaaggagcgcg	ACATACTGGA	102242
Query	1192	GCAGCACA	ATGTGAACCCGATGC	GCGGCTCCCACAGC	ACCGAAAGTATCC'	TGCGCGACAC	1251
Sbjct	102241	GCAGCACA	ATGTGAACCCGATGC	GCGGCTCCCACAGC	ACCGAAAGTATCC'	TGCGCGACAC	102182
Query	1252	GAGTCCAC	CGCCGAAGCCACCGC	TACCCAATAGGGCC	AGTAATCCGCCGC	CGTTGCCACC	1311
Sbjct	102181	GAGTCCAC	cdccdaadccaccdc	tycccyytydddcc	agtaatccccccc	cgttgccacc	102122
Query	1312	AAAGCGAC	GCAGCCAGCCGAGCG(CATCAGCTGGTACA(GTGGGCGTAGGCT	GCTCATCGTC	1371
Sbjct	102121	AAAGCGAC	gcagccagccgagcgo	catcagctggtacac	gtgggcgtaggct	GCTCATCGTC	102062
Query	1372	GACATCCA	CCTCCAATCAGGCCA(GTCCGCTGCCCTAC	GCCCAGTCCCATA	ATATTAGTCT	1431
Sbjct	102061	GACATCCA	cctccaatcaggcca	gtccactgccctac	GCCCAGTCCCATA	ATATTAGTCT	102002
Query	1432	GAACTCGG.	ACCTGGACTGCAGTT(CCAATATCTCGCTG(CTGAACTATGGCG'	TGGATCG 14	88
Sbjct	102001	GAACTCGG.	acctegactecaette	ccaatatctccctc	ctgyytty	tggatcg 10	1945

Range 3: 100883 to 101168

Score		Expect	Identities	Gaps	Strand	Frame	_
512 bits	(277)	1e-140()	283/286(99%)	0/286(0%)	Plus/Minus		_
Features	S :						
Query	1811	GGTTTCGTG	TCGATGCGTGAGTTTC	CGCACTTCTACACA	GACGACGGACTA	CAGTGTCCAG	1870
Sbjct	101168	GGTTTCGTG	tcgatgcgtgagtttc	cgcacttccacaca	dacdacddacta	CAGTGTCCAG	101109
Query	1871	TCCTCCACG	AAGTCGTCCAGCAGCA	AATTCGGAGATTGC	GTTTAGCATCAG	TGAGTCGACG	1930
Sbjct	101108	TCCTCCACG	AAGTCGTCCAGCAGCA	AATTCGGAGATTGC	GTTCAGCATCAG	TGAGTCGACG	101049
Query	1931	GCGGTCGGC	AGCAGTAGCGAGTACC	CAGCAGATTAGCCA	GTTGGTGTCGCA	CAGCCAGCGT	1990
Sbjct	101048	eceetceec	AGCAGTAGCGAGTACC	cadcadattadcca	œtteeteteek	CAGCCAGCGT	100989
Query	1991	CATATATCC	TCGAGCAGTAGCAGCT	GCACCACCACGAC	CACcagcagcag	cacaaccacc	2050
Sbjct	100988	catatatcc	tcgagcagtagcagct	rgcąccąccącgac	caccaccaccac	CACAACCACC	100929
Query	2051	ggctatggc	agcagcgaagtggagc	cagcagcagcagca	gcagcagc 20	96	
Sbjct	100928	ddctatddc	y y y y y y y y y y y y y y y y y y y	cygcrecygcygcy	.dcadcadc 10	0883	

Range 4: 102558 to 102749

Score	Expect	Identities	Gaps	Strand	Frame
350 bits(189)	9e-92()	191/192(99%)	0/192(0%)	Plus/Minus	

Features	S :		
Query	761	GTGATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAG	820
Sbjct	102749	GTGATCCAAACCTATACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAG	102690
Query	821	GTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGAC	880
Sbjct	102689	GTTTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGAC	102630
Query	881	AGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAG	940
Sbjct	102629	AGCGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAG	102570
Query	941	GATGCTGTGCGG 952	
Sbjct	102569	GATGCTGTGCGG 102558	

Range 5: 101705 to 101876

Score		Expect	Identities	Gaps	Strand	Frame	
307 bits(166)		6e-79()	170/172(99%)	0/172(0%)	Plus/Minus		_
Features	s:						
Query	1488	GCCTATCC	GTGCGTTCACGGTCAC	CGGATGAGAATAG	TCAGTGCTCCTTTG	ACTCGGCGT	1547
Sbjct	101876	GCCTATCC	gtgcgttcacggtcac	:cddatdadaatad:	tcagtgctccttd	ActcGGcGt	101817
Query	1548	TGAATCAC'	rcacgcgaggaggag	ACCAGCAACAGCA	ACATCAGCACCTGA	GGTCGTTTC	1607
Sbjct	101816	TGAATCAC!	rcacccaaccaccacc	accadcaacadca.	ACATCAGCATCTGA	GGTCATTTC	101757
Query	1608	CAAAGTTG	GCTGCGATGATGGACG	AAGACATGGACAA(GATGGTCAGCTACA	G 1659	
Sbjct	101756	CAAAGTTG	GCTGCGATGATGGACG	saadacatddacaac	gateeteaetaca	.g 101705	

Range 6: 109707 to 109870

Score		Expect	Identities	Gaps	Strand	Frame	
303 bits	(164)	7e-78()	164/164(100%)	0/164(0%)	Plus/Minus		_
Feature	s:						
Query	1	AAAAAGAG	GAAatatatatata	ta CAAGAATAAGTA	TCGAAACTCAAG'	TGGCCACATA	60
Sbjct	109870	AAAAAGAG	:GAAATATATATATATATA	TACAAGAATAAGTA	TCGAAACTCAAG'	TGGCCACATA	109811
Query	61	TATTTAGG	TGTGTGCTTCACGTTT	TTAATTTGTTTGCG	CGGGGTGAAAAA	GTTAAATAAT	120
Sbjct	109810	TATTTAGG	;tdtdtdcttcAcdttt	ttaatttgtttgcg	cdddtdaaaaa	GTTAAATAAT	109751
Query	121	ACACGGCG	GCTGGAAATAAAAAAGG	GGCGAAGCGACAAT	TCTCGA 164		
Sbjct	109750	ACACGGCG	GCTGGAAATAAAAAAG	ggcgaagcgacaat	rcrcdA 1097	07	

Range 7: 101449 to 101603

Score		Expect	Identities	Gaps	Strand	Frame	_
287 bits	(155)	7e-73()	155/155(100%)	0/155(0%)	Plus/Minus		_
Features	s:						
Query	1659	GCGCCGCA	ATCGACGACAAAACGC	AGACACCACTTTC	SACTGGTGGTGGT	'ATAGCTGGTG	1718
Sbjct	101603	GCGCCGCA	AtcGACGACAAAACGC	AGACACCACTTTC	sacteeteet	ATAGCTGGTG	101544
Query	1719	TTGCTGGT	GGAACTGGAGGAGCAG	GCGAAGGTGTAGCT	TGCTGCAGCGTCT	GGTGACGGGG	1778
Sbjct	101543	TTGCTGGT	GGAACTGGAGGAGCAG	GCGAAGGTGTAGC1	rgctgcagcgtct	GGTGACGGGG	101484
Query	1779	AAACTAAC	AGCAATCGCCACTCAA	ACGAATCGGGT 1	1813		
Sbjct	101483	AAACTAAC	AGCAATCGCCACTCAA	ACGAATCGGGT 1	101449		

Score		Expect	Identities	Gaps	Strand	Frame	
761 bits	(412)	0.0()	753/919(82%)	17/919(1%)	Plus/Plus		
Feature	s:						
Query	425	GGATCCTCGG	GCCACAAGAACAGT	'CTCAAGGGCACCAAGC'	TAGCGCGCCGGGC	CGCGTTCC	484
Sbjct	887	GGATCGTCCG	GCCATAAGAACAGT	'TTGAAGGGCACGAAAT'	rggcgcgacgago	ccccttcc	946
Query	485	TTTAAGGACGA	ACCTCATCGAGAAG 	ATTTCCCTGATGCGAA(CCACCAACAATA(CACTGGGT	544
Sbjct	947			SATCTCACTGATGCGCA(1006
Query	545			GCGCACCAAGCACGGCA			604
Sbjct	1007 605			ĊĠĊAATAAĠĊATĠCĊA			1066 664
Query Sbjct	1067			ACCCTGGAGACGCACG' 			1126
Query	665			CTCAAGAAGAAGCTGG			724
Sbjct	1127						1186
Query	725	ĄÇGĢŢÇĄŢTÇ:	ӷҫҫѧҭѧҫҫҫ	ŖĠĊŸŦĠŢŸĊŢĊĊĠŢĠŸ.	ГССАААССТАСАС	СССТĢААТ	784
Sbjct	1187	ACCGTCATAC		AGCATGTATTCCGTCA		CACTGAAC	1246
Query	785	GAAAACAGTG(CCATCATGAGCAGC	GCCACGCTGCAGGTTT	ACCAGAGC-CTGC	GCAAGCT	843
Sbjct	1247	GAGAACAGTG	CCATCATGAGCTCG	GCCACCCAGCAGGTGT	ATCA-ATCGCTTC	GCAAGCT	1305
Query	844	CATCAAGCTC	rgcgacgaggtgat 	GCTCTCCGAGGACAGC	GGCGAGTGCGCCT	CCCTGAG	903
Sbjct	1306	catcaagete:	tĠĊĠĂĊĠĂĠĠŦĠĂŦ	'ĠĊŦGAGĊĠAAAAGAĠĊ	accgaatgcgcc	rccctgag	1365
Query	904	CAACGAGAAT	GTGCGGGAAGTCAT 	TGATCTTCTCGAGGAT'	GCTGTGCGGAATO	CTCGTTAC	963
Sbjct	1366			'CĠĂŦĊŦĠĊŦĊĠĀĠĠĂŦ¢			1425
Query	964			GCAGGATCAGTGCGCC			1023
Sbjct	1426			ĠĊĀĠĠĀŤĊĀĠŤĠĊĀĊĠ! GGAGATCATGGGTGCG			1485 1079
Query Sbjct	1024 1486			GGAGATCATGGGTGCGC 			1545
Query	1080			AGTCATGC-G-C-GTT'			1131
Sbjct	1546			HA-T-ACGCCGGCCGAT			1602
Query	1132	ТĢÇСÇĀĢÇĢТ	 АСТТСӨТТӨССӨӨА	САТАĢСĢСТСАСĢССС	, , , , , , , , , , , , , , , , ,	АŢĄÇŢĢĢĄ	1191
Sbjct	1603	CGCGCAGCGA	ACGTCGCTGCCGGA	 .CATTGCGCTGACGCC		 ATACTGGA	1662
Query	1192	GCAGCACAATO	ĢŢĢĄĄĊĊĊĢĄŢĠĊĠ	; CGGCTCCCACAGCACC	Ģ AAAĢTATCÇTĞÇ	CGCGACAC	1251
Sbjct	1663	GCAGAGCAAT	GTGAATCCGATGCG	CGGCTCTCACAGCACC		CGCGACAC	1722
Query	1252	GAGTCCACCG	CCGAAGCCACCGCT	'ACCCAATAGGGCCAGT	AATCCGCCGCCGT	TTGCCACC	1311
Sbjct	1723	gygccccccc	ccayyerfectect	GCCCAATCGGTCGAGC	AATCCGCCGCCG	rtaccacc	1782
Query	1312	AAAGCGACGC	AGCCAGCCG 133	0			
Sbjct	1783	AAAGCGTCGC	AGCCAGCCG 180	1			

Range 2: 612 to 727

Score		Expect	Identities	Gaps	Strand	Frame	
78.7 bits	s(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus		
Features	S :						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGO	CCGGCACCTGTTC	CAG-T-GG-CATC	GGAGT-G	220
Sbjct	612	Accccaccatca	gttctccatccaccc	cccagtaattgctc	eege4ceeeeee	ggcgtcg	671
Query	221	G-G-CGGT-G	GCGGCTGCAGCAGC	AGCAGCAACAATAGO	CATCAACAGCGGC	AGC 271	
Sbjct	672	GCGTCGGCGTCG	GTGGCTGCAACAGC	AGCAGCAACAACAG	CATCAACAGTGGC.	AGC 727	

Score		Expect	Identities	Gaps	Strand	Frame	
761 bits	(412)	0.0()	753/919(82%)	17/919(1%)	Plus/Plus		
Feature	s:						
Query	425	GGATCCTCGG	GCCACAAGAACAGTC	TCAAGGGCACCAAGC'	TAGCGCGCCGGGC	GCGTTCC	484
Sbjct	888	GGATCGTCCG	GCCATAAGAACAGTT	tgaagggcacgaaat'	tggcgcgacgagc	gcgttcc	947
Query	485	TTTAAGGACG	ACCTCATCGAGAAGA	TTTCCCTGATGCGAA	CCACCAACAATAC	ACTGGGT	544
Sbjct	948	TTCAAGGACG.	Arctaatrgagaaga	tctcactdatdcdca	ccacaaacaacac	gctcggc	1007
Query	545	CGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA(CAAAGGCACCGCC 	CACCACC	604
Sbjct	1008	¢ dG T ¢ G ¢ ATT	cececacacacac	dcaataadcatdcca.	ccyyccccccccccccccc	çyççyçç	1067
Query	605	GAGGAGGTGC'	TACGGTCCACCCAAA 	CCCTGGAGACGCACG' 	TCAAGGACATTTC 	GAATGCC	664
Sbjct	1068	ĠĀĠĠĀĠĠŦĠĊ.	agċĠaተċċāċaċāgā	ĊĠĊŦĠĠĀĠĀĊĠĊĀĊĠ'	tcaaggacatatc	ĠĀĀŢĠĊĠ	1127
Query	665	CTGAAGCACT	TCCGGGATGTTATAC 	TCAAGAAGAAGCTGG. 	AGGTGTTGCCGGG 	CAACGGA 	724
Sbjct	1128	Ċ†CAAAĊAĊ†	†TĊĠCĠÀŤĠŤCÀŤÁĊ	ŤĊÁGAÁÁĠÁÁĠĊŤĠĠ.	^A AĠŦĠĊŦĠĊĊŦĠĠ	ĊĀĀTĠĠC	1187
Query	725	ACGGTCATTC'	TGGAAACCATAGCCA 	GCATGTACTCCGTGA' 	TCCAAACCTACAC 	CCTGAAT 	784
Sbjct	1188			ĠĊĀŢĠŢĀŢŢĊĊĠŢĊĀ			1247
Query	785			CCACGCTGCAGGTTT? 			843
Sbjct	1248			ĊĊĂĊCĊAĠĊĀĠĠŤĠŤ			1306
Query	844			CTCTCCGAGGACAGC(903
Sbjct	1307	ĊĂŤĊĂĂĠĊŤĊ'		CŤGAGCGÁAAÁGÁGC			1366
Query	904			$egin{aligned} GATCTTCTCGAGGAT^{(1)} & GAGGAT^{(2)} & GAGGAT^{(3)} & GAGGAT^{(4)} & GA$			963
Sbjct	1367			ĠĂŦĊŦĠĊŦĊĠĀĠĠĂŦ(1426
Query	964			CAGGATCAGTGCGCC'			1023
Sbjct	1427			ĊĂĠĠĂŦĊĂĠŦĠĊĂĊĠ'			1486
Query	1024			GAGATCATGGGTGCG			1079
Sbjct	1487			ĠĂŦĂŤĂĂŤĠĠĠĊĠĊĊ			1546 1131
Query	1080 1547			GTCATGC-G-C-GTT' 			1603
Sbjct	1132			-1-ACGCCGGCCGAT			1191
Query	1604			ATAGEGETEAEGECE 			1663
Sbjct Query	1192			GGCTCCCACAGCACC			1251
Sbjct	1664			GGCTCCCACAGCACC 			1723
Query	1252			GGC1C1CACAGCACC CCCAATAGGGCCAGT			1311
Sbjct	1724			CCCAATAGGGCCAGT 			1783
Query	1312	AAAGCGACGC					±,0 3
Sbjct	1784	AAAGCGTCGC					

Range 2: 613 to 728

Score		Expect	Identities	Gaps	Strand	Frame	
78.7 bits	s(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGO	CCGGCACCTGTTC	CAG-T-GG-CATC	GGAGT-G	220
Sbjct	613	AcGGCAGCATCA	gttctccatccd	cccagraartgctc	eege4ceeeeee	ggcgtcg	672
Query	221	G-G-CGGT-G	GCGGCTGCAGCAGCA	AGCAGCAACAATAG(CATCAACAGCGGC	AGC 271	
Sbjct	673	GCGTCGGCGTCG	GTGGCTGCAACAGC	rgcagcaacaacago	CATCAACAGTGGC.	AGC 728	

Drosophila mojavensis uncharacterized protein, transcript variant F (Dmoj\GI21607), mRNA

Sequence ID: **ref|XM_015161043.1|** Length: 5041 Number of Matches: 2 Range 1: 671 to 1585

