

# Basic Local Alignment Search Tool

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## Nucleotide Sequence (605 letters)

**RID** [CN9R2B19014](#) (Expires on 02-23 13:12 pm)

**Query ID** lcl|Query\_83179

**Description** None

**Molecule type** nucleic acid

**Query Length** 605

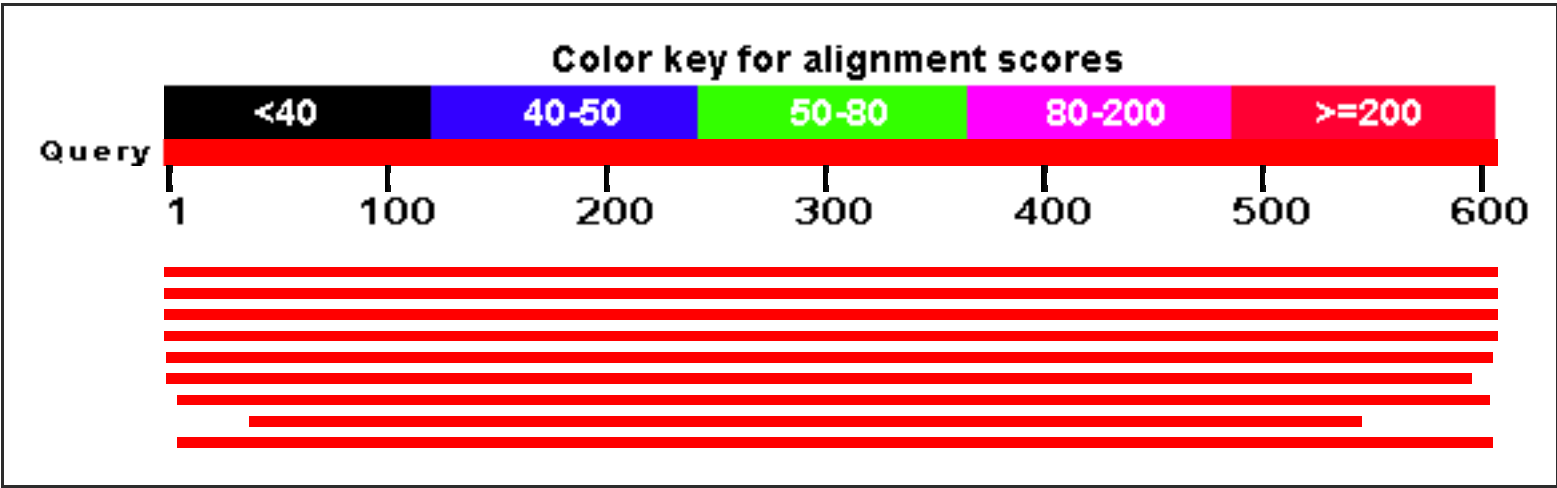
**Database Name** nr

**Description** Nucleotide collection (nt)

**Program** BLASTN 2.3.1+

## [Graphic Summary](#)

Distribution of 109 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila melanogaster chromosome X	1085	97069	100%	0.0	99%	<a href="#">AE014298.5</a>
Drosophila melanogaster mucin 14A (Muc14A), mRNA	1085	92355	100%	0.0	99%	<a href="#">NM_167482.4</a>
Drosophila melanogaster clone BACR32K23, complete sequence	1085	97069	100%	0.0	99%	<a href="#">AC010919.11</a>
Drosophila melanogaster 211000022280568 sequence	1018	7558	100%	0.0	97%	<a href="#">DS484375.1</a>
Drosophila melanogaster clone BACR03G18, complete sequence	601	1202	99%	6e-168	85%	<a href="#">AC009256.9</a>
Drosophila simulans GD17263 (Dsim\GD17263), mRNA	545	5367	99%	3e-151	84%	<a href="#">XM_002105681.1</a>
Drosophila yakuba uncharacterized protein (Dyak\GE27476), partial mRNA	468	1195	98%	7e-128	81%	<a href="#">XM_015189110.1</a>
Drosophila erecta uncharacterized protein (Dere\GG27179), partial mRNA	438	9280	98%	5e-119	82%	<a href="#">XM_015156007.1</a>
Drosophila yakuba uncharacterized protein (Dyak\GE28509), partial mRNA	431	1376	98%	9e-117	80%	<a href="#">XM_015190481.1</a>

Alignments

Drosophila melanogaster chromosome X  
Sequence ID: **gb|AE014298.5|** Length: 23542271 Number of Matches: 106  
Range 1: 16026820 to 16027424

Score	Expect	Identities	Gaps	Strand	Frame
1085 bits(587)	0.0()	599/605(99%)	0/605(0%)	Plus/Minus	
Features: <b>mucin 14A</b>					
Query 1		AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATA			60
Sbjct 16027424		AACTCTGACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATA			16027365
Query 61		GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC			120
Sbjct 16027364		GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGAATGAACTGC			16027305
Query 121		TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG			180
Sbjct 16027304		TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG			16027245
Query 181		TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA			240
Sbjct 16027244		TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA			16027185
Query 241		CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC			300
Sbjct 16027184		CAGAAATTGATGGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC			16027125
Query 301		TCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG			360
Sbjct 16027124		TCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG			16027065
Query 361		GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG			420

Sbjct	16027064	GCAC	TTCTGTCGTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	16027005
Query	421	TTGT	TAAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	16027004	TTGT	TAAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	16026945
Query	481	CTGC	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540
Sbjct	16026944	CTGC	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	16026885
Query	541	ATAG	TGTCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	16026884	GTAG	TGTCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	16026825
Query	601	TATTC	605	
Sbjct	16026824	TATTC	16026820	

Range 2: 16027984 to 16028588

Score	Expect	Identities	Gaps	Strand	Frame
1068 bits(578)	0.0()	596/605(99%)	0/605(0%)	Plus/Minus	
Features: mucin 14A					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATA	60	
Sbjct	16028588	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATA	16028529	
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120		
Sbjct	16028528	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	16028469		
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180		
Sbjct	16028468	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATCTTCCGATGTCTCCTCTTGAGCTG	16028409		
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240		
Sbjct	16028408	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	16028349		
Query	241	CAGAAATTGATAGTGTCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300		
Sbjct	16028348	CAGAAATTGATAGTGTCCTTGATCTTCTTGAGAAGTTTGTCTTCATTTACACTCTGAC	16028289		
Query	301	TCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCATG	360	
Sbjct	16028288	TCGAAAATATATTCTTTGTTTTTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCATG	16028229	
Query	361	GCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420		
Sbjct	16028228	GCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	16028169		
Query	421	TTGT	TAAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480	
Sbjct	16028168	TTGT	TAAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	16028109	
Query	481	CTGC	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540	
Sbjct	16028108	CTGC	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	16028049	
Query	541	ATAG	TGTCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600	
Sbjct	16028048	GTAG	TGTCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	16027989	
Query	601	TATTC	605		
Sbjct	16027988	TATTC	16027984		

Range 3: 16030603 to 16031207

Score	Expect	Identities	Gaps	Strand	Frame
1062 bits(575)	0.0()	595/605(98%)	0/605(0%)	Plus/Minus	
Features: mucin 14A					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATA	60	
Sbjct	16031207	AACTCGGACTCGAAAATATATTCTTTGTTTTTGAAC	TTGATTGAGAAGGTGATGTTGATA	16031148	
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120		
Sbjct	16031147	GTGTCCATGGCACTTCTGTCGTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	16031088		
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180		

Sbjct	16031087	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	16031028
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240
Sbjct	16031027	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	16030968
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	16030967	CAGAAATTGGTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC	16030908
Query	301	TCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	16030907	TCGAAAATATATTCTTTGGTTCTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	16030848
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	16030847	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	16030788
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	16030787	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	16030728
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540
Sbjct	16030727	CTGCACTTGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	16030668
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	16030667	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	16030608
Query	601	TATTC 605	
Sbjct	16030607	TATTC 16030603	

Drosophila melanogaster mucin 14A (Muc14A), mRNA

Sequence ID: **ref|NM\_167482.4|** Length: 48733 Number of Matches: 105

Range 1: 16058 to 16662

Score	Expect	Identities	Gaps	Strand	Frame
1085 bits(587)	0.0()	599/605(99%)	0/605(0%)	Plus/Minus	
Features:					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATA	60		
Sbjct	16662	AACTCTGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATA	16603		
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120		
Sbjct	16602	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGAATGAACTGC	16543		
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180		
Sbjct	16542	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	16483		
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240		
Sbjct	16482	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	16423		
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300		
Sbjct	16422	CAGAAATTGATGGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC	16363		
Query	301	TCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360		
Sbjct	16362	TCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	16303		
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420		
Sbjct	16302	GCACTTCTGTCGTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	16243		
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480		
Sbjct	16242	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	16183		
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540		
Sbjct	16182	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	16123		
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600		
Sbjct	16122	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	16063		
Query	601	TATTC 605			
Sbjct	16062	TATTC 16058			

Range 2: 17222 to 17826

Score		Expect	Identities	Gaps	Strand	Frame
1068 bits(578)		0.0()	596/605(99%)	0/605(0%)	Plus/Minus	
Features:						
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATA				60
Sbjct	17826	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATA				17767
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC				120
Sbjct	17766	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGTAAATGAACTGC				17707
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG				180
Sbjct	17706	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATCTTCCGATGTCTCCTCTTGAGCTG				17647
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA				240
Sbjct	17646	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA				17587
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC				300
Sbjct	17586	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAGTTTTGTCTTCATTTACACTCTGAC				17527
Query	301	TCGAAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG				360
Sbjct	17526	TCGAAAAATATATTCTTTGTTTTTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG				17467
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG				420
Sbjct	17466	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG				17407
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT				480
Sbjct	17406	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT				17347
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG				540
Sbjct	17346	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG				17287
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA				600
Sbjct	17286	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA				17227
Query	601	TATTC	605			
Sbjct	17226	TATTC	17222			

Range 3: 19670 to 20274

Score		Expect	Identities	Gaps	Strand	Frame
1062 bits(575)		0.0()	595/605(98%)	0/605(0%)	Plus/Minus	
Features:						
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATA				60
Sbjct	20274	AACTCGGACTCGAAAATATATTCTTTGTTTTTGAACCTTGATTGAGAAGGTGATGTTGATA				20215
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC				120
Sbjct	20214	GTGTCCATGGCACTTCTGTCGTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC				20155
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG				180
Sbjct	20154	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG				20095
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA				240
Sbjct	20094	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA				20035
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC				300
Sbjct	20034	CAGAAATTGGTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC				19975
Query	301	TCGAAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG				360
Sbjct	19974	TCGAAAAATATATTCTTTGGTTCTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG				19915
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG				420
Sbjct	19914	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG				19855
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT				480
Sbjct	19854	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT				19795
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG				540

Sbjct	19794	CTGCACTTGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	19735
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	19734	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	19675
Query	601	TATTC	605
Sbjct	19674	TATTC	19670

Drosophila melanogaster clone BACR32K23, complete sequence  
Sequence ID: **gb|AC010919.11|** Length: 198967 Number of Matches: 106  
Range 1: 153163 to 153767

Score	Expect	Identities	Gaps	Strand	Frame
1085 bits(587)	0.0()	599/605(99%)	0/605(0%)	Plus/Minus	
Features:					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATA	60		
Sbjct	153767	AACTCTGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATA	153708		
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120		
Sbjct	153707	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGTGAAATGAACTGC	153648		
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180		
Sbjct	153647	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	153588		
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240		
Sbjct	153587	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	153528		
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300		
Sbjct	153527	CAGAAATTGATGGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC	153468		
Query	301	TCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360		
Sbjct	153467	TCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATAGTGTCCATG	153408		
Query	361	GCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420		
Sbjct	153407	GCACTTCTGTGCTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	153348		
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480		
Sbjct	153347	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	153288		
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540		
Sbjct	153287	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	153228		
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600		
Sbjct	153227	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	153168		
Query	601	TATTC	605		
Sbjct	153167	TATTC	153163		

Range 2: 154327 to 154931

Score	Expect	Identities	Gaps	Strand	Frame
1068 bits(578)	0.0()	596/605(99%)	0/605(0%)	Plus/Minus	
Features:					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATA	60		
Sbjct	154931	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATA	154872		
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120		
Sbjct	154871	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGTGAAATGAACTGC	154812		
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180		
Sbjct	154811	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATCTTCCGATGTCTCCTCTTGAGCTG	154752		
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240		
Sbjct	154751	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	154692		

Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	154691	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAGTTTTGTCTTCATTTACACTCTGAC	154632
Query	301	TCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	154631	TCGAAAATATATTCTTTGTTTTTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATG	154572
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	154571	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	154512
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	154511	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	154452
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540
Sbjct	154451	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	154392
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	154391	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	154332
Query	601	TATTC	605
Sbjct	154331	TATTC	154327

Range 3: 156946 to 157550

Score	Expect	Identities	Gaps	Strand	Frame
1062 bits(575)	0.0()	595/605(98%)	0/605(0%)	Plus/Minus	
Features:					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTTGATA			60
Sbjct	157550	AACTCGGACTCGAAAATATATTCTTTGTTTTTGAACCTGATTGAGAAGGTGATGTTGATA			157491
Query	61	GTGTCCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC			120
Sbjct	157490	GTGTCCATGGCACTTCTGTCTGTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC			157431
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG			180
Sbjct	157430	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG			157371
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA			240
Sbjct	157370	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA			157311
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC			300
Sbjct	157310	CAGAAATTGGTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC			157251
Query	301	TCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATG			360
Sbjct	157250	TCGAAAATATATTCTTTGGTTCTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATG			157191
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG			420
Sbjct	157190	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG			157131
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT			480
Sbjct	157130	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT			157071
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG			540
Sbjct	157070	CTGCACTTGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG			157011
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA			600
Sbjct	157010	GTAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA			156951
Query	601	TATTC	605		
Sbjct	156950	TATTC	156946		

Drosophila melanogaster 211000022280568 sequence  
Sequence ID: **gb|DS484375.1|** Length: 2234 Number of Matches: 10  
Range 1: 60 to 664

Score	Expect	Identities	Gaps	Strand	Frame
1018 bits(551)	0.0()	587/605(97%)	0/605(0%)	Plus/Plus	

Features:

Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATA	60
Sbjct	60	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATA	119
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120
Sbjct	120	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGTGAAATGAACTGC	179
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180
Sbjct	180	TTTCTTCTGTTGTTAATTGAGGTAAGGAGTTTGAAAGTTCCGATGTCTCCTCTTGAGCTG	239
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240
Sbjct	240	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	299
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	300	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATATAAACTCGGAC	359
Query	301	TCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	360	TCGAAAATATATTCTTTGGTTCTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	419
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	420	GCACTTCTGTCATTTGATTTTCTTCTACACTGGATTCTTGAAATGAACTGCTCTCTTCTG	479
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	480	TTGTTAATTGAGGTAAGGATTTTGAAGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	539
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540
Sbjct	540	TTGCAATCGAACCTGTAAGTAATCTATTTGCTGTTGTACTTGATTGTGGGACAGATATTG	599
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	600	ATGGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGACTCGAAAATA	659
Query	601	TATTC	605
Sbjct	660	TATTC	664

