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NCBI/ BLAST/ blastn suite/ Formatting Results - CNA4YFRN014

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Blast report description

Nucleotide Sequence (467 letters)

RID <u>CNA4YFRN014</u> (Expires on 02-23 13:20 pm)

Query ID lcl|Query_186379 **Database Name** nr

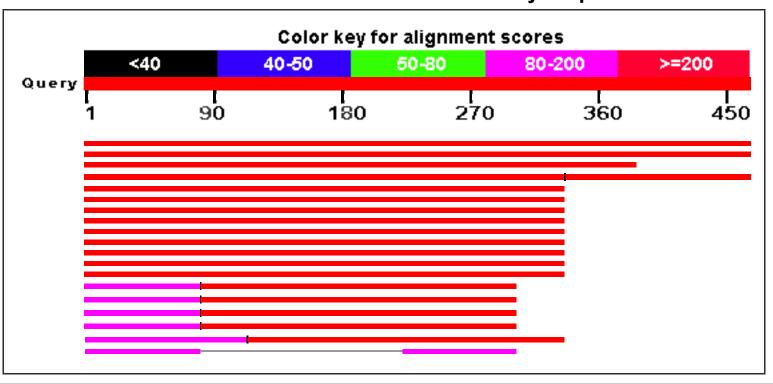
Description None **Description** Nucleotide collection (nt)

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

Query Length 467

□ Graphic Summary

Distribution of 52 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 transposon TART- C1 gag protein and pol protein genes, complete cds	560	1016	100%	8e-156	88%	AY600955.1
Drosophila melanogaster TART-B1 transposon putative single-stranded nucleic acid binding protein and putative reverse transcriptase genes, complete cds	538	1081	100%	4e-149	87%	<u>U14101.1</u>
Drosophila melanogaster chromosome Y Y_mapped_Scaffold_18_D1698 sequence	468	774	82%	5e-128	88%	CP007111.1
Drosophila melanogaster chromosome X; Y 211000022279810 sequence	449	998	100%	2e-122	91%	DS484314.1
Drosophila melanogaster clone BACR40C07, complete sequence	294	1147	71%	9e-76	82%	AC254617.2
Drosophila melanogaster 211000022279284 sequence	294	382	71%	9e-76	82%	DS484028.1
Drosophila melanogaster chromosome X	294	1147	71%	9e-76	82%	AE014298.5
Drosophila melanogaster chromosome 4	294	765	71%	9e-76	82%	AE014135.4
Drosophila melanogaster GH13568 full insert cDNA	294	382	71%	9e-76	82%	BT030106.1
Drosophila melanogaster clone BACN05O16, complete sequence	294	765	71%	9e-76	82%	AC010841.8
Drosophila melanogaster TART-A1 retrotransposon gag protein and pol protein genes, complete cds	294	382	71%	9e-76	82%	<u>AY561850.1</u>
Drosophila melanogaster GH16383 full insert cDNA	294	382	71%	9e-76	82%	<u>AY113347.1</u>
Drosophila melanogaster retrotransposon TART-A, clone 17G23	294	382	71%	9e-76	82%	AJ566116.1
Drosophila melanogaster sequence scaffold 211000022279209, complete sequence	292	382	64%	3e-75	84%	AC246448.1
Drosophila melanogaster 211000022278794 sequence	257	353	64%	1e-64	84%	DS484160.1
Drosophila melanogaster chromosome Y 211000022279532 sequence	252	347	64%	5e-63	84%	DS484103.1
Drosophila melanogaster chromosome Y 211000022278935 sequence	246	330	64%	3e-61	83%	DS485166.1
Drosophila melanogaster telomeric TART retrotransposon nonfunctional gag protein gene, partial sequence	231	319	71%	7e-57	79%	AY035776.1
Drosophila melanogaster 211000022278716 sequence	87.9	175	34%	2e-13	86%	DS484311.1

□ <u>Alignments</u>

Drosophila melanogaster transposon TART-C1 gag protein and pol protein genes, complete cds

Sequence ID: **gb|AY600955.1|** Length: 11124 Number of Matches: 2 Range 1: 826 to 1301

Score		Expect	Identities	Gaps	Strand	Frame
560 bits	(303)	8e-156()	422/478(88%)	13/478(2%)	Plus/Minus	
Feature	s:					
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTC	GTTGCATTAGTGTC	CATTATATTGTGTG	GGGGAGT 60
Sbjct	1301	ttaatttagcd	sgtttttgatgctgtd	scatcactactc	cttatgttgtgtg	GGTGAGT 1242
Query	61	TTATATGTGTT	TTGGCGGGAACTAGO	GTTTTGTGATGCT	ATGAGTTTG	TCTGTGT 114
Sbjct	1241	taatgtgtgtt	rttggcggaaaagag <i>i</i>	Atttdtdatdctgr	rgrrrrtgrgtttg	tctgtat 1182
Query	115	GGGTGAGTGTC	TCGGCTGCTTTG-TT	T-TGCAATAGGCTTT	TGGGTGCGGGGTG	AGGGGTC 172
Sbjct	1181	gggtgtgtgtg	cccdctdattccct	rgtg-aat-tgcttt	rtgrgtgaggggtg	AAATGTT 1124
Query	173	TTTGGCGGGCT	GTATTGGCTTGGTT7	CACCTAGGTGTGTC	TGTGTAGAAA-	TTATTTT 229
Sbjct	1123	tttggggact	reterteectre	rcacttreeteteae	stgtgaagagaaat	††A†††† 1064
Query	230	AGCGGTTTTTC	SATGCTTTGGTTGCAT	TAGTGTCATTATAT 	TGTGTGGGGGAGT	TTATATG 289
Sbjct	1063	Addddttttt	Atgcattggttgcat	rtagtgtcgttatat	rtĠtĠtĠĠĠĠĠĠĠ	ttatatd 1004
Query	290	TGTTTTGGCGG	GAACTAGGTTTTGT(GATGCTATGAGTTTG	TCTGTGTGGGTGA	GTGTCTC 349
Sbjct	1003	tettteeee	sgaactaggttttgt	satectateaette	stctgtgtgggtga	dtdtctc 944
Query	350	GGCTGCTTTGT	TTGCAATAGGCTTTT	GGGTGCGGGGTGAG	GGGTCTTTGGCGG	GCTGTAT 409
Sbjct	943	gectecttet	rttgcaataggcttt	reeeteeeeeree	egggtctttggggg	detetet 884
Query	410	TGGCTTGGTTT	CACCTAGGTGTGTCT	GTGTAGAAATTATT	TTAGCGGTTTTTG	ATGCT 467
Sbjct	883	tddc t t d d t t d	cacgtaggtgtaact	rgtgtagaaattatt	ŗŦŦĠĠĊĠĠŦŦŦŦŦĠ	AtGCt 826

Range 2: 735 to 1070

Score		Expect	Identities	Gaps	Strand	Frame	
455 bits	(246)	4e-124()	307/337(91%)	2/337(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTC	CATTATATTGTGTG	GGGGAGT	60
Sbjct	1070	ttattttagcg	GTTTTTAATGCATTG	gttgcattagtgtc	cottatattetete	GGGGAGT	1011
Query	61	TTATATGTGTT	TTGGCGGGAACTAGG'	TTTTGTGATGCTAT	GAGTTTGTCTGTG	TGGGTGA	120
Sbjct	1010	TTATATGTGTT	TTGGCGGGAACTAGG	rtttgtgatgctat	GAGTTTGTCTGTG	TGGGTGA	951
Query	121	GTGTCTCGGCT	GCTTTGTTTGCAATA(GGCTTTTGGGTGCG	GGGTGAGGGGTCT	TTGGCGG	180
Sbjct	950	gtgtctcgct	GCTTTGTTTGCAATA	ĠĠĊŦŦŦŦĠĠĠŦĠĊĠ	seeereaeeeere	ttggcgg	891
Query	181	GCTGTATTGGC	TTGGTTTCACCTAGG	TGTGTCTGTGTAGA	AATTATTTTAGCG	GTTTTTG	240
Sbjct	890	gctgtgttgc	ttggtttcacgtagg:	rgtaactgtgtaga	AATTATTTGGCG	\$GTTTTTG	831
Query	241	ATGCTTTGGTT	GCATTAGTGTCATTA	TATTGTGTGGGGGA	GTTTATATGTGTT	TTGGCGG	300
Sbjct	830	AtGCTTTGGTT	GCATTAATGTCGTCA:	rcttgtgtaggtci	dretacatetett	TTGTCGG	771
Query	301	GAACTAGGTTT	-TGTGATGCTATGAG	TTTGTCTGTGT 3	336		
Sbjct	770	GTAG-ATTTTT	ctgtgttactgtaat:	ተተተፍተራተፍተፍተ	'35		

Drosophila melanogaster TART-B1 transposon putative single-stranded nucleic acid binding protein and putative reverse transcriptase genes, complete cds

Sequence ID: gb|U14101.1|DMU14101 Length: 10654 Number of Matches: 3

Range 1: 1582 to 2057

Score		Expect	Identities	Gaps	Strand	Frame	
538 bits	(291)	4e-149()	418/478(87%)	13/478(2%)	Plus/Minus		
Features	S :						
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTC	ATTATATTGTGT	GGGGGAGT	60
Sbjct	2057	TTAATTTAGC	GTTTTTGATGCTGTG	GCTGCACTAGTGTA	GTTATGTTGTGT	GGGTGAGT	1998
Query	61	TTATATGTGTT	TTGGCGGGAACTAGG	TTTTGTGATGCT	ATGAGTTT	GTCTGTGT	114