Score Expect Identities Gaps Strand	d Frame
761 bits(412) 0.0() 753/919(82%) 17/919(1%) Plus/P	lus
Features:	
Query 425 GGATCCTCGGGCCACAAGAACAGTCTCAAGGGCACCAAGCTAGCGCGC	CGGGCGCGTTCC 484
Sbjct 671 GGATCGTCCGGCCATAAGAACAGTTTGAAGGGCACGAAATTGGCGCGA	CGAGCGCGTTCC 730
Query 485 TTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAACCACCAAC	AATACACTGGGT 544
Sbjet 731 treadgaegaretaatrgagaagateteaetgatgegeaeeaeaaae	AACACGCTCGGC 790
Query 545 CGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGGCACAAAGGCAC	CCGCCCACCACC 604
Sbjet 791 eggtegeartegeegeacher 791 eggtegeartegeege	cccccaccacc 850
Query 605 GAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCACGTCAAGGAC	ATTTCGAATGCC 664
Sbjet 851 ĠAĠĠAĠĠŦĠĊAĠĊĠAŦĊĊAĊAĊAĠĠĠĊĠĊŦĠĠAĠAĊĠĊĀĊĠŦĊĀĀĠĠĀĊ	ÁTATCGÁÁTGCG 910
Query 665 CTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGGAGGTGTTGG	CCGGGCAACGGA 724
Sbjet 911 čtchhačáčtttčácáhtátchtáctákahádáhádátádtáctá	ĊĊTĠĠĊĀĀTĠĠC 970
Query 725 ACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGATCCAAACC'	
Sbjct 971 ACCGTCATACTGGAGACCATTGCCAGCATGTATTCCGTCATCCAGTCG	
Query 785 GAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTTACCAGAGC	
Sbjct 1031 ĠAGAAĊĀĠŤĠĊĊĀŤĊĀŤĠĀĠĊŢĊĠĠĊĊĀĊĊĊĀĠĊĀĠĠŤĠŤĀŢĊĀ-ĀŢĊ	
Query 844 CATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCGGCGAGTG	
Sbjct 1090 ČAŤČÁÁĠČŤČŤĠČĠÁČĠÁĠĠŤĠÁŤĠČŤGAGČĠÁAAÁGÁĠČACČĠÁAŤĠ	
Query 904 CAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGG	
Sbjct 1150 TÄÄĊĠÄĠÄÄŤĠŤĊĊĠŢĠÄĠĠŤĊÄŤĊĠÄŤĊŤĠĊŤĊĠÄĠĠÄŤĠĊŤĠŤĠĊĠ	
Query 964 GCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCTTTCGCTAG	
Sbjct 1210 ACTGGCACAGGGCAAACTCAAGGAGCAGGATCAGTGCACGTTTCGCTA	
Query 1024 CTTGGGCGGCATTGGAGCGGCGGGGGAGATCATGGGTGCGGTCACCGC	
Sbjct 1270 ČCŤĠĠĠĊĠĠĊĀŤĊĠĠŢĠĊĊĠĊĊĠĊĊĠĀŢĀŤĀĀŤĠĠĠĊĠĊĊĠŤĠĀĊĊĠĊ	
Query 1080 GAGCGAGTGTTCCCGGTACTGGAGTCATGC-G-C-GTTTCGGCCGC	
Sbjct 1330 ĠĠĠĊĠĠĊĠĠĊĠĠĊĊĠĠ-ĀĊŤĠĊĀ-Ť-ĀĊĠĊĊĠĠĊĊĠĀŤĠĊĠĠĊĊĠĊ	
Query 1132 TGCCCAGCGTACTTCGTTGCCGGACATAGCGCTCACGCCCAAGGAGCG	
Sbjct 1387 CĠĊĠĊĀĠĊĠĀĀĊĠŤĊĠĊŤĠĊĊĠĠĀĊĀŤŦĠĊĠĊŤĠĀĊĠĊĊĊĀĀĠĠĀĠĊĠ	
Query 1192 GCAGCACAATGTGAACCCGATGCGCGGCTCCCACAGCACCGAAAGTATG Sbjct 1447 GCAGAGCAATGTGAATCCGATGCGCGGCTCTCACAGCACCGAGAGCAT	
Query 1252 GAGTCCACCGCCGAAGCCACCGCTACCCAATAGGGCCAGTAATCCGCCGSct 1507 GAGCCCGCCGAAAGCCGCCGCCGCCAATCGGTCGAGCAATCCGCCCGC	
Query 1312 AAAGCGACGCAGCCG 1330	GCCGITACCACC 1300
Sbjct 1567 AAAGCGTCGCAGCCG 1585	

Range 2: 396 to 511

Score		Expect	Identities	Gaps	Strand	Frame
78.7 bits	s(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus	_
Features	s:					
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGC	CCGGCACCTGTTC	CAG-T-GG-CATC	GGAGT-G 220
Sbjct	396	ACGGCAGCATCA	.gttctccatccacgc	ccagtaattgctc	eeqe4cqqeqqe	GGCGTCG 455
Query	221	G-G-CGGT-G	GCGGCTGCAGCAGCA	GCAGCAACAATAGO	CATCAACAGCGGC	AGC 271
Sbjct	456	dcdrcddcatcd	GTGGCTGCAACAGCA	dcagcaacaacag	catcaacagreec	AGC 511

Drosophila mojavensis uncharacterized protein, transcript variant D (Dmoj\GI21607), mRNA

Sequence ID: ref|XM_015161042.1| Length: 5014 Number of Matches: 2

Range 1: 887 to 1801

Score		Expect	Identities	Gaps	Strand	Frame	
761 bits	(412)	0.0()	753/919(82	%) 17/919(1%)	Plus/Plus		
Features	s:						
Query	425	GGATCCTCGG	GCCACAAGAAC	CAGTCTCAAGGGCACCAAG	CTAGCGCGCCGGGC	GCGTTCC	484
Sbjct	887	GGATCGTCCG	GCCATAAGAAC	ZAGTTTGAAGGGCACGAAA	ttggcgcgacgagc	:gcg44cc	946
Query	485	TTTAAGGACG	ACCTCATCGAC	SAAGATTTCCCTGATGCGA	ACCACCAACAATAC	ACTGGGT	544
Sbjct	947	ttcaaggacg.	Arctaatrgad	saagateteaetgatgege	accacadacacac	cectceec	1006
Query	545	CGCTCCCACT	CGCCGCACAG1	CCGCGCACCAAGCACGGC	ACAAAGGCACCGCC	CACCACC	604
Sbjct	1007	ĊĠĠŦĊĠĊĀŦŦŒ	ĊĠĊĊĠĊĀĊĀĠī	rcccccccccccccccccccccccccccccccccccccc	záccáágccgccgcc	ckáckáck	1066
Query	605	GAGGAGGTGC'	TACGGTCCACC	CCAAACCCTGGAGACGCAC	GTCAAGGACATTTC: 	GAATGCC	664
Sbjct	1067	ĠĀĠĠĀĠĠŦĠĊ	AGĊĠAŦĊĊĀĊ <i>Ā</i>	ACAGACGCTGGAGACGCAC	ĠŦĊĀĀĠĠĀĊĀŦĀŦĊ	ĊĠĀĀŢĠĊĠ	1126
Query	665			ATACTCAAGAAGAAGCTG			724
Sbjct	1127			CATACTCAGAAAGAAGCTC			1186
Query	725			AGCCAGCATGTACTCCGTG			784
Sbjct	1187			ĠĊĊĀĠĊĀŢĠŢĀŢŢĊĊĠŢĊ			1246
Query	785			CAGCGCCACGCTGCAGGTT			843
Sbjct	1247			CTCGĠĊĊĂĊCĊĀĠĊĀĠĠŤĠ			1305
Query	844			GATGCTCTCCGAGGACAG	1 111 111111		903
Sbjct	1306			ĠĂŦĠĊŦĠAĠĊĠĂAAĂĠĂĊ			1365 963
Query Sbjct	904 1366			CATTGATCTTCTCGAGGA 			1425
Query	964			AGGAGCAGGATCAGTGCGC			1023
Sbjct	1426						1485
Query	1024			CGGCGGAGATCATGGGTGC			1079
Sbjct	1486			CGCCGATATAATGGGCGC			1545
Query	1080	GAGCGAGT	GTTÇÇÇGGTAÇ	CTGGAGTCATGÇ-G-Ç-GT	TTCGGCCGCCGA	AT-ÇAĞC	1131
Sbjct	1546	GGGCGGCAGT	 GTGCCCGG-AC		 TGCGGCCGCGGCGG	 CTGCAGT	1602
Query	1132	ТĢСССАĢССТ	ĄÇTŢÇĢTŢĢÇÇ	СĢĢĀÇĀŢĀĢÇĢÇŢСĀÇĢÇÇ	ĊŖŖĠĠŖĠĊĠĊĠŖĊŖ	ТАСТССА	1191
Sbjct	1603	CGCGCAGCGA		 CGGACATTGCGCTGACGCC		TACTGGA	1662
Query	1192	ĢÇĄĢCAÇĄĄŢ(ĢŢĢĄ <mark>Ą</mark> СÇÇĢĄŢ	ӷҾҪҾҪҾҪҬҪСҪ҅҄҅ҲҪӒҾҾ	: ССФААА ФТАТССТОС	:ĢÇĢĄÇĄÇ	1251
Sbjct	1663	GCAGAGCAAT			CGAGAGCATACTGC	GCGACAC	1722
Query	1252	GAGTÇÇAÇÇG	ÇÇGAAGÇÇAÇÇ	CGCTACCCAATAGGGCCAG	таатссессес	TGCCACC	1311
Sbjct	1723	GAGCCCGCCG	CCAAAGCCGCC	GCTGCCCAATCGGTCGAG	CAATCCGCCGCCGT	TACCACC	1782
Query	1312	AAAGCGACGC	AGCCAGCCG	1330			
Sbjct	1783	AAAGCGTCGC	AGCCAGCCG	1801			

Range 2: 612 to 727

Score		Expect	Identities	Gaps	Strand	Frame
78.7 bits	s(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus	
Feature	s:					
Query	165	ACGGCAGCATCAG	GTTCTCCATCCACGC	CCCGGCACCTGTTCC	CAG-T-GG-CATC	GGAGT-G 220
Sbjct	612	ACGGCAGCATCAG	GTTCTCCATCCACGC	CCAGTAATTGCTCG	gggtcgggcggc	GGCGTCG 671
Query	221	G-G-CGGT-G	GCGGCTGCAGCAGC <i>I</i>	AGCAGCAACAATAGC	CATCAACAGCGGC	AGC 271

Drosophila mojavensis uncharacterized protein, transcript variant C (Dmoj\Gl21607), mRNA Sequence ID: **ref|XM_015161041.1|** Length: 4988 Number of Matches: 2

Range 1: 885 to 1799

Score		Expect	Identities	Gaps	Strand	Frame	
761 bits	(412)	0.0()	753/919(82	2%) 17/919(1%)	Plus/Plus		
Feature	S:						
Query	425	GGATCCTCGG	GCCACAAGAA	CAGTCTCAAGGGCACCAAGG	CTAGCGCGCCGGGC	GCGTTCC	484
Sbjct	885	GGATCGTCCG	GCCATAAGAA	CAGTTTGAAGGGCACGAAA	rtggcgcgacgagc	gcgttcc	944
Query	485	TTTAAGGACGA	ACCTCATCGA	GAAGATTTCCCTGATGCGAA	ACCACCAACAATAC	ACTGGGT	544
Sbjct	945	TTCAAGGACGA	ATCTAATTGA	gaagateteaetgatgege	yccycayycyycyc	gctcggc	1004
Query	545	CGCTCCCACTO	CGCCGCACAG'	TCCGCGCACCAAGCACGGCA	ACAAAGGCACCGCC	CACCACC	604
Sbjct	1005	CGGTCGCATTC	cgccgcacag	rcccccaaraaccarcca	yccyyecceccecc	ÇAÇÇAÇÇ	1064
Query	605	GAGGAGGTGC	TACGGTCCAC	CCAAACCCTGGAGACGCAC	GTCAAGGACATTTC	GAATGCC 	664
Sbjct	1065	gyggyggyggyggyggyggyggyggyggyggyggyggyg	agcgatccac	acadacectedadacecaco	stcaaggacatatc	ĠĀĀŦĠĊĠ	1124
Query	665	CTGAAGCACT	CCGGGATGT'	TATACTCAAGAAGAAGCTG(GAGGTGTTGCCGGG	CAACGGA 	724
Sbjct	1125	ctcaaacact:	trccccatct	catactcagaaaddaactc	saagtgetgeetge	CAATGGC	1184
Query	725	ACGGTCATTC	rggaaaccati	AGCCAGCATGTACTCCGTGA	ATCCAAACCTACAC	CCTGAAT 	784
Sbjct	1185	Accetcatac:	rĠĠĀGĀĊĊĀϮ'	rĠĊĊĀĠĊĀŦĠŦĀŦŦĊĊĠŦĊ	Atccagtcgtacac	AĊŦĠĀĀC	1244
Query	785	GAAAACAGTG(CCATCATGAG(CAGCGCCACGCTGCAGGTT'	FACCAGAGC-CTGG 	GCAAGCT 	843
Sbjct	1245	GAGAACAGTG	ccatcatgag	ctcgccaccaccaccaccaccaccaccaccaccaccaccacc	tarca-arccctrc	ĠĊĀĀĠĊŢ	1303
Query	844	CATCAAGCTC	rgcgacgagg' 	TGATGCTCTCCGAGGACAG(CGGCGAGTGCGCCT	CCCTGAG	903
Sbjct	1304	catcaagete:	tĠĊĠĀĊĠĀĠĠ'	tĠAtĠĊtGAGĊĠAAAAGAĠŒ	caccgaatgcgcct	ccctgyc	1363
Query	904	CAACGAGAATO	GTGCGGGAAG'	CATTGATCTTCTCGAGGA	rgctgtgcggaatc 	TCGTTAC	963
Sbjct	1364	TÁÁCGÁGÁÁT	ĠŦĊĊĠŦĠĀĠĠſ	rcatcgatctgctcgagga:	rĠĊϮĠϮĠĊĠĊĀĀϮŦ	†GĠ†CÁĊ	1423
Query	964	GCTGGCGCAG(GCAAGCTGA 	AGGAGCAGGATCAGTGCGC(CTTTCGCTACAGTG 	GATCTGG 	1023
Sbjct	1424	actĠĠĊaĊáĠ(GĠĊAAAĊTCA?	AĠĠAĠĊAĠĠATĊAĠTĠĊAĊ(GTTTĊĠĊTĂĊĂĠCĠ	ĠCGGŦĠĠ	1483
Query	1024	CTTGGGCGGC	ATTGGAGCGG(CGGCGGAGATCATGGGTGC(GTCACCGCCTC	GC-CGG-	1079
Sbjct	1484	ĊĊŦĠĠĠĊĠĠĊ	ÁTCĠĠTĠĊCĠ(ĊĊĠĊĊĠĂŦĂŤĂĂŤĠĠĠĊĠĊſ	CĠŤĠĂĊĊĠĊĊĠĊCA	ĠĊAĊĠĠC	1543
Query	1080	GAGCGAGTO	GTTCCCGGTA(CTGGAGTCATGC-G-C-GT'	ГТСGGССGССGА 	AT-CAGC	1131
Sbjct	1544	ĠĠĠĊĠĠĊÀĠŤſ	ĠŤĠĊĊĊĠĠ–ĀŒ	ĊŦĠĊĀ-Ŧ-ĀĊĠĊĊĠĠĊĊĠAſ	tGĊĠĠĊĊĠĊGGĊĠG	CTGCAGT	1600
Query	1132	TGCCCAGCGT	ACTTCGTTGC(CGGACATAGCGCTCACGCC(CAAGGAGCGCGACA 	TACTGGA	1191
Sbjct	1601	CĠĊĠĊĀĠĊĠĀ	ACGTCGCTGC(ĊĠĠĀĊĀŢŢĠĊĠĊŢĠĀĊĠĊĊŒ	ĊAAĠĠAĠĊĠĊĠAĊA	TÀCTGGÀ	1660
Query	1192	GCAGCACAAT(GTGAACCCGA' 	IGCGCGGCTCCCACAGCAC	CGAAAGTATCCTGC 	GCGACAC 	1251
Sbjct	1661	ĠĊĀĠAGĊĀĀŦŒ	ĠŦĠĂĂŦĊĊĠĂſ	ŢĠĊĠĊĠĠĊŢĊŢĊĂĊĂĠĊĂĊ(ĊĠĀĠĀĠĊĀŤĀĊŤĠĊ	ĠĊĠĂĊĂĊ	1720
Query	1252			CGCTACCCAATAGGGCCAG' 			1311
Sbjct	1721	ĠĀĠĊĊĠĊĊĠ	ĊĊAÄÄĠĊĊĠĊ	ĊĠĊϮĠĊĊĊĂĂϮĊĠĠŦĊĠĂĠŒ	CAATCCGCCGCCGT	ŤAĊĊÁĊĊ	1780
Query	1312	AAAGCGACGC	AGCCAGCCG	1330			
Sbjct	1781	AAAĠĊĠŦĊĠĊ	AĠĊĊĀĠĊĊĠ	1799			

Range 2: 610 to 725

Score		Expect	Identities	Gaps	Strand	Frame	
78.7 bits	s(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATCA	AGTTCTCCATCCACGO	CCCGGCACCTGTTCC	CAG-T-GG-CATC	GGAGT-G	220

Sbjct 610 ACGGCAGCATCAGTTCTCCATCCACGCCCAGTAATTGCTCGGGGTCGGGCGGCGGCGTCG 669

Query 221 G-G-CGG--T-GGCGGCTGCAGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGC 271

Sbjct 670 GCGTCGGCGTCGGTGGCTGCAACAGCAGCAGCAACAACAGCATCAACAGTGGCAGC 725

Drosophila mojavensis uncharacterized protein, transcript variant B (Dmoj\Gl21607), mRNA Sequence ID: **ref|XM_015161040.1|** Length: 4840 Number of Matches: 2 Range 1: 470 to 1384