Range 2: 642 to 1246

Score	Expect	Identities	Gaps	Strand	Frame
990 bits(536)	0.0()	582/605(96%)	0/605(0%)	Plus/Plus	

Features:

Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATA	60
Sbjct	642	AACTCTGACTCGAAAATATATTCTTTGGTTCTGAACCTTGATTGAGAAAGTGATGTTGATA	701
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120
Sbjct	702	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	761
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180
Sbjct	762	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTTTCCTCTTGAGCTG	821
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240
Sbjct	822	TTTGCTCTTCTGCAATCGAACCTGTAAGTAATCTATTTGCTGTTGTACTTGATTGTGGGA	881
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	882	CAGATATTGATGGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC	941
Query	301	TCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	942	TCGAAAATATGTTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	1001
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	1002	GCACTTCTGTCATTTGATTTTCTTCTGCGCTGGATTCTTGTAATGAACTGCGCTCTTCTG	1061
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	1062	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	1121
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540
Sbjct	1122	CTGCACTCGAACCTGTAAGTAATCTATTTGGTTGTTGCAAATGATTGTGGGACAGAAATTG	1181
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	1182	ATAGTGTCTTGTATCTTCTTGAGAAGTTTTGTCTTCATTTACACTCTGACTCGAAAATA	1241



Query 601 TATTC 605  
Sbjct 1242 TATTC 1246

Range 3: 351 to 955

Score	Expect	Identities	Gaps	Strand	Frame
979 bits(530)	0.0()	580/605(96%)	0/605(0%)	Plus/Plus	
Features:					
Query 1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATA	60		
Sbjct 351	AACTCGGACTCGAAAATATATTCTTTGGTTCTGAAC	TTGATTGAGAAAGTGATGTTGATA	410		
Query 61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTG	CACTGGATTCTTGAAATGAACTGC	120		
Sbjct 411	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTA	CACTGGATTCTTGAAATGAACTGC	470		
Query 121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAAT	GTTCCGATGTCTCCTCTTGAGCTG	180		
Sbjct 471	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAAAG	TTCCGATGTCTCCTCTTGAGCTG	530		
Query 181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTAT	TGGCTGTTGCAATTGATTGTGGGA	240		
Sbjct 531	TTTGCTCTTTTGCAATCGAACCTGTAAGTAATCTAT	TTGCTGTTGTACTTGATTGTGGGA	590		
Query 241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAAT	GTTGTCTTCATTTAAACTCGGAC	300		
Sbjct 591	CAGATATTGATGGTGTCTTGTATCTTCTTGAGAAAT	GTTGTCTTCATTTAAACTCTGAC	650		
Query 301	TCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360		
Sbjct 651	TCGAAAATATATTCTTTGGTTCTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCCATG	710		
Query 361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGAT	TCTTGAAATGAACTGCTCTCTTCTG	420		
Sbjct 711	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGAT	TCTTGAAATGAACTGCTCTCTTCTG	770		
Query 421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGAT	GTCTCCTCTTGAGCTGTTTGCTCTT	480		
Sbjct 771	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGAT	GTTTCCTCTTGAGCTGTTTGCTCTT	830		
Query 481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTT	GCAATTGATTGTGGGACAGAAATTG	540		
Sbjct 831	CTGCAATCGAACCTGTAAGTAATCTATTGCTGTT	GTACTTGATTGTGGGACAGATATTG	890		
Query 541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCT	TCAATTTAAACTCGGACTCGAAAATA	600		
Sbjct 891	ATGGTGTCTTGTATCTTCTTGAGAAATGTTGTCT	TCAATTTAAACTCTGACTCGAAAATA	950		
Query 601	TATTC	605			
Sbjct 951	TGTTC	955			

Range 4: 1521 to 2119

Score	Expect	Identities	Gaps	Strand	Frame
979 bits(530)	0.0()	576/599(96%)	0/599(0%)	Plus/Plus	
Features:					
Query 7	GACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCC	66		
Sbjct 1521	GACTCGAAAATATATTCTTTGTTATTGAAC	TTGATTGAGAAAGTGATGTTAAACTGTCC	1580		
Query 67	ATGGCACTTCTGTCATTTGATTTTCTTCTGCACT	GGATTCTTGAAATGAACTGCTCTCTT	126		
Sbjct 1581	ATGGCACTTCTGTCATTTGATTTTCTTCTGCACT	GGATTCTTGAAATGAACTGCTCTCTT	1640		
Query 127	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTT	CCGATGTCTCCTCTTGAGCTGTTTGCT	186		
Sbjct 1641	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTT	CCGATGTCTCCTCTTGAGCTGTTTGCT	1700		
Query 187	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCT	GTTGCAATTGATTGTGGGACAGAAA	246		
Sbjct 1701	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCT	GTTGCAAATGATTGTGGGACAGAAA	1760		
Query 247	TTGATAGTGTCTTGTATCTTCTTGAGAAATGTT	GTCTTCATTTAAACTCGGACTCGAAA	306		
Sbjct 1761	TTGATAGTGTCTTGTATCTTCTTGAGAAGTTT	TGTCTTCATTTACACTTTGACTCGAAA	1820		
Query 307	ATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTT	366		
Sbjct 1821	ATATATTCTTTGTTATTGAAC	TTGATTGAGAAAGTGATGTTAAACTGTCCATGGCACTT	1880		
Query 367	CTGTCATTTGATTTTCTTCTGCACTGGAT	TCTTGAAATGAACTGCTCTCTTCTGTTGTTA	426		

Sbjct	1881	CTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTA	1940
Query	427	ATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCAC	486
Sbjct	1941	ATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCAC	2000
Query	487	TCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTG	546
Sbjct	2001	TCGAACCTGTAAGTAAACTATTGGCTGTTGCAAATGATTGTGGGACAGAAATTGATAGTG	2060
Query	547	TCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATTC	605
Sbjct	2061	TCCTTGTATCTTCTTGAGAAGTTTGTCTTCATTTACACTCTGACTCGAAAATATATTC	2119

Range 5: 933 to 1537

Score	Expect	Identities	Gaps	Strand	Frame
957 bits(518)	0.0()	576/605(95%)	0/605(0%)	Plus/Plus	
Features:					
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATA	60		
Sbjct	933	AACTCTGACTCGAAAATATGTTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATA	992		
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120		
Sbjct	993	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCGCTGGATTCTTGTAATGAACTGC	1052		
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180		
Sbjct	1053	GCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	1112		
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGA	240		
Sbjct	1113	TTTGCTCTTCTGCACTCGAACCTGTAAGTAATCTATTGGTTGTTGCAAATGATTGTGGGA	1172		
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300		
Sbjct	1173	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAGTTTGTCTTCATTTACACTCTGAC	1232		
Query	301	TCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360		
Sbjct	1233	TCGAAAATATATTCTTTGTTTTTGAAC TTGATTGAGAAAGTGATGTTAAAACTGTCCATG	1292		
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420		
Sbjct	1293	GCACTTCTGTCATTTGATTTTCTTCTGCGCTGGATTCTTGTAATGAACTGCGCTCTTCTG	1352		
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480		
Sbjct	1353	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTTTCCTCTTGAGCTGTTTGCTCTT	1412		
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540		
Sbjct	1413	CTGCACTCGAACCTGTAAGTAATCTATTGGTTGTTGCAAATGATTGTGGGACAGAAATTG	1472		
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600		
Sbjct	1473	ATAGTGTCTTGTATCTTCTTGAGAAGTTTGTCTTCATTTACACTTTGACTCGAAAATA	1532		
Query	601	TATTC 605			
Sbjct	1533	TATTC 1537			

Range 6: 1225 to 1828

Score	Expect	Identities	Gaps	Strand	Frame
950 bits(514)	0.0()	574/604(95%)	0/604(0%)	Plus/Plus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATAG	61		
Sbjct	1225	ACTCTGACTCGAAAATATATTCTTTGTTTTTGAAC TTGATTGAGAAAGTGATGTTAAAC	1284		
Query	62	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCT	121		
Sbjct	1285	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCGCTGGATTCTTGTAATGAACTGCG	1344		
Query	122	CTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGT	181		
Sbjct	1345	CTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTTTCCTCTTGAGCTGT	1404		
Query	182	TTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGAC	241		
Sbjct	1405	TTGCTCTTCTGCACTCGAACCTGTAAGTAATCTATTGGTTGTTGCAAATGATTGTGGGAC	1464		

Query	242	AGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACT	301
Sbjct	1465	AGAAATTGATAGTGTCTTGTATCTTCTTGAGAAGTTTGTCTTCATTTACACTTTGACT	1524
Query	302	CGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGG	361
Sbjct	1525	CGAAAATATATTCTTTGTTATTGAACTTGATTGAGAAAGTGATGTTAAAACTGTCCATGG	1584
Query	362	CACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGT	421
Sbjct	1585	CACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGT	1644
Query	422	TGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTC	481
Sbjct	1645	TGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTC	1704
Query	482	TGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGA	541
Sbjct	1705	TGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAAATGATTGTGGGACAGAAATTGA	1764
Query	542	TAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATAT	601
Sbjct	1765	TAGTGTCTTGTATCTTCTTGAGAAGTTTGTCTTCATTTACACTTTGACTCGAAAATAT	1824
Query	602	ATTC	605
Sbjct	1825	ATTC	1828

Range 7: 1812 to 2233

Score	Expect	Identities	Gaps	Strand	Frame
680 bits(368)	0.0()	405/423(96%)	1/423(0%)	Plus/Plus	
Features:					
Query	7	GACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCC			66
Sbjct	1812	GACTCGAAAATATATTCTTTGTTATTGAACTTGATTGAGAAAGTGATGTTAAAACTGTCC			1871
Query	67	ATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT			126
Sbjct	1872	ATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT			1931
Query	127	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCT			186
Sbjct	1932	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCT			1991
Query	187	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAA			246
Sbjct	1992	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAAATGATTGTGGGACAGAAA			2051
Query	247	TTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAA			306
Sbjct	2052	TTGATAGTGTCTTGTATCTTCTTGAGAAGTTTTGTCTTCATTTACACTCTGACTCGAAA			2111
Query	307	ATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTT			366
Sbjct	2112	ATATATTCTTTGTTATTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTT			2171
Query	367	CTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTA			426
Sbjct	2172	CTGTCATTTGATTTTCTTCTGCGCTGGATTCTTGTAATGAACTGCGCTCTTCTGTTGT-A			2230
Query	427	ATT	429		
Sbjct	2231	ATT	2233		

Range 8: 1 to 373

Score	Expect	Identities	Gaps	Strand	Frame
651 bits(352)	0.0()	366/373(98%)	0/373(0%)	Plus/Plus	
Features:					
Query	233	TTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAA			292
Sbjct	1	TTGTGGGACAGAAATTGGCAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAA			60
Query	293	ACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAG			352
Sbjct	61	ACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAG			120
Query	353	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCT			412
Sbjct	121	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTGAATGAACTGCT			180
Query	413	CTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGT			472

Sbjct	181	TTCTTCTGTTGTTAATTGAGGTAAGGAGTTTGAAAGTTCCGATGTCTCCTCTTGAGCTGT	240
Query	473	TTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGAC	532
Sbjct	241	TTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGAC	300
Query	533	AGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACT	592
Sbjct	301	AGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATATAAACTCGGACT	360
Query	593	CGAAAATATATTC	605
Sbjct	361	CGAAAATATATTC	373

Range 9: 2098 to 2233

Score	Expect	Identities	Gaps	Strand	Frame
207 bits(112)	2e-49()	129/137(94%)	1/137(0%)	Plus/Plus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTC	TTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAG	61
Sbjct	2098	ACTCTGACTCGAAAATATATTC	TTTGTTATTGAAC	TTGATTGAGAAAGTGATGTTGATAG	2157
Query	62	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCT			121
Sbjct	2158	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCGCTGGATTCTTGTAATGAACTGCG			2217
Query	122	CTCTTCTGTTGTTAATT	138		
Sbjct	2218	CTCTTCTGTTGT-AATT	2233		

Range 10: 1 to 82

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	2e-29()	80/82(98%)	0/82(0%)	Plus/Plus	
Features:					
Query	524	TTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAA			583
Sbjct	1	TTGTGGGACAGAAATTGGCAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAA			60
Query	584	ACTCGGACTCGAAAATATATTC	605		
Sbjct	61	ACTCGGACTCGAAAATATATTC	82		

Drosophila melanogaster clone BACR03G18, complete sequence

Sequence ID: **gb|AC009256.9|** Length: 179931 Number of Matches: 2

Range 1: 2270 to 2858

Score	Expect	Identities	Gaps	Strand	Frame
601 bits(325)	6e-168()	512/602(85%)	14/602(2%)	Plus/Minus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTC	TTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAG	61
Sbjct	2858	ACTCTGACTCGAAAATATATTC	TTTGTTTTGAAC	TTGATTGAGCAGGTGATGTTGATAG	2799
Query	62	TGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCT			121
Sbjct	2798	AGTCCACGGCTCTTCTGTCATTTGATTTTCTTCTGCACTAGATTCTTGAAATGAAATGCT			2739
Query	122	CTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGT			181
Sbjct	2738	TTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAGTTCTGATGTTTCCTCTTGATTGT			2679
Query	182	TTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGAC			241
Sbjct	2678	TTGATCTTCGGAAC	TCAAATCTGTAAGTAGACTATTTGTTATTGTTATTGATTGAG--A-		2622
Query	242	AGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACT			301
Sbjct	2621	AG---TCGACAGTGTCTTGTATCCTCTAGAGAAGTTTGTCTTCATTTACACTCTGACT			2565
Query	302	CGAAAATATATTC	TTTG-CTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	2564	CGAAAATATAATGTTTGTCTT-TGAAC	TTGATTGAGGAGGTGAAGTTGATAGAGTCCACG		2506

Query	361	GCACTTCTGTTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	2505	GCTCTTCTGTTCATTTGAATTTGTTCTGCACTAGATTCTTGAAATGAAATGCTTTCTTCTG	2446
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	2445	TTGTTAATTGAGGTAAAGATTTTGAAAGTTCTGATGTTTCCTCTTGATTGTTTGATCTT	2386
Query	481	CTGCACTCGAACCTGTAAGTAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG	540
Sbjct	2385	CGGAACTCAAATCTGTAAGTAGACTATTTGTTATTGTTATTGATTGAG--A-AG---TCG	2332
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	2331	ACAGTGTCTTGTATCCTCTAGAGAAGTTTTGTCTTCATTTACACTCTGACTCGAAAATA	2272
Query	601	TA 602	
Sbjct	2271	TA 2270	

