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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CN9R2B19014

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Blast report description

Nucleotide Sequence (605 letters)

RID <u>CN9R2B19014</u> (Expires on 02-23 13:12 pm)

Query ID lcl|Query_83179 Database Name nr

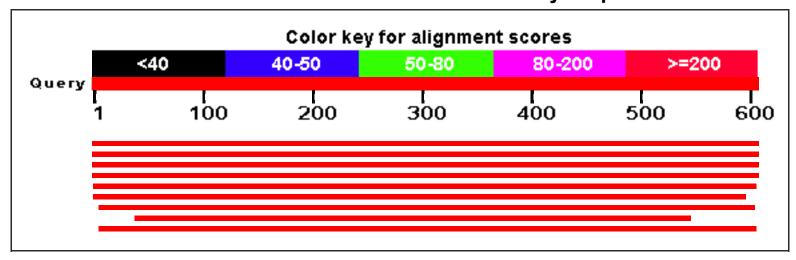
Description None **Description** Nucleotide collection (nt)

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

Query Length 605

□ Graphic Summary

Distribution of 109 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

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

□ <u>Alignments</u>

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 bit	ts(587)	0.0()	599/605(99%)	0/605(0%)	Plus/Minus		
Features: mucin 14A							
Query	1	AACTCGG	ACTCGAAAATATATTC	TTTGCTTGTGAAC	TTGATTGAGAAAG	TGATGTTGATA	60
Sbjct	16027424	AACTCTG	ACTCGAAAATATATTC	TTTGCTTGTGAAC	ttgattgagaaad	stgatgttgata	16027365
Query	61	GTGTCCA!	rggcacttctgtcatt	TGATTTTCTTCTG	CACTGGATTCTTG	GAAATGAACTGC	120
Sbjct	16027364	GTGTCCA'	rGGCACTTCTGTCATT	TGATTTTCTTCTG	CACTGGATTTTT	SAAATGAACTGC	16027305
Query	121	TCTCTTC	IGTTGTTAATTGAGGT	'AAGGATTTTGAAT	GTTCCGATGTCTC	CTCTTGAGCTG	180
Sbjct	16027304	4646446	tgttgttaattgaggt	·AAGGATTTTGAAT	ĠŦŦĊĊĠĂŦĠŦĊŦĊ	cctcttgagctg	16027245
Query	181	TTTGCTC	TTCTGCACTCGAACCT	GTAAGTAAACTAT	TGGCTGTTGCAA1	TGATTGTGGGA	240
Sbjct	16027244	tttgctc:	ttctccactccaacct	gtaagtaaactat	ተĠĠĊተĠተተĠĊልልተ	rtdattdtddda	16027185
Query	241	CAGAAAT'	rgatagtgtccttgta 	TCTTCTTGAGAAA	TGTTGTCTTCAT1	TAAACTCGGAC	300
Sbjct	16027184	CAGAAAT'	rdatgdtdtccttdta	tcttcttgagaaa	ተĠተተĠተĊተተĊልተሳ	rtaaactctgac	16027125
Query	301	TCGAAAA'	PATATTCTTTGCTTGT	GAACTTGATTGAG	AAAGTGATGTTG <i>A</i>	TAGTGTCCATG	360
Sbjct	16027124	tcgaaaa.	tatattettteet	ĠĀĀĊŦŦĠĀŦŦĠĀĠ	AAAGTGATGTTGA	rtygtgtgtgt	16027065
Query	361	GCACTTC	IGTCATTTGATTTTCT	TCTGCACTGGATT	CTTGAAATGAACT	GCTCTCTTCTG	420

Sbjct	16027064	GCACTTCTGTCGTTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	16027005
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	16027004	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	16026945
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	540
Sbjct	16026944	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	16026885
Query	541	ATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	16026884	GTAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	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 14							
Query	1	AACTCGO	GACTCGAAAATATATT(CTTTGCTTGTGAAC	TTGATTGAGAAA(GTGATGTTGATA	60
Sbjct	16028588	AACTCG	sactcgaaaatatatt	ctttgcttgtgaac	rtgattgagaaa	stgatgttgata	16028529
Query	61	GTGTCC	ATGGCACTTCTGTCATT	TTGATTTTCTTCTG(CACTGGATTCTT	GAAATGAACTGC	120
Sbjct	16028528	GTGTCC	ATGGCACTTCTGTCATT	TTGATTTTCTTCTG	CACTGGATTTTT	GAAATGAACTGC	16028469
Query	121	TCTCTTC	CTGTTGTTAATTGAGG	FAAGGATTTTGAAT(GTTCCGATGTCT(CCTCTTGAGCTG	180
Sbjct	16028468	464644	CTGTTGTTAATTGAGG	raaggattttgaato	cttccgatgtct	cctcttgagctg	16028409
Query	181	TTTGCTO	CTTCTGCACTCGAACCT	rgtaagtaaactat:	rggctgttgcaa'	TTGATTGTGGGA	240
Sbjct	16028408	tttgct	cttctgcactcgaacc	rgtaagtaaactat:	rddctdttdcaa'	rtgattgtgga	16028349
Query	241	CAGAAAT	TTGATAGTGTCCTTGT	ATCTTCTTGAGAAA?	rgttgtcttcat'	TTAAACTCGGAC	300
Sbjct	16028348	CAGAAA	rtgatagtgtccttgtz	ATCTTCTTGAGAAG:	rrttgtcttcat	TTACACTCTGAC	16028289
Query	301	TCGAAA	ATATATTCTTTGCTTG	rgaacttgattgag	AAAGTGATGTTG	ATAGTGTCCATG	360
Sbjct	16028288	TCGAAAZ	AtAtAttctttgrttr	rdaacttdattdadz	AAAGTGATGTTG	ATAGTGTCCATG	16028229
Query	361	GCACTTO	CTGTCATTTGATTTTC	TTCTGCACTGGATT(CTTGAAATGAAC'	TGCTCTCTTCTG	420
Sbjct	16028228	GCACTTO	chdachthadarthac	ttctccactccattc	cttgaaatgaac	tgctctcttctg	16028169
Query	421	TTGTTAZ	ATTGAGGTAAGGATTT	rgaatgttccgatg:	rctcctcttgag(CTGTTTGCTCTT	480
Sbjct	16028168	TTGTTAZ	ATTGAGGTAAGGATTT	rgaatgttccgatg	rctcctcttdag	chchrhdchchr	16028109
Query	481	CTGCACT	CGAACCTGTAAGTAA	ACTATTGGCTGTTG	CAATTGATTGTG	GGACAGAAATTG	540
Sbjct	16028108	CTGCAC1	rcgaacctgtaagtaaz	Actattggctgttg	CAATTGATTGTG	GGACAGAAATTG	16028049
Query	541	ATAGTGT	CCTTGTATCTTCTTG	AGAAATGTTGTCTT(CATTTAAACTCG	GACTCGAAAATA	600
Sbjct	16028048	GTAGTG	recttgtatettettg	AGAAATGTTGTCTT	CATTTAAACTCG	GACTCGAAAATA	16027989
Query	601	TATTC	605				
Sbjct	16027988	TATTC	16027984				