Score		Expect	Identities	Gaps	Strand	Frame	
761 bits	(412)	0.0()	753/919(829	%) 17/919(1%)	Plus/Plus		
Features	s:						
Query	425	GGATCCTCGG	GCCACAAGAAC	AGTCTCAAGGGCACCAAGC	TAGCGCGCCGGGC	GCGTTCC	484
Sbjct	470	GGATCGTCCG	GCCATAAGAAC	AGTTTGAAGGGCACGAAAT	TGGCGCGACGAGC	gcgttcc	529
Query	485	TTTAAGGACGA	ACCTCATCGAG	AAGATTTCCCTGATGCGAA	CCACCAACAATAC.	ACTGGGT	544
Sbjct	530	TTCAAGGACGA	Arctaattgag	AAGATCTCACTGATGCGCA	ccycyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyy	gctcggc	589
Query	545	CGCTCCCACTO	CGCCGCACAGT(CCGCGCACCAAGCACGGCA	CAAAGGCACCGCC	CACCACC	604
Sbjct	590	ccctcccartc	cdccdcacadt(ccececantadecatecca	rcyydccececec	caccacc	649
Query	605	GAGGAGGTGC	TACGGTCCACC	CAAACCCTGGAGACGCACG	TCAAGGACATTTC	GAATGCC 	664
Sbjct	650	gyggyggyggyggyggyggyggyggyggyggyggyggyg	agcgatccaca(cydyrain y charlen y	rtcaaggacatatc	ĠĀĀŦĠĊG	709
Query	665	CTGAAGCACT	CCGGGATGTT	ATACTCAAGAAGAAGCTGG	AGGTGTTGCCGGG	CAACGGA 	724
Sbjct	710	ctcaaacact:	trcccdatct	Atactcagaaaddaacctcc	saagtgetgeetge	CAATGGC	769
Query	725	ACGGTCATTC	rggaaaccata 	GCCAGCATGTACTCCGTGA	TCCAAACCTACAC	CCTGAAT 	784
Sbjct	770	ACCGTCATAC:	rĠĠĀGĀĊĊĀŤŦ	ĠĊĊĀĠĊĀŦĠŦĀŦŦĊĊĠŦĊĀ	.tccagtcgtacac.	AĊŦĠĀĀC	829
Query	785	GAAAACAGTGO	CCATCATGAGC	AGCGCCACGCTGCAGGTTT 	ACCAGAGC-CTGG	GCAAGCT 	843
Sbjct	830	ĠĀĠĀĀĊĀĠŦĠŒ	ccatcatgagc [,]	rcgĠċċāċcċāĠċāĠĠtgt	'ATĊA-ATĊGĊŤTĠ(ĠĊĀĀĠĊŢ	888
Query	844	CATCAAGCTC	rgcgacgaggt(GATGCTCTCCGAGGACAGC 	GGCGAGTGCGCCT!	CCCTGAG	903
Sbjct	889	ĊATĊAAĠĊTĊ!	rĠĊĠAĊĠAĠĠŦ(ĠAŢĠĊŢĠŖĠĊĠŖĸĸŖĠĠĊ	'ACĊĠĀATĠĊĠĊĊŦ	ĊĊĊŢĠĀĠ	948
Query	904			CATTGATCTTCTCGAGGAT 			963
Sbjct	949			ĊATCĠATĊTGĊTĊĠAĠĠAT			1008
Query	964	GCTGGCGCAG(GCAAGCTGAA(GGAGCAGGATCAGTGCGCC 	TTTCGCTACAGTG 	GATCTGG 	1023
Sbjct	1009			ĠĠĀĠĊĀĠĠĀŦĊĀĠŦĠĊĀĊĠ			1068
Query	1024			GGCGGAGATCATGGGTGCG			1079
Sbjct	1069			CĠĊCĠĂTĂŤAĂŤĠĠĠĊĠĊĊ			1128
Query	1080			TGGAGTCATGC			1131
Sbjct	1129			ŤĠĊÀ–Ť–ÀCĠĊĊĠĠĊĊĠAŤ			1185
Query	1132			GGACATAGCGCTCACGCCC 			1191
Sbjct	1186			ĠĠĂĊĂŤŦĠĊĠĊŤĠĂĊĠĊĊĊ			1245
Query	1192			GCGCGGCTCCCACAGCACC 			1251
Sbjct	1246			ĠĊĠĊĠĠĊϮĊŦĊĂĊĂĠĊĂĊĊ			1305
Query	1252			GCTACCCAATAGGGCCAGT 			1311
Sbjct	1306			ĠĊϮĠĊĊĊĂĂϮĊĠĠŦĊĠĂĠĊ	'AATĊĊĠĊĊĠĊĊĠĊ	ŤAĊĊÁĊĊ	1365
Query	1312	AAAGCGACGCA		1330			
Sbjct	1366	AAAĠĊĠŦĊĠĊ	AĠĊĊÁĠĊĊĠ	1384			

Range 2: 195 to 310

Score	Expect	Identities	Gaps	Strand	Frame
78.7 bits(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus	
Features:					

Query	165	ACGGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGTTCCAG-T-GG-CATCGGAGT-G	220
Sbjct	195	ACGGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGTTCCAG-T-GG-CATCGGAGT-G	254
Query	221	G-G-CGG-T-GGCGGCTGCAGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGC 27	1
Sbjct	255	G-G-CGGT-GGCGGCTGCAGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGC 27)

Drosophila mojavensis uncharacterized protein, transcript variant E (Dmoj\Gl21607), mRNA Sequence ID: **ref|XM_002010591.2|** Length: 5232 Number of Matches: 2 Range 1: 886 to 1800

Score		Expect	Identities	Gaps	Strand	Frame	
761 bits	(412)	0.0()	753/919(82%)	17/919(1%)	Plus/Plus		
Features	S :						
Query	425	GGATCCTCGG	GCCACAAGAACAGTCT	'CAAGGGCACCAAGC'	TAGCGCGCCGGGC	GCGTTCC	484
Sbjct	886	GGATCGTCCG	GCCATAAGAACAGTTI	'GAAGGGCACGAAAT'	rggcgcgacgagc	GCGTTCC	945
Query	485	TTTAAGGACG	ACCTCATCGAGAAGAT	TTCCCTGATGCGAA	CCACCAACAATAC	ACTGGGT	544
Sbjct	946	TTCAAGGACG	Arctaatrgagaagat	ctcactgatgcgcad	ccycyyycyycyc (cycycyc)	gctcggc	1005
Query	545	CGCTCCCACT	CGCCGCACAGTCCGCG	CACCAAGCACGGCAC	CAAAGGCACCGCC	CACCACC	604
Sbjct	1006	ccctcccart	cececacaetce	ckataagcatgccac	cyyęc c c c c c c c c c c c c c c c c c	çyççyçç	1065
Query	605	GAGGAGGTGC'	TACGGTCCACCCAAAC	CCTGGAGACGCACG!	FCAAGGACATTTC(GAATGCC 	664
Sbjct	1066	ĠĀĠĠĀĠĠŦĠĊ	AGĊĠATĊĊĀĊAĊĀĠĀĊ	GĊŦĠĠĀĠĀĊĠĊĀĊĠ?	rcaaggacatatco	ĠÀÀŤĠĊG	1125
Query	665		PCCGGGATGTTATACT 				724
Sbjct	1126	ĊŢĊĄĄĄĊĄĊŢ	trċĠċĠàtĠtcàtàċt	'ĊAGAAAĠAAĠĊŦĠĠ <i>i</i>	AAĠŦĠĊŦĠĊĊŦĠĠ(ĊĀĀTĠĠC	1185
Query	725	ACGGTCATTC	rggaaaccatagccag 	CATGTACTCCGTGAT		CCTGAAT 	784
Sbjct	1186	ACCGTCATAC:	rĠĠAGAĊĊATTĠĊĊAĠ	CATGTATTCCGTCAT	rccagrcgtacac;	AĊŢĠĀĀC	1245
Query	785		CCATCATGAGCAGCGC 				843
Sbjct	1246	ĠĀĠĀĀĊĀĠŦĠŒ		ĊĂĊĊĊĀĠĊĀĠĠŤĠŤ <i>I</i>			1304
Query	844		FGCGACGAGGTGATGC 			CCCTGAG 	903
Sbjct	1305			TGAGĊĠĀAAĀGĀĠĊ <i>i</i>		CCCTGAG	1364
Query	904		GTGCGGGAAGTCATTG				963
Sbjct	1365		ĠŤĊĊĠŦĠĂĠĠŤĊĂŤĊĠ				1424
Query	964		GCAAGCTGAAGGAGC				1023
Sbjct	1425		ĠĠĊŔŔĸĊŤĊŔŔĠĠŔĠĊ				1484
Query	1024		ATTGGAGCGGCGGCGG				1079
Sbjct	1485		ÁTCGGTGCCGCCGCCG GTTCCCGGTACTGGAG				1544 1131
Query Sbjct	1080 1545		GTGCCGGTACTGGAG				1601
Query	1132		ACTTCGTTGCCGGACA				1191
Sbjct	1602		ACGTCGTTGCCGGACA				1661
Query	1192		GTGAACCCGATGCGCG				1251
Sbjct	1662						1721
Query	1252		CCGAAGCCACCGCTAC				1311
Sbjct	1722		CCAAGCCACCGCTAC 				1781
Query	1312	AAAGCGACGC		.commicoorconder		INCOACC	1/01
Sbjct	1782	AAAGCGACGCAAAAGCGTCGCA					
טטטפנ	1/02	ANAGUGIUGU	AUCCAUCCU 1000				

Range 2: 611 to 726

Score	Expect	Identities	Gaps	Strand	Frame
78.7 bits(42)	5e-10()	93/116(80%)	9/116(7%)	Plus/Plus	_

Featur	es:		
Query	165	ACGGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGTTCCAG-T-GG-CATCGGAGT-G	220
Sbjct	611	ACGCAGCATCAGTTCTCCATCCACGCCCAGTAATTGCTCGGGGTCGGGCGGCGGCGTCG	670
Query	221	G-G-CGGT-GGCGGCTGCAGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGC 271	
Sbict	671	GCGTCGGCGTCGGTGCCTGCAACAGCAGCAGCAACAACAGCATCAACAGTGGCAGC 726	

Drosophila ananassae uncharacterized protein, transcript variant C (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905493.1|** Length: 5697 Number of Matches: 2 Range 1: 369 to 1046

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Feature	s:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGAT	TCCTCGGGCCACAAG	AACAGTCTCAAGG	GCACCAA	462
Sbjct	369	ACCACCAGCAC	CGCCAAGTGCCGGAT	CATCGGGCCATAAG	AACAGCCTAAAGG	GCACAAA	428
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTT <i>I</i>	AAGGACGACCTCATC	GAGAAGATTTCCC	TGATGCG	522
Sbjct	429	dctgdcaadga	ggggggggtgtttt	Aggacgacctgatc	GAGAAAATCTCCC	rtgatgeg	488
Query	523	AACCACCAACA	ATACACTGGGTCGC7	CCCACTCGCCGCAC	AGTCCGCGCACCA	AGCACGG	582
Sbjct	489	gyccyccyycy	AcAcgrtdddtadat	rcccartccccccacac	yę4ccecectecy yę4ccecec	rygcycee	548
Query	583	CACAAAGGCAC	CGCCCACCACCGAGG	GAGGTGCTACGGTCC	ACCCAAACCCTGG	GAGACGCA	642
Sbjct	549	ctgcaagccac	¢Ġ¢¢¢Ag¢AA¢ĠAĠ¢	saggtccagcgctcc	Acccagaccctcc	SAGACTCA	608
Query	643	CGTCAAGGACA	TTTCGAATGCCCTG <i>I</i>	AGCACTTCCGGGAT(GTTATACTCAAGA 	AGAAGCT	702
Sbjct	609	cctcaacca	tctccaatgccctc	Adcacttcccccata	stcatactcaaga	Adaadct	668
Query	703	GGAGGTGTTGC	CGGGCAACGGAACGG	GTCATTCTGGAAACC	ATAGCCAGCATGT 	ACTCCGT	762
Sbjct	669	ĠĠĀĀĠŦŦĊŦĠĊ	ĊĠĠĠĠĀĀŦĠĠĊĀĊĀĊ	stratcċtĠĠagaċċ <i>i</i>	AtaĠĊĊAĠĊAtĠt	Actccct	728
Query	763	GATCCAAACCT	ACACCCTGAATGAAA	AACAGTGCCATCATGA 	AGCAGCGCCACGC 	TGCAGGT	822
Sbjct	729	TÁTTCÁÁÁCCT	ÁTÁĊGĊŤĠÁÁCĠÁG <i>Ź</i>	\ATAĠŦĠĊĊACĊAŦĠ <i>i</i>	^A ĠĊTCĊĠĊĊAĊĠĊ	CAĠĊĀĠĠ甘	788
Query	823	TTACCAGAGCC	TGGGCAAGCTCATCA	\AGCTCTGCGACGAG(GTGATGCTCTCCG 	SAGGACAG	882
Sbjct	789	CTÁCCÁGÁGCC	TĠĠĠĊĂĂĠĊTĊĂTĊ <i>Ĭ</i>	\AĠĊŦĊŦĠĊĠAĊĠAĠ(ĠŦĠĂŦĠĊŦĊŦĊĊĠ	GĠĠĀGĀĠ	848
Query	883			GAGAATGTGCGGGAA(942
Sbjct	849	ĊĠAĊĠĀĠŦĠĊĠ	ĊĊŦĊĊĊŦŦĂĠĊĂĂĊĠ	SAGAACGTCCGGGAG(ĠŦĊĂŦĊĠĂŦĊŦŦĊ	ĊŢŢĠĀĠĠĀ	908
Query	943			GCGCAGGGCAAGCTG2			1002
Sbjct	909	ŤĠĊAĠŤĠAĠĠĀ	ÀTĊTĊĠTTÀĊCTTĠ(ĠĊĊĊŔĠĠĠĠŔŔĠĊŤĊ	AAĠĠAĠĊAĠĠAŦĊ	CÁĠŤĠĊAĊ	968
Query	1003			GGCGGCATTGGAGCG(1062
Sbjct	969			ĠĊĠĠĠĀŢŢĠĠĀĠĊŢſ	GCCGCCGAGATCA	ATĠĠĠĊĠĊ	1028
Query	1063	GGTCACCGCCT					
Sbjct	1029	CĠŤAÁĊAĠĊĊŤ	ĊCĊĊĠĠĠ 1046				

Range 2: 160 to 285

Score		Expect	Identities	Gaps	Strand	Frame	
124 bits	(67)	6e-24()	112/132(85%)	10/132(7%)	Plus/Plus		
Features	S :						
Query	164	AACGGCAGCA7	CAGTTCTCCATCCAC	CGCCCGGCACCTGTTC	CAGTGGCATCGG-	-AGTGGG	222
Sbjct	160	AACGGCAGCAT	rcagttctccatccac	cecceecacce	cygcedecece	cadcdd-	218
Query	223	CGGTGGCGGCT	GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	AACAATAGCATCAACA	GCGGCAGCTI	ACTCCAC	279
Sbjct	219	cggtggc	recyecyecyecyecy	AACAACAGCCTCAACA	gregcaacaect	Actcggc	275
Query	280	CGCCTGCACTC	CC 291				
Sbjct	276	ccc-cch-tc	cc 285				

Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF20837), mRNA

Sequence ID: **ref|XM_014905492.1|** Length: 5739 Number of Matches: 2 Range 1: 618 to 1295

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Feature	s:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGG	ATCCTCGGGCCACAA	GAACAGTCTCAAG	GGCACCAA	462
Sbjct	618	Accaccadcac	cccaactcccc	Atcatcgggccataa	gaacagcctaaag	GGCACAAA	677
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTT	TAAGGACGACCTCAT	CGAGAAGATTTCC	CTGATGCG	522
Sbjct	678	dctgdcaadga	ĠĠĠĠĠĠĠĊŦĊĊŦŦ	caaggacgacctgat	cdadaaaatctcc	ctgatgcg	737
Query	523	AACCACCAACA	ATACACTGGGTCG	CTCCCACTCGCCGCA	CAGTCCGCGCACC	AAGCACGG 	582
Sbjct	738	GĄCCĄCCĄĄCĄ	AcAcgrtgggtag	atcccattcccca	cadtccccccc.	AAGCACGG	797
Query	583	CACAAAGGCAC	CGCCCACCACCGA	GGAGGTGCTACGGTC	CACCCAAACCCTG(GAGACGCA	642
Sbjct	798	ĊTGCAAĠCĊAĊ	ĊĠĊĊĊAGĊAAĊĠA	.ĠĠĀĠĠϮCĊAGĊĠCϮĊ	ĊĂĊĊĊĂGĂĊĊĊŤĠ(ĠAĠAĊTĊA	857
Query	643	CGTCAAGGACA	TTTCGAATGCCCT	GAAGCACTTCCGGGA	TGTTATACTCAAG. 	AAGAAGCT 	702
Sbjct	858	ĊĠϮĊÀÀĠĠÀĊÀ	†C†ĊCÀÀ†ĠĊĊĊŤ	CAAĠĊAĊϮϮĊĊĠĠĠA	ŤĠŤCÀŤÀĊŤĊÀÀĠ.	ÄÄĠÄÄĠĊŢ	917
Query	703			GGTCATTCTGGAAAC			762
Sbjct	918			AĞTTÄTCČTĞĞAGÄČ			977
Query	763			AAACAGTGCCATCAT			822
Sbjct	978			GAATAGTGCCACCAT			1037
Query	823			CAAGCTCTGCGACGA			882
Sbjct	1038			ĊĂĂĠĊŦĊŦĠĊĠĂĊĠĂ			1097
Query	883			.CGAGAATGTGCGGGA 			942
Sbjct	1098			.cgagaacgtccggga			1157
Query	943			GGCGCAGGGCAAGCT			1002
Sbjct	1158			ĠĠĊĊĊĀĠĠĠĠĀĀĠĊŢ			1217
Query	1003			GGGCGGCATTGGAGC			1062
Sbjct	1218			ĠĠĠĊĠĠĠĂŤŤĠĠĂĠĊ	TGCCGCCGAGATC	ATGGGCGC	1277
Query	1063	GGTCACCGCCT					
Sbjct	1278	CĠŤAÁĊAĠĊĊŤ	CCCCGGG 1295				

Range 2: 410 to 534

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits	(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATC.	AGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG- <i>I</i>	AGTGGGC	223
Sbjct	410	ACGGCAGCATC.	AGTTCTCCATCCAC	GCCCGGCACCTGCTCC	AGCGGCGGCZ	AGCGG-C	468
Query	224	GGTGGCGGCTG	CAGCAGCAGCA 	ACAATAGCATCAACAG	CGGCAGCTAC	CTCCACC	280
Sbjct	469	ĠĠŦĠĠĊŦĠ	cagcagcagcagca	Acaacagcctcaacag	TGGCAACAGCTAG	ctcggcc	525
Query	281	GCCTGCACTCC	291				
Sbjct	526	gcc-gcy-4cc	534				