Range 2: 2555 to 3143

Score	Expect	Identities	Gaps	Strand	Frame
601 bits(325)	6e-168()	512/602(85%)	14/602(2%)	Plus/Minus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTCTTTG-CTTGTGAAC TTGATTGAGAAAGTGATGTTGATA			60
Sbjct	3143	ACTCTGACTCGAAAATATAATGTTTGTCTT-TGAAC TTGATTGAGGAGGTGAAGTTGATA			3085
Query	61	GTGTCCATGGCACTTCTGTTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC			120
Sbjct	3084	GAGTCCACGGCTCTTCTGTTCATTTGATTTTGTTCCTGCACTAGATTCTTGAAATGAAATGC			3025
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG			180
Sbjct	3024	TTTCTTCTGTTGTTAATTGAGGTAAGGAATTTGAAAGTTCTGATGTTTCCTCTTGATTTG			2965
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAACTATTGGCTGTTGCAATTGATTGTGGGA			240
Sbjct	2964	TTTGATCTTCTGCACTCAATTCTGTAAGGAGACTATTTGTTATTGTTATTGATTG-----			2910
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC			300
Sbjct	2909	-AGAAGTCAACAGTGTCTTGTATCCTCTAGAGAAGTTTTGTCTTCATTTACACTCTGAC			2851
Query	301	TCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGAAAGTGATGTTGATAGTGTCCATG			360
Sbjct	2850	TCGAAAATATATTCTTTGTTTGTGAAC TTGATTGAGCAGGTGATGTTGATAGAGTCCACG			2791
Query	361	GCACTTCTGTTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG			420
Sbjct	2790	GCTCTTCTGTTCATTTGATTTTCTTCTGCACTAGATTCTTGAAATGAAATGCTTTCTTCTG			2731
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT			480
Sbjct	2730	TTGTTAATTGAGGTAAAGATTTTGAAAGTTCTGATGTTTCCTCTTGATTGTTTGATCTT			2671
Query	481	CTGCACTCGAACCTGTAAGTAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG			540
Sbjct	2670	CGGAACTCAAATCTGTAAGTAGACTATTTGTTATTGTTATTGATTGAG--A-AG---TCG			2617
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA			600
Sbjct	2616	ACAGTGTCTTGTATCCTCTAGAGAAGTTTTGTCTTCATTTACACTCTGACTCGAAAATA			2557
Query	601	TA 602			
Sbjct	2556	TA 2555			

Drosophila simulans GD17263 (Dsim\GD17263), mRNA  
Sequence ID: **ref|XM\_002105681.1|** Length: 2988 Number of Matches: 14  
Range 1: 2193 to 2754

Score	Expect	Identities	Gaps	Strand	Frame
545 bits(295)	3e-151()	500/594(84%)	34/594(5%)	Plus/Minus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTCTT--TGCTTGTGAAC TTGATTGAGAAAGTGATGTTGAT			59
Sbjct	2754	ACTCGGACTCGAAAATATATTATTCGTG-TT-TGAAC TTAATTGAAAAAGTGATGTTGAT			2697
Query	60	AGTGTCCATGGCACTTCTGTTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTG			119

Sbjct	2696	ATTGTCCATGGCACTTCTGTAAATTGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTG	2637
Query	120	CTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCT	179
Sbjct	2636	CTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCCTCTTGCTTT	2577
Query	180	GTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGG	239
Sbjct	2576	GTTTGATCTTCTGCACTCAAATCTGTAAGTAAACTATTGTTGTTGTTTTTGATTG----	2521
Query	240	ACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGA	299
Sbjct	2520	--AGAAATTGATACCGTCCTTGTATCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGA	2463
Query	300	CTCGAAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCAT	359
Sbjct	2462	CTC-----T-GA--C--T-CTT-TG---TT-CTT--G--A---A-CTTGATTGTGTCCAA	2427
Query	360	GGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCT	419
Sbjct	2426	GGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTTTCTTCT	2367
Query	420	GTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCT	479
Sbjct	2366	GTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCTCTCGAATTGTTTGATCT	2307
Query	480	TCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATT	539
Sbjct	2306	TCTGCACTCGAATATGTAAGTAAACTATGTGCTGCTGTACTTGATTGTGGGAAGGAAGTT	2247
Query	540	GATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTC	593
Sbjct	2246	GATAGTGTCTTGTGTCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGACTC	2193

Range 2: 2460 to 2959

Score	Expect	Identities	Gaps	Strand	Frame
542 bits(293)	4e-150()	440/510(86%)	14/510(2%)	Plus/Minus	
Features:					
Query	88	TTTCTTCTGCACTG-GA-TTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAA			145
Sbjct	2959	TTTCTTCTG--TTGTGAGTTCTTGAAATGAACTTATTTCTCCTCTTGTAGATTGAGGTAG			2902
Query	146	GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGT			205
Sbjct	2901	AGCTTTTGAAGTTCTGATGTCTCTTCTTGAATTGTATGCTCTTCTGCACTTGAAACTGT			2842
Query	206	AAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATC			265
Sbjct	2841	AAGTAAACTATTTGCTGTTGTACTTGATTGTGAGAAAGAATTTGATAGTGTCTTGTATC			2782
Query	266	TTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTT--TGCTTGT			323
Sbjct	2781	TTCTTGAGAAATGTTGTCTTCATTTACACTCGGACTCGAAAATATATTATTCGTG-TT-T			2724
Query	324	GAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCT			383
Sbjct	2723	GAACTTAATTGAAAAAGTGATGTTGATATTGTCCATGGCACTTCTGTAATTGGATTTTCT			2664
Query	384	TCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTT			443
Sbjct	2663	TCCGCACTGGATTCTTGGAATGAACTGCTTTCTTCTGTTGTTAATTGAGGTAAAGATTTT			2604
Query	444	GAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAA			503
Sbjct	2603	GAAAGTTCCGATGTTTCCTCTTGCTTTGTTTGATCTTCTGCACTCAAATCTGTAAGTAAA			2544
Query	504	CTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGA			563
Sbjct	2543	CTATTTGTTGTTGTTTTTGATTG-----AGAAATTGATACCGTCCTTGTATCTTCTTGA			2490
Query	564	GAAATGTTGTCTTCATTTAAACTCGGACTC	593		
Sbjct	2489	GATGTTTTGTCTTCATTTACACTCTGACTC	2460		

Range 3: 48 to 604

Score	Expect	Identities	Gaps	Strand	Frame	
536 bits(290)	2e-148()	495/589(84%)	34/589(5%)	Plus/Minus		
Features:						
Query	7	GACTCGAAAATATATTCTT--TGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGT				64
Sbjct	604	GACTCGAAAATATATTATTCGTG-TT-TGAACTTAATTGAAAAAGTGATGTTGATATTGT				547

Query	65	CCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTC	124
Sbjct	546	CCATGGCACTTCTGTAAATTGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTGCTTTC	487
Query	125	TTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTG	184
Sbjct	486	TTCTGTTGTTAATTGAGGTAAAGATTTTGAAGTTCCGTTGTTTCCTCTTGCTTTGTTTG	427
Query	185	CTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGA	244
Sbjct	426	ATCTTCTGCACTCAAATCGGTAAAGTAAACTATTTGTTGTTGTTCTTGATTG-----AGA	373
Query	245	AATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGA	304
Sbjct	372	AATTGATACCGTCCTTGTATCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGACTC--	315
Query	305	AAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCAC	364
Sbjct	314	---T-GA--C--T-CTT-TG---TT-CTT--G--A---A-CTTGATTGTGTCCATGGCAC	277
Query	365	TTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424
Sbjct	276	TTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTTTCTTCTGTTGT	217
Query	425	TAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGC	484
Sbjct	216	TAATTGAGGTAAAGATTTTGAAGTTCCGATGTTTCCTCTCGAATTGTTTGATCTTCTGC	157
Query	485	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAG	544
Sbjct	156	ACTCGAATATGTAAGTAAACTATGTGCTGCTGTACTTGATTGTGGGAAGGAAGTTGATAG	97
Query	545	TGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTC	593
Sbjct	96	TGTCCTTGTGTCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGACTC	48

Range 4: 1608 to 2091

Score	Expect	Identities	Gaps	Strand	Frame
523 bits(283)	1e-144()	424/492(86%)	10/492(2%)	Plus/Minus	
Features:					
Query	104	TTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGA			163
Sbjct	2091	TTCTTGAAATGAACTTTTTTCTCCTCTTGTAGATTGAGGTAGAGCTTTTGAACGTTCTGA			2032
Query	164	TGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGT			223
Sbjct	2031	TGTCTCTTCTTGAATTGTATGCTCTTCTGCACTTGAAACTGTAAGTAAACTATTTGCTGT			1972
Query	224	TGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTC			283
Sbjct	1971	TTTACTTGATTGTGGGAAGGAAGTTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTC			1912
Query	284	TTCATTTAAACTCGGACTCGAAAATATATTCTT--TGCTTGTGAACCTGATTGAGAAAGT			341
Sbjct	1911	TTCATTTACACTCGGACTCGAAAATATATTATTCGTG-TT-TGAACCTAATTGAAAAAGT			1854
Query	342	GATGTTGATAGTGTCCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGA			401
Sbjct	1853	GATGTTGATAGTGTCCAAGGCACTTCTGTAATAGGATTTTCTTCCGCACTGGATTCTTGG			1794
Query	402	AATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCC			461
Sbjct	1793	AATGAACTGCTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAGTTCCGATGTTTCC			1734
Query	462	TCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATT			521
Sbjct	1733	TCTTGCTTTGTTTGATCTTCTGCACTCAAATCTGTAAGTAAACTATTTGTTGTTGTTTTT			1674
Query	522	GATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTT			581
Sbjct	1673	GATTG-----AGAAATCGATACCGTCCTTGTATCTTCTTGAGATGTTTTGTCTTCATTT			1620
Query	582	AAACTCGGACTC	593		
Sbjct	1619	ACACTCTGACTC	1608		

Range 5: 1037 to 1509

Score	Expect	Identities	Gaps	Strand	Frame
514 bits(278)	8e-142()	416/482(86%)	12/482(2%)	Plus/Minus	
Features:					
Query	104	TTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGA			163

Sbjct	1509	TTCTTGAAATGAAC TTATTTCTCCTCTTG TAGATTGAGGTAGAGCTTTTGAAAGTTCTGA	1450
Query	164	TGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGT	223
Sbjct	1449	TGTCTCTTCTCGAATTGTATGCTCTTCTGCACTTGAAACTGTAAGTAAACTATTTGCTGT	1390
Query	224	TGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGATCTTCTTGAGAAATGTTGTC	283
Sbjct	1389	TGTACTTGATTGTGGGAAAGAAGTTGATAGTGTCTTGATCTTCTTGAGAAATGTTGTC	1330
Query	284	TTCATTTAAACTCGGACTCGAAAATATATTCTT--TGCTTGTGAAC TTGATTGAGAAAGT	341
Sbjct	1329	TTCATTTACACTCGGACTCGAAAATATATTATTCGTG-TT-TGAAC TTAATTGAAAAAGT	1272
Query	342	GATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGA	401
Sbjct	1271	GATGTTGATAGTGTCCATGGCACTTCTGTAATTGGATTTTCTTCCGCACTGGATTCTTGG	1212
Query	402	AATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCC	461
Sbjct	1211	AATGAACTGCTTCTCTTCTGTTGTTAATTGAGGTAAGATTTTGAAGTTCCGATGTTTCC	1152
Query	462	TCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATT	521
Sbjct	1151	TCTTGCTTTGTTTGATCTTCTGCACTCAAATCTGTAAGTAAACTATTTGTTGTTGTTTTT	1092
Query	522	GATTGTGGGACAGAAATTGATAGTGTCTTGATCTTCTTGAGAAATGTTGT-CTTCATT	580
Sbjct	1091	GATTG-----AGAAATCAAAACTGCCCTTGATCTTCTTGAGAAGTTTGTTCCT-ATT	1039
Query	581	TA 582	
Sbjct	1038	TA 1037	

Range 6: 1300 to 1902

Score	Expect	Identities	Gaps	Strand	Frame
488 bits(264)	5e-134()	502/615(82%)	24/615(3%)	Plus/Minus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTCCTT--TGCTTGTGAAC TTGATTGAGAAAGTGATGTTGAT			59
Sbjct	1902	ACTCGGACTCGAAAATATATTATTCGTG-TT-TGAAC TTAATTGAAAAAGTGATGTTGAT			1845
Query	60	AGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTG			119
Sbjct	1844	AGTGTCCAAGGCACTTCTGTAATAGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTG			1785
Query	120	CTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCT			179
Sbjct	1784	CTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAGTTCCGATGTTTCCTCTTGCTTT			1725
Query	180	GTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGG			239
Sbjct	1724	GTTTGATCTTCTGCACTCAAATCTGTAAGTAAACTATTTGTTGTTGTTTTTGATTG----			1669
Query	240	ACAGAAATTGATAGTGTCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGA			299
Sbjct	1668	--AGAAATCGATACCGTCCTTGATCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGA			1611
Query	300	CTC-GAAAATATATTCCTTTG-CTTG-TGAAC TTGATTG-A-GAAAGTGATGTTGATAGT-			353
Sbjct	1610	CTCTGACTCTTTGTTCTTGAAC TTGATTGTGTCCATGGCACTTCTGTCAT-TTGATTTTC			1552
Query	354	GTC--CA-TGGCACTTCTGTCATTTG-ATTTTCTTCTGCACTGGATTCTTGAAATGAACT			409
Sbjct	1551	TTCTGCACTGG-A-TTCT-TGAAATGAAC TTTCTTTTGTTGTGTGTTCTTGAAATGAACT			1495
Query	410	GCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGC			469
Sbjct	1494	TATTTCTCCTCTTG TAGATTGAGGTAGAGCTTTTGAAGTTCTGATGTCTCTTCTCGAAT			1435
Query	470	TGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGG			529
Sbjct	1434	TGTATGCTCTTCTGCACTTGAAACTGTAAGTAAACTATTTGCTGTTGTACTTGATTGTGG			1375
Query	530	GACAGAAATTGATAGTGTCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGG			589
Sbjct	1374	GAAAGAAGTTGATAGTGTCTTGATCTTCTTGAGAAATGTTGTCTTCATTTACACTCGG			1315
Query	590	ACTCGAAAATATATT	604		
Sbjct	1314	ACTCGAAAATATATT	1300		

Range 7: 1882 to 2440

Score	Expect	Identities	Gaps	Strand	Frame
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464 bits(251)      9e-127()      463/564(82%)      19/564(3%)      Plus/Minus

Features:

Query	55	TTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	114
Sbjct	2440	TTGATTGTGTCCAAGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	2381
Query	115	AACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTT	174
Sbjct	2380	AACTGCTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAGTTCCGATGTTTCCTCTC	2321
Query	175	GAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATT	234
Sbjct	2320	GAATTGTTTGATCTTCTGCACTCGAATATGTAAGTAAACTATGTGCTGCTGTACTTGATT	2261
Query	235	GTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAAC	294
Sbjct	2260	GTGGGAAGGAAGTTGATAGTGTCTTGTGTCTTCTTGAGATGTTTTGTCTTCATTTACAC	2201
Query	295	TCGGACTC-GAAAATATATTCTTTGCTTGTGAACTTG---ATTG-A-GAAAGTGATGTTG	348
Sbjct	2200	TCTGACTCTGACTCTTTGTTCTT-GAATTTGATTGTGTCCATGGCACTTCTGTCAT-TTG	2143
Query	349	ATAGT-GTC--CA-TGGCACTTCTGTCATTTG-A-T--TTTCTTCTGCACTGGATTCTTG	400
Sbjct	2142	ATTTTCTTCTGCACTGG-A-TTCT-TGAAATGAACTGCTTTCTTTTGTTGTGTGTTCTTG	2086
Query	401	AAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTC	460
Sbjct	2085	AAATGAACTTTTTTCTCCTCTTGTAGATTGAGGTAGAGCTTTTGAACGTTCTGATGTCTC	2026
Query	461	CTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAAT	520
Sbjct	2025	TTCTTGAAATGTATGCTCTTCTGCACTTGAAACTGTAAGTAAACTATTTGCTGTTTTACT	1966
Query	521	TGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATT	580
Sbjct	1965	TGATTGTGGGAAGGAAGTTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATT	1906
Query	581	TAAACTCGGACTCGAAAATATATT	604
Sbjct	1905	TAACTCGGACTCGAAAATATATT	1882