Sbjct	1997	TAATGTGTGTTTTGGCGGAAAAGAGATTTTGTGATGCTGTTTTTTTT	1938
Query	115	GGGTGAGTGTCTCGGCTGCTTTG-TT-TGCAATAGGCTTTTTGGGTGCGGGGTGAGGGGTC	172
Sbjct	1937	GGGTGTGTGTCCCGGCTGATTCGCTTGTG-AAT-TGCTTTTGTGTGAGGGGTGAAATGTT	1880
Query	173	TTTGGCGGGCTGTATTGGCTTGGTTTCACCTAGGTGTGTCTGTGTAGAAA-TTATTTT	229
Sbjct	1879	tttggcggactgtgttggcttgatttcactttggtgtgagtgtgaagagaaatttattt	1820
Query	230	AGCGGTTTTTGATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGGAGTTTATATG	289
Sbjct	1819	AGCGGTTTTTAATGCATTGGTTGCATTAGTGTCGTTATATTGTGTGGGGTGTGTTTATATG	1760
Query	290	TGTTTTGGCGGGAACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGTGGGTGAGTGTCTC	349
Sbjct	1759	TGTTTTGGCGGGAACGAGGTTTTGTGATGCTGTGAGTTTGTCTGTGTGGGGTAAGTGTCTC	1700
Query	350	GGCTGCTTTGTTTGCAATAGGCTTTTTGGGTGCGGGGTGAGGGGTCTTTTGGCGGGCTGTAT	409
Sbjct	1699	GTCAGCTTTGTGTGCAATAGGCTTTTGGGTGCGGGGTGAGGGGGTCTTTGGCCGGGCTGTAT	1640
Query	410	TGGCTTGGTTTCACCTAGGTGTGTCTGTGTAGAAATTATTTTAGCGGTTTTTTGATGCT 4	67
Sbjct	1639	tggcttggtttcacctaggtgtgtctgtgtagaaattattttagcggtttttgatgct 1	582

Range 2: 1484 to 1826

Score		Expect	Identities	Gaps	Strand	Frame	
446 bits	(241)	2e-121()	310/344(90%)	2/344(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTC	CATTATATTGTGTG	GGGGAGT	60
Sbjct	1826	TTATTTTAGCG	GTTTTTAATGCATTG	GTTGCATTAGTGT	CGTTATATTGTGTG	GGTGTGT	1767
Query	61	TTATATGTGTT	TTGGCGGGAACTAGG'	TTTTGTGATGCTA1	GAGTTTGTCTGTC	STGGGTGA	120
Sbjct	1766	ተተልተልተĠተĠተተ	rttggcgggaacgagg	ttttgtgatgctg1	rgagttttgtctgtd	stgggtaa	1707
Query	121	GTGTCTCGGCT	GCTTTGTTTGCAATA(GGCTTTTGGGTGC	GGGTGAGGGGTCT	TTTGGCGG	180
Sbjct	1706	dtdtctcdtca	.dctttdtgtddaata	ĠĠĊŦŦŦŦĠĠĠŦĠĊĊ	edddadddddddddddddddddddddddddddddddddd	rttggcgg	1647
Query	181	GCTGTATTGGC	TTGGTTTCACCTAGG'	TGTGTCTGTGTAG <i>F</i>	AATTATTTTAGCO	GTTTTTG	240
Sbjct	1646	gctgtyttgc	tttggtttcacctagg	tĠtĠtĊtĠtĠtAĠ <i>ŧ</i>	AAATTATTTAGCC	schhhhhhc	1587
Query	241	ATGCTTTGGTT	GCATTAGTGTCATTA'	TATTGTGTGGGGG <i>F</i>	AGTTTATATGTGTT	TTTGGCGG	300
Sbjct	1586	Atgetttgett	'dcattaatdtcgtca'	tcttgtgtaggtg	rdtctacatdtdt	тттфтсфф	1527
Query	301	GAACTAGGTTT	'-TGTGATGCTATGAG'	TTTGTCTGTGTGGG	STGAG 343		
Sbjct	1526	ĠTÅG-ÅTTŤŤ	ctdtdrtcctgtrar:	t t t d t d t d t d t d t d t d t d t	CTGAG 1484		

Range 3: 1484 to 1604

Score		Expect	Identities	Gaps	Strand	Frame	
97.1 bits(52)		3e-16()	99/122(81%)	2/122(1%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAG	CGGTTTTTGATGCTT	TGGTTGCATTAGTG	TCATTATATTGTG	TGGGGGAGT	60
Sbjct	1604	TTATTTTAG	CGGTTTTTGATGCTT	rGGTTGCATTAATG:	regreateriging	TAGGTGTGT	1545
Query	61	TTATATGTG'	TTTTGGCGGGAACTAG	GTTT-TGTGATGC	PATGAGTTTGTCT	GTGTGGGTG	119
Sbjct	1544	CTACATGTG	rtttgregggrag-an	rrtttctgtgrtcc	tgtrartttgtct	GTGTAGCTG	1486
Query	120	AG 121					
Sbjct	1485	AG 1484					

Drosophila melanogaster chromosome Y Y_mapped_Scaffold_18_D1698 sequence Sequence ID: **gb|CP007111.1|** Length: 34521 Number of Matches: 2 Range 1: 1343 to 1738

Score Expect Identities Gaps	Strand Frame
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468 bits	(253)	5e-128()	350/396(88%)	9/396(2%)	Plus/Minus	
Features	s:					
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTGG	TTGCATTAGTGTC	ATTATATTGTGTGGGGGAGT	60
Sbjct	1738	TTAATTTAGCG	GTTTTTGATGCTGTGG	ctdcactagtgtc	GTTATGTTGTGTGGGTGAGT	1679
Query	61	TTATATGTGTT	TTGGCGGGAACTAGGT	TTTGTGATGCT	ATGAGTTTGTCTGTGT	114
Sbjct	1678	taatgtgtgtt	ttggcggaaaagat	tttgtgatgctgt	GTTTTTGTGTTTGTCTGTAT	1619
Query	115	GGGTGAGTGTC	rcggctgctttgtttg	CAATAGGCTTTTG	GGTGCGGGGTGAGGGGTCTT	174
Sbjct	1618	gggtgrgtgtg	cceecteattcectte	rgattrgcttttg	rgtgaggggtgaaargtrtt	1559
Query	175	TGGCGGGCTGT	ATTGGCTTGGTTTCAC	CTAGGTGTGTCTG	TGTAGAAA-TTATTTTAG	231
Sbjct	1558	†ggcgggctgt	gttggcttggtttcac	TTTGGTGTGAGTG	tgaagagaaatttatttag	1499
Query	232	CGGTTTTTGAT	GCTTTGGTTGCATTAG 	TGTCATTATATTG	TGTGGGGGAGTTTATATGTG	291
Sbjct	1498	ĊĠĠϮϮϮϮϮĠĂϮċ	ĠĊŦŦŦĠĠŦŦĠĊĂŦŦĂĠ	tgtcattatattg	tgtgggggagtttatatgtg	1439
Query	292	TTTTGGCGGGA	ACTAGGTTTTGTGATG 	CTATGAGTTTGTC	TGTGTGGGTGAGTGTCTCGG	351
Sbjct	1438	††††ddcdddai	Actaggttttgtgatg	ĊŦĀŦĠĀĠŦŦŦĠŦĊ	tereteere	1379
Query	352	CTGCTTTGTTT(GCAATAGGCTTTTGGG 	TGCGGGGTG 38	7	
Sbjct	1378	ĊŦĠĊŦŦŦĠŦŦŦ	ĠĊĀĀŦĀĠĠĊŦŦŦŦĠĠĠ	tgcggggtg 13	43	

Range 2: 1343 to 1507

Score		Expect	Identities	Gaps	Strand	Frame	
305 bits	(165)	4e-79()	165/165(100%)	0/165(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGC	GGTTTTTGATGCTTTG	GTTGCATTAGTGTC	ATTATATTGTGT	rgggggagt	60
Sbjct	1507	ttattttagc	GGTTTTTGATGCTTTG	central designation of the second	ATTATATTGTGT	rgggggagt	1448
Query	61	TTATATGTGT	TTTGGCGGGAACTAGG	TTTTGTGATGCTAT	GAGTTTGTCTGT	rgtgggtga 	120
Sbjct	1447	TTATATGTGT	tttggcgggaactagg	rtttgtgatgctat	ĠĀĠŦŦŦĠŦĊŦĠŢ	rgtgggtga	1388
Query	121	GTGTCTCGGC	TGCTTTGTTTGCAATA	GGCTTTTGGGTGCG	GGGTG 165		
Sbjct	1387	ĠŦĠŦĊŦĊĠĠĊ	ተ ĠĊተተተĠተተተĠĊAAተA	ჅĠĊϮϮϮϮĠĠĠϮĠĊĠ	dddtd 1343		

Drosophila melanogaster chromosome X; Y 211000022279810 sequence Sequence ID: **gb|DS484314.1|** Length: 2381 Number of Matches: 3 Range 1: 1936 to 2271

Score		Expect	Identities	Gaps	Strand	Frame	
449 bits	(243)	2e-122()	306/337(91%)	2/337(0%)	Plus/Minus		
Features	s:						
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTC	CATTATATTGTGTG	GGGGAGT	60
Sbjct	2271	TTATTTTAGCG	GTTTTTAATGCATTG	GTTGCATTAGTGTC	CGTTATATTGTGTC	GGTGTGT	2212
Query	61	TTATATGTGTT	TTGGCGGGAACTAGG	TTTTGTGATGCTAT	rgagtttgtctgt(GTGGGTGA	120
Sbjct	2211	++++++++++++++++++++++++++++++++++++	TTGGCGGGAACGAGG	thttgtgatgctg	rgagtttgtctgtd	STGGGTAA	2152
Query	121	GTGTCTCGGCT	GCTTTGTTTGCAATA	GGCTTTTGGGTGC	GGGTGAGGGGTCT	TTTGGCGG	180
Sbjct	2151	gtgtctcgtca	detttdtgtgtdeaata	œdetttttedettec	eddatdadddatca	rttggcgg	2092
Query	181	GCTGTATTGGC	TTGGTTTCACCTAGG	TGTGTCTGTGTAG <i>I</i>	AATTATTTTAGCO	GTTTTTG	240
Sbjct	2091	gctgtattgc	ttggtttcacctagg	rtgtgtctgtgtagz	AAATTATTTTAGC	GGTTTTTG	2032
Query	241	ATGCTTTGGTT	GCATTAGTGTCATTA	TATTGTGTGGGGG	AGTTTATATGTGTT	TTTGGCGG	300
Sbjct	2031	Atgetttgett	gcattaatgtcgtca	tcttgtgtaggtg	rgtctacatgtgtd	rttgrcgg	1972
Query	301	GAACTAGGTTT	-TGTGATGCTATGAG	TTTGTCTGTGT 3	336		
Sbjct	1971	GTAG-ATTTTT	ctdtdttcctattat	rtttgtctgtgt	1936		