Range 3: 16030603 to 16031207

Score		Expect	Identities	Gaps	Strand	Frame	
1062 bit	s(575)	0.0()	595/605(98%)	0/605(0%)	Plus/Minus		
Features mucin 1							
Query	1	AACTCGGA	CTCGAAAATATATTCTT	TGCTTGTGAACT	TGATTGAGAAAGT	GATGTTGATA	60
Sbjct	16031207	AACTCGGA	ctcgaaaatatattctt	rtgrttrtgaact	tgattgagaaggt	GATGTTGATA	16031148
Query	61	GTGTCCAT	GGCACTTCTGTCATTTG	ATTTTCTTCTGC.	ACTGGATTCTTGA	AATGAACTGC	120
Sbjct	16031147	GTGTCCAT	ĠĠĊĀĊŦŦĊŦĠŦĊĠŦŦŦĠ	:Attttcttctcc	Actggattcttga	AATGAACTGC	16031088
Query	121	TCTCTTCT	GTTGTTAATTGAGGTAA 	GGATTTTGAATG	TTCCGATGTCTCC	TCTTGAGCTG	180

Sbjct	16031087	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	16031028
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	240
Sbjct	16031027	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	16030968
Query	241	CAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	16030967	CAGAAATTGGTAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCTGAC	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	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	540
Sbjct	16030727	ctgcactrgaacctgtaagtaaactattggctgttgcaattgattgtgggacagaaattg	16030668
Query	541	ATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	16030667	GTAGTGTCCTTGTATCTTCATGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	16030608
Query	601	TATTC 605	
Sbjct	16030607	tattc 16030603	

Gaps

Frame

Strand

Drosophila melanogaster mucin 14A (Muc14A), mRNA

Expect

Sequence ID: **ref|NM_167482.4|** Length: 48733 Number of Matches: 105 Range 1: 16058 to 16662

Identities

Score

1085 bit	s(587)	0.0()	599/605(99%)	0/605(0%)	Plus/Minus	
Feature	s:					
Query	1	AACTCGGACT	'CGAAAATATATTCTTT	GCTTGTGAACTTG	ATTGAGAAAGTGATGTTGATA	60
Sbjct	16662	AACTCTGACT	rcgaaaatatatatcttt	ĠĊŦŦĠŦĠĂĂĊŦŦĠ	AttgAgAAAGtgAtgttgAtA	16603
Query	61	GTGTCCATGG	GCACTTCTGTCATTTGA	TTTTCTTCTGCAC	TGGATTCTTGAAATGAACTGC	120
Sbjct	16602	ĠŦĠŦĊĊĀŦĠĠ	;cacttctctctcatttca	ttttcttctgcac	rtggattttttgaaatgaactgc	16543
Query	121	TCTCTTCTGT	TGTTAATTGAGGTAAG! 	GATTTTGAATGTT 	CCGATGTCTCCTCTTGAGCTG	180
Sbjct	16542	tctcttctgt	rtĠttAAttĠAĠĠtAAĠ	ĠĂϮϮϮϮĠĂĂϮĠϮϮ	cccatctctctcttcacctc	16483
Query	181				CTGTTGCAATTGATTGTGGGA	240
Sbjct	16482	TTTGCTCTTC			ĊŢĠŢŢĠĊĀĀŢŢĠĀŢŢĠŢĠĠĠĀ	16423
Query	241				TGTCTTCATTTAAACTCGGAC	300
Sbjct	16422				TĠTĊTTĊĂTTTĂĂĂĊTĊTĠĂĊ	16363
Query	301				GTGATGTTGATAGTGTCCATG	360
Sbjct	16362				ĠŢĠĀŢĠŢŢĠĀŢĀĠŢĠŢĊĊĀŢĠ	16303
Query	361				GAAATGAACTGCTCTCTTCTG	420
Sbjct	16302		CGTTTGATTTTCTTCT			16243
Query	421 16242				CCTCTTGAGCTGTTTGCTCTT	480 16183
Sbjct	481				TTGATTGTGGGACAGAAATTG	540
Query Sbjct	16182		ACCTGTAAGTAAACTA 		TTGATTGTGGGACAGAAATTG	16123
Query	541				TTAAACTCGGACTCGAAAATA	600
Sbjct	16122				TTAAACTCGGACTCGAAAATA	16063
Query	601	TATTC 605		AIGIIGICIICAI	TIMMOTOGOCTOGNAMIA	10003
Sbjct	16062					
	10002	111110 100				

Range 2: 17222 to 17826

Score		Expect	Identities	Gaps	Strand	Frame	
1068 bit	s(578)	0.0()	596/605(99%)	0/605(0%)	Plus/Minus		
Feature	s:						
Query	1	AACTCGGAC'	rcgaaaatatattcttt	GCTTGTGAACTTG	GATTGAGAAAGTGA	TGTTGATA	60
Sbjct	17826	AACTCGGAC	rcgaaaatatattctt	rddtdaadttd	attgagaaaagtga	tgttgata	17767
Query	61	GTGTCCATG	GCACTTCTGTCATTTG <i>A</i>	ATTTTCTTCTGCAC	TGGATTCTTGAAA	TGAACTGC	120
Sbjct	17766	ĠŦĠŦĊĊĀŦĠ	ĠĊĂĊŦŦĊŦĠŦĊĂŦŦŦĠ	\rhodothera	ctggatttttgaaa	.tgaactgc	17707
Query	121	TCTCTTCTG	TTGTTAATTGAGGTAAG	GATTTTGAATGTT	CCGATGTCTCCTC	TTGAGCTG	180
Sbjct	17706	†c†c††c†c	trgttaattgaggtaad	sgattttgaatctt	rccgatgtctctc	ttgagctg	17647
Query	181	TTTGCTCTT	CTGCACTCGAACCTGT <i>A</i> 	AGTAAACTATTGG	CTGTTGCAATTGA	TTGTGGGA	240
Sbjct	17646	TTTGCTCTT	ĊŦĠĊĀĊŦĊĠĀĀĊĊŦĠŦĀ	AÁĠŦĀĀĀĊŦĀŦŦĠĠ	sctgttgcaattga	.TTĠTĠĠĠĀ	17587
Query	241		ATAGTGTCCTTGTATCT 				300
Sbjct	17586	ĊĀĠĀĀĀŤŤĠ	ATAGTGTCCTTGTATCT	TTĊTTĠAĠAAGTTT	ŢĠŦĊŦŦĊĂŦŦŦĀC	ÀĊŤĊŦĠĂĊ	17527
Query	301		FATTCTTTGCTTGTGA <i>F</i> 				360
Sbjct	17526		ŗattctttctttctt				17467
Query	361		FCATTTGATTTTCTTCT 	GCACTGGATTCTT: 			420
Sbjct	17466	ĠĊĂĊŤŤĊŤĠſ		GCACTGGATTCTT			17407
Query	421		GAGGTAAGGATTTTGAA 				480
Sbjct	17406		ĠAĠĠϮAAĠĠAϮϮϮϮĠAA 				17347
Query	481		AACCTGTAAGTAAACT <i>A</i> 				540
Sbjct	17346		AACCTGTAAGTAAACT <i>i</i>				17287
Query	541		$ ext{TTGTATCTTCTTGAGAA} \ ig ig ig ig ig ig ig ig $				600
Sbjct	17286		ĬŦĠŦĂŦĊŦŦĊŦŦĠĂĠĂŹ -	AATGTTGTCTTCAT	"I"I'AAAC'TCGGACT	CGAAAATA	17227
Query	601	TATTC 605					
Sbjct	17226	TATTC 173	222				