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Feature	s:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGA	TCCTCGGGCCACAAG.	AACAGTCTCAAG(GGCACCAA	462
Sbjct	617	Accaccadcac	cgccaagtgccgda	.tcatcgggccataag.	AACAGCCTAAAG	GCACAAA	676
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTT	AAGGACGACCTCATC	GAGAAGATTTCC	CTGATGCG	522
Sbjct	677	dctgdcaadga	ĠĠĠĠĠĠĠĠĊŦĊĊŦŦĊ	AAGGACGACCTGATC	gagaaaatctcc	ctgatgcg	736
Query	523	AACCACCAACA	ATACACTGGGTCGC	TCCCACTCGCCGCAC.	AGTCCGCGCACC	AAGCACGG	582
Sbjct	737	GACCACCAACA	ACACGTTGGGTAGA	.tcccartcgccgcac	Adtccccccc	AAGCACGG	796
Query	583	CACAAAGGCAC	CGCCCACCACCGAG	GAGGTGCTACGGTCC.	ACCCAAACCCTG(GAGACGCA	642
Sbjct	797	ĊTGCÅÅĠCĊÅĊ	ĊĠĊĊĊĀĠĊĀĀĊĠĀĠ	ĠĀĠĠŦĊĊĀĠĊĠĊŦĊĊ.	Acccagaccctg Acccagaccctg	GAGACTCA	856
Query	643	CGTCAAGGACA	TTTCGAATGCCCTG	AAGCACTTCCGGGAT	GTTATACTCAAGA 	AAGAAGCT 	702
Sbjct	857	ĊĠϮĊAAĠĠAĊA	TCTCCAATGCCCTC	AAGCACTTCCGGGAT	ĠϮĊĂϮĂĊϮĊĂĂĠĀ	AAĠAAĠĊŢ	916
Query	703	GGAGGTGTTGC	CGGGCAACGGAACG	GTCATTCTGGAAACC.	ATAGCCAGCATG' 	PACTCCGT	762
Sbjct	917			ĠŤŦĂŤĊĊŤĠĠĀĠĀĊĊ.			976
Query	763			AACAGTGCCATCATG. 			822
Sbjct	977			AATAGTGCCACCATG.			1036
Query	823			AAGCTCTGCGACGAG			882
Sbjct	1037	CTACCAGAGCC			GTGATGCTCTCC		1096
Query	883			GAGAATGTGCGGGAA			942
Sbjct	1097			ĠĀĠĀĀCĠŦĊĊĠĠĠĀĢ			1156
Query	943			GCGCAGGGCAAGCTG.			1002
Sbjct	1157			ĠĊĊĊĀĠĠĠĠĀĀĠĊŤĊ.			1216
Query	1003			GGCGGCATTGGAGCG			1062
Sbjct	1217			ĠĠĊĠĠĠĀŤŤĠĠĀĠĊŦ	GCCGCCGAGATC/	ATGGGCGC	1276
Query	1063	GGTCACCGCCT					
Sbjct	1277	CĠŤAÁĊAĠĊĊŤ	CCCCGGG 1294				

Range 2: 409 to 533

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits	(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATO	CAGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG-A	AGTGGGC	223
Sbjct	409	ACGGCAGCATO	CAGTTCTCCATCCAC	SCCCGGCACCTGCTCC	AGCGGCGGCZ	AGCGG-C	467
Query	224	GGTGGCGGCT	GCAGCAGCAGCAGCA	ACAATAGCATCAACAG	CGGCAGCTAC	CTCCACC	280
Sbjct	468	GGTGGCTC	GCAGCAGCAGCAZ	Acadecteaacad	TGGCAACAGCTAG	ctceecc	524
Query	281	GCCTGCACTC	291				
Sbjct	525	GCC-GCA-TCC	533				

Drosophila ananassae uncharacterized protein, transcript variant D (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905491.1|** Length: 6011 Number of Matches: 2 Range 1: 683 to 1360

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Feature	s:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGATC	CCTCGGGCCACAAGA	AACAGTCTCAAGG	GCACCAA 	462

Sbjct	683	ACCACCAGCACCGCCAAGTGCCGGATCATCGGGCCATAAGAACAGCCTAAAGGGCACAAA	742
Query	463	GCTAGCGCGCGGGCGCGTTCCTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCG	522
Sbjct	743	GCTGGCAAGGAGGGCGCCTCCTTCAAGGACGACCTGATCGAGAAAATCTCCCTGATGCG	802
Query	523	AACCACCAACAATACACTGGGTCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGG	582
Sbjct	803	GACCACCAACACGTTGGGTAGATCCCATTCGCCGCACAGTCCGCGCTCCAAGCACGG	862
Query	583	CACAAAGGCACCGCCCACCACGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCA	642
Sbjct	863	CTGCAAGCCACCGCCAGCAACGAGGAGGTCCAGCGCTCCACCCAGACCCTGGAGACTCA	922
Query	643	CGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCT	702
Sbjct	923	CGTCAAGGACATCTCCAATGCCCTCAAGCACTTCCGGGATGTCATACTCAAGAAGAAGCT	982
Query	703	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	762
Sbjct	983	GGAAGTTCTGCCGGGGAATGGCACAGTTATCCTGGAGACCATAGCCAGCATGTACTCCGT	1042
Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822
Sbjct	1043	TATTCAAACCTATACGCTGAACGAGAATAGTGCCACCATGAGCTCCGCCACGCAGCAGGT	1102
Query	823	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Sbjct	1103	CTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGGGGAGAG	1162
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	1163	CGACGAGTGCGCCTCCCTTAGCAACGAGAACGTCCGGGAGGTCATCGATCTTCTTGAGGA	1222
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002
Sbjct	1223	TGCAGTGAGGAATCTCGTTACCTTGGCCCAGGGGAAGCTCAAGGAGCAGGATCAGTGCAC	1282
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1283	CTTTCGGTATGGTGGCGCCGGTCTGGGCGGGATTGGAGCTGCCGCCGAGATCATGGGCGC	1342
Query	1063	GGTCACCGCCTCGCCGGG 1080	
Sbjct	1343	CGTAACAGCCTCCCGGG 1360	

Range 2: 475 to 599

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits(66) 2e-23()		2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Features	S :						
Query	165	ACGGCAGCATC	AGTTCTCCATCCAC	GCCCGGCACCTGTTCC.	AGTGGCATCGG- <i>I</i>	AGTGGGC	223
Sbjct	475	Acccaccatc	agtteteeateeac	scccggcacctgctcc.	adcedecedeca	yecee-c	533
Query	224	GGTGGCGGCTG	CAGCAGCAGCAGCA	ACAATAGCATCAACAG	CGGCAGCTAC	CTCCACC	280
Sbjct	534	GGTGGCTG	cagcagcagcagca	ACAACAGCCTCAACAG	TGGCAACAGCTAG	ctcggcc	590
Query	281	GCCTGCACTCC	291				
Sbjct	591	dcc-dca-tcc	599				

Drosophila ananassae uncharacterized protein, transcript variant K (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905490.1|** Length: 3083 Number of Matches: 2 Range 1: 622 to 1299

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Feature	s:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGATC	CTCGGGCCACAAG	AACAGTCTCAAG(GGCACCAA	462
Sbjct	622	ACCACCAGCAC	CGCCAAGTGCCGGATC	CATCGGGCCATAAGA	AACAGCCTAAAG	GGCACAAA	681
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTTAA	AGGACGACCTCATCO	GAGAAGATTTCC	CTGATGCG	522
Sbjct	682	GCTGGCAAGGA	dedecectecttead	deaceaccteatco	GAGAAAATCTCC	ctgatgcg	741
Query	523	AACCACCAACA	ATACACTGGGTCGCTC	CCACTCGCCGCAC	AGTCCGCGCACC	AAGCACGG	582
Sbjct	742	GACCACCAACA	ACACGTTGGGTAGATC	ccentceccecac	Agtccccccct	AAGCACGG	801

Query	583	CACAAAGGCACCGCCCACCACGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCA	642
Sbjct	802	CTGCAAGCCACCGCCAGCAACGAGGAGGTCCAGCGCTCCACCCAGACCCTGGAGACTCA	861
Query	643	CGTCAAGGACATTTCGAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCT	702
Sbjct	862	CGTCAAGGACATCTCCAATGCCCTCAAGCACTTCCGGGATGTCATACTCAAGAAGAAGCT	921
Query	703	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	762
Sbjct	922	GGAAGTTCTGCCGGGGAATGGCACAGTTATCCTGGAGACCATAGCCAGCATGTACTCCGT	981
Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822
Sbjct	982	TATTCAAACCTATACGCTGAACGAGAATAGTGCCACCATGAGCTCCGCCACGCAGCAGGT	1041
Query	823	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Sbjct	1042	ctaccagagcctgggcaagctcatcaagctctgcgacgaggtgatgctctccggggagag	1101
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	1102	CGACGAGTGCGCCTCCCTTAGCAACGAGAACGTCCGGGAGGTCATCGATCTTCTTGAGGA	1161
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002
Sbjct	1162	tgcagtgaggaatctcgttaccttggcccaggggaagctcaaggagcaggatcagtgcac	1221
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1222	ctttcggtatggtggcgccggtctgggcggattggagctgccgcgagatcatgggcgc	1281
Query	1063	GGTCACCGCCTCGCCGGG 1080	
Sbjct	1282	cgtaacagcctccccgg 1299	

Range 2: 414 to 538

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits(66)		2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATC	AGTTCTCCATCCACG	CCCGGCACCTGTTCC	AGTGGCATCGG-	ĄĢTĢĢGÇ	223
Sbjct	414	ACGGCAGCATC	AGTTCTCCATCCACG	cccgcacctgctcc	AGCGGCGGC.	AGCGG-C	472
Query	224		CAGCAGCAGCAA	CAATAGCATCAACAG	CGGCAGCTA	СТССАСС	280
Sbjct	473	ggtggctg	cagcagcagcagcaa	.caacagcctcaacag	TGGCAACAGCTA	ctceecc	529
Query	281	GCCTGCACTCC	291				
Sbjct	530	gcc-gcy-tcc	538				

Drosophila ananassae uncharacterized protein, transcript variant J (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905489.1|** Length: 5948 Number of Matches: 2 Range 1: 620 to 1297

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Features	S:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGAT	CCTCGGGCCACAAGA	ACAGTCTCAAG	GGCACCAA	462
Sbjct	620	ACCACCAGCAC	ccccaagtgccgdate	CATCGGGCCATAAGA	ACAGCCTAAAG	GGCACAAA	679
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTTA	AGGACGACCTCATCO	AGAAGATTTCC	CTGATGCG	522
Sbjct	680	GCTGGCAAGGA	dedececetectech	AGGACGACCTGATC	sadaaaatctcc	ctdatdcd	739
Query	523	AACCACCAACA	ATACACTGGGTCGCT	CCCACTCGCCGCAC	AGTCCGCGCACC	AAGCACGG	582
Sbjct	740	GĄCCĄCCĄĄCĄ	Acacgttgggtagat	cccartccccccc	zet e e e e e e e e e e e e e e e e e e	AAGCACGG	799
Query	583	CACAAAGGCAC	CGCCCACCACCGAGG	AGGTGCTACGGTCC <i>I</i>	ACCCAAACCCTG(GAGACGCA	642
Sbjct	800	CTGCAAGCCAC	cccccaccaaccacca	AGGTCCAGCGCTCC	rcccaeacccte	GAGACTCA	859
Query	643	CGTCAAGGACA	TTTCGAATGCCCTGA	AGCACTTCCGGGAT(GTTATACTCAAG	AAGAAGCT	702
Sbjct	860	cctcaaca	rtctccaatgccctca	agcacttccgggatd	stcatactcaag	AAGAAGCT	919

Query	703	GGAGGTGTTGCCGGGCAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGT	762
Sbjct	920	GGAAGTTCTGCCGGGGAATGGCACAGTTATCCTGGAGACCATAGCCAGCATGTACTCCGT	979
Query	763	GATCCAAACCTACACCCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGT	822
Sbjct	980	TATTCAAACCTATACGCTGAACGAGAATAGTGCCACCATGAGCTCCGCCACGCAGCAGGT	1039
Query	823	TTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAG	882
Sbjct	1040	CTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGGGGAGAG	1099
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	1100	CGACGAGTGCGCCTCCCTTAGCAACGAGAACGTCCGGGAGGTCATCGATCTTCTTGAGGA	1159
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002
Sbjct	1160	TGCAGTGAGGAATCTCGTTACCTTGGCCCAGGGGAAGCTCAAGGAGCAGGATCAGTGCAC	1219
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1220	CTTTCGGTATGGTGGCGCGGTCTGGGCGGGATTGGAGCTGCCGCCGAGATCATGGGCGC	1279
Query	1063	GGTCACCGCCTCGCCGGG 1080	
Sbjct	1280	CGTAACAGCCTCCCGGG 1297	

Range 2: 412 to 536

S	core		Expect	Identities	Gaps	Strand	Frame	
12	22 bits	(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Fe	eatures	S :						
Qι	ıery	165	ACGGCAGCATC	AGTTCTCCATCCAC	GCCCGGCACCTGTTCC.	AGTGGCATCGG- <i>I</i>	AGTGGGC	223
Sk	ojct	412	Accccaccatc	AGTTCTCCATCCAC	gcccgccacctgctcc.	AGCGGCGGCGGC	/qcqq-c	470
Qι	ery	224	GGTGGCGGCTG	CAGCAGCAGCA	ACAATAGCATCAACAG	CGGCAGCTAC	CTCCACC	280
Sk	ojct	471	ĠĠŦĠĠĊŦĠ	cagcagcagcagca	acaacagcctcaacag	rddcaacadctad	ctcggcc	527
Qι	ıery	281	GCCTGCACTCC	291				
Sk	ojct	528	ccc-ccy-tcc	536				

Drosophila ananassae uncharacterized protein, transcript variant I (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905488.1|** Length: 5759 Number of Matches: 2 Range 1: 620 to 1297

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Features	S :						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGA	TCCTCGGGCCACAAG	AACAGTCTCAAGG	GCACCAA	462
Sbjct	620	ACCACCAGCAC	CGCCAAGTGCCGGA	TCATCGGGCCATAAG	AACAGCCTAAAG	GCACAAA	679
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTT	AAGGACGACCTCATC	GAGAAGATTTCCC	CTGATGCG	522
Sbjct	680	GCTGGCAAGGA	gggcgcgctccttc	AAGGACGACCTGATC	gagaaaatctccc	ctgatgcg	739
Query	523	AACCACCAACA	ATACACTGGGTCGC	TCCCACTCGCCGCAC	AGTCCGCGCACC <i>I</i>	AAGCACGG	582
Sbjct	740	gaccaccaaca	AcAcgrtgggtaga	tcccartccccccac	AGTCCGCGCTCC <i>I</i>	Adcacdd	799
Query	583	CACAAAGGCAC	CGCCCACCACCGAG	GAGGTGCTACGGTCC	ACCCAAACCCTGG	GAGACGCA	642
Sbjct	800	ctgcaagccac	¢¢¢¢¢ag¢aa¢gag	gaggtccagcgctcc	acccagaccctdd	SAGACTCA	859
Query	643	CGTCAAGGACA	TTTCGAATGCCCTG	AAGCACTTCCGGGAT(GTTATACTCAAG <i>I</i>	AAGAAGCT	702
Sbjct	860	cetcyyey	tctccaatgccctc	AAGCACTTCCGGGAT	gtcatactcaag	Addaddt	919
Query	703	GGAGGTGTTGC	CGGGCAACGGAACG	GTCATTCTGGAAACC	ATAGCCAGCATGT	TACTCCGT	762
Sbjct	920	ddaadtrctdd	cggggyatggcycy	gtratcctggagacc:	AtAGCCAGCATG1	rActccct	979
Query	763	GATCCAAACCT	ACACCCTGAATGAA	AACAGTGCCATCATG	AGCAGCGCCACGC	CTGCAGGT	822
Sbjct	980	таттсааасст	ATACGCTGAACGAG	AATAGTGCCACCATG	agctccccccqcq	CAGCAGGT	1039
Query	823	TTACCAGAGCC	TGGGCAAGCTCATC	AAGCTCTGCGACGAG(GTGATGCTCTCC	SAGGACAG	882

Sbjct	1040	CTACCAGAGCCTGGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGGGGAGAG	1099
Query	883	CGGCGAGTGCGCCTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGA	942
Sbjct	1100	CGACGAGTGCGCCTCCCTTAGCAACGAGAACGTCCGGGAGGTCATCGATCTTCTTGAGGA	1159
Query	943	TGCTGTGCGGAATCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGC	1002
Sbjct	1160	tgcagtgaggaatctcgttaccttggcccaggggaagctcaaggagcaggatcagtgcac	1219
Query	1003	CTTTCGCTACAGTGGATCTGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1220	ctttcggtatggtggcgccggtctgggcggattggagctgccgcgagatcatgggcgc	1279
Query	1063	GGTCACCGCCTCGCCGGG 1080	
Sbjct	1280	CGTAACAGCCTCCCGGG 1297	

Range 2: 412 to 536

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits(66)		2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATC	CAGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG- <i>I</i>	AGTGGGC	223
Sbjct	412	AcGGCAGCATC	cagttctccatccac	GCCCGGCACCTGCTCC.	AGCGGCGGCZ	AGCGG-C	470
Query	224	GGTGGCGGCTG	GCAGCAGCAGCAI	ACAATAGCATCAACAG	CGGCAGCTA(CTCCACC	280
Sbjct	471	ĠĠţĠĠĊţĠ	scadcadcadcadca	ACAACAGCCTCAACAG	TGGCAACAGCTAG	ctcggcc	527
Query	281	GCCTGCACTCC	291				
Sbjct	528	gcc-gcy-4cc	536				

Drosophila ananassae uncharacterized protein, transcript variant H (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905487.1**| Length: 5788 Number of Matches: 2 Range 1: 619 to 1296