Score		Expect	Identities	Gaps	Strand	Frame	
448 bits	(242)	7e-122()	318/355(90%)	3/355(0%)	Plus/Minus		
Features	3 :						
Query	116	GGTGAGTGTCT	CGGCTGCTTTGTTTG	CAATAGGCTTTTGG	GTGCGGGGTGAGG	GGTCTTT	175
Sbjct	2381	ggtgrgtgtcc	cggctgattcgcttg	тдатттфстттфт	GTGAGGGGTGAAA	ѵҵҾҭҵҭҵҭ	2322
Query	176	GGCGGGCTGTA	TTGGCTTGGTTTCAC	CTAGGTGTGTCTGT	GTAGAAA-TT <i>A</i>	TTTTAGC	232
Sbjct	2321	GGCGGACTGTG	ttggcttgatttcac	TTTGGTGTGAGTGT	'GAAGAGAAATTTA	\t+t+ddc	2262
Query	233	GGTTTTTGATG	CTTTGGTTGCATTAG	TGTCATTATATTGT	GTGGGGGAGTTT <i>P</i>	TATGTGT	292
Sbjct	2261	GGTTTTTAATG	cattggttgcattag	ተ ĠተĊĠተተልተልተተĠተ	ĠŦĠĠĠŦĠŦĠŦŦŦ	\tatgtgt	2202
Query	293	TTTGGCGGGAA	CTAGGTTTTGTGATG	CTATGAGTTTGTCT	GTGTGGGTGAGTG	TCTCGGC	352
Sbjct	2201	tttggggggaa	.cgaggtttttgtgatg	ctgtgagtttgtct	dretededtaalete	;tctcgtc	2142
Query	353	TGCTTTGTTTG	CAATAGGCTTTTGGG	TGCGGGGTGAGGGG	TCTTTGGCGGGC1	'GTATTGG	412
Sbjct	2141	adctttdtgtgt	caataggcttttggg	teceeeetee	tctttggcgggci	'ĠŦĀŦŦĠĠ	2082
Query	413	CTTGGTTTCAC	CTAGGTGTGTCTGTG	TAGAAATTATTTTA 	GCGGTTTTTGATC	SCT 467	
Sbjct	2081	cttggtttcac	ctaggtgtgtctgtg	ተልĠልልልተተልተተተተል	ĠĊĠĠŦŦŦŦŦĠĀŦĠ	SCT 2027	

Range 3: 1936 to 2049

Score		Expect	Identities	Gaps	Strand	Frame	
100 bits(54)		2e-17()	95/115(83%)	2/115(1%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGO	CGGTTTTTGATGCTT'	TGGTTGCATTAGTG	TCATTATATTGTGT	[GGGGGAGT	60
Sbjct	2049	TTATTTTAG	CGGTTTTTGATGCTT	rggttgcattaatg	TCGTCATCTTGTGT	PAGGTGTGT	1990
Query	61	TTATATGTGT	TTTTGGCGGGAACTA	GGTTT-TGTGATGC	TATGAGTTTGTCTG	GTGT 114	
Sbjct	1989	ctacateter	rtttgrcgggrag-a	rrtttctgtgrtcc	ተልተتልتተተተፍተራተረ	STGT 1936	

Drosophila melanogaster clone BACR40C07, complete sequence Sequence ID: **gb|AC254617.2|** Length: 159272 Number of Matches: 6 Range 1: 16332 to 16667

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Features	S:						
Query	1	TTATTTTAG	CGGTTTTTGATGCTT	rggttgcattagtg:	rcattatattgtg7	TGGGGGAGT	60
Sbjct	16667	TTATTTTAC	CGTCTTTTGATGCTG	rgcttgcattagtg:	rcgttatattgtg:	TGGGTGAGT	16608
Query	61	TTATATGTG	TTTTGGCGGGAACTA(GGTTTTGTGATGCT	ATGAGTTTGTCTG7	TGTGGGTGA	120
Sbjct	16607	TTATATGTG:	rtttggtgggaaaaa	Gattttdtdacdct	stcggtttgtctg	rGTGTGTGT	16548
Query	121	GTGTCTCGG	CTGCTTTGTTTGCAAT	raggetttttgggtg(CGGGGTGAGGGGTC	CTTTGGCGG	180
Sbjct	16547	gtgtctrgg	ctgrtttgtttgrgg	tradctttttdddtd	addddaaddda	rtttggcgg	16488
Query	181	GCTGTATTG	GCTTGGTTTCACCTA(GGTGTGTCTGTGTA(GAAATTATTTTAGO	CGGTTTTTG	240
Sbjct	16487	GCTGTGTTG	GCTTGGTTTCATGTAG	GTTGTGAGTGTGAT	GAATCTATTTGGGC	CGGTTTTTG	16428
Query	241	ATGCTTTGG	TTGCATTAGTGTCAT	TATATTGTGTGGGGG	GAGTTTATATGTGT	TTTTGGCGG	300
Sbjct	16427	Atgctttgg:	ttgcattagtgtcato	cgtcttgtgtaggt	gretetacatete	rtttagtgg	16368
Query	301	G-AACTAGG	TTTTGTGATGCTATG <i>I</i>	AGTTTGTCTGTGT	336		
Sbjct	16367	GGAAATT-T	ttctgtgttgctgtaz	\rtqt&t&t&t&t	16332		

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAG	CGGTTTTTGATGCTT'	rggttgcattagtg:	rcattatattgtg'	TGGGGGAGT	60
Sbjct	28173	TTATTTTAC	CGTCTTTTGATGCTG	rgcttgcattagtg:	rcgttatattgtg	TGGGTGAGT	28114
Query	61	TTATATGTG	TTTTGGCGGGAACTA(GGTTTTGTGATGCT	ATGAGTTTGTCTG'	TGTGGGTGA	120
Sbjct	28113	TTATATGTG	TTTGGTGGGAAAAA	gattttgtgacgct	϶ϯϲͼͼϮϮϯͼϯϲϯͼ·	rgtgrgtgr	28054
Query	121	GTGTCTCGG	CTGCTTTGTTTGCAA'	TAGGCTTTTTGGGTG(CGGGGTGAGGGGT	CTTTGGCGG	180
Sbjct	28053	GTGTCTTGG	ĊŦĠŦŦŦŦĠŦŦŦĠŦĠŦĠ	rtagctttttgggtg	AGGGGTGAAGGGT'	rtttggcgg	27994
Query	181	GCTGTATTG	GCTTGGTTTCACCTA(GGTGTGTCTGTGTA	GAAATTATTTTAG(CGGTTTTTG	240
Sbjct	27993	gctgtgttg	gcttggtttcatgta	gttgtgagtgtgat	GAATCTATTTGGG	CGGTTTTTG	27934
Query	241	ATGCTTTGG	TTGCATTAGTGTCAT'	TATATTGTGTGGGGG	GAGTTTATATGTG'	TTTTGGCGG	300
Sbjct	27933	AtGCTTTGG	ttgcattagtgtcat	cgtcttgtgtaggt	gretetacatete	rtttagtgg	27874
Query	301	G-AACTAGG	TTTTGTGATGCTATG	AGTTTGTCTGTGT	336		
Sbjct	27873	ĠĠÅÅAŤT-T	ttctgtgttgtgta	ATTTTGTCTGTGT	27838		

Range 3: 39509 to 39844

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Features	S :						
Query	1	TTATTTTAG	CGGTTTTTGATGCTT	rggttgcattagtgt	CATTATATTGTG	TGGGGGAGT	60
Sbjct	39844	TTATTTTAC	CGTCTTTTGATGCTG	rgcttgcattagtg1	CGTTATATTGTG	TGGGTGAGT	39785
Query	61	TTATATGTG	TTTTGGCGGGAACTA(GTTTTGTGATGCTA	TGAGTTTGTCTG	TGTGGGTGA	120
Sbjct	39784	ttatatgtg:	rtrtggrgggaaaaa	Sattttgtgacgctg	stcggtttgtctg	rgtgtgtgt	39725
Query	121	GTGTCTCGG	CTGCTTTGTTTGCAAT	PAGGCTTTTGGGTGC	GGGGTGAGGGGT	CTTTGGCGG	180
Sbjct	39724	grgtctrgg(ctgrtttgtttgrgg	rtagetttttgggtga	rggggtgyagggt.	rtttggcgg	39665
Query	181	GCTGTATTG	GCTTGGTTTCACCTA(GTGTGTCTGTGTAG	GAAATTATTTTAG(CGGTTTTTG	240
Sbjct	39664	GCTGTGTTG	gcttggtttcatgtac	erteteaeteteare	SAATCTATTTGGG	CGGTTTTTG	39605
Query	241	ATGCTTTGG	TTGCATTAGTGTCAT	PATATTGTGTGGGGG	GAGTTTATATGTG'	TTTTGGCGG	300
Sbjct	39604	Atgctttgg:	ttgcattagtgtcatc	cgtcttgtgtaggtd	rgtctAcAtgtg:	rtttagtgg	39545
Query	301	G-AACTAGG	TTTTGTGATGCTATG <i>I</i>	AGTTTGTCTGTGT	336		
Sbjct	39544	GGAAATT-T'	ttctgtgttgctgtaz	\rተተተ ተተተተተ	39509		

Range 4: 16332 to 16444

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Features	s:						
Query	2	TATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTG7	CATTATATTGTGTG	GGGGGAGTT	61
Sbjct	16444	tatttgggc	ĠĠŦŦŦŦŦĠĂŦĠĊŦŦŦ	ĠĠŦŦĠĊĀŦŦĀĠŦĠſ	cktcgtcttgtgt	AGGTGTGTC	16385
Query	62	TATATGTGT	TTTGGCGGG-AACTA	GGTTTTGTGATGC	TATGAGTTTGTCTG	rgt 114	
Sbjct	16384	TACATGTGT	tttagtgggddatt	-rttctctttctct	rgtaartttgtctg	rGT 16332	