Range 3: 19670 to 20274

Score		Expect	Identities	Gaps	Strand	Frame	
1062 bit	s(575)	0.0()	595/605(98%)	0/605(0%)	Plus/Minus		
Features	s:						
Query	1	AACTCGGACTC	CGAAAATATATTCTT	TGCTTGTGAACTTG.	ATTGAGAAAGTGA	ATGTTGATA	60
Sbjct	20274	AACTCGGACTC	CGAAAATATATTCTT	tgrttrtgaacttg.	ATTGAGAAGGTGA	ATGTTGATA	20215
Query	61	GTGTCCATGGC	CACTTCTGTCATTTG	ATTTTCTTCTGCAC	TGGATTCTTGAA <i>F</i>	ATGAACTGC	120
Sbjct	20214	gtgtccatgg	cacttctctctctttc	Attttcttctccac	tggyttgy	ATGAACTGC	20155
Query	121	TCTCTTCTGTT	rgttaattgaggtaa 	GGATTTTGAATGTT	CCGATGTCTCCTC	CTTGAGCTG	180
Sbjct	20154	ተረተረተተረተሬተሳ	rgttaattgaggtaa	ddattttdaatdt	cceatetctct	cttgagctg	20095
Query	181	TTTGCTCTTCT	rgcactcgaacctgt 	AAGTAAACTATTGG	CTGTTGCAATTG <i>A</i>	ATTGTGGGA	240
Sbjct	20094	ተተተፅረተረተተረተ	rdcactcdaacctdt	AAGTAAACTATTGG	ĊŦĠŦŦĠĊĂĂŦŦĠ <i>Ĕ</i>	ATTGTGGGA	20035
Query	241	CAGAAATTGAT	PAGTGTCCTTGTATC	TTCTTGAGAAATGT	TGTCTTCATTTA <i>I</i> 	ACTCGGAC	300
Sbjct	20034	cagaaattggt	ragtgtccttgtatc	ttcttgagaaatgt	tgtcttcatta <i>t</i>	AAĊŦĊŦĠĀĊ	19975
Query	301	TCGAAAATATA	ATTCTTTGCTTGTGA 	ACTTGATTGAGAAA(GTGATGTTGATAG	TGTCCATG	360
Sbjct	19974	†¢ĠAAAA†A†A	Attcttdgttctga	ACTTGATTGAGAAA	ĠŦĠĀŦĠŦŦĠĀŦĀĠ	stgtccatg	19915
Query	361	GCACTTCTGTC	CATTTGATTTTCTTC	TGCACTGGATTCTT	GAAATGAACTGCT 	CTCTTCTG	420
Sbjct	19914	ĠĊĀĊŢŢĊŢĠŢĊ	catttgattttc	†ĠĊĀĊŢĠĠĀŢŢĊŢŢ	ĠĀĀĀŢĠĀĀĊŢĠĊŢ	rctcttctc	19855
Query	421	TTGTTAATTG <i>I</i>	AGGTAAGGATTTTGA 	ATGTTCCGATGTCT(CCTCTTGAGCTG1 	TTTGCTCTT	480
Sbjct	19854	t	Aggtaaggatttga	Atgttccgatgtct	cctcttdacctd	rttgctctt	19795
Query	481	CTGCACTCGAA	ACCTGTAAGTAAACT	ATTGGCTGTTGCAA'	TTGATTGTGGGAC	CAGAAATTG 	540

Sbjct	19794	CTGCACTTGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	19735
Query	541		600
Sbjct	19734	GTAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	19675
Query	601	TATTC 605	
Sbict	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 bit	ts(587)	0.0()	599/605(99%)	0/605(0%)	Plus/Minus		_
Feature	s:						
Query	1	AACTCGGAC'	rcgaaaatatattctt	TGCTTGTGAACTT	GATTGAGAAAGT(GATGTTGATA	60
Sbjct	153767	AACTCTGAC	tcgaaaatatattctt	ϮĠĊϮϮĠϮĠ⅄⅄ĊϮϮ	gattgagaaagt	GATGTTGATA	153708
Query	61	GTGTCCATG(GCACTTCTGTCATTTG 	ATTTTCTTCTGCA	CTGGATTCTTGAZ	AATGAACTGC	120
Sbjct	153707	ĠŦĠŦĊĊĂŦĠŒ	ĠĊĀĊŦŦĊŦĠŦĊĀŦŦŦĠ	ATTTTCTTCTGCA	ĊŦĠĠĂŦŦŦŦĠĀŹ	AATGAACTGC	153648
Query	121		ITGTTAATTGAGGTAA 			CTTGAGCTG	180
Sbjct	153647		PTGTTAATTGAGGTAA			rcttgagetg	153588
Query	181		CTGCACTCGAACCTGT				240
Sbjct	153587		ĊŢĠĊĂĊŢĊĠĂĂĊĊŢĠŢ		ĠĊŦĠŦŦĠĊĂĂŦŦ(153528 300
Query Sbjct	241 153527		$egin{array}{ll} ext{ATAGTGTCCTTGTATC} \ ert & ert & ert & ert & ert \ ert & ert \ ert & ert \ ert & ert \ \ ert \ ert \ ert \ \ \ \ ert \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$				153468
Query	301		PATTCTTTGCTTGTGA				360
Sbjct	153467						153408
Query	361	GCACTTCTG'	PCATTTGATTTTCTTC	TGCACTGGATTCT	TGAAATGAACTG	CTCTCTTCTG	420
Sbjct	153407	GCACTTCTG'	tcgtttgattttcttc	tgcactggattct	tgaaatgaactg	ctctcttctc	153348
Query	421	TTGTTAATTO	GAGGTAAGGATTTTGA 	ATGTTCCGATGTC	TCCTCTTGAGCT	GTTTGCTCTT	480
Sbjct	153347	ተተĠተተልልተተ	GAGGTAAGGATTTGA	Atgttccgatgtc	tcctcttdact	ĠŦŦŦĠĊŦĊŦŦ	153288
Query	481		AACCTGTAAGTAAACT 				540
Sbjct	153287	ĊŦĠĊĀĊŦĊĠ	AACCTGTAAGTAAACT	ATTĠĠĊTĠTTĠĊA	AttĠAttĠtĠĠĠ	Acagaaattg	153228
Query	541		TGTATCTTCTTGAGA 				600
Sbjct	153227		rtgtatcttcttgaga -	AATGTTGTCTTCA	TTTAAACTCGGAG	CTCGAAAATA	153168
Query	601	TATTC 60!					
Sbjct	153167	TATTC 15	3163				