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Features	S:						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGAT	CTCGGGCCACAAG	AACAGTCTCAAGO	GCACCAA	462
Sbjct	619	ACCACCAGCAC	CGCCAAGTGCCGGAT	CATCGGGCCATAAG	AACAGCCTAAAG	GGCACAAA	678
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTTA	AGGACGACCTCATC	GAGAAGATTTCC	CTGATGCG	522
Sbjct	679	GCTGGCAAGGA	.gggcgcgctccttcAz	AGGACGACCTGATC	GAGAAAATCTCC	CTGATGCG	738
Query	523	AACCACCAACA	ATACACTGGGTCGCT	CCACTCGCCGCAC	AGTCCGCGCACC <i>I</i>	AAGCACGG	582
Sbjct	739	GACCACCAACA	ACACGTTGGGTAGATO	CCCATTCGCCGCAC	AGTCCGCGCTCC	AAGCACGG	798
Query	583	CACAAAGGCAC	CGCCCACCACCGAGG	AGGTGCTACGGTCC	ACCCAAACCCTGC	GAGACGCA	642
Sbjct	799	CTGCAAGCCAC	CGCCCAGCAACGAGG	AGGTCCAGCGCTCC	Acccagaccctgo	GAGACTCA	858
Query	643	CGTCAAGGACA	TTTCGAATGCCCTGA	AGCACTTCCGGGAT(GTTATACTCAAGA	AAGAAGCT	702
Sbjct	859	cgtcaaggaca	.tctccAAtGccctcAz	y g c y c t t c c d d g y t c	gtcatactcaag	AAGAAGCT	918
Query	703	GGAGGTGTTGC	CGGGCAACGGAACGG	CATTCTGGAAACC	ATAGCCAGCATGT	PACTCCGT	762
Sbjct	919	GGAAGTTCTGC	cccccadatcccccccccccccccccccccccccccccc	tratcctddagacc	Atadecadeatd	ractccct	978
Query	763	GATCCAAACCT	ACACCCTGAATGAAA	ACAGTGCCATCATG	AGCAGCGCCACG(CTGCAGGT	822
Sbjct	979	таттсаласст	ATACGCTGAACGAGA	ATAGTGCCACCATG	AGCTCCGCCACGC	CAGCAGGT	1038
Query	823	TTACCAGAGCC	TGGGCAAGCTCATCA	AGCTCTGCGACGAG	GTGATGCTCTCC	GAGGACAG	882
Sbjct	1039	ctaccadadcc	tgggcaagctcatca	y g c t c t g c g y c g y g o	gtgytgctctcc	GGGAGAG	1098
Query	883	CGGCGAGTGCG	CCTCCCTGAGCAACG	AGAATGTGCGGGAA(GTCATTGATCTT(CTCGAGGA	942
Sbjct	1099	cgacgagtgcg	cctcccttagcaacg	y gyycetropedd y character a c	stcatcgatctt	CTTGAGGA	1158
Query	943	TGCTGTGCGGA	ATCTCGTTACGCTGG(CGCAGGGCAAGCTGA	AAGGAGCAGGAT(CAGTGCGC	1002

Sbjct	1159	TGCAGTGAGGAATCTCGTT	ACCTTGGCCCAGGGAAGCTCAAGGAGCAGGATCAGTGCAC	1218
Query	1003		GGCTTGGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGC	1062
Sbjct	1219	ctttcggtATggtggcgcc	GTCTGGGCGGATTGGAGCTGCCGCGAGATCATGGGCGC	1278
Query	1063	GGTCACCGCCTCGCCGGG	1080	
Sbict	1279	CGTAACAGCCTCCCCGGG	1296	

Range 2: 411 to 535

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits	(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATO	CAGTTCTCCATCCAC	GCCCGGCACCTGTTCC.	AGTGGCATCGG-	AGTGGGC	223
Sbjct	411	ACGGCAGCATO	cagtteteeateeace	scccddcacctdctcc.	AGCGGCGGC	AGCGG-C	469
Query	224	GGTGGCGGCTG	GCAGCAGCAGCAI	ACAATAGCATCAACAG	CGGCAGCTA	CTCCACC	280
Sbjct	470	GGTGGCTC	SCAGCAGCAGCAZ	ACAACAGCCTCAACAG	TGGCAACAGCTA	CTCGGCC	526
Query	281	GCCTGCACTC	291				
Sbjct	527	ecc-ecy-tcc	535				

Drosophila ananassae uncharacterized protein, transcript variant G (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905486.1|** Length: 5435 Number of Matches: 2 Range 1: 617 to 1294

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Features	S :						
Query	403	ĄÇÇĄÇÇGĢÇĄÇ	ҪѦҪҪСѦ҅Ҫҭ҅ҪҪҪ	, ĢĄŢÇСŢÇĢĢĢÇÇĄCĄĄ	ĢĄĄÇĄĢTÇŢСĄĄĢ	ĢĢÇĄÇCĄĄ	462
Sbjct	617	ACCACCAGCAC			 GAACAGCCTAAAG	 GGCACAAA	676
Query	463	ĢÇŢAĢÇGCĢCC	<mark>ĢĢĢÇĢ</mark> ÇĢТŢÇÇŢ	TTAAGGACGACCTCAT	CGAGAAGATTTCC	CTGATGCG	522
Sbjct	677	GCTGGCAAGGA	ggggggggtct	TCAAGGACGACCTGAT	CGAGAAAATCTCC	CTGATGCG	736
Query	523	AACCACCAACA	ATACACTGGGTC	GCTCCCACTCGCCGCA	CAGTCCGCGCACC.	AAGCACGG	582
Sbjct	737	GACCACCAACA	ACACGTTGGGTA	GATCCCATTCGCCGCA	CAGTCCGCGCTCC.	AAGCACGG	796
Query	583	CACAAAGGCAC	CGCCCACCACCG.	AGGAGGTGCTACGGTC	CACCCAAACCCTG	GAGACGCA	642
Sbjct	797	CTGCAAGCCAC	CGCCCAGCAACG.	AGGAGGTCCAGCGCTC	CACCCAGACCCTG	GAGACTCA	856
Query	643	CGTCAAGGACA	TTTCGAATGCCC	TGAAGCACTTCCGGGA'	rgttatactcaag.	AAGAAGCT	702
Sbjct	857	CGTCAAGGACA	tctccaatgccc	tcaagcacttccggga:	rgtcatactcaag.	AAGAAGCT	916
Query	703	GGAGGTGTTGC	CGGGCAACGGAA	CGGTCATTCTGGAAAC	CATAGCCAGCATG	TACTCCGT	762
Sbjct	917	ggaagttctgc	cddddaatddca	cagttatcctggagaco	catadccadcatd	tactccgt	976
Query	763	GATCCAAACCT	ACACCCTGAATG	AAAACAGTGCCATCAT(GAGCAGCGCCACG	CTGCAGGT	822
Sbjct	977	TATTCAAACCT	ATACGCTGAACG.	AGAATAGTGCCACCAT	GAGCTCCGCCACG	CAGCAGGT	1036
Query	823	TTACCAGAGCC	TGGGCAAGCTCA	TCAAGCTCTGCGACGA	GGTGATGCTCTCC	GAGGACAG	882
Sbjct	1037	ctaccadadcc	teeecaaectea	tcaagctctgcgacga	GGTGATGCTCTCC	GGGGAGAG	1096
Query	883	CGGCGAGTGCG	CCTCCCTGAGCA	ACGAGAATGTGCGGGA	AGTCATTGATCTT	CTCGAGGA	942
Sbjct	1097	cgacgagtgcg	cctcccttagca	acdadaacdtccddda	ggtcatcgatctt	CTTGAGGA	1156
Query	943	TGCTGTGCGGA	ATCTCGTTACGC	TGGCGCAGGGCAAGCT	GAAGGAGCAGGAT	CAGTGCGC	1002
Sbjct	1157	TGCAGTGAGGA	AtctccttAcct	tggcccagggaagct	CAAGGAGCAGGAT	CAGTGCAC	1216
Query	1003	CTTTCGCTACA	GTGGATCTGGCT	TGGGCGGCATTGGAGC(GGCGGCGGAGATC	ATGGGTGC	1062
Sbjct	1217	ctttccctarc	дтерсерсе раз	tgggcgggattggagc:	rdccdccdadatc	Atgggcgc	1276
Query	1063	GGTCACCGCCT	CGCCGGG 108	0			
Sbjct	1277	cdtaacadcct	ccccddd 129	4			

Range 2: 409 to 533

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits	(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATC	AGTTCTCCATCCAC	GCCCGGCACCTGTTCC	AGTGGCATCGG	AGTGGGC	223
Sbjct	409	ACGGCAGCATC	AGTTCTCCATCCAC	GCCGGCACCTGCTCC	AGCGGCGGCGC.	AGCGG-C	467
Query	224	GGTGGCGGCTG	CAGCAGCAGCAGCAZ	ACAATAGCATCAACAG	CGGCAGCTA	CTCCACC	280
Sbjct	468	ddtddctd	cagcagcagca _z	Acaacagcctcaacag	TGGCAACAGCTA	Ç4ÇGGÇÇ	524
Query	281	GCCTGCACTCC	291				
Sbjct	525	dcc-dch-tcc	533				

Drosophila ananassae uncharacterized protein, transcript variant F (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905485.1|** Length: 5832 Number of Matches: 2 Range 1: 618 to 1295

			Gaps	Strand	Frame	
710 bits(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Features:						
Query 403	ACCACCGGCAC	CACCCAGTGCCGG.	ATCCTCGGGCCACAAG	AACAGTCTCAAGO	GCACCAA	462
Sbjct 618	ACCACCAGCAC	CGCCAAGTGCCGG.	ATCATCGGGCCATAAG	AACAGCCTAAAG	GCACAAA	677
Query 463	GCTAGCGCGCCC	GGGCGCGTTCCTT	TAAGGACGACCTCATC	GAGAAGATTTCCC	CTGATGCG	522
Sbjct 678	gctggcaaggac	gegegegeteet	caaggacgacctgatc	dadaaaatctcc	ctgytgcg	737
Query 523	AACCACCAACAA	ATACACTGGGTCG 	CTCCCACTCGCCGCAC	AGTCCGCGCACCI	AAGCACGG	582
Sbjct 738	GÁCCÁCCÁÁCÁZ	ACAĊGTTĠĠĠŦAĠ.	atcccartcccccc	AĠŦĊĊĠĊĠĊŦĊĊ <i>Ĭ</i>	AAĠĊĀĊĠĠ	797
Query 583	CACAAAGGCACO	CGCCCACCACCGA 	GGAGGTGCTACGGTCC 	ACCCAAACCCTGC	GAGACGCA	642
.	ĊTGCĂĂĠCĊĂĊ	ĊĠĊĊĊĠĠĊĀĀĊĠĀ	ĠĠĀĠĠŦĊĊĀĠĊĠĊŦĊĊ	ACCCAGACCCTG(SAĠĀĊŦĊĀ	857
2 2			GAAGCACTTCCGGGAT			702
,			CAAĠĊAĊŢŢĊĊĠĠĠĀŢ		AAGAAGCT	917
~ 1			GGTCATTCTGGAAACC			762
,			AĞTTÁTCCTĞĞAGACC			977
~ 1			AAACAGTGCCATCATG 			822 1037
,			CAAGCTCTGCGACGAG			882
- 1		TGGGCAAGCTCAT			GGGAGAG	1097
_			ÇGAGAATGTGÇGGGAA			942
~ 1						1157
_	ŢĢĊŢĢŢĢĊĢĢĀ <i>I</i>	ATÇTÇĞTTAÇGCT	ĢĢÇGÇĄĢĢGCĄĄĢÇTG	AAGGAGCAGGATO	CAGTGCGC	1002
Sbjct 1158	TGCAGTGAGGAZ		 GGCCAGGGGAAGCTC	 AAGGAGCAGGATO	CAGTGCAC	1217
Query 1003	СТТТСССТАСАС	ĢŢĢĢATÇTĢĢCTŢ	ĢĢĢÇĢĢС ĀŢŢĢĢĀĢÇG	ĢÇGĢÇGĢĀĢĀŢÇ <i>I</i>	АŢĢĢĢŢĢÇ	1062
Sbjct 1218	CTTTCGGTATGO		 GGGCGGGATTGGAGCT	GCCGCCGAGATC	ATGGGCGC	1277
Query 1063	GGTCACCGCCTC	CGCCGGG 1080				
Sbjct 1278	CGTAACAGCCTC	CCCGGG 1295				

Range 2: 410 to 534

Score	Expect	Identities	Gaps	Strand	Frame
122 bits(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus	

Features	S:		
Query	165	ACGGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGTTCCAGTGGCATCGG-AGTGGGC	223
Sbjct	410	AcGGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGCTCCAGCGGCGGCGGCAGCGG-C	468
Query	224	GGTGGCGGCTGCAGCAGCAGCAACAATAGCATCAACAGCGGCAGCTACTCCACC	280
Sbjct	469	GGTGGCTGCAGCAGCAGCAACAACAGCCTCAACAGTGGCAACAGCTACTCGGCC	525
Query	281	GCСТGСАСТСС 291	
Sbjct	526	GCC-GCA-TCC 534	

Drosophila ananassae uncharacterized protein, transcript variant E (Dana\GF20837), mRNA Sequence ID: **ref|XM_014905484.1|** Length: 5857 Number of Matches: 2 Range 1: 619 to 1296

Score		Expect	Identities	Gaps	Strand	Frame	
710 bits	(384)	0.0()	580/678(86%)	0/678(0%)	Plus/Plus		
Features	S :						
Query	403	ACCACCGGCAC	CACCCAGTGCCGGA	TCCTCGGGCCACAAG	AACAGTCTCAAG(GGCACCAA	462
Sbjct	619	ACCACCAGCAC	CGCCAAGTGCCGGA	TCATCGGGCCATAAG	AACAGCCTAAAG	GGCACAAA	678
Query	463	GCTAGCGCGCC	GGGCGCGTTCCTTI	'AAGGACGACCTCATC	GAGAAGATTTCC	CTGATGCG	522
Sbjct	679	dctgdcaadga	ggggggggtgtt	:AAGGACGACCTGATC	GAGAAAATCTCC	ctdatdcd	738
Query	523	AACCACCAACA	ATACACTGGGTCGC	TCCCACTCGCCGCAC	AGTCCGCGCACC	AAGCACGG 	582
Sbjct	739	gaccaccaaca	AcAcgttgggtaga	rtcccattcccccc	AGTCCGCGCTCC	AAGCACGG	798
Query	583	CACAAAGGCAC	CGCCCACCACCGAG	GAGGTGCTACGGTCC	ACCCAAACCCTG(GAGACGCA	642
Sbjct	799	ĊTGCÅÅĠCĊÅĊ	ĊĠĊĊĊAGĊAAĊĠĀĠ	sĠĀĠĠŦĊĊĀĠĊĠĊŦĊĊ <i>ĭ</i>	Acccagaccctg	ЗАĠАĊТĊА	858
Query	643	CGTCAAGGACA	TTTCGAATGCCCTG	GAAGCACTTCCGGGAT(GTTATACTCAAG 	AAGAAGCT 	702
Sbjct	859	ĊĠŦĊĀĀĠĠĀĊĀ	tctccaatgcctc	:AAGCACTTCCGGGAT(gtcatactcaag	AAĠAAĠĊϮ	918
Query	703	GGAGGTGTTGC	CGGGCAACGGAACG	GTCATTCTGGAAACC 	ATAGCCAGCATG' 	PACTCCGT	762
Sbjct	919	ĠĠŔĸĠŤŦĊŤĠĊ	ĊĠĠĠĠĀĀŦĠĠĊĀĊĀ	ĠŢŢŖŢĊŢĠĠŖĠĊĊ	ÁTÁĠĊĊÁĠĊÁTĠ!	ŤÁĊŤĊĊĠŤ	978
Query	763			AACAGTGCCATCATGA 			822
Sbjct	979			SAATAĠTĠĊĊACĊATĠ <i>i</i>			1038
Query	823			CAAGCTCTGCGACGAGG	GTGATGCTCTCC(GAGGACAG 	882
Sbjct	1039	CTÁCCÁGÁGCC		'AAGCTCTGCGACGAG		ĠĠĠĀĠĀĠ	1098
Query	883			GAGAATGTGCGGGAAG			942
Sbjct	1099			ĠĀĠĀĀCĠŤCĊĠĠĠĀGŒ			1158
Query	943			GCGCAGGGCAAGCTGA			1002
Sbjct	1159			ĠĊĊĊĀĠĠĠĠĀĀĠĊŤĊ			1218
Query	1003			GGCGGCATTGGAGCG			1062
Sbjct	1219			ĠĠĊĠĠĠĀŤŤĠĠĀĠĊŦſ	GCCGCCGAGATC?	ATGGGCĠĊ	1278
Query	1063	GGTCACCGCCT					
Sbjct	1279	CĠŤAÁĊAĠĊĊŤ	ĊCĊĊĠĠĠ 1296				

Range 2: 411 to 535

Score		Expect	Identities	Gaps	Strand	Frame	
122 bits	(66)	2e-23()	111/131(85%)	10/131(7%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATO	CAGTTCTCCATCCACG	GCCGGCACCTGTTCC	AGTGGCATCGG- <i>I</i>	AGTGGGC	223
Sbjct	411	ACGGCAGCATO	cagttctccatccacc	scccggcacctgctcc	ygcgggggggg	AGCGG-C	469
Query	224	GGTGGCGGCT	GCAGCAGCAGCAA	CAATAGCATCAACAG	CGGCAGCTAC	CTCCACC	280
Sbjct	470	GGTGGCT	GCAGCAGCAGCAA	chacadcetcaacad	TGGCAACAGCTAG	ctcggcc	526

Query 281 GCCTGCACTCC 291 Sbjct 527 GCC-GCA-TCC 535

Drosophila grimshawi GH24527 (Dgri\GH24527), mRNA

Sequence ID: **ref|XM_001991970.1**| Length: 4638 Number of Matches: 2 Range 1: 718 to 1632