Range 5: 27838 to 27950

Score	Expect	Identities	Gaps	Strand	Frame
87.9 bits(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus	
Features:					

reatures:

Query	2	ŢĄŢŢŢŢĀĢÇĢĢŢŢŢŢŢĢĄŢĢÇŢŢŢĢĢŢŢĢŢĢŢĢŢÇĄŢŢAŢŦŢŢŢŢŢŢĠŢĠĢĠĢĀĢŢŢ	61
Sbjct	27950	TATTTGGGCGGTTTTTGATGCTTTGGTTGCATTAGTGTCATCGTCTTGTGTAGGTGTCTC	27891
Query	62	TATATGTGTTTTGGCGGG-AACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGT 114	
Sbict	27890	TACATGTGTTTTAGTGGGGAAATT-TTTCTGTGTTGCTGTAATTTTGTCTGTGT 27838	

Range 6: 39509 to 39621

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Feature	s:						
Query	2	TATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTGT	CATTATATTGTGTG	GGGGGAGTT	61
Sbjct	39621	TATTTGGGC	GGTTTTTGATGCTTT	GGTTGCATTAGTG1	CATCGTCTTGTGT	AGGTGTGTC	39562
Query	62	TATATGTGT	TTTGGCGGG-AACTA	GGTTTTGTGATGCT	TATGAGTTTGTCTG	rgr 114	
Sbjct	39561	TACATGTGT	TTTAGTGGGGAAATT	-rttctgtgrtgct	rgtaartttgtctg	rgt 39509	

Drosophila melanogaster 211000022279284 sequence

Sequence ID: **gb|D\$484028.1|** Length: 3196 Number of Matches: 2 Range 1: 1252 to 1587

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTGT	CATTATATTGTGTG	GGGGAGT	60
Sbjct	1587	TTATTTTACC	GTCTTTTGATGCTGT	GCTTGCATTAGTGT(CGTTATATTGTGTG	GGTGAGT	1528
Query	61	TTATATGTGT'	TTTGGCGGGAACTAG	GTTTTGTGATGCTA	rgagtttgtctgtc	TGGGTGA	120
Sbjct	1527	ተተልተልተۈተۈተ	rttggtgggaaaad.	attttgtgacgctg	tcggtttgtgtctgt	stgrgtgr	1468
Query	121	GTGTCTCGGC	rgctttgtttgcaat.	AGGCTTTTGGGTGC	GGGGTGAGGGGTCT	TTGGCGG	180
Sbjct	1467	gtgtctrggc	ŀĠ┰ϮϮϮĠϮϮϮĠ┰ĠĠϮ [;]	radctttttdddtdao	GGGGTGAAGGGTTT	rttggcgg	1408
Query	181	GCTGTATTGG	CTTGGTTTCACCTAG	GTGTGTCTGTGTAG	AAATTATTTTAGCG	GTTTTTG	240
Sbjct	1407	GCTGTGTTGG	cttggtttcatgtag	rtdtdagtdtdatd	AATCTATTTGGGCC	GTTTTTG	1348
Query	241	ATGCTTTGGT	rgcattagtgtcatt. 	ATATTGTGTGGGGG	AGTTTATATGTGTT	TTGGCGG	300
Sbjct	1347	Argetrreger	tgcattagtgtcatc	gtcttgtgtaggtg	rgtctycytgtgt	TTAGTGG	1288
Query	301	G-AACTAGGT	TTTGTGATGCTATGA	GTTTGTCTGTGT (336		
Sbjct	1287	GGAAATT-TT:	tctgtgttgctgtaa	ተተተተፍተረተፍተፍተ	1252		

Range 2: 1252 to 1364

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Feature	s:						
Query	2	TATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGT(CATTATATTGTGTG	GGGGAGTT	61
Sbjct	1364	TATTTGGGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTG	CATCGTCTTGTGTA	GGTGTGTC	1305
Query	62	TATATGTGTT	TTGGCGGG-AACTAG	GTTTTGTGATGCT	ATGAGTTTGTCTGT	GT 114	
Sbjct	1304	TACATGTGTT		TTTCTGTGTTGCT	GTAATTTTGTCTGT	 GT 1252	

Drosophila melanogaster chromosome X

Sequence ID: **gb|AE014298.5|** Length: 23542271 Number of Matches: 6 Range 1: 16332 to 16667

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Features 107797	s: bp at 3' s	ide: uncharac	cterized protein, iso	form C			
Query	1	TTATTTTAGO	CGGTTTTTGATGCTTT	GGTTGCATTAGTG	TCATTATATTGTG7	TGGGGGAGT	60
Sbjct	16667	TTATTTTAC	CGTCTTTTGATGCTGT	cttgcattagtg	rcgttatattgtg	rGGGTGAGT	16608
Query	61	TTATATGTGT	TTTTGGCGGGAACTAG	GTTTTGTGATGCT	ATGAGTTTGTCTG7	TGTGGGTGA	120
Sbjct	16607	TTATATGTGT	rtttggtggddaaad	attttgtgacgct	gtcggtttgtctg	rGTGTGTGT	16548
Query	121	GTGTCTCGG	CTGCTTTGTTTGCAAT	AGGCTTTTGGGTG	CGGGGTGAGGGGTC	CTTTGGCGG	180
Sbjct	16547	GTGTCTTGG	chgrhhhghhhdragh	TAGCTTTTGGGTG	addddadddda	rtttggcgg	16488
Query	181	GCTGTATTGO	GCTTGGTTTCACCTAG	GTGTGTCTGTGTA	GAAATTATTTTAGO	CGGTTTTTG	240
Sbjct	16487	gctgtgttg	Schröghthcarghad	rtdtdagtdtdar	GAATCTATTTGGGC	cggtttttg	16428
Query	241	ATGCTTTGGT	TTGCATTAGTGTCATT	ATATTGTGTGGGG	GAGTTTATATGTGT	TTTTGGCGG	300
Sbjct	16427	ATGCTTTGG	rtgcattagtgtcatc	GtCttGtGtAGGT	grgtctacatgtg	TTTAGTGG	16368
Query	301	G-AACTAGG	TTTTGTGATGCTATGA	GTTTGTCTGTGT	336		
Sbjct	16367	GGAAATT-TI	rtctgtgttgctgtaa	ттттбтстбтбт	16332		

Range 2: 27838 to 28173

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Features 96291 b	s: p at 3' si	de: uncharac	terized protein, isof	orm C			
Query	1	TTATTTTAG	CGGTTTTTGATGCTT	rggttgcattagtg:	TCATTATATTGTG	rgggggagt	60
Sbjct	28173	TTATTTTAC	cgrcttttgatgctg	rgcttgcattagtg	rcgttatattgtg	rgggtgagt	28114
Query	61	TTATATGTG'	TTTTGGCGGGAACTA(GGTTTTGTGATGCT	ATGAGTTTGTCTG	rgtgggtga 	120
Sbjct	28113	ttatatdtg	rtttggtgggaaaa	gattttgtgacgcto	gtcggtttgtctg	rgtgtgtgt	28054
Query	121	GTGTCTCGG(CTGCTTTGTTTGCAA!	TAGGCTTTTGGGTG(CGGGGTGAGGGGT	CTTTGGCGG	180
Sbjct	28053	ĠŦĠŦĊŦŦĠĠŒ	ĊŦĠŦŦŦŦĠŦŦŦĠŦĠŦĠ	tradctttttdddtd	aĠĠĠĠŦĠAaĠĠĠŦſ	rtttggcg	27994
Query	181	GCTGTATTG	GCTTGGTTTCACCTA(GGTGTGTCTGTGTA(GAAATTATTTTAG(CGGTTTTTG	240
Sbjct	27993	ĠĊŦĠŦĠŦŦĠ	ĠĊϮϮĠĠϮϮϮĊĂŦĠϮĂſ	ĠŦŦĠŦĠAGŦĠŦĠAŦ¢	ĠÅÅTCŤÅŤŤŤGGĠG	cggtttttg	27934
Query	241	ATGCTTTGG'	TTGCATTAGTGTCATT	FATATTGTGTGGGGG	GAGTTTATATGTGT 	PTTTGGCGG	300
Sbjct	27933	ATĠĊŢŢŢĠĠ	trĠĊAtrAĠtĠtĊAto	CGTCTTGTGTAGGT	ĠTĠTCTACATĠTĠ:	ГТТТАĞТĞĞ	27874
Query	301	G-AACTAGG	ΓΤΤΤGTGATGCTATG₽ 	AGTTTGTCTGTGT	336		
Sbjct	27873	ĠĠÅĀĀŤŢŢ	trctgtgttgtal	ATTTTGTCTGTGT	27838		

Range 3: 39509 to 39844

Score		Expect	Identities	Gaps	Strand	Frame			
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus				
Features: 84620 bp at 3' side: uncharacterized protein, isoform C									
Query	1	TTATTTTAGO	CGGTTTTTGATGCTTT	GGTTGCATTAGTG	CATTATATTGTG	rgggggagt	60		
Sbjct	39844	TTATTTACC	cgrcttttgatgctgt	gcttgcattagtg	tcgttatattgtg	rgggtgagt	39785		
Query	61	TTATATGTGT	TTTTGGCGGGAACTAG	GTTTTGTGATGCT <i>I</i>	ATGAGTTTGTCTG	rgtgggtga	120		
Sbjct	39784	TTATATGTGT	rtttggtgggaaaad	attttgtgacgcto	stcggtttgtctg	rgtgtgtgt	39725		
Query	121	GTGTCTCGG(CTGCTTTGTTTGCAAT	AGGCTTTTGGGTG(CGGGGTGAGGGGT	CTTTGGCGG	180		
Sbjct	39724	gtgtcttgg	ctgrtttgtttgrggt	radctttttdddtd	addddtdaadddt	rtttggcgg	39665		
Query	181	GCTGTATTGO	GCTTGGTTTCACCTAG	GTGTGTCTGTGTA(GAAATTATTTTAG(CGGTTTTTG	240		
Sbjct	39664	gctgtgttg	scttggtttcatgtag	rtgtgagtgtgato	SAATCTATTTGGGG	cggtttttg	39605		
Query	241	ATGCTTTGGT	TTGCATTAGTGTCATT	ATATTGTGTGGGG	GAGTTTATATGTG	TTTTGGCGG	300		