Range 2: 154327 to 154931

Score		Expect	Identities	Gaps	Strand	Frame	_
1068 bit	s(578)	0.0()	596/605(99%)	0/605(0%)	Plus/Minus		_
Features	S :						
Query	1	AACTCGGACT	rcgaaaatatattctt	TGCTTGTGAACTT	GATTGAGAAAGT	GATGTTGATA	60
Sbjct	154931	AACTCGGAC	rcgaaaatatattett	rtgcttgtgaactt	GATTGAGAAAGT	GATGTTGATA	154872
Query	61	GTGTCCATGO	GCACTTCTGTCATTTG	ATTTTCTTCTGCA	CTGGATTCTTGA	AATGAACTGC	120
Sbjct	154871	GTGTCCATGO	Scacttctgtcatttg	attttcttctcca	ctggatttttga	AATGAACTGC	154812
Query	121	TCTCTTCTGT	TTGTTAATTGAGGTAA 	GGATTTTGAATGT	TCCGATGTCTCC'	ICTTGAGCTG	180
Sbjct	154811	†c†c††c†G	ttgttaattgaggtaa	.ddattttdaatct	tccgatgtctcc	tcttgagctg	154752
Query	181	TTTGCTCTT(CTGCACTCGAACCTGT	'AAGTAAACTATTG(GCTGTTGCAATT(GATTGTGGGA	240
Sbjct	154751	tttgctctt	ctgcactcgaacctgt	'AAGTAAACTATTG	\$ctgttgcaatt	ĠATTĠTĠĠĠĀ	154692

Query	241	CAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	154691	CAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAGTTTTGTCTTCATTTACACTCTGAC	154632
Query	301	TCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	154631	tcgaaaatatattctttgttttgaacttgattgactagatagtgatgttgatagtgtccatg	154572
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	154571	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	154512
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	154511	trgtraatrgaggtaaggatrtrgaatgtreegatgtetetetetetaggetetet	154452
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	540
Sbjct	154451	ctgcactcgaacctgtaagtaaactattgcctgttgcaattgattg	154392
Query	541	ATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	154391	GTAGTGTCCTTGTATCTTCAGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	154332
Query	601	TATTC 605	
Sbjct	154331	ተልተተር 154327	

Range 3: 156946 to 157550

Score		Expect	Identities	Gaps	Strand	Frame	
1062 bit	ts(575)	0.0()	595/605(98%)	0/605(0%)	Plus/Minus		
Feature	s:						
Query	1	AACTCGGAC	TCGAAAATATATTCTT	TTGCTTGTGAACTT	GATTGAGAAAGT(GATGTTGATA	60
Sbjct	157550	AACTCGGAC	TCGAAAATATATTCTT	TTGTTTTTGAACTT	GATTGAGAAGGT	GATGTTGATA	157491
Query	61	GTGTCCATG	GCACTTCTGTCATTTG	SATTTTCTTCTGCA	CTGGATTCTTGA	AATGAACTGC	120
Sbjct	157490	GTGTCCATG	gcacttctgtcgttd	sattttetteta	ĊŦĠĠĀŦŦĊŦŦĠĀZ	AATGAACTGC	157431
Query	121	TCTCTTCTG	TTGTTAATTGAGGTAA	AGGATTTTGAATGT	TCCGATGTCTCC	CTTGAGCTG	180
Sbjct	157430	ተረተረተተረተራ	ttgttaattgaggtaa	AGGATTTTGAATGT	tcccatctcc.	rcttgagctg	157371
Query	181	TTTGCTCTT	CTGCACTCGAACCTGT	TAAGTAAACTATTG 	GCTGTTGCAATT(GATTGTGGGA	240
Sbjct	157370	ተተተፍረተረተተ	ctgcactcgaacctgt	raagtaaactattg	ĠĊŦĠŦŦĠĊĂĂŦŦŒ	GATTGTGGGA	157311
Query	241	CAGAAATTG	ATAGTGTCCTTGTATC	CTTCTTGAGAAATG	TTGTCTTCATTT	AAACTCGGAC	300
Sbjct	157310	cagaaattg	GTAGTGTCCTTGTATC	cttcttgagaaatg	††d†c††cA††t	AAACTCTGAC	157251
Query	301	TCGAAAATA	TATTCTTTGCTTGTGA	AACTTGATTGAGAA 	AGTGATGTTGATA	AGTGTCCATG	360
Sbjct	157250	tċĠAAAAtA	†A††¢†††G††¢¢	AACTTGATTGAGAA	AĠŢĠĀŢĠŢŢĠĀŢ	AĠŦĠŦĊĊĂŦĠ	157191
Query	361	GCACTTCTG	TCATTTGATTTTCTTC	CTGCACTGGATTCT 	TGAAATGAACTG(CTCTCTTCTG	420
Sbjct	157190		†CÀTTTGÀTTTCTTC				157131
Query	421		GAGGTAAGGATTTTG <i>A</i> 				480
Sbjct	157130	ተተĠተተልልተተ	ĠĀĠĠŦĀĀĠĠĀŦŦŦŦĠĀ	AATĠTTĊĊĠATĠTĊ	TĊĊŦĊŦŦĠĀĠĊŦŒ	STTTGCTCTT	157071
Query	481		AACCTGTAAGTAAACT 				540
Sbjct	157070	ĊŢĠĊĀĊŢŢĠ	AAĊĊϮĠϮAAĠϮAAAĊϮ	rATTĠĠĊTĠTTĠĊA	ATTĠATTĠTĠĠĠ <i>ā</i>	ACAGAAATTG	157011
Query	541	ATAGTGTCC	$ ext{TTGTATCTTCTTGAGA} $	AATGTTGTCTTCA 	TTTAAACTCGGA(CTCGAAAATA 	600
Sbjct	157010		ŢŢĠŢĄŢĊŢŢĊŢŢĠĄĠ <i>Ŗ</i>	\AATĠŦŦĠŦĊŦŦĊA	ŤŤŤÁÁÁĊŤĊĠĠÁ(ĊŢĊĠĀĀĀĀŢĀ	156951
Query	601	TATTC 60					
Sbjct	156950	TATTC 15	6946				