Range 8: 315 to 712

Score	Expect	Identities	Gaps	Strand	Frame
453 bits(245)	2e-123()	354/406(87%)	10/406(2%)	Plus/Minus	
Features:					
Query	190	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG			249
Sbjct	712	CTGCACTCGAATATGTAAGTAAACTATTTGCTGTTGTACTTGATTGTGGGAAAGAAGTTG			653
Query	250	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA			309
Sbjct	652	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTACAGTCTGACTCGAAAATA			593
Query	310	TATTCTT--TGCTTGTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTC			367
Sbjct	592	TATTATTCGTG-TT-TGAACCTAATTGAAAAGTGATGTTGATATTGTCCATGGCACTTC			535
Query	368	TGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAA			427
Sbjct	534	TGTAATTGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTGCTTTCTTCTGTTGTTAA			475
Query	428	TTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACT			487
Sbjct	474	TTGAGGTAAAGATTTTGAAGTTCCGTTGTTTCTCTTGCTTTGTTTGATCTTCTGCACT			415
Query	488	CGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGT			547
Sbjct	414	CAAATCGGTAAGTAAACTATTTGTTGTTGTTCTTGATTG-----AGAAATTGATACCGT			361
Query	548	CCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTC		593	
Sbjct	360	CCTTGATCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGACTC		315	

Range 9: 48 to 295

Score	Expect	Identities	Gaps	Strand	Frame	
320 bits(173)	2e-83()	223/248(90%)	0/248(0%)	Plus/Minus		
Features:						
Query	55	TTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG				114

Sbjct	295	TTGATTGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	236
Query	115	AACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTT	174
Sbjct	235	AACTGCTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCCTCTC	176
Query	175	GAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATT	234
Sbjct	175	GAATTGTTTGATCTTCTGCACTCGAATATGTAAGTAAACTATGTGCTGCTGTACTTGATT	116
Query	235	GTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAAC	294
Sbjct	115	GTGGGAAGGAAGTTGATAGTGTCTTGTGTCTTCTTGAGATGTTTTGTCTTCATTTACAC	56
Query	295	TCGGACTC	302
Sbjct	55	TCTGACTC	48

Range 10: 1037 to 1320

Score	Expect	Identities	Gaps	Strand	Frame
303 bits(164)	2e-78()	252/293(86%)	12/293(4%)	Plus/Minus	
Features:					
Query	2	ACTCGGACTCGAAAATATATTCTT--TGCTTGTGAACTTGATTGAGAAAGTGATGTTGAT			59
Sbjct	1320	ACTCGGACTCGAAAATATATTATTCGTG-TT-TGAACTTAATTGAAAAAGTGATGTTGAT			1263
Query	60	AGTGTCCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTG			119
Sbjct	1262	AGTGTCCATGGCACTTCTGTAATTGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTG			1203
Query	120	CTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCT			179
Sbjct	1202	CTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAGTTCCGATGTTTCCTCTTGCTTT			1143
Query	180	GTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGG			239
Sbjct	1142	GTTTGATCTTCTGCACTCAAATCTGTAAGTAAACTATTTGTTGTTGTTTTTGATTG----			1087
Query	240	ACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGT-CTTCATTTA			291
Sbjct	1086	--AGAAATCAAACTGCCCTTGTATCTTCTTGAGAAGTTTTGTTCTT-ATTTA			1037

Range 11: 2734 to 2959

Score	Expect	Identities	Gaps	Strand	Frame
252 bits(136)	7e-63()	198/228(87%)	4/228(1%)	Plus/Minus	
Features:					
Query	379	TTTCTTCTGCACTG-GA-TTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAA			436
Sbjct	2959	TTTCTTCTG--TTGTGAGTTCTTGAAATGAACTTATTTCTCCTCTTGTAGATTGAGGTAG			2902
Query	437	GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGT			496
Sbjct	2901	AGCTTTTGAAAGTTCTGATGTCTCTTCTTGAATTGTATGCTCTTCTGCACTTGAAACTGT			2842
Query	497	AAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATC			556
Sbjct	2841	AAGTAAACTATTTGCTGTTGTACTTGATTGTGAGAAAGAATTTGATAGTGTCCTTGTATC			2782
Query	557	TTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATT			604
Sbjct	2781	TTCTTGAGAAATGTTGTCTTCATTTACACTCGGACTCGAAAATATATT			2734

Range 12: 589 to 712

Score	Expect	Identities	Gaps	Strand	Frame
174 bits(94)	2e-39()	114/124(92%)	0/124(0%)	Plus/Minus	
Features:					
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTG			540
Sbjct	712	CTGCACTCGAATATGTAAGTAAACTATTTGCTGTTGTACTTGATTGTGGGAAAGAAGTTG			653
Query	541	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA			600
Sbjct	652	ATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTACAGTCTGACTCGAAAATA			593
Query	601	TATT	604		

Sbjct 592 TATT 589

Range 13: 2095 to 2173

Score	Expect	Identities	Gaps	Strand	Frame
130 bits(70)	4e-26()	76/79(96%)	0/79(0%)	Plus/Minus	

Features:

Query	55	TTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	114
Sbjct	2173	TTGATTGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	2114
Query	115	AACTGCTCTCTTCTGTTGT	133
Sbjct	2113	AACTGCTTTCTTTTGTGT	2095

Range 14: 1513 to 1588

Score	Expect	Identities	Gaps	Strand	Frame
115 bits(62)	1e-21()	74/79(94%)	3/79(3%)	Plus/Minus	

Features:

Query	55	TTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	114
Sbjct	1588	TTGATTGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	1529
Query	115	AACTGCTCTCTTCTGTTGT	133
Sbjct	1528	AACTT-TCT-TT-TGTTGT	1513

Drosophila yakuba uncharacterized protein (Dyak\GE27476), partial mRNA  
Sequence ID: **ref|XM\_015189110.1|** Length: 784 Number of Matches: 4  
Range 1: 88 to 682

Score	Expect	Identities	Gaps	Strand	Frame
468 bits(253)	7e-128()	485/599(81%)	8/599(1%)	Plus/Minus	

Features:

Query	7	GACTCGAAAATATATTCTTT--GCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGT	64
Sbjct	682	GACTTG-AAA-ATATTCTTTCAGTTTGTGTACTTGATGGAAGAAGCTTTGTTGATAGTGT	625
Query	65	CCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTC	124
Sbjct	624	CCATGGCACTTCTGTCATTTGATTTTCTTCTTCACTGGATTCTTTAAGTGAACGCTTTC	565
Query	125	TTCTGTTGTTAATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTT	183
Sbjct	564	TTCTGTTGTAGATTGAGGTAAAGGAGTTAAAAA-TTCCGTTGTTTCCTCTTTAATTGTTT	506
Query	184	GCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAG	243
Sbjct	505	GATCTTCTGCACTCGAAACTGTGGGAAAACATTTGCCATTGTACTTGATTGAAAATTAG	446
Query	244	AAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCG	303
Sbjct	445	ATATCGATAGTGTCTTGTATCTTCTTCAGATGTTCTATCTTCATCTACACTTTGACTTG	386
Query	304	AAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCA	363
Sbjct	385	AAAATATACTTTCAGTTTGTGTACTTGATTGAGGAAGCTTTGTTGATAGTGTCCATGGCC	326
Query	364	CTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTG	423
Sbjct	325	CTTCTGTCATTTGATTTTCTTCTTCACTGGATTCTTGAAATGAACTGCTTTCCTTCTGTTG	266
Query	424	TTAATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCT	482
Sbjct	265	TGGATTGAGGTAAAGGATTTAAAAA-TTCCGTTGTTTCCTCTTGAATTGTTTGAATTTCT	207
Query	483	GCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGAT	542
Sbjct	206	GCACTCGGAACAGTAGGTAAACTATTTGCCATTGTACTTGATTGAAAAGGAGATATCGAT	147
Query	543	AGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATAT	601
Sbjct	146	AGTGTCTTGTATCTTCTTCAGATGTTCTATCTTTATTTACACTTTGACTTGAAAATAT	88

Range 2: 1 to 391

Score	Expect	Identities	Gaps	Strand	Frame
340 bits(184)	2e-89()	327/396(83%)	10/396(2%)	Plus/Minus	
Features:					
Query	7	GACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCC	66	
Sbjct	391	GACTTGAAAATATACTTTCAGTTTGTGTACTT	GATTGAGGAAGCTTTGTTGATAGTGTCC	332	
Query	67	ATGGCACTTCTGTCAATTTGATTTTCTTCTG	CACTGGATTCTTGAAATGAACTGCTCTCTT	126	
Sbjct	331	ATGGCCCTTCTGTCAATTTGATTTTCTTCTT	CACTGGATTCTTGAAATGAACTGCTTTCTT	272	
Query	127	CTGTTGTTAATTGAGGTAA-GGATTTTGAAT	GTTCCGATGTCTCCTCTTGAGCTGTTTGC	185	
Sbjct	271	CTGTTGTGGATTGAGGTAAAGGA-TTTAAAA	ATTCCGTTGTTTCCTCTTGAATTGTTTGA	213	
Query	186	TCTTCTGCACTCGAACCTGTAAGTAAACTAT	TGGCTGTTGCAATTGATTGTGGGACAGAA	245	
Sbjct	212	ATTTCTGCACTCGGAACAGTAGGTAAACTAT	TTGCCATTGTACTTGATTGAAAAGGAGAT	153	
Query	246	ATTGATAGTGTCTTGTATCTTCTTGAGAAAT	G-T-TGTCTTCATTTAAACTCGGACTCG	303	
Sbjct	152	ATCGATAGTGTCTTGTATCTTCTTCAGA--	TGTTCTATCTTTATTTACACTTTGACTTG	95	
Query	304	AAAATATATTCTTT--GCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGG	361	
Sbjct	94	AAAATAT--TCTTTCAGTTTGTGTACTT	GATGGAAGAAGCTTTGTTGATAGTGTCCATGG	37	
Query	362	CACTTCTGTCAATTTGATTTTCTTCTGCACT	GGATTTC	397	
Sbjct	36	CACTTCTGTCAATTTGATTTTCTTCTTCACT	GGATTTC	1	

Range 3: 378 to 776

Score	Expect	Identities	Gaps	Strand	Frame
278 bits(150)	1e-70()	321/404(79%)	10/404(2%)	Plus/Minus	
Features:					
Query	204	GTAAGTAAACTATTGGCTGTTGCAATTGATT	GTGGGACAGAAATTGATAGTGTCTTGTA	263	
Sbjct	776	GTAGGTAAACTATTGCGCATTGTACTTGATT	GAAAATTAGATATCGATAGTGTCTTGTA	717	
Query	264	TCTTCTTGAGAAATG-T-TGTCTTCATTTAA	ACTCGGACTCGAAAATATATTCTTT--GC	319	
Sbjct	716	TCTTCTTCAGA--TGTTCTATCTTTATTTAC	ACTTTGACTTGAAAATAT--TCTTTCAGT	661	
Query	320	TTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCAATTTGATT	379	
Sbjct	660	TTGTGTACTTGATGGAAGAAGCTTTGTTGAT	AGTGTCCATGGCACTTCTGTCAATTTGATT	601	
Query	380	TTCTTCTGCACTGGATTCTTGAAATGAACT	GCTCTCTTCTGTTGTTAATTGAGGTAA-GG	438	
Sbjct	600	TTCTTCTTCACTGGATTCTTTAAGTGAACT	GCTTTCTTCTGTTGTAGATTGAGGTAAAGG	541	
Query	439	ATTTTGAATGTTCCGATGTCTCCTCTTGAG	CTGTTTGCTCTTCTGCACTCGAACCTGTAA	498	
Sbjct	540	AGTTAAAAA-TTCCGTTGTTTCCTCTTTAAT	TGTTTGATCTTCTGCACTCGAAACTGTGG	482	
Query	499	GTAAACTATTGGCTGTTGCAATTGATTGTGG	GACAGAAATTGATAGTGTCTTGATCTT	558	
Sbjct	481	GAAAACTATTTGCCATTGTACTTGATTGAAA	ATTAGATATCGATAGTGTCTTGATCTT	422	
Query	559	CTTGAGAAATGTTGTCTTCATTTAAACTCGG	ACTCGAAAATATA	602	
Sbjct	421	CTTCAGATGTTCTATCTTCATCTACACTTTG	ACTTGAAAATATA	378	

Range 4: 1 to 100

Score	Expect	Identities	Gaps	Strand	Frame
108 bits(58)	2e-19()	88/102(86%)	4/102(3%)	Plus/Minus	
Features:					
Query	7	GACTCGAAAATATATTCTTT--GCTTGTGAAC	TTGATTGAGAAAGTGATGTTGATAGTGT	64	
Sbjct	100	GACTTG-AAA-ATATTCTTTCAGTTTGTGTAC	TTGATGGAAGAAGCTTTGTTGATAGTGT	43	
Query	65	CCATGGCACTTCTGTCAATTTGATTTTCTTCT	GCACTGGATTTC	106	

Sbjct 42 CCATGGCACTTCTGTCATTTGATTTTCTTCTTCACTGGATTC 1

Drosophila erecta uncharacterized protein (Dere\GG27179), partial mRNA  
Sequence ID: **ref|XM\_015156007.1|** Length: 6171 Number of Matches: 50  
Range 1: 4009 to 4513

Score	Expect	Identities	Gaps	Strand	Frame
438 bits(237)	5e-119()	419/508(82%)	7/508(1%)	Plus/Minus	
Features:					
Query 40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99			
Sbjct 4513	ATTGAGGAAGTGATGTTGATAATGTCCCTGGCACTTCTGACATTTGATTTTCTTCTGCAC	4454			
Query 100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTT	159			
Sbjct 4453	TGGATTCTTGGAATGAAATGCTTTCTTCTGTTGTGGATTGAGGTAAAGATTTTGAATTTT	4394			
Query 160	CCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGG	219			
Sbjct 4393	CCGTGGTTTCCTTTTGAATTGTTTGATCCTCTGCACTCGAAACTGTAAGTAAACTATTTT	4334			
Query 220	CTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGT	279			
Sbjct 4333	CTGTTGCATATGATTGAGGGAACGAGATTGATAGTGTCTTGTATCTTCTTGAGATGTTT	4274			
Query 280	TGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTG-CTT-GTGAAC TTGATTGAGA	337			
Sbjct 4273	TATCTTCTTCTACACTTTGACTGGAAAATGTACTTTTAGTCTTCGT-A-CTTAGTTGATG	4216			
Query 338	AAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTC	397			
Sbjct 4215	GTGTGATGTTGATAATGTCCATGGCAATTCAGACATTTGATTTTCTTTTCACTGGATTC	4156			
Query 398	TTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATG-	456			
Sbjct 4155	TTGGAATGAAATGCTTTCATCTGTTGTAAATTGAGGTAAAGATTTTGAATTTCCG-TGA	4097			
Query 457	TCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTG	516			
Sbjct 4096	TTTCCTTTTGCATTGTTTGATCTATTGCACTCGAAACTGTTAGTAAACTATTTTCTATTG	4037			
Query 517	CAATTGATTGTGGGACAGAAATTG-ATA	543			
Sbjct 4036	CATATGATTGAGGGAACGAGATTGTATA	4009			