Sbjct 39604 ATGCTTTGGTTGCATTAGTGTCATCGTCTTGTGTAGGTGTCTACATGTGTTTTAGTGG

301 Query GGAAATT-TTTCTGTGTTGCTGTAATTTTGTCTGTGT Sbjct 39544

Range 4: 16332 to 16444

Score	Expect	Identities	Gaps	Strand	Frame
87.9 bits(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus	

Features: 108020 bp at 3' side: uncharacterized protein, isoform C

Query	2	TATTTTAGCGGTTTTTGATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGA	- T T -	61
Sbjct	16444	TATTTGGGCGGTTTTTGATGCTTTGGTTGCATTAGTGTCATCGTCTTGTGTAGGTGT	rĠϮC	16385
Query	62	+ + + + + + + + + + + + + + + + + + +	114	
Sbjct	16384	tacatetetttaeteegeaaatt-tttctetetetetetaattttetetetet	16332	

Range 5: 27838 to 27950

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		_
Feature: 96514 b		de: uncharac	terized protein, iso	form C			
Query	2	TATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTGT	rcattatattgtgt	GGGGGAGTT	61
Sbjct	27950	TATTTGGGC	GGTTTTTGATGCTTT	ggttgcattagtg	rcatcgtcttgtgt	AGGTGTGTC	27891
Query	62	TATATGTGT'	TTTGGCGGG-AACTA	GGTTTTGTGATGCT	TATGAGTTTGTCTG	TGT 114	
Sbjct	27890	TACATGTGT'		-TTTCTGTGTTGC	rgtaarttttgtctg	TGT 27838	

Range 6: 39509 to 39621

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Features 84843 b	s: p at 3' si	de: uncharac	terized protein, iso	form C			
Query	2	TATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTG'	TCATTATATTGTGT	GGGGGAGTT	61
Sbjct	39621	TATTTGGGC	GGTTTTTGATGCTTT	GGTTGCATTAGTG	TCATCGTCTTGTGT.	AGGTGTGTC	39562
Query	62	TATATGTGT	TTTGGCGGG-AACTA	.GGTTTTGTGATGC	TATGAGTTTGTCTG	TGT 114	
Sbjct	39561	TACATGTGT	TTTAGTGGGGAAATT	ֈ–ՠֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈֈ	tgtaartttgtctg	TGT 39509	

Drosophila melanogaster chromosome 4

Sequence ID: gb|AE014135.4| Length: 1348131 Number of Matches: 4

Range 1: 1330908 to 1331243

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits((159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Plus		
Features	S :						
Query	1	TTATTTTA	GCGGTTTTTGATGCTT	rggttgcattagtg	TCATTATATTG7	GTGGGGGAGT	60
Sbjct	1330908	TTATTTTA	CCGTCTTTTGATGCTG	rgcttgcattagtg	tcgttatattg	GTGGGTGAGT	1330967
Query	61	TTATATGT	GTTTTGGCGGGAACTA(GTTTTGTGATGCT	ATGAGTTTGTCT	GTGTGGGTGA	120
Sbjct	1330968	ttatatgt	GTTTTGGTGGGAAAAA	sattttgtgacgct	ctccctttct	cdtdtdtdtdt	1331027
Query	121	GTGTCTCG	GCTGCTTTGTTTGCAAT	PAGGCTTTTGGGTG	CGGGGTGAGGG	TCTTTGGCGG	180
Sbjct	1331028	gtgtcttg	ĠĊŦĠŦŦŦŦĠŦŦŦĠŦĠ	rtagetttttgggtg	adddtdaadd	strtttddddd	1331087

Query	181	GCTGTATTGGCTTGGTTTCACCTAGGTGTGTCTGTGTAGAAATTATTTTAGCGGTTTTTTG	240
Sbjct	1331088	GCTGTGTTGGCTTGGTTCATGTAGTTGTGAGTGTGATGAATCTATTTGGGCGGTTTTTTG	1331147
Query	241	ATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGAGTTTATATGTGTTTTTGGCGG	300
Sbjct	1331148	ATGCTTTGGTTGCATTAGTGTCATCGTCTTGTGTAGGTGTGTCTACATGTGTTTTTAGTGG	1331207
Query	301	G-AACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGT 336	
Sbjct	1331208	GGAAATT-TTTCTGTGTTGCTGTAATTTTGTCTGTGT 1331243	

Range 2: 1343890 to 1344225

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Plus		
Features	s :						
Query	1	TTATTTTA	GCGGTTTTTGATGCT	TTGGTTGCATTAGTG	GTCATTATATTG7	GTGGGGGAGT	60
Sbjct	1343890	$\frac{1}{2}$	ccgrcttttgatgct	GTGCTTGCATTAGTG	stegttatattel	GTGGGTGAGT	1343949
Query	61	TTATATGT	GTTTTGGCGGGAACT	AGGTTTTGTGATGCT	'ATGAGTTTGTC'	TGTGTGGGTGA	120
Sbjct	1343950	ttatatgt	GTTTTGGTGGGAAAA	Agattttgtgacgct	rgtcggtttgtcj	rgtgtgtgtgt	1344009
Query	121	GTGTCTCG	GCTGCTTTGTTTGCA	ATAGGCTTTTGGGTG	GCGGGGTGAGGG	GTCTTTGGCGG	180
Sbjct	1344010	GTGTCTTG	GCTGTTTTGTTGTG	GTTAGCTTTTGGGTG	SAGGGGTGAAGGG	strtttddddd	1344069
Query	181	GCTGTATT	GGCTTGGTTTCACCT	AGGTGTGTCTGTGTA	GAAATTATTT <i>I</i>	AGCGGTTTTTG	240
Sbjct	1344070	gctgtgtt	œĠĊŦŦĠĠŦŦŦĊĂŦĠŦ	AGTTGTGAGTGTGAT	rgaatctatttgo	scccctttttc	1344129
Query	241	ATGCTTTG	GTTGCATTAGTGTCAT	TTATATTGTGTGGGG	GAGTTTATATGT	TGTTTTGGCGG	300
Sbjct	1344130	AtGCTTTG	gttgcattagtgtca	rcgtcttgtgtaggi	rgrgtctacatgi	rgttttagtgg	1344189
Query	301	G-AACTAG	GTTTTGTGATGCTAT(GAGTTTGTCTGTGT	336		
Sbjct	1344190	GGAAATT-	rttctgtgttgctgt	AATTTTGTCTGTGT	1344225		

Range 3: 1331131 to 1331243

Score		Expect	Identities	Gaps	Strand	Frame	_
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Plus		
Feature	s:						
Query	2	TATTTTAG	GCGGTTTTTTGATGCTT	TGGTTGCATTAGT	GTCATTATATTGT(GTGGGGGAGTT	61
Sbjct	1331131	TATTTGG	CGGTTTTTGATGCTT	TGGTTGCATTAGT	GTCATCGTCTTGT	GTAGGTGTGTC	1331190
Query	62	TATATGTO	GTTTTGGCGGG-AACT	CAGGTTTTGTGATG	CTATGAGTTTGTC'	TGTGT 114	
Sbjct	1331191	TACATGTO	STTTTAGTGGGGAAA1	T-TTTCTGTGTTG	CTGTAATTTTGTC'	TGTGT 13312	243

Range 4: 1344113 to 1344225

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Plus		
Feature	s:						
Query	2	TATTTTAC	GCGGTTTTTGATGCTT	TTGGTTGCATTAGTO	GTCATTATATTGT	GTGGGGGAGTT	61
Sbjct	1344113	TATTTGG	GCGGTTTTTGATGCT1	TTGGTTGCATTAGT	GTCATCGTCTTGT	GTAGGTGTGTC	1344172
Query	62	TATATGTO	TTTTGGCGGG-AACT	TAGGTTTTGTGATG(CTATGAGTTTGTC	rgrgr 114	
Sbjct	1344173	TACATGT	sttttagreeggaaat	rr-rrrcrcrcrcrc	ctgtaattttgtc	rgtgt 13442	25

Drosophila melanogaster GH13568 full insert cDNA

Sequence ID: gb|BT030106.1| Length: 2725 Number of Matches: 2

Range 1: 1532 to 1867

Score Expect Identities Gaps Strand Frame

294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Plus	
Features	S :					
Query	1	TTATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTC <i>F</i>	ATTATATTGTGTGGGGGAGT	60
Sbjct	1532	TTATTTTACCG	TCTTTTGATGCTGTGC	CTTGCATTAGTGTC	STTATATTGTGTGGGTGAGT	1591
Query	61	TTATATGTGTT	TTGGCGGGAACTAGG	TTTTGTGATGCTATG	GAGTTTGTCTGTGTGGGTGA	120
Sbjct	1592	TTATATGTGTT	TTGGTGGGAAAAAGAT	rtttgtgacgctgtc	CGGTTTGTCTGTGTGTGTGT	1651
Query	121	Ģ ŢĢŢĊŢĊĢĢĊŢ	GCTTTGTTTGCAATAG	GCTTTTGGGTGCGG	GGGTGAGGGGTCTTTGGCGG	180
Sbjct	1652	GTGTCTTGGCT	GTTTTGTTTGTGGTT1	AGCTTTTGGGTGAG	GGTGAAGGGTTTTTGGCGG	1711
Query	181	GCTGTATTGGC	TTGGTTTCACCTAGGT	rgtgtctgtgtaga <i>r</i>	AATTATTTTAGCGGTTTTTG	240
Sbjct	1712	GCTGTGTTGGC	TTGGTTTCATGTAGT	rgtgagtgtgatgaz	ATCTATTTGGGCGGTTTTTG	1771
Query	241	ATGCTTTGGTT	GCATTAGTGTCATTAT	TATTGTGTGGGGGAG	GTTTATATGTGTTTTTGGCGG	300
Sbjct	1772	Argetttegtt	GCATTAGTGTCATCGT	rcttgtgtaggtgtd	STCTACATGTGTTTTTAGTGG	1831
Query	301	G-AACTAGGTT	TTGTGATGCTATGAGT	TTTGTCTGTGT 33	36	
Shict	1832	GGAAAHT_THH	$C^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}A^{\dagger}G^{\dagger}G^{\dagger}A^{\dagger}G^{\dagger}G^{\dagger}A^{\dagger}G^{\dagger}G^{\dagger}A^{\dagger}G^{\dagger}G^{\dagger}A^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}A^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G^{\dagger}G$	$\frac{1}{2}$	367	