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	

Feature	S:		
Query	1	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGA	60
Sbjct	60	AACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGA	119
Query	61	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGC	120
Sbjct	120	GTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTTTTGAAATGAACTGC	179
Query	121	TCTCTTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTG	180
Sbjct	180	trtcttctgttgttaattgaggtaaggagtttgaaagttccgatgtctcttcttgagctg	239
Query	181	TTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	240
Sbjct	240	trtgctcttctgcactcgaacctgtaagtaaactattggctgttgcaattgattg	299
Query	241	CAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGAC	300
Sbjct	300	cagaaattgatagtgtccttgtatcttcttgagaaatgttgtcttcatataaactcggac	359
Query	301	TCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATG	360
Sbjct	360	tcgaaaatatattctttggttctgaacttgattgagaaagtgatgttgatagtgtcatg	419
Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	420	ĠĊĂĊŦŦĊŦĠŦĊĂŦŦŦĠĂŦŦŦŦĊŦŦĊŦaĊĂĊŦĠĠĂŦŦĊŦŦĠĂĂĂŦĠĂĂĊŦĠĊŦĊŦĊŦŦĊŦĠ	479
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	480	trettaatteaetaaetaaetaaaetreteeaateteeteeteeteeteeteeteeteeteeteete	539
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	540
Sbjct	540	TTGCAATCGAACCTGTAAGTAATCTATTTGCTGTTGTACTTGATTGTGGGACAGATATTG	599
Query	541	ATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	600	AtgGtGtCcttGtAtcttcttGAGAAAtGttGtCttCAtttAAACtCTGACtCGAAAAtA	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	AACTCGGACTC	GAAAATATATTCTT	rgcttgtgaacttga:	rtgagaaagtgar	IGTTGATA	60
Sbjct	642	AACTCTGACTC	GAAAATATATTCTT	rggttctgaacttga	rtgagaaagtgar	rgttgata	701
Query	61	GTGTCCATGGC	ACTTCTGTCATTTG	ATTTTCTTCTGCACT(GGATTCTTGAAAT	rgaactgc	120
Sbjct	702	GTGTCCATGGC.	ActtctctctcAtttc	ATTTCTTCTGCACT	GGATTCTTGAAA	rgaactgc	761
Query	121	TCTCTTCTGTT	GTTAATTGAGGTAAG	GGATTTTGAATGTTC	CGATGTCTCCTC	TTGAGCTG	180
Sbjct	762	†¢†¢††¢†¢††	GTTAATTGAGGTAAG	GGATTTTGAATGTTC	cgatgtttcctc	rtgagetg	821
Query	181	TTTGCTCTTCT	GCACTCGAACCTGT	AAGTAAACTATTGGC'	rgttgcaattga:	TTGTGGGA	240
Sbjct	822	TTTGCTCTTCT	GCAATCGAACCTGT	AAGTAATCTATTTGC:	rGTTGTACTTGA:	rtgtggga	881
Query	241	CAGAAATTGAT.	AGTGTCCTTGTATC	TTCTTGAGAAATGTT(GTCTTCATTTAA	ACTCGGAC	300
Sbjct	882	CAGATATTGAT	GGTGTCCTTGTATC	rtcttgagaaatgtt	ĠŦĊŦŦĊĀŦŦŦĀĀZ	ACTCTGAC	941
Query	301	TCGAAAATATA	TTCTTTGCTTGTGA	ACTTGATTGAGAAAG'	rgatgttgatag:	FGTCCATG	360
Sbjct	942	tcgaaaatatg	ተተ ረተተተ <u>ፈ</u> ረተተፈተፈ	ACTTGATTGAGAAAG	rdatdttdatad:	rgtccatg	1001
Query	361	GCACTTCTGTC	ATTTGATTTTCTTC	rgcactggattcttg	AAATGAACTGCT(CTCTTCTG	420
Sbjct	1002	GCACTTCTGTC.	ATTTGATTTTCTTC	rdcgctddattcttd	raatgaactgcgo	ctcttctc	1061
Query	421	TTGTTAATTGA	GGTAAGGATTTTGA	ATGTTCCGATGTCTC	CTCTTGAGCTGT	TTGCTCTT	480
Sbjct	1062	ተተፍተተልልተተፍል	GGTAAGGATTTTGA	AtdttccdAtdtctc	ctcttgagctgt	rtgctctt	1121
Query	481	CTGCACTCGAA	CCTGTAAGTAAACT	ATTGGCTGTTGCAAT'	rgattgtgggac <i>i</i>	AGAAATTG	540
Sbjct	1122	ctgcactcgaa	cctgtaagtaarct	Attggttgttgcaaa	rdattdtdddacz	AGAAATTG	1181
Query	541	ATAGTGTCCTT	GTATCTTCTTGAGA	AATGTTGTCTTCATT	FAAACTCGGACT(CGAAAATA	600
Sbjct	1182	ATAGTGTCCTT	GTATCTTCTTGAGAZ	AGTTTTGTCTTCATT	TACACTCTGACT	CGAAAATA	1241