Range 2: 2434 to 2938

Score	Expect	Identities	Gaps	Strand	Frame
366 bits(198)	2e-97()	410/512(80%)	15/512(2%)	Plus/Minus	
Features:					
Query 40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99			
Sbjct 2938	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTTCTGTCATTTGATTTTCTTCTGCAC	2879			
Query 100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT-TA--ATTGAGGTAAGGATTTTGA-A	155			
Sbjct 2878	TGGATTCTTGAAAGTGAAC TCCTTCTTCGGTTGTATATTGTTGTGGGACAGAAATCGATA	2819			
Query 156	TGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTA	215			
Sbjct 2818	CCGTCC-TTGTATCTTCTTGAGATGTTT--T-ATCTTCATTCGAAACTGTAAGTAAACTA	2763			
Query 216	TTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAA	275			
Sbjct 2762	TTTTCTGTTGCATATGATTGAGGGAACGAGATTGATAGTGTCTTGTATCTTCTTGAGAT	2703			
Query 276	ATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTG-CTT-GTGAAC TTGATT	333			
Sbjct 2702	GTTTTATCTTCTTCTACACTTTGACTGGAAAATGTACTTTTAGTCTTCGT-A-CTTAGTT	2645			
Query 334	GAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGG	393			
Sbjct 2644	GATGGTGTGATGTTGATAATGTCCATGGCAATTCAGACATTTGATTTTCTTTTCACTGG	2585			
Query 394	ATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCG	453			
Sbjct 2584	ATTCTTGGAATGAAATGCTTTCATCTGTTGTAAATTGAGGTAAAGATTTTGAATTTCCG	2525			
Query 454	ATG-TCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCT	512			
Sbjct 2524	-TGATTTCTTTTGCATTGTTTGATCTATTGCACTCGAAACTGTTAGTAAACTATTTTCT	2466			

Query 513 GTTGC AATTGATTGTGGGACAGAAATTG-ATA 543  
Sbjct 2465 ATTGCATATGATTGAGGGAACGAGATTGTATA 2434

Range 3: 5737 to 6115

Score	Expect	Identities	Gaps	Strand	Frame
313 bits(169)	3e-81()	316/387(82%)	10/387(2%)	Plus/Minus	
Features:					
Query 40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99			
Sbjct 6115	ATTGAGGAAGTGATGTTGATAATGTCCATGGCAATTCAGTCATTTGATTTTCTTTTGCAC	6056			
Query 100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTT	159			
Sbjct 6055	TGGATTCTTTGAGGGAAATGCTTTCTTCTGTTGTGGATTGAGGTAAAGATTTTGAAATTT	5996			
Query 160	CCGATGTCTCCTCTTGAGC--TGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATT	217			
Sbjct 5995	CCGTGGATTCCCT-TT-CGCATTTTTTTGATCCTCTGCACTCGAAACTGTAAGTAAACTATT	5938			
Query 218	GGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAAT	277			
Sbjct 5937	TTCTGTTGCATATGATTGAGGGAACGAGATTGATAGTGTCCTTAGATATTCTTGAGATGC	5878			
Query 278	GTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATTGAGA	337			
Sbjct 5877	TTTATCTTCTTCTACACTTTGACTGGAAAGTATA--CTTT--TAGT--TTTTAATTGAGG	5824			
Query 338	AAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCT	397			
Sbjct 5823	AAGTG TAGTTGATAGTGCCCATGGCACTTCTGTCATTTGATTTTCTTCTCCACTGGATTG	5764			
Query 398	TTGAAATGAACTGCTCTCTTCTGTTGT	424			
Sbjct 5763	TTGAAGTGAAC TGCTTTTTTCTGTTGT	5737			

Range 4: 1 to 337

Score	Expect	Identities	Gaps	Strand	Frame
302 bits(163)	7e-78()	282/340(83%)	6/340(1%)	Plus/Minus	
Features:					
Query 37	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTG	96			
Sbjct 337	TTGATTGAGGAAGTGATGTTGATAATGTCCATGGCACTTCTGTCATTTGATTTTCTTCTG	278			
Query 97	CACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAAT	156			
Sbjct 277	CACTGAATTCTTGAAAGTGAAC TGCTTTCTTTTGTGTAGATTGAGGTAAAGACTTTGAAA	218			
Query 157	GTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTAT	216			
Sbjct 217	TTTCCGTGGTTTCCTTTTGCACTGTTTGATCCTCTGCACTCGAAACTGTAAGTAAACTAT	158			
Query 217	TGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAA	276			
Sbjct 157	TTGGTGTTGAACCTAGTTGAGGTAAAGAAATCGATATTGTCCTTGTATCTTTT TGAGA--	100			
Query 277	TGTTGTC---TTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC TTGATT	333			
Sbjct 99	TGTT-TCATTTTCATCTACACTTTGACTGGAAAATATACTTTCAGTTT TAGTACTTAACT	41			
Query 334	GAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCAT	373			
Sbjct 40	TAGTAAGAGATGTTGATAGTGTCCATGGCACTTCTGTCAT	1			

Range 5: 4245 to 4513

Score	Expect	Identities	Gaps	Strand	Frame
281 bits(152)	9e-72()	230/269(86%)	0/269(0%)	Plus/Minus	
Features:					
Query 331	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	390			
Sbjct 4513	ATTGAGGAAGTGATGTTGATAATGTCCCTGGCACTTCTGACATTTGATTTTCTTCTGCAC	4454			
Query 391	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTT	450			

Sbjct	4453	TGGATTCTTGGAATGAAATGCTTTCTTCTGTTGTGGATTGAGGTAAAGATTTTGAAATTT	4394
Query	451	CCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGG	510
Sbjct	4393	CCGTGGTTTCCTTTTGAATTGTTTGATCCTCTGCACTCGAAACTGTAAGTAAACTATTTT	4334
Query	511	CTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGT	570
Sbjct	4333	CTGTTGCATATGATTGAGGGAACGAGATTGATAGTGTCTTGTATCTTCTTGAGATGTTT	4274
Query	571	TGTCTTCATTTAAACTCGGACTCGAAAAT	599
Sbjct	4273	TATCTTCTTCTACACTTTGACTGGAAAAT	4245

Range 6: 2275 to 2638

Score	Expect	Identities	Gaps	Strand	Frame
279 bits(151)	3e-71()	304/377(81%)	14/377(3%)	Plus/Minus	
Features:					
Query	49	GTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTT			108
Sbjct	2638	GTGATGTTGATAATGTCCATGGCAATTCAGACATTTGATTTTCTTTTTCCTGCACTGGATTCTT			2579
Query	109	GAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATG-TC			167
Sbjct	2578	GGAATGAAATGCTTTCATCTGTTGTAAATTGAGGTAAAGATTTTGAATTTCCG-TGATT			2520
Query	168	TCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCA			227
Sbjct	2519	TCCTTTTGCATTGTTTGATCTATTGCACTCGAAACTGTAGTAAACTATTTTCTATTGCA			2460
Query	228	ATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCA			287
Sbjct	2459	TATGATTG-AGG---G-AA-CG--A--G--ATTGTATATTCCTGAGATGCTTTATCTTCA			2412
Query	288	TTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTT			347
Sbjct	2411	TCTACACTTTGACTGGAAAATATTCTTTTTGTTTTAGTACTTGATTGAGGAAGAGATGTT			2352
Query	348	GATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAA			407
Sbjct	2351	AATAGTGTCCATGGCACTTCTGTCATTTGATTTTTTTCTGCACTGGATTGTTGAAGTGAA			2292
Query	408	CTGCTCTCTTCTGTTGT	424		
Sbjct	2291	CTGCTTTTTTCTGTTGT	2275		

Range 7: 3850 to 4213

Score	Expect	Identities	Gaps	Strand	Frame
279 bits(151)	3e-71()	304/377(81%)	14/377(3%)	Plus/Minus	
Features:					
Query	49	GTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTT			108
Sbjct	4213	GTGATGTTGATAATGTCCATGGCAATTCAGACATTTGATTTTCTTTTTCCTGCACTGGATTCTT			4154
Query	109	GAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATG-TC			167
Sbjct	4153	GGAATGAAATGCTTTCATCTGTTGTAAATTGAGGTAAAGATTTTGAATTTCCG-TGATT			4095
Query	168	TCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCA			227
Sbjct	4094	TCCTTTTGCATTGTTTGATCTATTGCACTCGAAACTGTAGTAAACTATTTTCTATTGCA			4035
Query	228	ATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCA			287
Sbjct	4034	TATGATTG-AGG---G-AA-CG--A--G--ATTGTATATTCCTGAGATGCTTTATCTTCA			3987
Query	288	TTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTT			347
Sbjct	3986	TCTACACTTTGACTGGAAAATATTCTTTTTGTTTTAGTACTTGATTGAGGAAGAGATGTT			3927
Query	348	GATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAA			407
Sbjct	3926	AATAGTGTCCATGGCACTTCTGTCATTTGATTTTTTTCTGCACTGGATTGTTGAAGTGAA			3867
Query	408	CTGCTCTCTTCTGTTGT	424		
Sbjct	3866	CTGCTTTTTTCTGTTGT	3850		

Range 8: 3516 to 3856

Score	Expect	Identities	Gaps	Strand	Frame
270 bits(146)	2e-68()	278/343(81%)	4/343(1%)	Plus/Minus	
Features:					
Query	220	CTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCC	TTGTATCTTCTTGAGAAATG	278	
Sbjct	3856	CTGTTGTAGATTG-TTGTGGGAGAGAAATCGATAGTGTCC	TTGTATCTTCTTTAGATGTT	3798	
Query	279	TTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAAC	TTGATTGAGAA	338	
Sbjct	3797	TTATCTTCTTCTACACTTTGACTGGAAAATATACTTTCAGCTTTAGTACTTAATTTAGGA	3738		
Query	339	AGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCT	398		
Sbjct	3737	AGTGATGTAGATAATGCCCATTTGTAATTCAGTATTTTGATTTTCTTCTGCACTGGATTCT	3678		
Query	399	TGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTC	458		
Sbjct	3677	TGAAGTGAAC	TGCTTTCTTTTGTGTTAGATTGAGGTAAAGACTTTGAAATTTCCGTGGTT	3618	
Query	459	TCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCA	518		
Sbjct	3617	TCCTCTTGCACTGTTTGATCCTCTGCACTCGAAACTGTAAGTAAACTATTTGCTGTTGAA	3558		
Query	519	ATTGATTGTGGGACAGAAATTGATAGTGTCC-TTGTATCTTCT	560		
Sbjct	3557	CTTAATTGAGGAAAAGATGTTGATGGTGTCCATTGCA-CTTCT	3516		

Range 9: 63 to 337

Score	Expect	Identities	Gaps	Strand	Frame
259 bits(140)	4e-65()	233/278(84%)	6/278(2%)	Plus/Minus	
Features:					
Query	328	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTG	387		
Sbjct	337	TTGATTGAGGAAGTGATGTTGATAATGTCCATGGCACTTCTGTCATTTGATTTTCTTCTG	278		
Query	388	CACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAAT	447		
Sbjct	277	CACTGAATTCTTGAAAGTGAAC	TGCTTTCTTTTGTGTTAGATTGAGGTAAAGACTTTGAAA	218	
Query	448	GTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTAT	507		
Sbjct	217	TTTCCGTGGTTTCCTTTTGCACTGTTTGATCCTCTGCACTCGAAACTGTAAGTAAACTAT	158		
Query	508	TGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCC	TTGTATCTTCTTGAGAAA	567	
Sbjct	157	TTGGTGTTGAACCTAGTTGAGGTAAAGAAATCGATATTGTCCTTGTATCTTTTTTGAGA--	100		
Query	568	TGTTGTC---TTCATTTAAACTCGGACTCGAAAATATA	602		
Sbjct	99	TGTT-TCATTTTCATCTACACTTTGACTGGAAAATATA	63		

Range 10: 2670 to 3215

Score	Expect	Identities	Gaps	Strand	Frame
230 bits(124)	3e-56()	421/562(75%)	29/562(5%)	Plus/Minus	
Features:					
Query	51	GATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGA	110		
Sbjct	3215	GATATTGATGGTGTCCATTGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGG	3156		
Query	111	AATGAACTGCTCTCTTCTGTTGTTAATTG-AG-GTAAG-GATTTTGAATGT-TCCGATGT	166		
Sbjct	3155	AATGAAATGCTTTCCTTTGTTGTAGATTGTTGTGGGAGAGAAATCGATGGTGTCC-ATGT	3097		
Query	167	CTCCTCTTGAGCTGTTTGCTCTTCT--GCACTCGAACCTGTAAGTAAACTATTGGCTGTT	224		
Sbjct	3096	ATCTTCTTGAGATGTTTTATCTTCTTTGTA-T---TCTTG-AAGTGAAC	TGCTTTCTTTT	3042	
Query	225	GCAATTGATTGTGGGACAGAAATTGATAGTGTCC	TTGTATCTTCTTGAGAAATGTTGTCT	284	
Sbjct	3041	GTTGTAGATTGAGGTAAAGACTTTGA-AATTTCCGTGGTT-TCCTTTTGCACTGTT-TGA	2985		
Query	285	TCATTTAAACTCG-GACTCGAAAATATATTCT-TTGCTTGTGAAC-TTGATTGAGAAAGT	341		
Sbjct	2984	TCCTCTGCACTCGAAACT-GTGAGTA-A-ACTATTGTTTTTAGTCTTTAATTGAGGAAGC	2928		
Query	342	GATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGA	401		
Sbjct	2927	GATGTTGATAGTGTCCATGGCATTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGA	2868		



Query	402	AATGAACTGCTCTCTTCTGTTGT-TA--ATTGAGGTAAGGATTTTGA-ATGTTCCGATGT	457
Sbjct	2867	AGTGAACCTCCTTTCTTCGGTTGTATATTGTTGTGGGACAGAAATCGATACCGTCC-TTGT	2809
Query	458	CTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGC	517
Sbjct	2808	ATCTTCTTGAGATGTTT--T-ATCTTCATTTCGAAACTGTAAGTAAACTATTTTCTGTTGC	2752
Query	518	AATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTC	577
Sbjct	2751	ATATGATTGAGGGAACGAGATTGATAGTGTCTTGTATCTTCTTGAGATGTTTTATCTTC	2692
Query	578	ATTTAAACTCGGACTCGAAAAT	599
Sbjct	2691	TTCTACACTTTTGA	2670