Score		Expect	Identities	Gaps	Strand	Frame	
667 bits	(361)	0.0()	733/916(80%)	11/916(1%)	Plus/Plus		
Features	s:						
Query	425	GGATCCTCGG	GCCACAAGAACAGTCT	CAAGGGCACCAAGC	тафсфссссф	СССТТСС	484
Sbjct	718	GGATCGTCGG	GGCATAAGAACAGTTT	'GAAGGGTACGAAAT'	TGGCGAAGCGAG	CGCGCTCC	777
Query	485	TTTAAGGACG	ACCTCATCGAGAAGAT	TTCCCTGATGCGAA	CCACCAACAATAO	CACTGGGT	544
Sbjct	778	TTCAAGGACG	ATCTGATTGAGAAGA1	ctcactgatgcgca	ccacaaacaata	crctgggt	837
Query	545	CGCTCCCACT	CGCCGCACAGTCCGCG	GCACCAAGCACGGCA	CAAAGGCACCGC	CCACCACC	604
Sbjct	838	CGATCACATT	ceceeracaetceece	chachagcatggag	cyyydccececec	CAACCACC	897
Query	605	GAGGAGGTGC'	TACGGTCCACCCAAAC	CCTGGAGACGCACG	TCAAGGACATTT(CGAATGCC	664
Sbjct	898	GAAGAGGTCC	agcgatccacacagac	:GCTGGAGACGCACG	tcaaggatatato	CGAATGCG	957
Query	665	CTGAAGCACT	TCCGGGATGTTATACT	CAAGAAGAAGCTGG.	AGGTGTTGCCGG(GCAACGGA 	724
Sbjct	958	ctcaagcact:	trcgrgytgtcytyc	rcaaaaadaaactdd	AGGTACTGCCGG	SCAATGGT	1017
Query	725	ACGGTCATTC	TGGAAACCATAGCCAG	CATGTACTCCGTGA	TCCAAACCTACA(CCTGAAT	784
Sbjct	1018	Acccttchtac'	tĠĠAGAĊĊAϮτĠĊĊĀĠ	scatgtartccgtca	trcagaagtatad	CGCTGAAT	1077
Query	785	GAAAACAGTG(CCATCATGAGCAGCGC	CACGCTGCAGGTTT.	ACCAGAGC-CTGC	GCAAGCT	843
Sbjct	1078	GAGAACAGTG	ccatcatgagctcagc	ccacaccaccaccaccaccac.	ATCA-ATCTCTTC	GGCAAGCT	1136
Query	844	CATCAAGCTC'	TGCGACGAGGTGATGC 	CTCTCCGAGGACAGC	GGCGAGTGCGCCT	CCCTGAG	903
Sbjct	1137	ċatċaaĠċtċ	tĠĊĠĀĊĠĀĠĠŦĠĀŦĠĊ	ctcagcgagaagagc	ĠĠĊĠĀĠŦĠĊĠĊĊſ	tccctcag	1196
Query	904	CAACGAGAAT(GTGCGGGAAGTCATTG 	GATCTTCTCGAGGAT(GCTGTGCGGAAT(CTCGTTAC	963
Sbjct	1197	ĊAATĠAĠAAŤ	ĠŦĠĊĠĊĠĀĠĠŦĊĀŦŦĠ	SATCTCCTCGAGGAT(ĠĊAĠϮĊĊĠĊĂĂϮĊ	ctggtcac	1256
Query	964	GCTGGCGCAG(GGCAAGCTGAAGGAGC 	CAGGATCAGTGCGCC' 	TTTCGCTACAGT(GGATCTGG 	1023
Sbjct	1257	AĊŤAĠĊĠĊĀĠ(ĠĠĊAAAĊϮĠAAĠĠAĠĊ	ĊĀĠĠĀŦĊĀĀŦĠĊĠĊĠ	†††¢ĠĊ†ÀTGĠC¢	ĠĠŦŦĊŦĠĠ	1316
Query	1024	CTTGGGCGGC	ATTGGAGCGGCGGCGG 	GAGATCATGGGTGCG	GTCACCGCCTCG(CCGGGAGC	1083
Sbjct	1317	ATTĠĠĠŢĠĠĊ	ATTĠĠTĠĊCĠĊCĠĊCĠ	SACATAATĠĠĠĊĠĊĊ	ĠϮŦĂĊĊĠĊAGĊA <i>I</i>	AĊTĠCĀĠĊ	1376
Query	1084	GAGTGTTC	CC-GGTACTG-GAGTC 	CATGCGCGTTTCG(GCCGCCGAATCAC 	GCTGCC	1135
Sbjct	1377	AGĠTĠGAATG(GĊTĠĠϮGGϮĠŦĠĂŦĠĊ	CGTACGCCGTTGGAT	ĠĊAĠĊŦĠĊĀGĊĀŒ	ĠĊĠĠŦĠĠĊ	1436
Query	1136	-CAGCGTACT	TCGTTGCCGGACATAG 	CGCTCACGCCCAAG!	GAGCGCGACATA(CTGGAGCA	1194
Sbjct	1437		ŤĊĠĊŤAĊĊAĠĂĊĂŤŦĠ				1496
Query	1195		AACCCGATGCGCGGCT 				1254
Sbjct	1497		AATĊĊĠATĠĊĠĊĠĠĊ1				1556
Query	1255		AAGCCACCGCTACCC <i>A</i> 				1314
Sbjct	1557	CĊĊĠĊĊĠĊĊA	AAGCCACCGCTGCCCG	SATCĠĠTĊĊAĠCAAT(ĊĊĠĊĊAĊĊĠŦŦĀĊ	CCACCAAA	1616
Query	1315	GCGACGCAGC	CAGCCG 1330				
Sbjct	1617	ĠĊĠŦĊĠĊĀĠĊ	ckśccś 1632				

Range 2: 437 to 537

Score	Expect	Identities	Gaps	Strand	Frame
99.0 bits(53)	4e-16()	90/107(84%)	6/107(5%)	Plus/Plus	

Features:

Query	165	ĄÇĢĢÇĄĢÇĄŢÇĄĢŢŢÇŢÇÇĄŢÇÇĄÇĢÇÇGĢÇĄCCŢĢŢŢÇCAĢTĢĢCAŢÇĢĢAĢŢGGGÇĢ	224
Sbjct	437	ACGGCAGCATCAGTTCTCCATCCACGCCCGGCACCTGTTCCAGTGGCATCGGAGTGGGCG	490
Query	225	ĢŢĢĢÇĢĢÇTĢÇAĢÇAĢÇAĢÇAAÇAATAĢÇAŢÇAAÇAĢCĢĢÇAĢÇ 271	
Sbict	491		

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant L (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185781.1**| Length: 4903 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	S :						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC'	TCAAGGGCACCAAGC	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	647	CGGATCTTCGG	GGCATAAGAACAGCC'	TCAAGGGAACGAAGC	rtggcacgacggg	CACGCTC	706
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA'	TTTCCCTGATGCGAA	CCACCAACAATA	CACTGGG 	543
Sbjct	707	ctttaaagacg	Acctgatcgaaaaga	tatccctgatgcga	rççyççyyçyycy	çeçteçe	766
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	767	†¢¢¢†¢¢¢å¢†	ceccecycycycycec	gryceyyddau	ccegtetchage	çeççecç	826
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA	CCCAAACCCTGGAGA	CGCACGTCAAGG	ACATTTC	657
Sbjct	827	TTĊGAAĊĠAĠĠ	AGGTGCAGCGCTCCA	cacagaccctggaga	rcecycetcy	ATATATĊ	886
Query	658	GAATGCCCTGA	AGCACTTCCGGGATG	TTATACTCAAGAAGA	AGCTGGAGGTGT	TGCCGGG	717
Sbjct	887	daatdccctca	ydcychtuced a gan y	ttattctgaagaaga	AgctcgAggtgc	4gcccee	946
Query	718	CAACGGAACGG	TCATTCTGGAAACCA'	TAGCCAGCATGTACT	CCGTGATCCAAA	CCTACAC	777
Sbjct	947	cyyrdecycee	tcatcctggagacca	trdccadcatdtart	cccttratccaaa	сстатас	1006
Query	778	CCTGAATG	AAAACAGTGCCATCA'	TGAGCAGCGCCACGC	TGCAGGTTTACC	AGAGCCT	834
Sbjct	1007	ccactdaatd	AGAACAGTGCCATCA'	tgygctcegc	adcaddtctacc	AATCCCT	1066
Query	835	GGGCAAGCTCA	TCAAGCTCTGCGACG	AGGTGATGCTCTCCG	AGGACAGCGGCG	AGTGCGC	894
Sbjct	1067	ddddaaactca	tcaaactctgcgacg	addtdatdctctcd	gycgydygggggg	AGTGCCC	1126
Query	895	CTCCCTGAGCA	ACGAGAATGTGCGGG.	AAGTCATTGATCTTC	TCGAGGATGCTG	TGCGGAA	954
Sbjct	1127	ctccctaagca	AcGATAA†G†GCGCG.	AGGTTATCGATCTAC	tcgyggycgcyg	TGAGGAA	1186
Query	955	TCTCGTTACGC	TGGCGCAGGGCAAGC'	TGAAGGAGCAGGATC	AGTGCGCCTTTC	GCTACAG	1014
Sbjct	1187	tctcgtaaccc	TGGCCCAGGGTAAAC'	TAAAGGAGCAGGATC	AGTGCGCCTTTC	GCTACAG	1246
Query	1015	TGGATC-TG	GCTTGGGCGGCATTG	GAGCGGCGGCGAGA	TCATGGGTGCGG	TCAC 10	68
Sbjct	1247	ceecectcee	gcctgggcggcyttg	gegcegcagcegaga	ttatgggtgcgg	tcac 13	03

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant K (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185780.1|** Length: 4659 Number of Matches: 1 Range 1: 262 to 918

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	S :						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC	TCAAGGGCACCAAGC	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	262	CGGATCTTCGG	GGCATAAGAACAGCC	CAAGGGAACGAAGC	TGGCACGACGGG	CACGCTC	321
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA	TTTCCCTGATGCGAA	CCACCAACAATA	.CACTGGG	543
Sbjct	322	ctttaaagacg	Acctgatcgaaaaga	ratecetgatgegga	ccaccaacaaca	cecteee	381
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	382	tcgctcccact	cdccdcacadtccdc	STACGAAGCATGGCG	CCGGTGTCAAGC	çeççecç	441
Query	601	C-ACCGAGG	AGGTGCTACGGTCCAC	CCCAAACCCTGGAGA	CGCACGTCAAGG	ACATTTC	657

Sbjct	442	TTĊĠĂAĊĠĂĠĠĂĠĠŤĠĊAĠĊĠĊŤĊĊĂĊAĊĀĠĀĊĊĊŤĠĠĀĠĀĊĠĊĀĊĠŤĊĀĀĠĠĀŦĀŤĀŤĊ	501
Query	658	GAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGGAGGTGTTGCCGGG	717
Sbjct	502	GAATGCCCTCAAGCACTTTCGGGACGTTATTCTGAAGAAGAAGCTCGAGGTGCTGCCCGG	561
Query	718	CAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGATCCAAACCTACAC	777
Sbjct	562	CAATGGCACGGTCATCCTGGAGACCATTGCCAGCATGTATTCCGTTATCCAAACGTATAC	621
Query	778	CCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTTACCAGAGCCT	834
Sbjct	622	cccactgaatgagaacagtgccatcatgagctcggccacgcagcaggtctaccaatccct	681
Query	835	GGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCGGCGAGTGCGC	894
Sbjct	682	GGGGAAACTCATCAAACTCTGCGACGAGGTGATGCTCTCCGACGAGAGCGGCGAGTGCCC	741
Query	895	CTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGGAA	954
Sbjct	742	CTCCCTAAGCAACGATAATGTGCGCGAGGTTATCGATCTACTCGAGGACGCAGTGAGGAA	801
Query	955	TCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCTTTCGCTACAG	1014
Sbjct	802	tctcgtaaccctggcccagggtaaactaaaggagcaggatcagtgcgcctttcgctacag	861
Query	1015	TGGATC-TGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGTGCGGTCAC 10	68
Sbjct	862	CGCCGCCTCCGGCCTGGGCGCATTGGGGCCGCAGCCGAGATTATGGGTGCGGTCAC 91	8

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant J (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185779.1|** Length: 5044 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTO	CTCAAGGGCACCAAGC	CTAGCGCGCCGGG	CGCGTTC	483
Sbjct	647	cccatcatcatcatcatcatcatcatcatcatcatcatca	GGCATAAGAACAGC	ctcaagggaacgaagd	ctggcacgacggg	CACGCTC	706
Query	484	CTTTAAGGACG.	ACCTCATCGAGAAGA	ATTTCCCTGATGCGA	ACCACCAACAATA	CACTGGG	543
Sbjct	707	CTTTAAAGACG.	ACCTGATCGAAAAG	ATATCCCTGATGCGGA	ACCACCAACAACA	CGCTGGG	766
Query	544	TCGCTCCCACT	CGCCGCACAGTCCG(CGCACCAAGCACGGC <i>A</i>	ACAAAGG-CAC	CGCCCAC	600
Sbjct	767	†cectcce	ceceecycacaetce	CGTACGAAGCATGGCG	SCCGGTGTCAAGC	çeççecç	826
Query	601	C-ACCGAGG	AGGTGCTACGGTCC	ACCCAAACCCTGGAG <i>A</i>	ACGCACGTCAAGG	ACATTTC	657
Sbjct	827	TTCGAACGAGG	AGGTGCAGCGCTCC <i>I</i>	Acacagaccctggaga	rcecycetcyye?	ATATATC	886
Query	658	GAATGCCCTGA	AGCACTTCCGGGAT(GTTATACTCAAGAAGA	AGCTGGAGGTGT	TGCCGGG	717
Sbjct	887	GAATGCCCTCA	AGCACTTTCGGGACO	GTTATTCTGAAGAAGA	AAGCTCGAGGTGC	4gcccgg	946
Query	718	CAACGGAACGG	TCATTCTGGAAACC	ATAGCCAGCATGTACT	CCGTGATCCAAA	CCTACAC	777
Sbjct	947	CAATGGCACGG	tcatcctddagacc	Atroccadcatetari	rcccttatccaaa	cgtatac	1006
Query	778	CCTGAATG	AAAACAGTGCCATC <i>I</i>	ATGAGCAGCGCCACGC	TGCAGGTTTACC	AGAGCCT	834
Sbjct	1007	ccactdaatd	agaacagtgccatc <i>i</i>	Atgagctcggccacgc	caddaddtctadd	AATCCCT	1066
Query	835	GGGCAAGCTCA	TCAAGCTCTGCGAC(GAGGTGATGCTCTCC	GAGGACAGCGGCG	AGTGCGC	894
Sbjct	1067	ddddaaactca	tcaaactctgcgaco	SAGGTGATGCTCTCCG	gacgagagcggcg	AGTGCCC	1126
Query	895	CTCCCTGAGCA	ACGAGAATGTGCGG(GAAGTCATTGATCTTC	TCGAGGATGCTG	TGCGGAA	954
Sbjct	1127	ctccctaagca	AcGATAATGTGCGCC	SAGGTTATCGATCTAC	ctcdaddacdcad	TGAGGAA	1186
Query	955	TCTCGTTACGC	TGGCGCAGGGCAAG(CTGAAGGAGCAGGATC	CAGTGCGCCTTTC	GCTACAG	1014
Sbjct	1187	tctcctaaccc	tggcccagggtaaa	ctaaaggagcaggatd	cadtdddddtttd	GCTACAG	1246
Query	1015	TGGATC-TG	GCTTGGGCGGCATT(GGAGCGGCGGAG <i>F</i>	ATCATGGGTGCGG	TCAC 10	68
Sbjct	1247	ceecectcee	ĠĊĊŦĠĠĠĠĠĠĠĊĀŦŦŒ	gggccgcagccgag <i>i</i>	ıtratdddtdddd	TCAC 13	03

Sequence ID: **ref|XM_015185778.1|** Length: 5203 Number of Matches: 1 Range 1: 806 to 1462

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Feature	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC'	TCAAGGGCACCAAGC	CTAGCGCGCCGGG	ССССТТС	483
Sbjct	806	CGGATCTTCGG	GGCATAAGAACAGCC'	TCAAGGGAACGAAGC	TGGCACGACGGG	CACGCTC	865
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA'	TTTCCCTGATGCGAA	ACCACCAACAATA	CACTGGG 	543
Sbjct	866	ctttaaagacg	AcctgAtcgAAAAgA	tatccctdatdcdg	rccyccyycyycy	çeçteçe	925
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGC <i>F</i> 	CAAAGG-CAC	CGCCCAC	600
Sbjct	926	tccctcct	ceccecacacacac	ĠŦĀĊĠĀĀĠĊĀŦĠĠĊĠ	sccggtgtcaagc	ççççecç	985
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA	CCCAAACCCTGGAGA 	ACGCACGTCAAGG.	ACATTTC 	657
Sbjct	986	TTĊĠĀAĊĠĀĠĠ	AĠĠŦĠĊAGĊĠCŦĊĊĀ	ĊAĊÁGÁĊĊĊŤĠĠÁĠŹ	AĊĠĊĀĊĠŦĊĀĀĠĠ.	ATATATĊ	1045
Query	658	GAATGCCCTGA	AGCACTTCCGGGATG'	TTATACTCAAGAAG <i>A</i> 	AGCTGGAGGTGT'	TGCCGGG	717
Sbjct	1046	ĠĀĀŦĠĊĊĊŦĊĀ	AĠĊAĊϮϮϮĊĠĠĠACĠ [,]	††A††C†GAAGAAGA	AÁĠĊϮCĠÁĠĠϮĠC'	rĠĊĊCĠĠ	1105
Query	718		TCATTCTGGAAACCA'				777
Sbjct	1106		·TĊATCĊTĠĠAGAĊĊA'				1165
Query	778		AAAACAGTGCCATCA'				834
Sbjct	1166		ÁGÁÁCÁĠŤĠĊĊÁŤĊÁ'				1225
Query	835		TCAAGCTCTGCGACG.				894
Sbjct	1226	GGGGAAACTCA			GACGAGAGCGGCG.		1285
Query	895		ACGAGAATGTGCGGG.				954
Sbjct	1286		Accaraatchecec.				1345
Query	955		TGGCGCAGGGCAAGC'				1014
Sbjct	1346		ŤĠĠĊĊĊĀĠĠĠŦĀĀĀĊ'				1405
Query	1015		GCTTGGGCGGCATTG				
Sbjct	1406	CGGCGCCTCCG	ĠĊĊŦĠĠĠĊĠĠĊĂŦŦĠ	GGGCCGCAGCCGÁGÁ	ATTATGGGTGCGG	TCAC 14	62