Query 601 TATTC 605
Sbjct 1242 TATTC 1246

Range 3: 351 to 955

Score		Ex	pect	Identities	Gaps	Strand	Frame	
979 bits	(530)	0.0	()	580/605(96%)	0/605(0%)	Plus/Plus		
Features	s:							
Query	1	AACTCGG	SACTCGA <i>I</i>	AATATATTCTTT	GCTTGTGAACTTGATT	TGAGAAAGTGAT(GTTGATA	60
Sbjct	351	AACTCGC	SACTCGAZ	AAATATATTCTTT	rggttctgaacttgatr	rgagaaagtgato	STTGATA	410
Query	61	GTGTCCA	TGGCACT	TTCTGTCATTTGA	TTTTCTTCTGCACTGC	SATTCTTGAAAT(GAACTGC	120
Sbjct	411	GTGTCCA	ATGGCAC1	rtctgtcatttga	\trttcttctacactcd	SATTCTTGAAATO	GAACTGC	470
Query	121	TCTCTTC	TGTTGTT	TAATTGAGGTAAG	GATTTTGAATGTTCCC	GATGTCTCCTCTT	TGAGCTG	180
Sbjct	471	ተረተረተተረ	ctdttdtd	rAATTGAGGTAAG	sdattttdaaadttcc	satgteteetet	rgagetg	530
Query	181	TTTGCTC	TTCTGC <i>E</i>	ACTCGAACCTGTA	AGTAAACTATTGGCT(GTTGCAATTGATT	TGTGGGA	240
Sbjct	531	ተተተፍርተረ	cttrtgc	AatcGAAcctGtA	Addaarctatttgctd	strgrycttgyt	rgtgggy	590
Query	241	CAGAAAT	TGATAGT	GTCCTTGTATCT	TCTTGAGAAATGTTGT	CTTCATTTAAA(CTCGGAC	300
Sbjct	591	ĊAĠATA¹	rtĠAtGĠi	rgtccttgtatct	rtcttgagaaatgttg	rcttcatttaaac	CTCTGAC	650
Query	301	TCGAAA?	TATATTC	CTTTGCTTGTGAA	CTTGATTGAGAAAGT(GATGTTGATAGTO	GTCCATG	360
Sbjct	651	tcgaaaa	ላተልተልተተረ	cttdgttctgaa	cttgattgagaaagt	satgttgatagtd	stccatg	710
Query	361	GCACTTC	TGTCATI	TTGATTTTCTTCT 	GCACTGGATTCTTGAZ	ATGAACTGCTCT	CTTCTG	420
Sbjct	711	ĠĊĀĊŦŦĊ	ctgtcatt	rtgattttcttct	rĠĊĀĊŦĠĠĀŦŦĊŦŦĠĀŹ	Adreaderecte	tcttctc	770
Query	421	TTGTTA <i>I</i>	TTGAGGT	TAAGGATTTTGAA 	TGTTCCGATGTCTCCT	CTTGAGCTGTTT	rgctctt 	480
Sbjct	771	††g††A	\tr\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\d\	raaggattttgaa	tgttccgatgtttcc	rcttgagctgtt	rĠĊϮĊϮϮ	830
Query	481				$\Delta ext{TTGGCTGTTGCAATTC} \ \ \ \ \ \ \ \ \ $			540
Sbjct	831	ctccaat	ccgyycci	rĠtAAĠtAATĊtA	tractical	sattgtgggacac	SATATTG	890
Query	541	ATAGTGT	CCTTGT <i>I</i>	ATCTTCTTGAGAA	ATGTTGTCTTCATTT	AAACTCGGACTCC	GAAAATA 	600
Sbjct	891	Atggtgt	rccttdf	Atcttcttgagaa	AtgttgtcttcAttt	AAActcrGActc	AAAAAA	950
Query	601	TATTC	605					
Sbjct	951	тдттс	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	s:						
Query	7	GACTCGAAAAT	'ATATTCTTTGCTTGT	GAACTTGATTGAGA	AAGTGATGTTGAT	TAGTGTCC	66
Sbjct	1521	GACTCGAAAAT	'ATATTCTTTGTTATT	GAACTTGATTGAGA	AAGTGATGTTAAA	ACTGTCC	1580
Query	67	ATGGCACTTCT	GTCATTTGATTTTCT'	TCTGCACTGGATTC	TTGAAATGAACTG	SCTCTCTT	126
Sbjct	1581	Atgckttct	ŀĠŦĊĀŦŦŦĠĀŦŦŦŦĊŦ	tctgcactggattc	rtgaaatgaactd	schchchh	1640
Query	127	CTGTTGTTAAT	TGAGGTAAGGATTTT	GAATGTTCCGATGT(CTCCTCTTGAGC1	GTTTGCT	186
Sbjct	1641	ctcttcttaat	rtgaggtaaggattt	gaatgttccgatgt	ctcctcttgagct	rgtttgct	1700
Query	187	CTTCTGCACTC	GAACCTGTAAGTAAA	CTATTGGCTGTTGC	AATTGATTGTGGG	SACAGAAA 	246
Sbjct	1701	cttctcckctc	:daacctdtaadtaaa	ctattggctgttgc	AAATGATTGTGGG	SACAGAAA	1760
Query	247	TTGATAGTGTC	CTTGTATCTTCTTGA	GAAATGTTGTCTTC	ATTTAAACTCGG <i>A</i>	ACTCGAAA	306
Sbjct	1761	ttgatagtgtc	cttgtatcttcttga	gaagttttgtcttc	AtttACACtTTGA	ActcGAAA	1820
Query	307	ATATATTCTTT	GCTTGTGAACTTGAT	TGAGAAAGTGATGT'	rgatagtgtccat	GGCACTT	366
Sbjct	1821	ልተልተልተተ ረተተተ	grtartgaacttgat	tgagaaagtgatgt:	taaaactgtccat	rddcactt	1880
Query	367	CTGTCATTTGA	ATTTTCTTCTGCACTG	GATTCTTGAAATGA 	ACTGCTCTCTTCT	GTTGTTA	426

Sbjct	1881	CTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGTTA	1940
Query	427	ATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCAC	486
Sbjct	1941	ATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCAC	2000
Query	487	TCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	546
Sbjct	2001	TCGAACCTGTAAGTAAACTATTGGCTGTTGCAAATGATTGTGGGGACAGAAATTGATAGTG	2060
Query	547	TCCTTGTATCTTCAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATATATTC	605
Shict	2061	+CC++G+A+C++C++GAGAAG++++G+C++CA++++ACAC+C+GAC+CGAAAA+A+A+A+	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	S:						
Query	1	AACTCGGACTC	GAAAATATATTCTTT	GCTTGTGAACTTGA	TTGAGAAAGTGA:	PGTTGATA	60
Sbjct	933	AACTCTGACTC	:GAAAATATGTTCTTT	GCTTGTGAACTTGA	rtgagaaagtga:	rgttgata	992
Query	61	GTGTCCATGGC	ACTTCTGTCATTTGA	TTTTCTTCTGCACT(GGATTCTTGAAA?	rgaactgc 	120
Sbjct	993	ĠŦĠŦĊĊĂŦĠĠĊ	cactrotedecate	######################################	ggytter and see grant and s	rgyyctec	1052
Query	121	TCTCTTCTGTT	GTTAATTGAGGTAAG	GATTTTGAATGTTC	CGATGTCTCCTC'	TTGAGCTG	180
Sbjct	1053	GCTCTTCTGTT	'ĠϮϮልልተተĠልĠĠተልልĠ	ĠĂŦŦŦŦĠĂĂŦĠŦŦĊŒ	cdatdtctctct	rtgagctg	1112
Query	181	TTTGCTCTTCT	GCACTCGAACCTGTA	AGTAAACTATTGGC	rgttgcaattgat 	TTGTGGGA	240
Sbjct	1113	†††dc†c††c†	'ĠĊĀĊŢĊĠĀĀĊĊŢĠŢĀ	AĠTAATĊTATTĠĠT:	rĠttĠĊAAAtĠA:	ŗţĠţĠĠĀ	1172
Query	241	CAGAAATTGAT	'AGTGTCCTTGTATCT 	TCTTGAGAAATGTT(GTCTTCATTTAA <i>I</i> 	ACTCGGAC	300
Sbjct	1173	ĊAĠAAATTĠAT	'AĠTĠTĊĊTTĠTATĊT	TCTTGAGAAGTTTTC	ĠŦĊŦŦĊĀŦŦŦĀCĀ	AĊŢĊŢĠĀĊ	1232
Query	301		TTCTTTGCTTGTGAA				360
Sbjct	1233		.ttctttgtttttAA				1292
Query	361		:ATTTGATTTTCTTCT 				420
Sbjct	1293		'ÀTTTĠÀTTTTĊTTĊT				1352
Query	421		GGTAAGGATTTTGAA. 				480
Sbjct	1353		ĠĠϮĂĂĠĠĂϮϮϮϮĠĂĂ				1412
Query	481		CCTGTAAGTAAACTA 				540
Sbjct	1413		cctctaadtaatcta				1472
Query	541		'GTATCTTCTTGAGAA 				600
Sbjct	1473		ĠŦĂŦĊŦŦĊŦŦĠĀĠĀĀ	GTTŤŤĠŤĊŤŤĊĂŤŤ:	PACĂCTTTĠĂĊŤ(CGAAAATA	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	S :						
Query	2	ACTCGGACTCG	SAAAATATATTCTTTC	CTTGTGAACTTGATT	GAGAAAGTGAT	GTTGATAG	61
Sbjct	1225	ACTCTGACTCG	sAAAATATATTCTTTC	rttrtgaacttgatt	GAGAAAGTGAT	GTTAAAAC	1284
Query	62	TGTCCATGGCA	CTTCTGTCATTTGAT	TTTCTTCTGCACTGG	ATTCTTGAAAT	GAACTGCT	121
Sbjct	1285	TGTCCATGGCA	\chtctgtc\https://	rtttcttctgcgctgg	AttcttcttdtAt	GAACTGCG	1344
Query	122	CTCTTCTGTTC	GTTAATTGAGGTAAGG	ATTTTGAATGTTCCG	ATGTCTCCTCT	TGAGCTGT	181
Sbjct	1345	ctcttctctctc	sttaattgaggtaagd	attttdaatgttcc	ATGTTTCCTCT	TGAGCTGT	1404
Query	182	TTGCTCTTCTC	GCACTCGAACCTGTAA	GTAAACTATTGGCTG	TTGCAATTGAT	TGTGGGAC	241
Sbjct	1405	††dc†c††c†d	scactcgaacctgtaa	dtaarctatteerte	rtgcaaatgat	tgtgggyç	1464