Range 2: 1755 to 1867

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Plus		
Feature	Features:						
Query	2	TATTTTAGCGG	TTTTTGATGCTTTG(GTTGCATTAGTGTC <i>I</i>	ATTATATTGTGTG	GGGGAGTT	61
Sbjct	1755	TATTTGGGCGG	;+++++GA+GC+++GG	GTTGCATTAGTGTC	Atcgtcttgtgta	GGTGTGTC	1814
Query	62	TATATGTGTTT	TGGCGGG-AACTAG	GTTTTGTGATGCTAT	rgagtttgtctgt	GT 114	
Sbjct	1815	tacatetett	TAGTGGGGAAATT-	rttctgtgrtgctg	raartttgtetgt	GT 1867	

Drosophila melanogaster clone BACN05O16, complete sequence Sequence ID: **gb|AC010841.8|** Length: 83903 Number of Matches: 4 Range 1: 3907 to 4242

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Features	S :						
Query	1	TTATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTGT	CATTATATTGTGTG	GGGGAGT	60
Sbjct	4242	TTATTTTACC	GTCTTTTGATGCTGT	GCTTGCATTAGTGT	cgttatattgtgtd	GGTGAGT	4183
Query	61	TTATATGTGT	TTTGGCGGGAACTAG	GTTTTGTGATGCTA	TGAGTTTGTCTGTG	STGGGTGA	120
Sbjct	4182	ttatatgtgt:	rttggtgggaaaad	attttgtgacgctg	+cg $+$ d	stgrgtgr	4123
Query	121	GTGTCTCGGC	rgctttgtttgcaat	AGGCTTTTGGGTGC	GGGGTGAGGGGTCT	TTTGGCGG	180
Sbjct	4122	GTGTCTTGGC	rgrtttgtttgtgt	TAGCTTTTGGGTGA	GGGGTGAAGGGTTT	rttggcgg	4063
Query	181	GCTGTATTGG(CTTGGTTTCACCTAG	GTGTGTCTGTGTAG	AAATTATTTTAGCO	GTTTTTG	240
Sbjct	4062	\$\delta \text{def} \delta \text{def} \def \def \def \def \def \def \def \def	cttggtttcatgtag	rtgtgagtgtgarg	AATCTATTTGGGCC	sG++++++G	4003
Query	241	ATGCTTTGGTT	rgcattagtgtcatt	ATATTGTGTGGGGG	AGTTTATATGTGTT	TTTGGCGG	300
Sbjct	4002	AtGCTTTGGT	rdcattadtdtcatc	gtcttgtgtaggtg	rgtctacatgtgtt	rttagtgg	3943
Query	301	G-AACTAGGT	TTTGTGATGCTATGA	GTTTGTCTGTGT	336		
Sbjct	3942	GGAAATT-TT:	tctgtgttgctgtaa	ттттстстст	3907		

Range 2: 16889 to 17224

Score	Expect	Identities	Gaps	Strand	Frame
294 bits(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus	

Features	S:		
Query	1	TTATTTTAGCGGTTTTTGATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGGAGT	60
Sbjct	17224	TTATTTTACCGTCTTTTGATGCTGTGCTTGCATTAGTGTCGTTATATTGTGTGGGGTGAGT	17165
Query	61	TTATATGTGTTTTGGCGGGAACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGTGGGTGA	120
Sbjct	17164	ttAtAtGtGttttGGTGGGAAAAAGAttttGtGACGCtGtCGGtttGtCtGtGtGTGTGT	17105
Query	121	GTGTCTCGGCTGCTTTGTTTGCAATAGGCTTTTTGGGTGCGGGGTGAGGGGTCTTTTGGCGG	180
Sbjct	17104	GTGTCTTGGCTGTTTTGTTGGTTAGCTTTTGGGTGAGGGGTGAAGGGTTTTTTGGCGG	17045
Query	181	GCTGTATTGGCTTGGTTTCACCTAGGTGTGTCTGTGTAGAAATTATTTTAGCGGTTTTTTG	240
Sbjct	17044	GCTGTGTTGGCTTGGTTTCATGTAGTTGTGAGTGTGATGAATCTATTTGGGCCGGTTTTTG	16985
Query	241	ATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGGAGTTTATATGTGTTTTGGCGG	300
Sbjct	16984	AtGCTTTGGTTGCATTAGTGTCATCGTCTTGTGTAGGTGTGTCTACATGTGTTTTAGTGG	16925
Query	301	G-AACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGT 336	
Sbjct	16924	ĠĠĀĀĀŦŢ-ŢŦŦĊŦĠŦĠŢŦĠĊŦĠŦĀĀŢŦŦŦĠŦĊŦĠŦĠŦ 16889	

Range 3: 3907 to 4019

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Feature	s:						
Query	2	TATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGTC	CATTATATTGTGTG	GGGGAGTT	61
Sbjct	4019	tatttgggcg	GTTTTTGATGCTTTG	GTTGCATTAGTGTC	CATCGTCTTGTGTA	GGTGTGTC	3960
Query	62	TATATGTGTT	TTGGCGGG-AACTAG	GTTTTGTGATGCT	ATGAGTTTGTCTGT(GT 114	
Sbjct	3959	tacatetetr	rtagregegaaatt-	THETGTGTTGET	GTAATTTTGTCTGT(GT 3907	

Range 4: 16889 to 17001

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		_
Features	s:						
Query	2	TATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTG	CATTATATTGTGT(GGGGGAGTT	61
Sbjct	17001	TATTTGGGC	GGTTTTTGATGCTTT	GGTTGCATTAGTG	tcatcgtcttgtgt	AGGTGTGTC	16942
Query	62	TATATGTGT	TTTGGCGGG-AACTA	GGTTTTGTGATGCT	TATGAGTTTGTCTG	TGT 114	
Sbjct	16941	tacatetet	tttagtgggddatt	-TTTCTGTGTTGCT	tgtaartttgtctg	tgt 16889	

Drosophila melanogaster TART-A1 retrotransposon gag protein and pol protein genes, complete cds Sequence ID: **gb|AY561850.1|** Length: 13424 Number of Matches: 2 Range 1: 2289 to 2624

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Features	S :						
Query	1	TTATTTTAGC	GGTTTTTGATGCTTT	GGTTGCATTAGTGT	CATTATATTGTGT	GGGGGAGT	60
Sbjct	2624	TTATTTTACC	GTCTTTTGATGCTGT	GCTTGCATTAGTGT	cgttatattgtgt	GGGTGAGT	2565
Query	61	TTATATGTGT'	TTTGGCGGGAACTAG(GTTTTGTGATGCTA	TGAGTTTGTCTGT	GTGGGTGA	120
Sbjct	2564	TTATATGTGT	tttggtgggaaaad <i>i</i>	attttgtgacgctg	tcggtttgtgtgt	gtgtgtgt	2505
Query	121	GTGTCTCGGC'	TGCTTTGTTTGCAAT <i>I</i>	AGGCTTTTGGGTGC	GGGGTGAGGGGTC	TTTGGCGG	180
Sbjct	2504	GTGTCTTGGC'	rgrtttgtttgtgt	radctttttdddtda	dddddadddta	TTTGGCGG	2445
Query	181	GCTGTATTGG	CTTGGTTTCACCTAG(GTGTGTCTGTGTAG.	AAATTATTTTAGC 	GGTTTTTG	240
Sbjct	2444	\$\$\delta\$\delta\$\delta\$\delta\$	cttggtttcatgtag	rtgtgagtgtgatg	AATCTATTTGGGC	cgtttttg	2385

Query	241	ATĢÇTTTGĢTTĢÇATTAĢTĢTÇATTATATTĢTĢTGĢĢG		300
Sbjct	2384			2325
Query	301	G-AACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGT	336	
Sbict	2324	GGAAATT-TTTCTGTGTTGCTGTAATTTTGTCTGTGT	2289	

Range 2: 2289 to 2401

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Features	s:						
Query	2	TATTTTAGCG	GTTTTTGATGCTTTG	GTTGCATTAGTGT	CATTATATTGTGTG	GGGGAGTT	61
Sbjct	2401	†A†††GGGCG	ĠŦŦŦŦŦĠĀŦĠĊŦŦŦĠ	GTTGCATTAGTGT(CATCGTCTTGTGTA	GGTGTGTC	2342
Query	62	TATATGTGTT	TTGGCGGG-AACTAG	GTTTTGTGATGCT	ATGAGTTTGTCTGT	GT 114	
Sbjct	2341	TACATGTGTT	rtagtggggaaatt-	·TTTCTGTGTTGCT	gtaartttgtetgt	GT 2289	

Drosophila melanogaster GH16383 full insert cDNA

Sequence ID: **gb|AY113347.1**| Length: 1334 Number of Matches: 2 Range 1: 218 to 553