Range 11: 5050 to 5469

Score	Expect	Identities	Gaps	Strand	Frame
230 bits(124)	3e-56()	329/426(77%)	21/426(4%)	Plus/Minus	
Features:					
Query	35	ACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTC			94
Sbjct	5469	ACTTAATTTAGGAAGTGATGTCGATAATGCCCATTGTAATTCAGTCTTTTGATTTTCTTT			5410
Query	95	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGA			154
Sbjct	5409	TGCACTGGATTCTTGGAAGGAAATGGTTTCTTCTGTTGTGGATTGAGGTAAAGATTTTGA			5350
Query	155	ATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACT			214
Sbjct	5349	AATTTCCGTGGATTCCTTTTGCATTGTTTGATCCTCTGCACTCGAAACTGTAAGTAAACT			5290
Query	215	ATT--GGCT-G--TT-GCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTC			268
Sbjct	5289	ATTTTTTTTAGTTTTAGTACTTGATTGAGGAAGTGATGTTGATAGTGTCCATGTCAC TTC			5230
Query	269	TTGAGAAATGTTG-TCTTCATTTAAACTCGGA--CTCGAAAATATATTC-TTTGCTTGT-			323
Sbjct	5229	-T--GTCAT-TTGATTTTCTTCTGCACT-GGATTCTTGAAGTGAAATGCTTTTTTTTTTTA			5175
Query	324	GAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCT			383
Sbjct	5174	GTTTTTAATTGAGGAAGTGATGTTGATAATGTCCCTGGCACTTCTGTCATTTGATTTTCT			5115
Query	384	TCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCT---GTTGTTAATTGAGGTAAG-GA			439
Sbjct	5114	TCTGCACTGGATTCTTGAAAGTGAAGTCTTTCTTTTTTAGTTTTTGATTGAGG-AAGTGA			5056
Query	440	TTTTGA			445
Sbjct	5055	TGTTGA			5050

Range 12: 1420 to 1718

Score	Expect	Identities	Gaps	Strand	Frame
222 bits(120)	6e-54()	247/306(81%)	17/306(5%)	Plus/Minus	
Features:					
Query	129	GTTGTTAATTGAGGTAAG-GATTTTG--AATGTTCCGATGTCTCCTCT-TGAGCTGTTTG			184
Sbjct	1718	GTTTTTTAATTGAGG-AAGTGATGTTGATAATG-TCC-ATGTCACCTCTGTCA TTTGATTT			1662
Query	185	CTCTTCTGCACTCGA-ACCTGTAAGT-AA--ACTATTGGCTGTTGCA-ATTGATTGTGGG			239
Sbjct	1661	-TCTTCTGCACTGGATTCCTG-AAGTGAAGTGC TTTTTTCTGTTGAAGATTG-TTGTAGC			1605
Query	240	ACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGA			299
Sbjct	1604	AGAAAAATCGATAGTGTCTTGTATCTTCTTGAGATGTTTTATCTTCATCTACACTTTGA			1545
Query	300	CTCGAAAATATATTCTTT-GCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCA			358
Sbjct	1544	CTGGAAAATATA-CCTTTAGTTTTAGTACTTGATTGAGGAAGCGATGTTGATAGTGTCCA			1486
Query	359	TGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTC			418
Sbjct	1485	CGGCATTTCTGTCATTTGATTTTCTTCTGCACTGGATTCCTGAAGTGAAGTCTTTCTTC			1426
Query	419	TGTTGT	424		
Sbjct	1425	TGTTGT	1420		

Range 13: 336 to 794

Score		Expect	Identities	Gaps	Strand	Frame
211 bits(114)		1e-50()	362/476(76%)	40/476(8%)	Plus/Minus	
Features:						
Query	129	GTTGTTAATTGAGGTAAG-GATTTT	184			
Sbjct	794	GTTTTTAATTGAG-AAAGTGATGTTGATAATG-TCC-ATGTCAC	738			
Query	185	CTCTTCTGCACTCGA-ACCTGTAAGTAACT--ATT-GGCTGTTGCA-ATTGATTGTGGG	239			
Sbjct	737	-TCTTCTGCACTGGATTCC	681			
Query	240	ACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGA	299			
Sbjct	680	AGAGAAATCGATACCGTCCTTGTATCTTCTTGAGATGTTTTATCTTCACCTACACTTTGT	621			
Query	300	CTCGAAAATATATTCTTTGCTTGTGAAC	359			
Sbjct	620	CTGGAAAATATA--CTTT--TAGT--CTTTAATTGAGGAAGCGATGTTGATAGTGTCCAT	567			
Query	360	GGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCT	419			
Sbjct	566	GGCATTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAAGTGAAC	507			
Query	420	GTTGT--TA---A-TTGAGGTAAG-GATTTTGAATGT-TCCGATGTCTCCTCT-TGAGCT	470			
Sbjct	506	GTTGTAGTACTTAATTGAGG-AAGAGATGTTGATGGTGTCC-ATTGCACTTCTGTCATTT	449			
Query	471	GTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTA-TTGG--CTGTTGCA-ATTGATTG	526			
Sbjct	448	GATTT-TCTTCTGCACTGTATTCTTGAAAGTGAAC	391			
Query	527	TGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAA-ATGTTGTCTTCATTT	581			
Sbjct	390	TGGGAGTGTAAATCGATAGTGTCTTGTATCTTCTTGAGATGAT-TTATCTTCTTTT	336			

Range 14: 1619 to 1840

Score		Expect	Identities	Gaps	Strand	Frame
211 bits(114)		1e-50()	191/228(84%)	6/228(2%)	Plus/Minus	
Features:						
Query	196	TCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTG	255			
Sbjct	1840	TCGAAACTGTAAGTAAACTATTTTCTGTTGCATATGATTGAGGGAACGAGATTGATAGTG	1781			
Query	256	TCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCT	315			
Sbjct	1780	TCCTTGATTTTCTTGAGATGTTTTATCTTCTTCTACACTGTGACTGGAAAATATA--CT	1723			
Query	316	TTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTT	375			
Sbjct	1722	TT--TAGT--TTTTAATTGAGGAAGTGATGTTGATAATGTCCATGTCACTTCTGTCATTT	1667			
Query	376	GATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTG	423			
Sbjct	1666	GATTTTCTTCTGCACTGGATTCTTGAAAGTGAAC	1619			

Range 15: 1909 to 2201

Score		Expect	Identities	Gaps	Strand	Frame
211 bits(114)		1e-50()	240/300(80%)	11/300(3%)	Plus/Minus	
Features:						
Query	150	TTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGT	209			
Sbjct	2201	TTTGAAATTTCCGTGGTTTCCTCTTGCACTGTTTGATCCTCTGCACTCGAAACTGTAAGT	2142			
Query	210	AAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCT	269			
Sbjct	2141	AAAATATTTGCTGTTGAACCTAGTTGGGGTAAAGAAATCGATATTGTCCTTGTATCTTTT	2082			
Query	270	TGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTT	329			
Sbjct	2081	TGAGATATTTCATTTTCATCTACACTTTGACTGGAAAATATA--CTTT-C-AGT--CTTT	2028			
Query	330	GATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCA	389			
Sbjct	2027	AATTGAGGAAGCGATGTTGATAGTGTCCATGTCACTTCTGTCATTTGATTTTCTTCTGCA	1968			
Query	390	CTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT-T--AATTGAGGTAAG-GATTTTGA	445			

Sbjct

1967

CTGGATTCTTGAGGTGAACGGATTTCTTTTTTAGTCTTTAATTGAGG-AAGCGATGTTGA

1909

Range 16: 4876 to 5271

Score	Expect	Identities	Gaps	Strand	Frame
211 bits(114)	1e-50()	312/405(77%)	24/405(5%)	Plus/Minus	
Features:					
Query	35	ACTTGATTGAGAAAGTGATGTTGATAGTGTC	ACTTGATTGAGAAAGTGATGTTGATAGTGTC	ACTTGATTGAGAAAGTGATGTTGATAGTGTC	94
Sbjct	5271	ACTTGATTGAGGAAGTGATGTTGATAGTGTC	ACTTGATTGAGGAAGTGATGTTGATAGTGTC	ACTTGATTGAGGAAGTGATGTTGATAGTGTC	5212
Query	95	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCT---	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCT---	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCT---	150
Sbjct	5211	TGCACTGGATTCTTGAAAGTGAAATGCTTTTTTTTTTTAGTTTTTTAATTGAGG-AAGTGATG	TGCACTGGATTCTTGAAAGTGAAATGCTTTTTTTTTTTAGTTTTTTAATTGAGG-AAGTGATG	TGCACTGGATTCTTGAAAGTGAAATGCTTTTTTTTTTTAGTTTTTTAATTGAGG-AAGTGATG	5153
Query	151	TTGA-A-TGTTCCGATGTCTCCTCT-TGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAA	TTGA-A-TGTTCCGATGTCTCCTCT-TGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAA	TTGA-A-TGTTCCGATGTCTCCTCT-TGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAA	207
Sbjct	5152	TTGATAATGTCCC--TGGCACTTCTGTCAATTTGATTT-TCTTCTGCACTGGATTCTTGAA	TTGATAATGTCCC--TGGCACTTCTGTCAATTTGATTT-TCTTCTGCACTGGATTCTTGAA	TTGATAATGTCCC--TGGCACTTCTGTCAATTTGATTT-TCTTCTGCACTGGATTCTTGAA	5096
Query	208	GTAAACTATTGGCTGTTGCAA---TTGATTGTGGGACAGAAATTGATAGTGTCTTGTAT	GTAAACTATTGGCTGTTGCAA---TTGATTGTGGGACAGAAATTGATAGTGTCTTGTAT	GTAAACTATTGGCTGTTGCAA---TTGATTGTGGGACAGAAATTGATAGTGTCTTGTAT	264
Sbjct	5095	GTGAACTGCTTTCTTTTTTTAGTTTTTTGATTGAGGAAGTGATGTTGATAGTGCCCATGGCA	GTGAACTGCTTTCTTTTTTTAGTTTTTTGATTGAGGAAGTGATGTTGATAGTGCCCATGGCA	GTGAACTGCTTTCTTTTTTTAGTTTTTTGATTGAGGAAGTGATGTTGATAGTGCCCATGGCA	5036
Query	265	CTTCTTGAGAAATG-TTGTCTTCATTTAAACTCGGACTC--GAAAATATATTCTTTGCTT	CTTCTTGAGAAATG-TTGTCTTCATTTAAACTCGGACTC--GAAAATATATTCTTTGCTT	CTTCTTGAGAAATG-TTGTCTTCATTTAAACTCGGACTC--GAAAATATATTCTTTGCTT	321
Sbjct	5035	CTTCT-GTCATTTGATTTTCTAC-TGCA--CT-GGATTCTTGAAGTGAAATGCTTTGTTT	CTTCT-GTCATTTGATTTTCTAC-TGCA--CT-GGATTCTTGAAGTGAAATGCTTTGTTT	CTTCT-GTCATTTGATTTTCTAC-TGCA--CT-GGATTCTTGAAGTGAAATGCTTTGTTT	4981
Query	322	GTGAA-CTTG-ATTGAGAAAGTGATGTTGATAGTGTC	GTGAA-CTTG-ATTGAGAAAGTGATGTTGATAGTGTC	GTGAA-CTTG-ATTGAGAAAGTGATGTTGATAGTGTC	379
Sbjct	4980	TTTAGTCTTTAATTGAGGAAGCGATGTTGATAGTGTC	TTTAGTCTTTAATTGAGGAAGCGATGTTGATAGTGTC	TTTAGTCTTTAATTGAGGAAGCGATGTTGATAGTGTC	4921
Query	380	TTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	TTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	TTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424
Sbjct	4920	TTCTTCTGCACTGGATTCTTGAAAGTGAACTCCTTTCTTCGGTTGT	TTCTTCTGCACTGGATTCTTGAAAGTGAACTCCTTTCTTCGGTTGT	TTCTTCTGCACTGGATTCTTGAAAGTGAACTCCTTTCTTCGGTTGT	4876

Range 17: 3516 to 3778

Score	Expect	Identities	Gaps	Strand	Frame
209 bits(113)	4e-50()	214/264(81%)	2/264(0%)	Plus/Minus	
Features:					
Query	7	GACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTC	GACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTC	GACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTC	66
Sbjct	3778	GACTGGAAAATATACTTTCAGCTTTAGTACTTAATTTAGGAAGTGATGTAGATAATGCCC	GACTGGAAAATATACTTTCAGCTTTAGTACTTAATTTAGGAAGTGATGTAGATAATGCCC	GACTGGAAAATATACTTTCAGCTTTAGTACTTAATTTAGGAAGTGATGTAGATAATGCCC	3719
Query	67	ATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT	ATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT	ATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT	126
Sbjct	3718	ATTGTAATTCAGTATTTTGATTTTCTTCTGCACTGGATTCTTGAAAGTGAACTGCTTTCTT	ATTGTAATTCAGTATTTTGATTTTCTTCTGCACTGGATTCTTGAAAGTGAACTGCTTTCTT	ATTGTAATTCAGTATTTTGATTTTCTTCTGCACTGGATTCTTGAAAGTGAACTGCTTTCTT	3659
Query	127	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCT	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCT	CTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCT	186
Sbjct	3658	TTGTTGTAGATTGAGGTAAAGACTTTGAAATTTCCGTGGTTTCCTCTTGCACTGTTTGAT	TTGTTGTAGATTGAGGTAAAGACTTTGAAATTTCCGTGGTTTCCTCTTGCACTGTTTGAT	TTGTTGTAGATTGAGGTAAAGACTTTGAAATTTCCGTGGTTTCCTCTTGCACTGTTTGAT	3599
Query	187	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAA	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAA	CTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAA	246
Sbjct	3598	CCTCTGCACTCGAAACTGTAAGTAAACTATTTGCTGTTGAACTTAATTGAGGAAAAGATG	CCTCTGCACTCGAAACTGTAAGTAAACTATTTGCTGTTGAACTTAATTGAGGAAAAGATG	CCTCTGCACTCGAAACTGTAAGTAAACTATTTGCTGTTGAACTTAATTGAGGAAAAGATG	3539
Query	247	TTGATAGTGTCCTTGTATCTTCT	TTGATAGTGTCCTTGTATCTTCT	TTGATAGTGTCCTTGTATCTTCT	269
Sbjct	3538	TTGATGGTGTCCATTGCA-CTTCT	TTGATGGTGTCCATTGCA-CTTCT	TTGATGGTGTCCATTGCA-CTTCT	3516