Query	242	AGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACT	301
Sbjct	1465	AGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAGTTTTGTCTTCATTTACACTTTGACT	1524
Query	302	CGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGG	361
Sbjct	1525	cgaaaatatattctttgttattgaacttgattgagaaagtgatgttaaaactgtccatgg	1584
Query	362	CACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGT	421
Sbjct	1585	cactrotedtcattroattrotedtecactegattotteaaaateaactectotetotet	1644
Query	422	TGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTC	481
Sbjct	1645	TGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTC	1704
Query	482	TGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	541
Sbjct	1705	TGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAAATGATTGTGGGACAGAAATTGA	1764
Query	542	TAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATAT	601
Sbjct	1765	TAGTGTCCTTGTATCTTCAGAGAAGTTTTGTCTTCATTTACACTTTGACTCGAAAATAT	1824
Query	602	ATTC 605	
Sbjct	1825	ATTC 1828	

Range 7: 1812 to 2233

Score		E	xpect	Identities	Gaps	Strand	Frame	
680 bits	(368)	0	.0()	405/423(96%)	1/423(0%)	Plus/Plus		
Features	S :							
Query	7	GACTO	CGAAAAT	ATATTCTTTGCTTGT	GAACTTGATTGAGA	AAGTGATGTTGAT	AGTGTCC	66
Sbjct	1812	GACT	CGAAAAT	AtAttctttdrtarto	GAACTTGATTGAGA	AAGTGATGTTAAA	Actitic	1871
Query	67	ATGG(CACTTCT	GTCATTTGATTTTCT	rctgcactggattc	TTGAAATGAACTG	SCTCTCTT	126
Sbjct	1872	ATGG	CACTTCT	GTCATTTGATTTCT:	rctgcactggattc	TTGAAATGAACTG	SCTCTCTT	1931
Query	127	CTGT	rgttaat:	rgaggtaaggatttt	GAATGTTCCGATGT	CTCCTCTTGAGCT	GTTTGCT	186
Sbjct	1932	ctgt:	rgttaat:	rdaddtaaddatttt	SAATGTTCCGATGT	ctcctcttdagct	rgtttgct	1991
Query	187	CTTC	TGCACTC	GAACCTGTAAGTAAA(CTATTGGCTGTTGC	AATTGATTGTGGG	GACAGAAA	246
Sbjct	1992	cttc:	tecycte	GAACCTGTAAGTAAA	ctattggctgttgc	AAATGATTGTGGG	SACAGAAA	2051
Query	247	TTGA:	FAGTGTC	CTTGTATCTTCTTGA(GAAATGTTGTCTTC	ATTTAAACTCGG <i>A</i>	ACTCGAAA	306
Sbjct	2052	TTGA:	ragtgtc	CTTGTATCTTCTTGA	GAAGTTTTGTCTTC	ATTTACACTCTGA	ACTCGAAA	2111
Query	307	ATATA	ATTCTTT(GCTTGTGAACTTGAT	rgagaaagtgatgt 	TGATAGTGTCCAT	GGCACTT	366
Sbjct	2112	ATATA	Attett	GTTATTGAACTTGAT:	rgagaaagtgatgt	tgatagtgtccat	rddcactt	2171
Query	367	CTGT	CATTTGA:	TTTTCTTCTGCACTG(GATTCTTGAAATGA	ACTGCTCTCTTCT	GTTGTTA	426
Sbjct	2172	ctgt	CATTTGA:	ŀ ተተተċተተċተĠċĠċተĠ‹	sattettetaatea	Actdccctcttct	rGTTGT_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	S :						
Query	233	TTGTGGGACAGA	AATTGATAGTGTCCTT	rgtatcttcttgag <i>i</i>	AATGTTGTCTT(CATTTAA	292
Sbjct	1	TTGTGGGACAGA	AATTGGCAGTGTCCT	rGTATCTTCTTGAGA	AAATGTTGTCTTC	CATTTAA	60
Query	293	ACTCGGACTCGA	AAATATATTCTTTGC	TTGTGAACTTGATTG	GAGAAAGTGATGT	TTGATAG	352
Sbjct	61	ACTCGGACTCGA	AAATATATTCTTTGC	rtgtgaacttgattd	SAGAAAGTGATG	rtgatag	120
Query	353	TGTCCATGGCAC	TTCTGTCATTTGATT	TTCTTCTGCACTGG <i>I</i>	ATTCTTGAAATGA	AACTGCT	412
Sbjct	121	tgtccatggcac	trctgtcatttgatt	rtcttctgcactgg	Attrttgaaatga	AACTGCT	180
Query	413	CTCTTCTGTTGT	TAATTGAGGTAAGGAT	TTTGAATGTTCCG <i>I</i>	ATGTCTCCTCTT(SAGCTGT	472