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant H (Dpse\GA16131), mRNA Sequence ID: ref|XM_015185777.1| Length: 4831 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTO	CTCAAGGGCACCAAGC	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	647	CGGATCTTCGG	GGCATAAGAACAGC	CTCAAGGGAACGAAGC	TGGCACGACGGG	CACGCTC	706
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA	ATTTCCCTGATGCGAA	CCACCAACAATA	CACTGGG	543
Sbjct	707	CTTTAAAGACG.	ACCTGATCGAAAAGA	Atatecetgatgegga	CCACCAACAACA	cctcc	766
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	CGCACCAAGCACGGCA	CAAAGG-CAC	ÇGÇÇCAÇ	600
Sbjct	767	†cgc†cccac†	CGCCGCACAGTCCGC	CGTACGAAGCATGGCG	CCGGTGTCAAGC	çeççecç	826
Query	601	C-ACCGAGG	AGGTGCTACGGTCC	ACCCAAACCCTGGAGA	CGCACGTCAAGG	ACATTTC	657
Sbjct	827	TTCGAACGAGG.	AGGTGCAGCGCTCC	ACACAGACCCTGGAGA	CGCACGTCAAGG	ATATATC	886
Query	658	GAATGCCCTGA	AGCACTTCCGGGATC	GTTATACTCAAGAAGA	AGCTGGAGGTGT	TGCCGGG	717
Sbjct	887	GAATGCCCTCA	AGCACTTTCGGGAC	GTTATTCTGAAGAAGA	AGCTCGAGGTGC	TGCCCGG	946
Query	718	CAACGGAACGG	TCATTCTGGAAACC	ATAGCCAGCATGTACT	CCGTGATCCAAA	CCTACAC	777
Sbjct	947	CAATGGCACGG	TCATCCTGGAGACC	ATTGCCAGCATGTATT	CCGTTATCCAAA	CGTATAC	1006
Query	778	CCTGAATG	AAAACAGTGCCATCA	ATGAGCAGCGCCACGC	TGCAGGTTTACC	AGAGCCT	834

Sbjct	1007	CCCACTGAATGAGAACAGTGCCATCATGAGCTCGGCCACGCAGCAGGTCTACCAATCCCT	1066
Query	835	GGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCGGCGAGTGCGC	894
Sbjct	1067	GGGGAAACTCATCAAACTCTGCGACGAGGTGATGCTCTCCGACGAGAGCGGCGAGTGCCC	1126
Query	895	CTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGGAA	954
Sbjct	1127	CTCCCTAAGCAACGATAATGTGCGCGAGGTTATCGATCTACTCGAGGACGCAGTGAGGAA	1186
Query	955	TCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCTTTCGCTACAG	1014
Sbjct	1187	tctcgtaaccctggcccagggtaaactaaaggagcaggatcagtgcgcctttcgctacag	1246
Query	1015	TGGATC-TGGCTTGGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGCGGTCAC 10	68
Sbjct	1247	cgcccccccgcctggccdcattgggcccccagccgagattatgggtgcgctcac 13	03

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant G (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185776.1|** Length: 3890 Number of Matches: 1 Range 1: 731 to 1387

Gaps

Strand

Frame

Identities

Expect

Score

OCOILE		Expect	identities	Oaps	Ottaila	i raine	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Feature	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC'	TCAAGGGCACCAAGC	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	731	cccatcutccc	:GGCATAAGAACAGCC'	rcaagggaacgaagd	tggcacgacggg	Caccctc	790
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA'	TTTCCCTGATGCGAA	CCACCAACAATA	CACTGGG	543
Sbjct	791	ctttaaagacd	:Acctgatcgaaaaga	tatccctgatgcgg	rccyccyycyycy	çeçteçe	850
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	851	tccctcct	ckkak	ĠŦĀĊĠĀĀĠĊĀŦĠĠĊĠ	ccggrgtcaagc	çeççecç	910
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA(CCCAAACCCTGGAGA 	CGCACGTCAAGG.	ACATTTC 	657
Sbjct	911		:AĠĠŦĠĊAGĊĠCŦĊĊA(970
Query	658		AGCACTTCCGGGATG' 	1111 11 111111			717
Sbjct	971		AĠĊĀĊŦŤŦĊĠĠĠĀCĠ [,]				103
Query	718		'TCATTCTGGAAACCA' 				777
Sbjct	1031		ŢĊĀŢĊĊŢĠĠĀĠĀĊĊĀ'				109
Query	778		GAAAACAGTGCCATCA'				834
Sbjct	1091		;AGAAĊAĠŤĠĊĊAŤĊA'				115
Query	835		TCAAGCTCTGCGACG				894
Sbjct	1151		TCAAACTCTGCGACG				121
Query	895 1211		ACGAGAATGTGCGGG 				954 127
Sbjct	955		TGGCGCAGGGCAAGC'				101
Query Sbjct	1271		TGGCGCAGGGCAAGC 	1			133
Query	1015		GCTTGGGCGGCATTG				
Sbjct	1331		GCCTGGGCGGCATTG				
22,00	1001	33333331300					J ,

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant F (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185775.1|** Length: 4879 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	S:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTCT	CAAGGGCACCAAGC	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	647	cedaterteed	GGCATAAGAACAGCC1	CAAGGGAACGAAGC	TGGCACGACGGG	CACGCTC	706

Query	484	CTTTAAGGACGACCTCATCGAGAAGATTTCCCTGATGCGAACCACCAACAATACACTGGG	543
Sbjct	707	CTTTAAAGACGACCTGATCGAAAAGATATCCCTGATGCGGACCACCAACAACACGCTGGG	766
Query	544	TCGCTCCCACTCGCCGCACAGTCCGCGCACCAAGCACGGCACAAAGG-CACCGCCCAC	600
Sbjct	767	tcgctcccactcgcccccccccccccccccccccccccc	826
Query	601	C-ACCGAGGAGGTGCTACGGTCCACCCAAACCCTGGAGACGCACGTCAAGGACATTTC	657
Sbjct	827	TTCGAACGAGGAGGTGCAGCGCTCCACACAGACCCTGGAGACGCACGTCAAGGATATATC	886
Query	658	GAATGCCCTGAAGCACTTCCGGGATGTTATACTCAAGAAGAAGCTGGAGGTGTTGCCGGG	717
Sbjct	887	GAATGCCCTCAAGCACTTTCGGGACGTTATTCTGAAGAAGAAGCTCGAGGTGCTGCCCGG	946
Query	718	CAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGATCCAAACCTACAC	777
Sbjct	947	CAATGGCACGGTCATCCTGGAGACCATTGCCAGCATGTATTCCGTTATCCAAACGTATAC	1006
Query	778	CCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTTACCAGAGCCT	834
Sbjct	1007	CCCACTGAATGAGAACAGTGCCATCATGAGCTCGGCCACGCAGCAGGTCTACCAATCCCT	1066
Query	835	GGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCGGCGAGTGCGC	894
Sbjct	1067	GGGGAAACTCATCAAACTCTGCGACGAGGTGATGCTCTCCGACGAGAGCGGCGAGTGCCC	1126
Query	895	CTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGGAA	954
Sbjct	1127	ctccctaagcaacgataatgtgcgcgaggttatcgatctactcgaggacgcagtgaggaa	1186
Query	955	TCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCTTTCGCTACAG	1014
Sbjct	1187	TCTCGTAACCCTGGCCCAGGGTAAACTAAAGGAGCAGGATCAGTGCGCCTTTCGCTACAG	1246
Query	1015	TGGATC-TGGCTTGGGCGGCATTGGAGCGGCGGCGGAGATCATGGGTGCGGTCAC 10	68
Sbjct	1247	cgcccccccgcctggccgcattgggcccccagccgagattatgggtgcggtcac 13	03

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant E (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185774.1|** Length: 4924 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC	TCAAGGGCACCAAGC	TAGCGCGCGGG	CGCGTTC	483
Sbjct	647	CGGATCTTCGG	GGCATAAGAACAGCC	tcaagggaacgaagc	tggcacgacgg	CACGCTC	706
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA	TTTCCCTGATGCGAA	CCACCAACAATA	CACTGGG	543
Sbjct	707	ctttaaagacg	Acctgatcgaaaaga	tateeetgatgega	ccaccaacaaca	cecteee	766
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	767	tegeteeeket	ceceecycacaetecec	dracgaagcarggcg	CCGGTGTCAAGC	çeççecç	826
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA	CCCAAACCCTGGAGA	.CGCACGTCAAGG	ACATTTC	657
Sbjct	827	TTCGAACGAGG	AGGTGCAGCGCTCCA	.cacagaccctggaga	.cccacgtcaagg	ATATATC	886
Query	658	GAATGCCCTGA	AGCACTTCCGGGATG	TTATACTCAAGAAGA	AGCTGGAGGTGT'	TGCCGGG	717
Sbjct	887	daatdccctca	AGCACTTTCGGGACG	ttattctgaagaaga	'ygcpcgyggtgc	teccee	946
Query	718	CAACGGAACGG	TCATTCTGGAAACCA	TAGCCAGCATGTACT	CCGTGATCCAAA	CCTACAC	777
Sbjct	947	CAATGGCACGG	tcatcctggagacca	treccaecatetart	cccttatccaaa	CGTATAC	1006
Query	778	CCTGAATG	AAAACAGTGCCATCA	TGAGCAGCGCCACGC	TGCAGGTTTACC	AGAGCCT	834
Sbjct	1007	CCCACTGAATG	AGAACAGTGCCATCA	tgageteggeeaege	addaddtctadd	AATCCCT	1066
Query	835	GGGCAAGCTCA	TCAAGCTCTGCGACG	AGGTGATGCTCTCCG	AGGACAGCGGCG	AGTGCGC	894
Sbjct	1067	ddddaaactca	tcaaactctgcgacg	addtdatdctctcc	acdagadcddcd.	Agtgccc	1126
Query	895	CTCCCTGAGCA	ACGAGAATGTGCGGG	AAGTCATTGATCTTC	TCGAGGATGCTG	TGCGGAA	954
Sbjct	1127	ctccctaagca	AcGATAATGTGCGCG	AGGTTATCGATCTAC	tcgyggycgcyg	tgaggaa	1186
Query	955	TCTCGTTACGC	TGGCGCAGGGCAAGC	TGAAGGAGCAGGATC	AGTGCGCCTTTC	GCTACAG	1014
Sbjct	1187	tctcgtaaccc	tggccagggtaaac	taaaggagcaggatc	AGTGCGCCTTTC	GCTACAG	1246

Ouery	1015	TGGATC-TGGCTTGGGCGGCATTGGAGCGGCGGGGGAGATCATGGGTGCGGTCAC	1068
~ - 1		CGGCGCCTCCGGCCTGGGCGGCATTGGGGCCGCAGCCGAGATTATGGGTGCGGTCAC	
Sbjct	1247	CĠĠCĠĊĊŤĊĊĠĠĊĊŤĠĠĠĊĠĠĊĂŤŤĠĠĠĠĊĊĠĊAĠĊĊĠĀĠĂŤŦĂŤĠĠĠŤĠĊĠĠŤĊĀĊ	1303

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant D (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185773.1|** Length: 5295 Number of Matches: 1 Range 1: 898 to 1554

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	S :						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC'	TCAAGGGCACCAAGG	CTAGCGCGCCGGG	CGCGTTC	483
Sbjct	898	cggatcttcgg	GGCATAAGAACAGCC	rcaagggaacgaagd	ctggcacgacggg	CACGCTC	957
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA'	TTTCCCTGATGCGA	ACCACCAACAATA	CACTGGG	543
Sbjct	958	ctttaaagacg	acctgatcgaaaaga	ratccctgatgcgg	rccyccyycyycy	cctcc	1017
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGC <i>F</i>	ACAAAGG-CAC	CGCCCAC	600
Sbjct	1018	†¢¢¢†¢¢¢å¢†	ceceptack	gracgaagcarggco	sccggtgtcaagc	çeççecç	1077
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA	CCCAAACCCTGGAG <i>A</i>	ACGCACGTCAAGG	ACATTTC	657
Sbjct	1078	ттсвалсвав	addtdcagcdctccac	cacagaccctggaga	ycecycetcyyer	ATATATĊ	1137
Query	658	GAATGCCCTGA	AGCACTTCCGGGATG	TTATACTCAAGAAGA 	AGCTGGAGGTGT	TGCCGGG	717
Sbjct	1138	daatdccctca	.AgcActtttcgggAcg	ttáttétgáágáágá	AAGCTCGAGGTGC	ф	1197
Query	718	CAACGGAACGG	TCATTCTGGAAACCA' 	FAGCCAGCATGTACT	CCGTGATCCAAA	CCTACAC	777
Sbjct	1198	ĊAATĠĠCAĊĠĠ	tcatcctggagacca:	trĠĊĊĀĠĊĀŦĠŦĀŦſ	rccgttatccaaa	ĊĠŦĀŦĀĊ	1257
Query	778	CCTGAATG	AAAACAGTGCCATCA' 	FGAGCAGCGCCACGC	CTGCAGGTTTACC.	AGAGCCT	834
Sbjct	1258	ĊCCAĊŢĠĀĀŢĠ	:AGAAĊAĠTĠĊĊATĊA:	rdadctcgdcdaddd	cagcaggtctacc.	ААТСССТ	1317
Query	835	GGGCAAGCTCA	TCAAGCTCTGCGACGA	AGGTGATGCTCTCCG	GAGGACAGCGGCG.	AGTGCGC	894
Sbjct	1318	ĠĠĠĠÀÀAĊŦĊĀ	tcaactctctcdcacc	AĠĠŦĠAŦĠĊŦĊŦĊĊĊ	ĠĀĊĠĀĠĀĠĊĠĠĊĠ.	AĠŦĠĊĊĊ	1377
Query	895		ACGAGAATGTGCGGGA				954
Sbjct	1378	ĊŦĊĊĊŦĸĂĠĊĀ	Acgaraatgtgcgcg	AGĠŦŦĂŦĊĠĂŦĊŦĀĊ	ctcgaggacgcag	†ĠaĠĠĀĀ	1437
Query	955	TCTCGTTACGC	TGGCGCAGGGCAAGC'	FGAAGGAGCAGGATO	CAGTGCGCCTTTC	GCTACAG	1014
Sbjct	1438	tċtċĠtaAċcċ	tdgcccagggtaaac	taaaggagcaggatd	cagtgcccctttc	ĠĊŦĀĊĀĠ	1497
Query	1015	TGGATC-TG	GCTTGGGCGGCATTG	GAGCGGCGGCGAGA 	ATCATGGGTGCGG	TCAC 10	68
Sbjct	1498	cęęcectce	cctcccccccccccccccccccccccccccccccccccc	ĠĠĠĊĊĠĊĀĠĊĊĠĀĠĀ	AtratĠĠĠtĠĊĠĠ	TCAC 15	54

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA16131), mRNA Sequence ID: **ref|XM_015185772.1|** Length: 4546 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Features	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC	TCAAGGGCACCAAGC	PAGCGCGCCGGG	CGCGTTC	483
Sbjct	647	CGGATCTTCGG	GGCATAAGAACAGCC	TCAAGGGAACGAAGC	rggcacgacggg	CACGCTC	706
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA	TTTCCCTGATGCGAA	CCACCAACAATA	.CACTGGG	543
Sbjct	707	CTTTAAAGACG	ACCTGATCGAAAAGA	TATCCCTGATGCGGA	CCACCAACAACA	cgctggg	766
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	767	tccctccact	cececacacactcec	GTACGAAGCATGGCG	CCGGTGTCAAGC	çeççecç	826
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA	.CCCAAACCCTGGAGA(CGCACGTCAAGG	ACATTTC	657
Sbjct	827	TTCGAACGAGG	AGGTGCAGCGCTCCA	.cacagaccctggaga	cgcycgtcyydd	ATATATC	886
Query	658	GAATGCCCTGA	AGCACTTCCGGGATG	TTATACTCAAGAAGA	AGCTGGAGGTGT	TGCCGGG	717

Sbjct	887	GAATGCCCTCAAGCACTTTCGGGACGTTATTCTGAAGAAGAAGCTCGAGGTGCTGCCCG	946
Query	718	CAACGGAACGGTCATTCTGGAAACCATAGCCAGCATGTACTCCGTGATCCAAACCTACAC	777
Sbjct	947	CAATGGCACGGTCATCCTGGAGACCATTGCCAGCATGTATTCCGTTATCCAAACGTATAC	1006
Query	778	CCTGAATGAAAACAGTGCCATCATGAGCAGCGCCACGCTGCAGGTTTACCAGAGCCT	834
Sbjct	1007	CCCACTGAATGAGAACAGTGCCATCATGAGCTCGGCCACGCAGCAGGTCTACCAATCCCT	1066
Query	835	GGGCAAGCTCATCAAGCTCTGCGACGAGGTGATGCTCTCCGAGGACAGCGGCGAGTGCGC	894
Sbjct	1067	GGGGAAACTCATCAAACTCTGCGACGAGGTGATGCTCTCCGACGAGAGCGGCGAGTGCCC	1126
Query	895	CTCCCTGAGCAACGAGAATGTGCGGGAAGTCATTGATCTTCTCGAGGATGCTGTGCGGAA	954
Sbjct	1127	CTCCCTAAGCAACGATAATGTGCGCGAGGTTATCGATCTACTCGAGGACGCAGTGAGGAA	1186
Query	955	TCTCGTTACGCTGGCGCAGGGCAAGCTGAAGGAGCAGGATCAGTGCGCCTTTCGCTACAG	1014
Sbjct	1187	TCTCGTAACCCTGGCCCAGGGTAAACTAAAGGAGCAGGATCAGTGCGCCTTTCGCTACAG	1246
Query	1015	TGGATC-TGGCTTGGGCGCATTGGAGCGGCGGCGGAGATCATGGGTGCGGTCAC 10	68
Sbjct	1247	cgcccccccgcctgggcgcattgggcccccagccgagattatgggtgcggtcac 13	03

Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant C (Dpse\GA16131), mRNA Sequence ID: **ref|XM_001355540.3|** Length: 4759 Number of Matches: 1 Range 1: 647 to 1303

Score		Expect	Identities	Gaps	Strand	Frame	
621 bits	(336)	2e-173()	552/657(84%)	12/657(1%)	Plus/Plus		
Feature	s:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC	TCAAGGGCACCAAGC	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	647	cggatcttcgg	GGCATAAGAACAGCC'	TCAAGGGAACGAAGC	TGGCACGACGGG	CACGCTC	706
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGA	TTTCCCTGATGCGA#	CCACCAACAATA	CACTGGG	543
Sbjct	707	ctttaaagacd	acctgatcgaaaaga	tatccctgatgcgg	rccyccyycyycy	cctcc	766
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC	GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	767	tccctccact	ceccecycycycycec	gracgaagcarggc	ccggtgtcaagc	ççççecç	826
Query	601	C-ACCGAGG	AGGTGCTACGGTCCA	CCCAAACCCTGGAGA	CGCACGTCAAGG	ACATTTC	657
Sbjct	827	TTĊGÅAĊĠÅĠĠ	addtdcadcdctcca	cacagaccctggaga	rçeçyçetçyye	ATATATĊ	886
Query	658	GAATGCCCTGA	AGCACTTCCGGGATG'	TTATACTCAAGAAGA 	AGCTGGAGGTGT	TGCCGGG	717
Sbjct	887	ĠĀĀŦĠĊĊĊŦĊĀ	.AĠĊAĊϮϮͲĊĠĠĠACĠ [,]	††A††C†GAAGAAGA	.AĠĊ†CĠAĠĠ†ĠC	tgcccgg	946
Query	718	CAACGGAACGG	TCATTCTGGAAACCA'	TAGCCAGCATGTACT	CCGTGATCCAAA	CCTACAC	777
Sbjct	947	ĊĀĀTĠĠCĀĊĠĠ	tĊATCĊTĠĠAGAĊĊA'	†TĠĊĊÀĠĊÀ†Ġ†ÀTİ	rccgtratccaaa	ĊĠŤÅŦÅĊ	1006
Query	778	CCTGAATG	AAAACAGTGCCATCA' 	TGAGCAGCGCCACGC 	TGCAGGTTTACC: 	AGAGCCT	834
Sbjct	1007	ĊCCAĊŢĠĂĀŢĠ	'AGAACAGTGCCATCA'	ŤĠĀĠĊTCGĠĊĊĀĊĠĊ	CAĠĊĀĠĠϮCϮĀĊĊ	AATCĊĊŢ	1066
Query	835		TCAAGCTCTGCGACG.	1			894
Sbjct	1067		.TĊĀĀĀĊTĊŦĠĊĠĀĊĠ.				1126
Query	895	CTCCCTGAGCA	ACGAGAATGTGCGGG. 	$egin{array}{c c c c c c c c c c c c c c c c c c c $	TCGAGGATGCTG 	TGCGGAA	954
Sbjct	1127		.ÀĊĠÀTÀÀŤĠŤĠĊĠĊĠ.				1186
Query	955		'TGGCGCAGGGCAAGC' 	1			1014
Sbjct	1187		'TĠĠĊCĊAĠĠĠTAAAĊ'				1246
Query	1015		GCTTGGGCGGCATTG				
Sbjct	1247	CGGCGCCTCCG	ŀĠĊĊŦĠĠĠĊĠĠĊĂŦŦĠŀ	GGGCCGCAGCCGAGA	\TTATĠĠĠŦĠĊĠĠ	TCAC 13	03

Score		Expect	Identities	Gaps	Strand	Frame	
616 bits	(333)	8e-172()	551/657(84%)	12/657(1%)	Plus/Plus		
Features	3:						
Query	424	CGGATCCTCGG	GCCACAAGAACAGTC	rcaagggcaccaagc	TAGCGCGCCGGG	CGCGTTC	483
Sbjct	546	CGGATCTTCGG	GGCATAAGAACAGCC	rcaagggaacgaagc	tggcacgacgcg	CACGCTC	605
Query	484	CTTTAAGGACG	ACCTCATCGAGAAGAT	TTTCCCTGATGCGAA	CCACCAACAATA	CACTGGG	543
Sbjct	606	ctttaaagacg	Acctgatcgaaaaga	ratccctgatgcgga	.ccyccyycyycy	cctcc	665
Query	544	TCGCTCCCACT	CGCCGCACAGTCCGC(GCACCAAGCACGGCA	CAAAGG-CAC	CGCCCAC	600
Sbjct	666	tccctcct	cececacacacacacacacacacacacacacacacacac	gracgaagcarggcg	ccggrgtcyagc	ççççecç	725
Query	601	C-ACCGAGG	AGGTGCTACGGTCCAC	CCCAAACCCTGGAGA	CGCACGTCAAGG	ACATTTC	657
Sbjct	726	TTĊGÅAĊĠÅĠĠ	AĠĠŦĠĊAGĊĠĊŦĊĊĀĊ	cacagactctggaga	.cccacctca	ATATATĊ	785
Query	658	GAATGCCCTGA	AGCACTTCCGGGATGT	FTATACTCAAGAAGA 	AGCTGGAGGTGT	TGCCGGG	717
Sbjct	786	ĠĀĀŢĠĊĊĊŢĊĀ	AĠĊĀĊŦŦŦĊĠĠĠĀĊĠſ	ttatrctgaagaaga	AĠĊϮĊĠĀĠĠϮĠĊ	tgcccgg	845
Query	718	CAACGGAACGG	TCATTCTGGAAACCAT	FAGCCAGCATGTACT 	CCGTGATCCAAA	CCTACAC	777
Sbjct	846	ĊAATĠĠCAĊĠĠ	†CA†CC†GGAGACCA1	trĠĊĊĀĠĊĀŦĠŦĀŦŦ	ĊĊĠϮͲÅϮĊĊĂĂĂ	ĊĠŤÅŦÅĊ	905
Query	778	CCTGAATG	AAAACAGTGCCATCAT	rgagcagcgccacgc 	TGCAGGTTTACC	AGAGCCT	834
Sbjct	906	ĊCCAĊŤĠÄÄŤĠ	ÁGÁÁCÁĠŤĠĊĊÁŤĊÁ1	ŗĠĀĠĊŦCGĠĊĊĀĊĠĊ	AĠĊĀĠĠŤĊŤĀĊĊ	ÄATCĊĊŢ	965
Query	835	GGGCAAGCTCA	TCAAGCTCTGCGACGA	AGGTGATGCTCTCCG 	AGGACAGCGGCG	AGTGCGC	894
Sbjct	966	ĠĠĠĠĀĀĀĊŦĊĀ	†ĊAAAĊ†Ċ†ĠĊĠAĊĠ <i>I</i>	AĠĠŦAAŦĠĊŦĊŦĊĊĠ	ACĠAGAĠĊĠĠĊĠ	AĠŦĠĊĊĊ	1025
Query	895	CTCCCTGAGCA	ACGAGAATGTGCGGGA	AAGTCATTGATCTTC 	TCGAGGATGCTG	TGCGGAA	954
Sbjct	1026	ĊŢĊĊĊŢĸĸĠĊĸ	AĊĠATAATĠTĠĊĠCĠ <i>I</i>	\AĠ†TA†CĠA†Ċ†AĊ	TĊĠĀĠĠĀCĠĊĀĠ	†ĠAĠĠĀĀ	1085
Query	955	TCTCGTTACGC	TGGCGCAGGGCAAGCT	rgaaggagcaggatc 	AGTGCGCCTTTC	GCTACAG	1014
Sbjct	1086	†Ċ†ĊĠ†AÅĊCĊ	ŤĠĠĊCĊĀĠĠĠŦĀĀĀĊī	[†] AAAĠĠAĠĊAĠĠA†Ċ	AĠŦĠĊĠĊĊŦŦŦĊ	ĠĊŦÀĊĀĠ	1145
Query	1015	TGGATC-TG	GCTTGGGCGGCATTG(GAGCGGCGGCGAGA 	TCATGGGTGCGG		
Sbjct	1146	cĠĠcŦċcŦccĠ	ĠĊĊŦĠĠĠĠĠĠĠAŦŦĠĊ	ĠĠĠĊĊĠĊAĠĊĊĠĀĠĀ	.tratĠĠĠtĠĊĠĠ	rtcac 12	02

Drosophila busckii chromosome X sequence

Sequence ID: **gb|CP012528.1|** Length: 23724088 Number of Matches: 1 Range 1: 14063570 to 14063901

Score		Expect	Identities	Gaps	Strand	Frame	
278 bits	(150)	4e-70()	273/333(82%)	5/333(1%)	Plus/Plus		
Features C3G	S:						
Query	431	TCGGGC	CACAAGAACAGTCTCAA	AGGGCACCAAGCTAG	cececeeece	GTTCCTTTAAG	490
Sbjct	14063570	4cgggg	CATAAGAACAGCCTGAA	AGGGCACCAAATTGG	CGCGACGTGCAC	GCAGCTTCAAG	14063629
Query	491	GACGAC	CTCATCGAGAAGATTTC	CCTGATGCGAACCA	CCAACAATACAC	TGGGTCGCTCC	550
Sbjct	14063630	GACGATO	ctaatrgagaaaatctd	cactgatgcgcacca	rccyycyycycec	tegeecectec	14063689
Query	551	CACTCGO	CGCACAGTCCGCGCAC	CCAAGCACGGC-	ACAAAGGCACCG	CCCACCACCGA	606
Sbjct	14063690	CATTCC	ccccacactccccccac	scaataagcacggcc	ac-yygccecc	ccaagcaatga	14063748
Query	607	GGAGGTO	CTACGGTCCACCCAAA	ACCCTGGAGACGCAC	GTCAAGGACATT	TCGAATGCCCT	666
Sbjct	14063749	GGAAGT	scagcgctccacgcaa	усветсвувусска	rgtcaaggacata	tcgaatgctct	14063808
Query	667	GAAGCA(CTTCCGGGATGTTATAC	CTCAAGAAGAAGCTG	GAGGTGTTGCCG	GGCAACGGAAC	726
Sbjct	14063809	caagca	rttcccccatctcatac	ctcaagaagaagctc	daagtgctgcc	regeryyce	14063868
Query	727	GGTCATT	CTGGAAACCATAGCCA	AGCATGTACTC 75	9		
Sbjct	14063869	CĠŦĊĀŦſ	ctggagaccattgcc	AĠĊĀŦĠŦĀĊŦĊ 14	063901		

Sequence ID: ref|XM_002106295.1| Length: 582 Number of Matches: 1

Range 1: 491 to 578

Score		Expect	Identities	Gaps	Strand	Frame	
128 bits	(69)	5e-25()	82/88(93%)	1/88(1%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGO	CCGGCACCTGTT	CCAGTGGC-ATCG	GAGTGGGC	223
Sbjct	491	ACGGCAGCATCA	GTTCTCCATCCACGC	CCGGCACCTGTT	CCAGTGGCAATCA	'GAGTGGGC	550
Query	224	GGTGGCGGCTGC	AGCAGCAGCAAC	CA 251			
Sbjct	551	GGTGGCAGCTGC	TGCAGCTTCAGCAAC	A 578			

Drosophila virilis uncharacterized protein, transcript variant E (Dvir\GJ16545), mRNA

Sequence ID: ref|XM_015169995.1| Length: 4786 Number of Matches: 1

Range 1: 485 to 579

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	8e-13()	84/101(83%)	6/101(5%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACG	CCCGGCACCTGTTCC	AGTGGCATCGGA	GTGGGCG	224
Sbjct	485	ACGGCAGCATCA	GTTCTCCATCCACG	CCAGCAACTGCTCG-	-eceeceec	gtcggcg	541
Query	225	GTGGCGGCTGCA	GCAGCAGCAGCAAC	AATAGCATCAACAGC	265		
Sbjct	542	GCTGCGGCAGCA	.dcadcadcadcaaca	AGCATCAACAGC	579		

Drosophila virilis uncharacterized protein, transcript variant D (Dvir\GJ16545), mRNA

Sequence ID: ref|XM_015169994.1| Length: 4807 Number of Matches: 1

Range 1: 485 to 579

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	8e-13()	84/101(83%)	6/101(5%)	Plus/Plus		
Features	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGC	CCGGCACCTGTTCC	AGTGGCATCGGAG	TGGGCG	224
Sbjct	485	ACGGCAGCATCA	GTTCTCCATCCACGC	CCAGCAACTGCTCG	-qcqqqcqqcd	rcggcg	541
Query	225	GTGGCGGCTGCA	GCAGCAGCAGCAACA	ATAGCATCAACAGC	265		
Sbjct	542	GCTGCGGCAGCA	.GCAGCAGCAGCAACA	AGCATCAACAGC	579		

Drosophila virilis uncharacterized protein, transcript variant C (Dvir\GJ16545), mRNA

Sequence ID: ref|XM_015169993.1| Length: 4811 Number of Matches: 1

Range 1: 486 to 580

Score		Expect	Identities	Gaps	Strand Fr	ame
87.9 bits	s(47)	8e-13()	84/101(83%)	6/101(5%)	Plus/Plus	
Feature	s:					
Query	165	ACGGCAGCATC	AGTTCTCCATCCACGC	CCCGGCACCTGTTCC	AGTGGCATCGGAGTGGG	SCG 224
Sbjct	486	ACGGCAGCATCA	AGTTCTCCATCCACGC	CCAGCAACTGCTCG	-GCGGGCGGCGTCGG	GCG 542
Query	225	GTGGCGGCTGC	AGCAGCAGCAACA	AATAGCATCAACAGC	265	
Sbjct	543	GCTGCGGCAGCA	AGCAGCAGCAACA	AGCATCAACAGC	580	

Sequence ID: ref|XM_015169992.1| Length: 4752 Number of Matches: 1

Range 1: 427 to 521

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	8e-13()	84/101(83%)	6/101(5%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACG(CCCGGCACCTGTTCC	AGTGGCATCGGA	\GTGGGCG	224
Sbjct	427	ACGGCAGCATCA	GTTCTCCATCCACGO	CCAGCAACTGCTCG	-gcgggcggc	GTCGGCG	483
Query	225	GTGGCGGCTGCA	.GCAGCAGCAGCAAC	AATAGCATCAACAGC	265		
Sbjct	484	GCTGCGGCAGCA	.GCAGCAGCAGCAAC	AGCATCAACAGC	521		

Drosophila virilis uncharacterized protein, transcript variant G (Dvir\GJ16545), mRNA

Sequence ID: ref|XM_015169991.1| Length: 4493 Number of Matches: 1

Range 1: 168 to 262

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	8e-13()	84/101(83%)	6/101(5%)	Plus/Plus		
Features	S :						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACG	CCCGGCACCTGTTCCA	AGTGGCATCGG	AGTGGGCG	224
Sbjct	168	ACGGCAGCATCA	gttctccatccacg	CCCAGCAACTGCTCG-	-gcgggcgg	cetceece	224
Query	225	GTGGCGGCTGCA	GCAGCAGCAGCAAC	AATAGCATCAACAGC	265		
Sbjct	225	GCTGCGGCAGCA	GCAGCAGCAGCAAC	AGCATCAACAGC	262		

Drosophila virilis uncharacterized protein, transcript variant F (Dvir\GJ16545), mRNA

Sequence ID: ref|XM_002057044.2| Length: 4782 Number of Matches: 1

Range 1: 484 to 578

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits(47)		8e-13()	84/101(83%)	6/101(5%)	Plus/Plus		
Feature	s:						
Query	165	ACGGCAGCATCA	GTTCTCCATCCACGO	CCGGCACCTGTTC	CAGTGGCATCGGAGT	rgggcg	224
Sbjct	484	ACGGCAGCATCA	GTTCTCCATCCACGC	CCAGCAACTGCTC	e-gcggecggcg1	rceece	540
Query	225	GTGGCGGCTGCA	GCAGCAGCAGCAAC <i>I</i>	AATAGCATCAACAGO	265		
Sbjct	541	GCTGCGGCAGCA	.GCAGCAGCAGCAAC <i>I</i>	AGCATCAACAGO	578		

 $Drosophila\ willistoni\ uncharacterized\ protein,\ transcript\ variant\ B\ (Dwil\backslash GK25837),\ partial\ mRNA$

Sequence ID: ref|XM_015177223.1| Length: 4519 Number of Matches: 1

Range 1: 126 to 156

Score		Expect	Identities	Gaps	Strand	Frame	
58.4 bits(31)		6e-04()	31/31(100%)	0/31(0%)	Plus/Plus		
Features:							
Query	Query 163 GAACGGCAGCATCAGTTCTCCATCCACGCCC			GCCC 193			
Sbjct	126	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCC 156			

Drosophila willistoni uncharacterized protein, transcript variant C (Dwil\GK25837), partial mRNA

Sequence ID: ref|XM_002071466.2| Length: 4387 Number of Matches: 1

Range 1: 126 to 156

Score		Expect	Identities	Gaps	Strand	Frame
58.4 bits(31)		6e-04()	31/31(100%)	0/31(0%)	Plus/Plus	
Feature	s:					
Query	163	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCC 193		
Sbjct	126	GAACGGCAGCAT	CAGTTCTCCATCCAC	GCCC 156		