Range 18: 3268 to 3466

Score	Expect	Identities	Gaps	Strand	Frame
196 bits(106)	3e-46()	175/207(85%)	10/207(4%)	Plus/Minus	
Features:					
Query	220	CTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGA-AAT	CTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGA-AAT	CTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGA-AAT	277
Sbjct	3466	CTGTTGTAGATTG-TTGTGGGAGTGTAATCGATAGTGTCCTTGTATCTTCTTGAGATGAT	CTGTTGTAGATTG-TTGTGGGAGTGTAATCGATAGTGTCCTTGTATCTTCTTGAGATGAT	CTGTTGTAGATTG-TTGTGGGAGTGTAATCGATAGTGTCCTTGTATCTTCTTGAGATGAT	3408
Query	278	GTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGA	GTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGA	GTTGTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGA	337
Sbjct	3407	-TTATCTTCTTCTACACTTTGAGTGGAATAATA--CTTT--TAGT--CTTTAATTGAGG	-TTATCTTCTTCTACACTTTGAGTGGAATAATA--CTTT--TAGT--CTTTAATTGAGG	-TTATCTTCTTCTACACTTTGAGTGGAATAATA--CTTT--TAGT--CTTTAATTGAGG	3355
Query	338	AAGTGATGTTGATAGTGTCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTC	AAGTGATGTTGATAGTGTCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTC	AAGTGATGTTGATAGTGTCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTC	397
Sbjct	3354	AAGTGATGTTGATAGTGTCATGGCATTTCTGTCAATTTGATTTTCTTCTGCACTGGATTC	AAGTGATGTTGATAGTGTCATGGCATTTCTGTCAATTTGATTTTCTTCTGCACTGGATTC	AAGTGATGTTGATAGTGTCATGGCATTTCTGTCAATTTGATTTTCTTCTGCACTGGATTC	3295

Query398TTGAAATGAACTGCTCTCTTCTGTTGT424

Sbjct3294TTGAAGTGAAGTGCCTTCTTCTGTTGT3268

Range 19: 400 to 787

Score	Expect	Identities	Gaps	Strand	Frame
193 bits(104)	4e-45()	305/399(76%)	25/399(6%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	787	ATTGAGAAAGTGATGTTGATAATGTCCATGTCACCTTCTGTCATTTGATTTTCTTCTGCAC			728
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTA--AG-GATTTTGA-A			155
Sbjct	727	TGGATTCCTGAAGTGAAGTGCCTTCTTCTGTTGTAGATTGTTGTGGGAGAGAAATCGATA			668
Query	156	TGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTA			215
Sbjct	667	CCGTCCT-TGTATCTTCTTGAGATGTTTTATCTTCA-C-CTACACTTTGTCTGGAAAATA			611
Query	216	TTGGCTGTT-GCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGT-ATCTTCTTGAG			273
Sbjct	610	TA--CTTTTAGTCTTTAATTGAGGAAGCGATGTTGATAGTGTCCATGGCAT-TTCT-GTC			555
Query	274	AAATG-TTGTCTTCATTTAAACTCGGACTC--GAA---AA-TATATTCTTTGCTTGT-GA			325
Sbjct	554	ATTTGATTTTCTTC-TGCA--CT-GGATTCCTGAAGTGAAGTGCCTTTTTTTAGTTGTAGT			499
Query	326	ACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTC			385
Sbjct	498	ACTTAATTGAGGAAGAGATGTTGATGGTGTCCATTGCACTTCTGTCATTTGATTTTCTTC			439
Query	386	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424		
Sbjct	438	TGCACTGTATTCTTGAAGTGAAGTGCCTTCTTCTGTTGT	400		

Range 20: 1228 to 1463

Score	Expect	Identities	Gaps	Strand	Frame
189 bits(102)	6e-44()	199/244(82%)	13/244(5%)	Plus/Minus	
Features:					
Query	186	TCTTCTGCACTCGA-ACCTGTAAGTAAACT--ATT-GGCTGTTGCA-ATTGATTGTGGGA			240
Sbjct	1463	TCTTCTGCACTGGATTCCTG-AAGTGAAGTGCCTTCTTCTGTTGTAGATTG-TTGTGGGA			1406
Query	241	CAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC			300
Sbjct	1405	GAGAAATCGATACCGTCCTTGTATCTTCTTGAGATGTTTTATCTTCACCTACACTTGTGTC			1346
Query	301	TCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATG			360
Sbjct	1345	TGGAAAATATA--CTTT--TAGT--CTTTAATTGAGGAAGCGATGTTGATAGTGTCCATG			1292
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG			420
Sbjct	1291	GCATTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAGTGAAGTGCCTTCTTCGG			1232
Query	421	TTGT	424		
Sbjct	1231	TTGT	1228		

Range 21: 4814 to 5071

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	6e-39()	208/262(79%)	14/262(5%)	Plus/Minus	
Features:					
Query	328	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTG			387
Sbjct	5071	TTGATTGAGGAAGTGATGTTGATAGTGCCCATGGCACTTCTGTCATTTGATTTTCTACTG			5012
Query	388	CACTGGATTCTTGAAATGAACTGCT--CTCTTCT-GTTGTTAATTGAGGTAAG-GATTTT			443
Sbjct	5011	CACTGGATTCTTGAAGTGAATGCTTTGTTTTTTAGTCTTTAATTGAGG-AAGCGATGTT			4953
Query	444	GAATGT-TCCGATGTCTCCTCT-TGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTA			501

Sbjct	4952	GATAGTGTCC-ATGGCATTTCTGTCAATTTGATTT-TCTTCTGCACTGGATTCTTGAAGTG	4895
Query	502	AACT--ATT-GGCTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCT	557
Sbjct	4894	AACTCCTTTCTTCGGTTGTATATTG-TTGTGGGACAGAAATCGATACCGTCCTTGTATCT	4836
Query	558	TCTTGAGAAATGTTGTCTTCAT	579
Sbjct	4835	TCTTGAGATGTTTTATCTTCAT	4814

Range 22: 4814 to 5071

Score	Expect	Identities	Gaps	Strand	Frame
172 bits(93)	6e-39()	208/262(79%)	14/262(5%)	Plus/Minus	
Features:					
Query	37	TTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCAATTTGATTTTCTTCTG			96
Sbjct	5071	TTGATTGAGGAAGTGATGTTGATAGTGCCCATGGCACTTCTGTCAATTTGATTTTCTACTG			5012
Query	97	CACTGGATTCTTGAAATGAACTGCT--CTCTTCT-GTTGTTAATTGAGGTAAG-GATTTT			152
Sbjct	5011	CACTGGATTCTTGAAAGTGAAATGCTTTGTTTTTTAGTCTTTAATTGAGG-AAGCGATGTT			4953
Query	153	GAATGT-TCCGATGTCTCCTCT-TGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTA			210
Sbjct	4952	GATAGTGTCC-ATGGCATTTCTGTCAATTTGATTT-TCTTCTGCACTGGATTCTTGAAGTG			4895
Query	211	AACT--ATT-GGCTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCT			266
Sbjct	4894	AACTCCTTTCTTCGGTTGTATATTG-TTGTGGGACAGAAATCGATACCGTCCTTGTATCT			4836
Query	267	TCTTGAGAAATGTTGTCTTCAT	288		
Sbjct	4835	TCTTGAGATGTTTTATCTTCAT	4814		

Range 23: 4594 to 4812

Score	Expect	Identities	Gaps	Strand	Frame
169 bits(91)	8e-38()	180/222(81%)	9/222(4%)	Plus/Minus	
Features:					
Query	230	TGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATT			289
Sbjct	4812	TGATTGAGGAAACGAAATCGATAGTGTCAATTGTATTTGCTTGAGATGTTTTATCTTCATC			4753
Query	290	TAAACTCGGACTCGAAAATATATTC-TTT-GCTTGTGAAC TTGATTGAGAAAGTGATGTT			347
Sbjct	4752	TACACTTTGACT-GGAGA-ATATTCTTTTAGTTTTAGTACTTGATTGAGGAAGTGATGTT			4695
Query	348	GATAGTGTCCATGGCACTTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAA			407
Sbjct	4694	GATAGTGTCCATGTCAC TTCTGTCAATTTGATTTTCTTCTGCACTGGATTCTTGAGGTGAA			4635
Query	408	CTGCTCTCTTCTGTTGT-T--AATTGAGGTAAG-GATTTTGA	445		
Sbjct	4634	CGGATTTCTTTTTTTAGTCTTTAATTGAGG-AAGCGATGTTGA	4594		

Range 24: 336 to 595

Score	Expect	Identities	Gaps	Strand	Frame
156 bits(84)	6e-34()	208/265(78%)	19/265(7%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCAATTTGATTTTCTTCTGCAC			99
Sbjct	595	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCAATTTCTGTCAATTTGATTTTCTTCTGCAC			536
Query	100	TGGATTCTTGAAATGAACTGCTCTTCTGTTGT--TA---A-TTGAGGTAAG-GATTTT			152
Sbjct	535	TGGATTCTTGAAAGTGAACTGCTTTTTTTTAGTTGTAGTACTTAATTGAGG-AAGAGATGTT			477
Query	153	GAATGT-TCCGATGTCTCCTCT-TGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTA			210
Sbjct	476	GATGGTGTCC-ATTGCACTTCTGTCAATTTGATTT-TCTTCTGCACTGTATTCTTGAAGTG			419
Query	211	AACTA-TTGG--CTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCT			266
Sbjct	418	AACTGCTTTCTTCTGTTGTAGATTG-TTGTGGGAGTGTAATCGATAGTGTCTTGTATCT			360
Query	267	TCTTGAGAA-ATGTTGTCTTCATTT	290		

Sbjct

359

TCTTGAGATGAT-

TTATCTTCTTTT

336

Range 25: 1420 to 1546

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(82)	8e-33()	113/128(88%)	2/128(1%)	Plus/Minus	
Features:					
Query	7	GACTCGAAAATATATTCTTT-GCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTC			65
Sbjct	1546	GACTGGAAAATATA-CCTTTAGTTTTAGTACTTGATTGAGGAAGCGATGTTGATAGTGTC			1488
Query	66	CATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCT			125
Sbjct	1487	CACGGCATTTCTGTCATTTGATTTTCTTCTGCACTGGATTCCTGAAGTGAAGTCTTTCT			1428
Query	126	TCTGTTGT	133		
Sbjct	1427	TCTGTTGT	1420		

Range 26: 3268 to 3361

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(82)	8e-33()	90/94(96%)	0/94(0%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	3361	ATTGAGGAAGTGATGTTGATAGTGTCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			3302
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	133		
Sbjct	3301	TGGATTCTTGAAAGTGAAGTGAAGTCTTTCTTCTGTTGT	3268		

Range 27: 694 to 787

Score	Expect	Identities	Gaps	Strand	Frame
147 bits(79)	4e-31()	89/94(95%)	0/94(0%)	Plus/Minus	
Features:					
Query	331	ATTGAGAAAGTGATGTTGATAGTGTCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			390
Sbjct	787	ATTGAGAAAGTGATGTTGATAATGTCCATGTCACCTTCTGTCATTTGATTTTCTTCTGCAC			728
Query	391	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424		
Sbjct	727	TGGATTCTTGAAAGTGAAGTGAAGTCTTTCTTCTGTTGT	694		

Range 28: 2275 to 2401

Score	Expect	Identities	Gaps	Strand	Frame
147 bits(79)	4e-31()	111/127(87%)	0/127(0%)	Plus/Minus	
Features:					
Query	7	GACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTC			66
Sbjct	2401	GACTGGAAAATATTCTTTTTGTTTTAGTACTTGATTGAGGAAGAGATGTTAATAGTGTC			2342
Query	67	ATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT			126
Sbjct	2341	ATGGCACTTCTGTCATTTGATTTTTTTTCTGCACTGGATTGTTGAAGTGAAGTCTTTTTT			2282
Query	127	CTGTTGT	133		
Sbjct	2281	CTGTTGT	2275		

Range 29: 3850 to 3976

Score	Expect	Identities	Gaps	Strand	Frame
147 bits(79)	4e-31()	111/127(87%)	0/127(0%)	Plus/Minus	

Features:

Query	7	GACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCC	66
Sbjct	3976	GACTGGAAAATATATTCTTTTGTTTTAGTACTTGATTGAGGAAGAGATGTTAATAGTGTCC	3917
Query	67	ATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT	126
Sbjct	3916	ATGGCACTTCTGTCATTTGATTTTTTTCTGCACTGGATTGTTGAAGTGAAGTCTTTTTT	3857
Query	127	CTGTTGT	133
Sbjct	3856	CTGTTGT	3850

Range 30: 5149 to 5271

Score	Expect	Identities	Gaps	Strand	Frame
147 bits(79)	4e-31()	110/124(89%)	5/124(4%)	Plus/Minus	

Features:

Query	326	ACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTC	385
Sbjct	5271	ACTTGATTGAGGAAGTGATGTTGATAGTGTCCATGTCACTTCTGTCATTTGATTTTCTTC	5212
Query	386	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCT---GTTGTTAATTGAGGTAAG-GATT	441
Sbjct	5211	TGCACTGGATTCTTGAAAGTGAAATGCTTTTTTTTTTAGTTTTTAATTGAGG-AAGTGATG	5153
Query	442	TTGA	445
Sbjct	5152	TTGA	5149

Range 31: 3460 to 3569

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(77)	5e-30()	99/110(90%)	0/110(0%)	Plus/Minus	

Features:

Query	315	TTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATT	374
Sbjct	3569	TTTGCTGTTGAACTTAATTGAGGAAAAGATGTTGATGGTGTCCATTGCACTTCTGTCATT	3510
Query	375	TGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424
Sbjct	3509	TGATTTTCTTCTGCACTGTATTCTTGAAGTGAAGTCTTTCTTCTGTTGT	3460

Range 32: 3460 to 3569

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(77)	5e-30()	99/110(90%)	0/110(0%)	Plus/Minus	

Features:

Query	24	TTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATT	83
Sbjct	3569	TTTGCTGTTGAACTTAATTGAGGAAAAGATGTTGATGGTGTCCATTGCACTTCTGTCATT	3510
Query	84	TGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	133
Sbjct	3509	TGATTTTCTTCTGCACTGTATTCTTGAAGTGAAGTCTTTCTTCTGTTGT	3460

Range 33: 1228 to 1321

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	2e-29()	88/94(94%)	0/94(0%)	Plus/Minus	

Features:

Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99
Sbjct	1321	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTTCTGTCATTTGATTTTCTTCTGCAC	1262
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	133
Sbjct	1261	TGGATTCTTGAAGTGAAGTGCCTTCTTCGGTTGT	1228

Range 34: 400 to 505

Score	Expect	Identities	Gaps	Strand	Frame
139 bits(75)	6e-29()	96/106(91%)	1/106(0%)	Plus/Minus	
Features:					
Query	29	TTGT-GAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGAT			87
Sbjct	505	TTGTAGTACTTAATTGAGGAAGAGATGTTGATGGTGTCCATTGCACCTTCTGTCATTTGAT			446
Query	88	TTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT		133	
Sbjct	445	TTTCTTCTGCACTGTATTCTTGAAAGTGAACCTGCTTTCTTCTGTTGT		400	

Range 35: 4495 to 4612

Score	Expect	Identities	Gaps	Strand	Frame
137 bits(74)	2e-28()	105/119(88%)	5/119(4%)	Plus/Minus	
Features:					
Query	331	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			390
Sbjct	4612	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTCTGTCATTTGATTTTCTTCTGCAC			4553
Query	391	TGGATTCTTGAAATGAACTGCTCTCTTCT---GTTGTTAATTGAGGTAAG-GATTTTGA			445
Sbjct	4552	TGGATTCTTGAAGTGAACCTGCTTTCTTTTCTAGTTTCTTAATTGAGG-AAGTGATGTTGA			4495