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Plus		
Features	S :						
Query	1	TTATTTTAGCGG	STTTTTGATGCTTTGG	TTGCATTAGTGTCAT	TATATTGTGTG	GGGGAGT	60
Sbjct	218	ттаттттассст	cttttgatgctgtgc	ttgcattagtgtcgt	·ϮልϮልϮϮĠϮĠϮĠ	GGTGAGT	277
Query	61	TTATATGTGTTT	TGGCGGGAACTAGGT	TTTGTGATGCTATGA	GTTTGTCTGTG'	TGGGTGA	120
Sbjct	278	ተተልተልተۈተۈተተተ	rtggrgggaaaaadat	tttgtgycgctatce	ĸĠŦŦŦĠŦĊŦĠŦĠ	rgrgtgr	337
Query	121	GTGTCTCGGCTG	CTTTGTTTGCAATAG	GCTTTTGGGTGCGGG	GTGAGGGGTCT	TTGGCGG	180
Sbjct	338	gtgtctrggctg	rtttgtttgtggtta	GCTTTTGGGTGAGGG	dtdaaddttt'	rtggcgg	397
Query	181	GCTGTATTGGCT	TGGTTTCACCTAGGT	GTGTCTGTGTAGAAA	TTATTTTAGCG	GTTTTTG 	240
Sbjct	398	gctgtgttgct	rtddtttcargtadrt	gtgagtgtgatgaat	ctatttgggcg	Ġ ተተተተተ Ġ	457
Query	241	ATGCTTTGGTTG	CATTAGTGTCATTAT	ATTGTGTGGGGGAGT	TTATATGTGTT'	TTGGCGG	300
Sbjct	458	Ardetrrddrd	cattagtgtcatcgt	cttdtdtaddtdtd	'ctacatgtgtt'	rtagtgg	517
Query	301	G-AACTAGGTTT	TGTGATGCTATGAGT	TTGTCTGTGT 336	!		
Sbjct	518	GGAAATT-TTTC	tgtgttgctgtaatt	र्मर्दर्मर्टमदर्मदर्म 553			

Range 2: 441 to 553

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Plus		
Feature	s:						
Query	2	TATTTTAGCGGT	TTTTGATGCTTTGG	TTGCATTAGTGTCA:	TTATATTGTGTGG	GGGAGTT	61
Sbjct	441	TATTTGGGCGGT	rtttdatgetttgg:	rtgcattagtgtca	rcgtcttgtgtag	GTGTGTC	500
Query	62	TATATGTGTTTT	GGCGGG-AACTAGG	TTTTGTGATGCTAT	GAGTTTGTCTGTG	т 114	
Sbjct	501	TACATGTGTTT	'AGTGGGGAAATT-T:	rtctgtgttgctgt	AATTTTGTCTGTG	T 553	

Drosophila melanogaster retrotransposon TART-A, clone 17G23

Sequence ID: **emb|AJ566116.1|** Length: 15576 Number of Matches: 2 Range 1: 4464 to 4799

Score		Expect	Identities	Gaps	Strand	Frame	
294 bits	(159)	9e-76()	278/337(82%)	2/337(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGC	GGTTTTTGATGCTTTC	GTTGCATTAGTGT	CATTATATTGTGTG	ЗĢĢGĢĀĢŢ	60
Sbjct	4799	TTATTTTACC	GTCTTTTGATGCTGT	CTTGCATTAGTGT	CGTTATATTGTGTG	GGTGAGT	4740
Query	61	TTATATGTGT	TTTGGCGGGAACTAGG	GTTTTGTGATGCTA	TGAGTTTGTCTGTG	TGGGTGA	120
Sbjct	4739	TTATATGTGT	TTTGGTGGGAAAAAGA	ATTTGTGACGCTG	tcggtttgtctgtd	;tgrgtgr	4680
Query	121	GTGTCTCGGC	TGCTTTGTTTGCAAT <i>I</i>	AGGCTTTTGGGTGC	GGGGTGAGGGGTCT	TTGGCGG	180
Sbjct	4679	gtgtctrggc	tĠrtttĠtttĠrggtı	radctttttdddtda	GGGGTGAAGGGTTT	rttggcgg	4620
Query	181	GCTGTATTGG	CTTGGTTTCACCTAGO	GTGTGTCTGTGTAG	AAATTATTTTAGCG	GTTTTTG	240
Sbjct	4619	GCTGTGTTGG	cttggtttcatgtag	rtgtgagtgtgatg	AATCTATTTGGGCC	;GTTTTTG	4560
Query	241	ATGCTTTGGT	TGCATTAGTGTCATT <i>F</i>	ATATTGTGTGGGGG	AGTTTATATGTGTT	TTGGCGG	300
Sbjct	4559	Atgetttegt	tgcattagtgtcatco	stcttgtgtaggtg	rdtctAcAtdtdt1	rtagtgg	4500
Query	301	G-AACTAGGT	TTTGTGATGCTATGAG	GTTTGTCTGTGT	336		
Sbjct	4499	GGAAATT-TT	tctgtgttgtaai	rtttgtctgtgt	4464		

Range 2: 4464 to 4576

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits	s(47)	2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Feature	s:						
Query	2	TATTTTAGCG	GTTTTTGATGCTTTC	GTTGCATTAGTGTG	CATTATATTGTGTG	GGGGAGTT	61
Sbjct	4576	tatttgggcg	GTTTTTGATGCTTTG	GTTGCATTAGTGTG	CATCGTCTTGTGTA	GGTGTGTC	4517
Query	62	TATATGTGTT	TTGGCGGG-AACTAG	GTTTTGTGATGCT	ATGAGTTTGTCTGT	GT 114	
Sbjct	4516	tacatetett	ttagtgggaaatt-	-rttctgtgrtgcto	gtaartttgtctgt	GT 4464	

Drosophila melanogaster sequence scaffold 211000022279209, complete sequence Sequence ID: **gb|AC246448.1|** Length: 21921 Number of Matches: 2

▶ See 1 more title(s) Range 1: 18834 to 19132

Score		Expect	Identities	Gaps	Strand	Frame	
292 bits	(158)	3e-75()	252/299(84%)	0/299(0%)	Plus/Plus		
Features	S:						
Query	5	TTTAGCGGTT	TTTGATGCTTTGGTT	GCATTAGTGTCATT	ATATTGTGTGGG(GGAGTTTAT	64
Sbjct	18834	TTTACCGGTT	rttcgatgctgtggtt	gcatcagtgtcgttz	AtAttGtGtGGG	rgagtttat	18893
Query	65	ATGTGTTTTG	GCGGGAACTAGGTTT	TGTGATGCTATGAG	TTTGTCTGTGTG(GTGAGTGT	124
Sbjct	18894	ATGCGTTTTG	GTGGGAAAAAGATTT	tgtgycgctttggg	ͰϮϮĠϮĊϮĠϮĠϮĠ	GGTGTGTGT	18953
Query	125	CTCGGCTGCT	TTGTTTGCAATAGGC	TTTTGGGTGCGGGG	rgaggggtcttt	GCGGGCTG	184
Sbjct	18954	CTTGGCTGTT	rttgtttgtggttagc	ttttggatgagggg	rdaacddtttttc	GGTGGGCTA	19013
Query	185	TATTGGCTTG	GTTTCACCTAGGTGT	GTCTGTGTAGAAATT	PATTTTAGCGGTT	TTTTGATGC	244
Sbjct	19014	tgttggcttg	gtttcaccaaggtgt	gagtgtgatgaart:	tatttgagcggt	rtttgatge	19073
Query	245	TTTGGTTGCA	TTAGTGTCATTATAT	TGTGTGGGGGAGTT	PATATGTGTTTT(GCGGGAA	303
Sbjct	19074	tttggttgc	ttagtgtcattgtct	tgtgtaggtgtgtc	tacatgtgattt	GACTGGAA	19132

Range 2: 19052 to 19132

Score	Expect	Identities	Gaps	Strand	Frame
89.8 bits(48)	5e-14()	70/81(86%)	0/81(0%)	Plus/Plus	

Fea	tures	:			
Que	ry	1	TTATTTTAGCGGTTTTTGATGC	TTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGAGT	60
Sbj	ct	19052	TTATTTGAGCGGTTTTTGATGC	tttggttgcattagtgtcattgtcttgtgtaggtgtgt	19111
Que	ry	61	TTATATGTGTTTTTGGCGGGAA	81	
Sbj	ct	19112	CTACATGTGATTTGACTGGAA	19132	

Drosophila melanogaster 211000022278794 sequence

Sequence ID: **gb|D\$484160.1|** Length: 2783 Number of Matches: 2 Range 1: 2413 to 2674

Score		Expect	Identities	Gaps	Strand	Frame	
257 bits	(139)	1e-64()	221/262(84%)	0/262(0%)	Plus/Plus		
Feature	s:						
Query	42	TTATATTGTGT	GGGGGAGTTTATA	TGTGTTTTGGCGGGAA	CTAGGTTTTGTG	ATGCTATG	101
Sbjct	2413	TTATATTGTGT	rdddrdadrffafa	TGCGTTTTGGTGGGAA	AAAGATTTTGTG	ACGCTTTG	2472
Query	102	AGTTTGTCTGT	GTGGGTGAGTGTC	TCGGCTGCTTTGTTTG	CAATAGGCTTTT	GGGTGCGG	161
Sbjct	2473	ggtttgtctgt	੶ĠŦĠĠĠŦĠŦĠŦĠŦĊ	ϮͲĠĠĊϮĠͲϮϮϮĠϮϮϯĠ	TGGTTAGCTTT	GGATGAGG	2532
Query	162	GGTGAGGGGTC	TTTGGCGGGCTGT.	ATTGGCTTGGTTTCAC	CTAGGTGTGTCT	GTGTAGAA	221
Sbjct	2533	GGTGAACGGTT	rtttggrgggctat	gttggcttggtttcac	caacctctcact	GTGATGAA	2592
Query	222	ATTATTTTAGC	GGTTTTTGATGCT	TTGGTTGCATTAGTGT	CATTATATTGTG	TGGGGGAG	281
Sbjct	2593	TTTATTTGAGC	:ĠĠŦŦŦŦŦĠĀŦĠĊŦ	ttggttgcattagtgt	cattgtcttgtg	TAGGTGTG	2652
Query	282	TTTATATGTGT	TTTGGCGGGAA	303			
Sbjct	2653	tctacatgtga	tttggctggaa	2674			

Range 2: 2594 to 2674

Score		Expect	Identities	Gap	วร	Strand	Frame	
95.3 bits(51)		1e-15()	71/81(88%	o) 0/8 ²	1(0%)	Plus/Plus		
Feature	s:							
Query	1	TTATTTTAGCG	GTTTTTGATGC	TTTGGTTGCA'	TTAGTGT	CATTATATTGT	GTGGGGGAGT	60
Sbjct	2594	TTATTTGAGCGC	GTTTTTGATGC	'TTTGGTTGCA'	TTAGTGT	ckttgtcttgt	GTAGGTGTGT	2653
Query	61	TTATATGTGTT	TTGGCGGGAA	81				
Sbjct	2654	CTACATGTGATT	TTGGCTGGAA	2674				

Drosophila melanogaster chromosome Y 211000022279532 sequence Sequence ID: **gb|DS484103.1|** Length: 2899 Number of Matches: 2 Range 1: 2641 to 2899

Score		Expect	Identities	Gaps	Strand	Frame	
252 bits	(136)	5e-63()	218/259(84%)	0/259(0%)	Plus/Minus		
Features	s:						
Query	45	TATTGTGTGG	GGGAGTTTATATGTG7	TTTTGGCGGGAACT <i>I</i>	AGGTTTTGTGATG	CTATGAGT	104
Sbjct	2899	TATTGTGTGG	GTGAGTTTATATGCG	rtttggtgggaaaa	AGATTTTGTGACG	CTTTGGGT	2840
Query	105	TTGTCTGTGT	GGGTGAGTGTCTCGG(CTGCTTTGTTTGCA <i>I</i>	ATAGGCTTTTGGG'	TGCGGGGT	164
Sbjct	2839	tretetetetete	geeteretetetreed	ctgrtttgtttgrg	gttadcttttdda'	rgaggggt	2780
Query	165	GAGGGGTCTT	rggcgggctgtattg(GCTTGGTTTCACCT	AGGTGTGTCTGTG'	TAGAAATT 	224
Sbjct	2779	dacddtrtt'	rddredddrataethdd	scttggtttcacca	AGGTGTGAGTGTG	атфааттт	2720
Query	225	ATTTTAGCGG'	TTTTTGATGCTTTGG7	TTGCATTAGTGTCAT	TTATATTGTGTGG(GGGAGTTT 	284
Sbjct	2719	AtttgAgcgg	rttttgatgctttgg	rtgcattagtgtcat	ttgtcttgtgtag	дтфтфтст	2660

Query	285	ATATGTGTTTTTGGCGGGAA	303
Sbjct	2659		2641

Range 2: 2641 to 2721

Score		Expect	Identities	Gaps	Strand	Frame	
95.3 bits	s(51)	1e-15()	71/81(88%)	0/81(0%)	Plus/Minus		
Feature	s:						
Query	1	TTATTTTAGCG	GTTTTTGATGC	TTTGGTTGCATTAG	TGTCATTATATTGT	STGGGGGAGT	60
Sbjct	2721	TTATTTGAGCG	GTTTTTGATGC	tttggttgcattag	tgtcattgtcttgt	TAGGTGTGT	2662
Query	61	TTATATGTGTT	TTGGCGGGAA	81			
Sbjct	2661	ctacatgtgat	TTGGCTGGAA	2641			

Drosophila melanogaster chromosome Y 211000022278935 sequence

Sequence ID: gb|DS485166.1| Length: 1222 Number of Matches: 2

Range 1: 563 to 830

Score		Expect	Identities	Gaps	Strand	Frame	
246 bits	(133)	3e-61()	223/268(83%)	0/268(0%)	Plus/Plus		
Feature	s:						
Query	36	GTGTCATTATAT	TGTGTGGGGGAGTTT	ATATGTGTTTTTGGC	GGGAACTAGGTTT	TTGTGAT	95
Sbjct	563	GTGTCGTTATAT	TGTGTGGGTGAGTTA	ATATGCGTTTTGGT	GGAAAAAGATT	rtgtgac	622
Query	96	GCTATGAGTTTG	TCTGTGTGGGTGAGT	GTCTCGGCTGCTTT(GTTTGCAATAGG	CTTTTGG	155
Sbjct	623	gctrtgggttd	᠄ᡶĊᡶĠᡶĠᡶĠĠĠĠŦĠŦĠŦ	ĠϯĊϮͲĠĠĊϮĠͲϮϮϮ	Strtgregttage	cttttgg	682
Query	156	GTGCGGGGTGAG	GGGTCTTTGGCGGGC'	IGTATTGGCTTGGT	TTCACCTAGGTGT	TGTCTGT	215
Sbjct	683	ATGAGGGGTGAA	ceetrttteereec	ratgttggcttggt	rtcaccaaggtg	rGAGTGT	742
Query	216	GTAGAAATTATT	TTAGCGGTTTTTGAT	GCTTTGGTTGCATT <i>I</i>	AGTGTCATTATAT	TTGTGTG	275
Sbjct	743	GATGAATTTATT	rtgagcggtttttgat	ĠĊŦŦŦĠĠŦŦĠĊĂŦŦ	Adtdtcattgtc	rtgtgta	802
Query	276	GGGGAGTTTATA	TGTGTTTTGGCGGGA	A 303			
Sbjct	803	GGTGTCTCTACA	de de la company	A 830			

Range 2: 750 to 830

Score		Expect	Identities	i	Gaps	Strand	Frame	
84.2 bits	s(45)	2e-12()	69/81(85°	%)	0/81(0%)	Plus/Plus		
Feature	s:							
Query	1	TTATTTTAGCGGT	TTTTGATGC	TTTGGTT	GCATTAGTGTC	ATTATATTGTGT	GGGGGAGT	60
Sbjct	750	TTATTTGAGCGGT	TTTTGATGC	₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	GCATTAGTGTC	Attgtcttgtgt.	AGGTGTCT	809
Query	61	TTATATGTGTTTT	GGCGGGAA	81				
Sbjct	810	ctacatgggattt	GGCTGGAA	830				

Drosophila melanogaster telomeric TART retrotransposon nonfunctional gag protein gene, partial sequence Sequence ID: **gb|AY035776.1|** Length: 2913 Number of Matches: 2 Range 1: 530 to 866

Score	Expect	Identities	Gaps	Strand	Frame
231 bits(125)	7e-57()	268/338(79%)	5/338(1%)	Plus/Minus	
Features:					

Query 3 ATTTTAGCGGTTTTTGATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGGAGTTT 62

Sbjct	866		807
Query	63	ATATGTGTTTTGGCGGGAACTAGGTTTTGTGATG-CTATGAGTTT-GTCTGTGTGG-GTG	119
_	806	ATATOTOTTTTGGCGGAAAAAAGATTTTGTACCGCCTGTCGGTTTGGTCCGGGGGGTGTG	747
Sbjct			
Query	120	AGTGTCTCGGCTGCTTTGTTTGCAATAGGCTTTTTGGGTGCGGGGTGAGGGGTCTTTTGGCG	179
Sbjct	746	TĠŦĠŦĊŦŦĠĠĊŦĠŦŦŦŦĠŦŦĠŦĠĠŦŦAĠĊŦŦŦĠĠĠŦĠAĠĠĠĠĠĠĠĠ	687
Query	180	GGCTGTATTGGCTTGGTTTCACCTAGGTGTGTCTGTGTAGAAATTATTTTAGCGGTTTTT	239
Sbjct	686	ĠĠĊϮĠϮĠϮϮĠĠĊϮϮĠĠϮϮϮĊÁŦĠϮÁĠŦŦĠϮĠAGϮĠϮĠAŦĠÁÁŦĊϮÁϮϮϮĠĠĊĊĠĠϮϮϮϮϮ	627
Query	240	GATGCTTTGGTTGCATTAGTGTCATTATATTGTGTGGGGGGGG	299
Sbjct	626	GATGCTTTGGTTGCATTAGTGTCATCGTCTTGTGTAGGTGTCTACATGTGTTTTAGTG	567
Query	300	GG-AACTAGGTTTTGTGATGCTATGAGTTTGTCTGTGT 336	
Shict	566	GGGAAAHT-THYCHGHGHGCHGHAATHHHGHCHGHGH 530	

Range 2: 530 to 642

Score		Expect	Identities	Gaps	Strand	Frame	
87.9 bits(47)		2e-13()	92/114(81%)	2/114(1%)	Plus/Minus		
Features	s:						
Query	2	TATTTTAGCGG'	TTTTTGATGCTTTGG	TTGCATTAGTGTC	ATTATATTGTGTGG	GGGAGTT	61
Sbjct	642	TATTTGGGCGG'	rtttdatgetttgg	ttgcattagtgtc	ATCGTCTTGTGTAG	GTGTGTC	583
Query	62	TATATGTGTTT	TGGCGGG-AACTAGG	TTTTGTGATGCTA	rgagtttgtctgtg'	г 114	
Sbjct	582	tacatetett	ragtgggaaatt-t	ttctgtgttgctg	taartttgtctgtg	T 530	

Drosophila melanogaster 211000022278716 sequence

Sequence ID: **gb|DS484311.1|** Length: 2383 Number of Matches: 2 Range 1: 508 to 588

Score		Expect	Identities	i	Gaps	Strand	Frame	
87.9 bits(47)		2e-13()	70/81(86°	%)	1/81(1%)	Plus/Plus		
Feature	s:							
Query	2	TATTTT-AGCGGT	TTTTGATGC	TTTGGT	rgcattagtgt(CATTATATTGTGTGT	GGGGGAGT	60
Sbjct	508	TATTTTGAGCGGT	TTTTGATGC	₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	rgcattagtgt	CATTGTCTTTTGT	AGGTGTGT	567
Query	61	TTATATGTGTTTT	GGCGGGAA	81				
Sbjct	568	CTAAATGTGATTT	GGCTGGAA	588				

Range 2: 508 to 588

Score		Expect	Identities	i	Gaps	Strand	Frame	
87.9 bits(47)		2e-13()	70/81(86°	%)	1/81(1%)	Plus/Plus		
Feature	s:							
Query	224	TATTTT-AGCGGT	TTTTGATGC	TTTGGT	TGCATTAGTGTC	CATTATATTGTGT	GGGGGAGT	282
Sbjct	508	TATTTTGAGCGGT	ttttgatgc	:TTTGG1	rtgcattagtgtc	cattgtcttttgt.	AGGTGTGT	567
Query	283	TTATATGTGTTTT	GGCGGGAA	303				
Sbjct	568	ctaaatgtgattt	GGCTGGAA	588				