Range 36: 4495 to 4612

Score	Expect	Identities	Gaps	Strand	Frame
137 bits(74)	2e-28()	105/119(88%)	5/119(4%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	4612	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTCTGTCATTTGATTTTCTTCTGCAC			4553
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCT---GTTGTTAATTGAGGTAAG-GATTTTGA			154
Sbjct	4552	TGGATTCTTGAAGTGAACCTGCTTTCTTTTCTAGTTTCTTAATTGAGG-AAGTGATGTTGA			4495

Range 37: 5050 to 5167

Score	Expect	Identities	Gaps	Strand	Frame
137 bits(74)	2e-28()	105/119(88%)	5/119(4%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	5167	ATTGAGGAAGTGATGTTGATAATGTCCCTGGCACTTCTGTCATTTGATTTTCTTCTGCAC			5108
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCT---GTTGTTAATTGAGGTAAG-GATTTTGA			154
Sbjct	5107	TGGATTCTTGAAGTGAACCTGCTTTCTTTTCTAGTTTCTTAATTGAGG-AAGTGATGTTGA			5050

Range 38: 4594 to 4716

Score	Expect	Identities	Gaps	Strand	Frame
135 bits(73)	8e-28()	108/124(87%)	5/124(4%)	Plus/Minus	
Features:					
Query	35	ACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTC			94
Sbjct	4716	ACTTGATTGAGGAAGTGATGTTGATAGTGTCCATGTCACTTCTGTCATTTGATTTTCTTC			4657
Query	95	TGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT-T--AATTGAGGTAAG-GATT			150
Sbjct	4656	TGCACTGGATTCTTGAGGTGAACGGATTCTTTTCTAGTCTTTAATTGAGG-AAGCGATG			4598
Query	151	TTGA		154	



Sbjct 4597 TTGA 4594

Range 39: 4876 to 4969

Score	Expect	Identities	Gaps	Strand	Frame
135 bits(73)	8e-28()	87/94(93%)	0/94(0%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	4969	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTTCTGTCATTTGATTTTCTTCTGCAC			4910
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	133		
Sbjct	4909	TGGATTCTTGAAGTGAACTCCTTTCTTCGGTTGT	4876		

Range 40: 5569 to 5662

Score	Expect	Identities	Gaps	Strand	Frame
135 bits(73)	8e-28()	87/94(93%)	0/94(0%)	Plus/Minus	
Features:					
Query	331	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			390
Sbjct	5662	ATTGAGGAAGTGATGTTGATAATGTCCCTGGCACTTCTGTCATTTGATTTTCTTCTGCAC			5603
Query	391	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424		
Sbjct	5602	TGGATTCTTGAAGTGAAATGCTTTTTTCTGTTGT	5569		

Range 41: 5569 to 5662

Score	Expect	Identities	Gaps	Strand	Frame
135 bits(73)	8e-28()	87/94(93%)	0/94(0%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	5662	ATTGAGGAAGTGATGTTGATAATGTCCCTGGCACTTCTGTCATTTGATTTTCTTCTGCAC			5603
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	133		
Sbjct	5602	TGGATTCTTGAAGTGAAATGCTTTTTTCTGTTGT	5569		

Range 42: 1061 to 1153

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(72)	3e-27()	86/93(92%)	0/93(0%)	Plus/Minus	
Features:					
Query	331	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			390
Sbjct	1153	ATTGAGGAAGTGATGTTGATAATGTCCATGTCACCTTCTGTCATTTGATTTTCTTCTGCAC			1094
Query	391	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTG	423		
Sbjct	1093	TGGATTCTTGAAGTGAACTGCTTTTTTCTGTTG	1061		

Range 43: 1061 to 1153

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(72)	3e-27()	86/93(92%)	0/93(0%)	Plus/Minus	
Features:					
Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC			99
Sbjct	1153	ATTGAGGAAGTGATGTTGATAATGTCCATGTCACCTTCTGTCATTTGATTTTCTTCTGCAC			1094
Query	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTG	132		

Sbjct

1093

TGGATTCTCTGAAGTGAAGTGCCTTTTTCTGTTG

1061

Range 44: 1619 to 1711

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(72)	3e-27()	86/93(92%)	0/93(0%)	Plus/Minus	

Features:

Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99
Sbjct	1711	ATTGAGGAAGTGATGTTGATAATGTCCATGTCACCTTCTGTCATTTGATTTTCTTCTGCAC	1652
Query	100	TGGATTCTTGAAATGAAGTGCCTCTCTTCTGTTG	132
Sbjct	1651	TGGATTCTCTGAAGTGAAGTGCCTTTTTCTGTTG	1619

Range 45: 1841 to 1927

Score	Expect	Identities	Gaps	Strand	Frame
128 bits(69)	1e-25()	81/87(93%)	0/87(0%)	Plus/Minus	

Features:

Query	331	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	390
Sbjct	1927	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTTCTGTCATTTGATTTTCTTCTGCAC	1868
Query	391	TGGATTCTTGAAATGAAGTGCCTCTCTT	417
Sbjct	1867	TGGATTCTCTGAAGTGAAGTGCCTTCTT	1841

Range 46: 1841 to 1927

Score	Expect	Identities	Gaps	Strand	Frame
128 bits(69)	1e-25()	81/87(93%)	0/87(0%)	Plus/Minus	

Features:

Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99
Sbjct	1927	ATTGAGGAAGCGATGTTGATAGTGTCCATGGCATTTCTGTCATTTGATTTTCTTCTGCAC	1868
Query	100	TGGATTCTTGAAATGAAGTGCCTCTCTT	126
Sbjct	1867	TGGATTCTCTGAAGTGAAGTGCCTTCTT	1841

Range 47: 5737 to 5830

Score	Expect	Identities	Gaps	Strand	Frame
124 bits(67)	2e-24()	85/94(90%)	0/94(0%)	Plus/Minus	

Features:

Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99
Sbjct	5830	ATTGAGGAAGTGATGTTGATAGTGCCCATGGCACTTCTGTCATTTGATTTTCTTCTCCAC	5771
Query	100	TGGATTCTTGAAATGAAGTGCCTCTCTTCTGTTGT	133
Sbjct	5770	TGGATTGTTGAAGTGAAGTGCCTTTTTCTGTTGT	5737

Range 48: 1909 to 2026

Score	Expect	Identities	Gaps	Strand	Frame
121 bits(65)	2e-23()	102/119(86%)	5/119(4%)	Plus/Minus	

Features:

Query	40	ATTGAGAAAGTGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCAC	99
Sbjct	2026	ATTGAGGAAGCGATGTTGATAGTGTCCATGTCACCTTCTGTCATTTGATTTTCTTCTGCAC	1967

Query	100	TGGATTCTTGAAATGAAC	TGCTCTCTGTTGT-T--AATTGAGGTAAG-GATTTTGA	154
Sbjct	1966	TGGATTCTTGAGGTGAAC	GGATTCTTTTTTAGTCTTTAATTGAGG-AAGCGATGTTGA	1909

Range 49: 3133 to 3215

Score	Expect	Identities	Gaps	Strand	Frame
110 bits(59)	5e-20()	75/83(90%)	0/83(0%)	Plus/Minus	

Features:

Query	342	GATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGA	401

Range 50: 1 to 76

Score	Expect	Identities	Gaps	Strand	Frame
63.9 bits(34)	4e-06()	64/78(82%)	4/78(5%)	Plus/Minus	

Features:

Query	7	GACTCGAAAATATATTCTTTGC-TTGT-GAACTTGATTGAGAAAGTGATGTTGATAGTGT	64

Drosophila yakuba uncharacterized protein (Dyak\GE28509), partial mRNA  
Sequence ID: **ref|XM\_015190481.1|** Length: 1451 Number of Matches: 4  
Range 1: 218 to 813

Score	Expect	Identities	Gaps	Strand	Frame
431 bits(233)	9e-117()	477/598(80%)	4/598(0%)	Plus/Minus	

Features:

Query	7	GACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCC	66
Sbjct	813	GACTTGAAAATATACTTTTAGTTTGAGTACTTGTTTGAGGAAGCTTTGTTGATAGTGTCC	754
Query	67	ATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACGCTCTCTT	126
Sbjct	753	ATGGCACTTCTGTCATTTGATTTTCTTCTTCACTAGATTCTTGAAATGAACGCTTTCTT	694
Query	127	CTGTTGTTAATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGC	185
Sbjct	693	CTGTTGTAGATTGAGGTAAAGGAGTTAAAAA-TTCCGTTGTTGCCCTCTTTAATTGTTTCA	635
Query	186	TCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAA	245
Sbjct	634	ATTTCTGCACTCGAAACTGTAGGTAAACTTTTTGCCATTGTACCTGATTGAAAAGGAGAT	575
Query	246	ATTGATAGTGTCCCTTGATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAA	305
Sbjct	574	ATCGATAGTGTCCCTTGATCTTCTTCAGATGTTCTATCTTCATCTACACTTTGACTTGAA	515
Query	306	AATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACT	365
Sbjct	514	AATATACTTTTAGTTTGAGTACTTGTTTGAGGAAGCTTTGTTGATAGTGTCCATGGCACT	455
Query	366	TCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACGCTCTCTTCTGTTGTT	425
Sbjct	454	TCTGTCATATGATTTTCTTCTTCACTGGATTCTTGAAATGAACGCTTTCTTCTGTTGTG	395
Query	426	AATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGC	484
Sbjct	394	GATTGAGGTAAAGGAGTTAAAAA-TTCCGTTGTTTTCTCTTTAATTGTTTCAATTTCTGC	336
Query	485	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAAATTGATAG	544
Sbjct	335	ACTCGAAACAGTAGGTAAACTATTTGCCATTGTACTTGATTGAAAAGGAGATATCGATAG	276
Query	545	TGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATA	602

Sbjct 275 TGTCCTTGTAICTTTCTTTAGATATTCTGTTTTTATCTTCACCTTGACTTGAAAAATATA 218

Range 2: 3 to 522

Score	Expect	Identities	Gaps	Strand	Frame
407 bits(220)	1e-109()	422/522(81%)	4/522(0%)	Plus/Minus	
Features:					
Query 7		GACTCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCC			66
Sbjct 522		GACTTGAAAATATACTTTTAGTTTGAGTACTTGTTTGAGGAAGCTTGTTGATAGTGTCC			463
Query 67		ATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT			126
Sbjct 462		ATGGCACTTCTGTCATATGATTTTCTTCTTCACTGGATTCTTGAAATGAACTGCTTTCTT			403
Query 127		CTGTTGTTAATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGC			185
Sbjct 402		CTGTTGTGGATTGAGGTAAAGGA-GTTAAAAATTCCGTTGTTTTCTCTTTAATTGTTTCA			344
Query 186		TCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTGTGGGACAGAA			245
Sbjct 343		ATTTCTGCACTCGAAACAGTAGGTAAACTATTTGCCATTGTACTTGATTGAAAAGGAGAT			284
Query 246		ATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAA			305
Sbjct 283		ATCGATAGTGTCTTGTATCTTCTTTAGATATTCTGTTTTTATCTTCACTTTGACTTGAA			224
Query 306		AATATATTCTTTGCTTGTGAACCTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCACT			365
Sbjct 223		AATATACTTTCAGTTTGTGTACTTGATTGAGGAAGCTTGTTGATAGTGTCCATGGCACT			164
Query 366		TCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTT			425
Sbjct 163		TCTGTCATTTGATTTTCTTCTTCACTGGATTCTTGAAATGAACTGCTTCCTTCTGTTGTG			104
Query 426		AATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGC			484
Sbjct 103		GATTGGGGTAAAGGAGTTAAAAA-TTCCGTTGTTTCCTCTTTAATTGTTTCAATTTCTGC			45
Query 485		ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	526		
Sbjct 44		ACTCGAAACAGTAGGTAAACTATTTGCCATTGTACTTGATTG	3		

Range 3: 509 to 1007

Score	Expect	Identities	Gaps	Strand	Frame
335 bits(181)	7e-88()	397/503(79%)	8/503(1%)	Plus/Minus	
Features:					
Query 104		TTCTTGAAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAA-GGATTTTGAATGTTCCG			162
Sbjct 1007		TTCTTGAACTGAACTGCTTTCTTCTGTTGTGGATTGAGGTAAAGGA-GTTAAAAATTTCTG			949
Query 163		ATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTG			222
Sbjct 948		TTGTTTTCTTTTGAATTGTTTGATCTTCTGCACTCGAAACAGTAGGCAAACCTATTGCCA			889
Query 223		TTGCAATTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATG-T-T			280
Sbjct 888		TTGTACTTGATTGAAAAGGAGATATCGATAGTGTCTTGTATCTTCTTTCAGA--TGTTC			831
Query 281		GTCTTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACCTGATTGAGAAAG			340
Sbjct 830		ATCTTCATCTACACTTTGACTTGAAAATATACTTTTAGTTTGAGTACTTGTTTGAGGAAG			771
Query 341		TGATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTG			400
Sbjct 770		CTTTGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTTCACTAGATTCTTG			711
Query 401		AAATGAACTGCTCTCTTCTGTTGTTAATTGAGGTAA-GGATTTTGAATGTTCCGATGTCT			459
Sbjct 710		AAATGAACTGCTTTCTTCTGTTGTAGATTGAGGTAAAGGAGTTAAAAA-TTCCGTTGTTG			652
Query 460		CCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAA			519
Sbjct 651		CCTCTTTAATTGTTTCAATTTCTGCACTCGAACTGTAGGTAAACTTTTTGCCATTGTAC			592
Query 520		TTGATTGTGGGACAGAAATTGATAGTGTCTTGTATCTTCTTGAGAAATGTTGTCTTCAT			579
Sbjct 591		CTGATTGAAAAGGAGATATCGATAGTGTCTTGTATCTTCTTTCAGATGTTCTATCTTCAT			532
Query 580		TTAAACTCGGACTCGAAAATATA	602		
Sbjct 531		CTACACTTTGACTTGAAAATATA	509		

Range 4: 3 to 231

Score	Expect	Identities	Gaps	Strand	Frame
202 bits(109)	7e-48()	190/230(83%)	2/230(0%)	Plus/Minus	
Features:					
Query	7	GACTCGAAAATATATTCTTTGCTTGTGAACCTTGATTGAGAAAGTGATGTTGATAGTGTCC			66
Sbjct	231	GACTTGAAAATATACTTTCAGTTTGTGTACTTGATTGAGGAAGCTTTGTTGATAGTGTCC			172
Query	67	ATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTT			126
Sbjct	171	ATGGCACTTCTGTCATTTGATTTTCTTCTTCACTGGATTCTTGAAATGAACTGCTTCCTT			112
Query	127	CTGTTGTTAATTGAGGTAA-GGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGC			185
Sbjct	111	CTGTTGTGGATTGGGGTAAAGGAGTTAAAAA-TTCCGTTGTTTCCTCTTTAATTGTTTCA			53
Query	186	TCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG			235
Sbjct	52	ATTTCTGCACTCGAAACAGTAGGTAAACTATTTGCCATTGTACTTGATTG			3