Sbjct	181	${\tt TTCTTCTGTTGATTGAGGTAAGGAGTTTGAAAGTTCCGATGTCTCCTTTGAGCTGT}$	240
Query	473	TTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	532
Sbjct	241	ttgctcttctgcactcgaacctgtaagtaaactattggctgttgcaattgattg	300
Query	533	AGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACT	592
Sbjct	301	AGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATATAAACTCGGACT	360
Query	593	CGAAAATATATTC 605	
Sbjct	361	CGAAATATATTC 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	s:						
Query	2	ACTCGGACTCG	SAAAATATATTCTTT(GCTTGTGAACTTGATT	TGAGAAAGTGAT	GTTGATAG	61
Sbjct	2098	Actctcd	;AAAATATATTCTTT	GTTATTGAACTTGAT	rdadaaadddat	GTTGATAG	2157
Query	62	TGTCCATGGCA	CTTCTGTCATTTGA	TTTTCTTCTGCACTG(GATTCTTGAAAT	GAACTGCT	121
Sbjct	2158	†g†cca†gca	cttctctctcatttca	ttttcttctgcgctg	SATTCTTGTAAT	GAACTGCG	2217
Query	122	CTCTTCTGTTG	TTAATT 138				
Sbjct	2218	ctcttctgttc	T-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		
Feature	s:						
Query	524	TTGTGGGACAGA	AATTGATAGTG	TCCTTGTATCTTCT	TGAGAAATGTTGTC	TTCATTTAA	583
Sbjct	1	ttgtgggacaga	AATTGGCAGTG	;tccttgtAtcttct;	rgagaaargttgtc	ttcatttaa	60
Query	584	ACTCGGACTCGA	AAATATATTC	605			
Sbjct	61	ACTCGGACTCGA	AAATATATTC	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	ACTCGGACTCG	GAAAATATATTCTTT	GCTTGTGAACTTGAT	TGAGAAAGTGATG	STTGATAG	61
Sbjct	2858	ACTCTGACTC	;AAAATATATTCTTT	GTTTTTGAACTTGAT	rtdadcagdtdatd	STTGATAG	2799
Query	62	TGTCCATGGC	CTTCTGTCATTTGA	TTTTCTTCTGCACTG	GATTCTTGAAATG	SAACTGCT	121
Sbjct	2798	AGTCCACGGCI	ccttctgtcatttga	rtttcttctgcactz	dattettgaaate	SAAATGCT	2739
Query	122	CTCTTCTGTTC	GTTAATTGAGGTAAG	GATTTTGAATGTTCC	GATGTCTCCTCTT	GAGCTGT	181
Sbjct	2738	$\tau\tau$	sttaattgaggtaaa	GATTTTGAAAGTTC1	rgytetaptar	rGATTTGT	2679
Query	182	TTGCTCTTCTC	GCACTCGAACCTGTA	AGTAAACTATTGGCT	GTTGCAATTGATT	GTGGGAC	241
Sbjct	2678	ttgatcttcg	saactcaaatctgta	AGTAGACTATTTGT	rattgrtattgatt	rgaga-	2622
Query	242	AGAAATTGATA	GTGTCCTTGTATCT	rcttgagaaatgtte 	TCTTCATTTAAAC	CTCGGACT	301
Sbjct	2621	ÁĠŤCĠÁCŹ	schick de la	rctagagaagtrttd	stcttcatttacad	ctctgact	2565
Query	302	CGAAAATATAT	TCTTTG-CTTGTGA	ACTTGATTGAGAAAG	GTGATGTTGATAGT	TGTCCATG	360
Sbjct	2564	ccaaaaatataa	\tgttdgrctt-tgA	Acttgattgaggg	stgaagttgataga	AGTCCACG	2506

Query	361	GCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTG	420
Sbjct	2505	GCTCTTCTGTCATTTGAATTTGTTCTGCACTAGATTCTTGAAATGAAATGCTTTCTTCTG	2446
Query	421	TTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTT	480
Sbjct	2445	TTGTTAATTGAGGTAAAGATTTTGAAAGTTCTGATGTTTCCTCTTGATTTGTTTG	2386
Query	481	CTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	540
Sbjct	2385	CGGAACTCAAATCTGTAAGTAGACTATTTGTTATTGTTATTGATTG	2332
Query	541	ATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGAAAATA	600
Sbjct	2331	ACAGTGTCCTTGTATCCTCTAGAGAAGTTTTGTCTTCATTTACACTCTGACTCGAAAATA	2272
Query	601	TA 602	
Sbict	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		
Feature	s:						
Query	2	ACTCGGACTC	GAAAATATATTCTTTC	G-CTTGTGAACTTGA	TTGAGAAAGTGAT	GTTGATA	60
Sbjct	3143	ACTCTGACTC	GAAAATATAATGTTTC	STCTT-TGAACTTGA	TTGAGGAGGTGAA	GTTGATA	3085
Query	61	GTGTCCATGG(CACTTCTGTCATTTGA	ATTTTCTTCTGCACT	GGATTCTTGAAAT	GAACTGC	120
Sbjct	3084	dadtccacdd	cretteteteattte	Atttgttctgcact	adattcttdaaat	GAAATGC	3025
Query	121	TCTCTTCTGT	rgttaattgaggtaac	GATTTTGAATGTTC	CGATGTCTCCTCT	TGAGCTG	180
Sbjct	3024	ተተተረተተረተ	rgttaattgaggtaad	sgaatttgaaagttc	тĠѦϮĠϮͲϮĊĊϮĊϮ	тфатттф	2965
Query	181	TTTGCTCTTC	FGCACTCGAACCTGT <i>A</i>	AAGTAAACTATTGGC	TGTTGCAATTGAT	TGTGGGA 	240
Sbjct	2964	†††da†c††c	rdcactcaattctgta	Adgagactattgt	tattgttattgat	ТĠ	2910
Query	241	CAGAAATTGA:	FAGTGTCCTTGTATCT	TTCTTGAGAAATGTT	GTCTTCATTTAAA	CTCGGAC	300
Sbjct	2909	-AĠAAGTCAA	cagtgtccttgtatcc	ctctagagaagtttt	ĠŦĊŦŦĊĀŦŦŦĀCĀ	ĊŢĊŢĠĂĊ	2851
Query	301	TCGAAAATATA 	ATTCTTTGCTTGTGA <i>P</i> 	ACTTGATTGAGAAAG 	TGATGTTGATAGT	GTCCATG	360
Sbjct	2850	TĊĠAAAATATA	\trctttgrttrtga#	ACTTGATTGAGCAGG	rgatgttgataga	ĠŦĊĊĀĊĠ	2791
Query	361	GCACTTCTGT(CATTTGATTTTCTTCT 	GCACTGGATTCTTG	AAATGAACTGCTC	TCTTCTG	420
Sbjct	2790		ĊĂŢŢŢĠĂŢŢŢŢĊŢŢĊŢ				2731
Query	421		AGGTAAGGATTTTGA <i>A</i> 				480
Sbjct	2730		ÅĠĠϮÄÄAĠĂϮϮϮϮĠĂÄ				2671
Query	481	CTGCACTCGAZ	ACCTGTAAGTAAACT <i>A</i> 	$\Delta TTGGCTGTTGCAAT \ \ \ \ \ \ \ \ \ \ \ \ \ $	TGATTGTGGGACA	GAAATTG 	540
Sbjct	2670		\TCTGTAAGTAGACTA				2617
Query	541	ATAGTGTCCTT		$\Delta ATGTTGTCTTCATT oxed{ }$	TAAACTCGGACTC	GAAAATA 	600
Sbjct	2616		ŗĠŦÀŦĊĊŦĊŦAĠĀĠĀ <i>Ŕ</i>	AGŤTŤŤĠŤĊŤŤĊÁŤŤ	TÁCÁCTCTGÁCTC	ĠÀÀÀÀTÀ	2557
Query	601	TA 602					
Sbjct	2556	тА 2555					

Drosophila simulans GD17263 (Dsim\GD17263), mRNA

Sequence ID: **ref|XM_002105681.1|** Length: 2988 Number of Matches: 14 Range 1: 2193 to 2754

	Expect	Identities	Gaps	Strand	Frame	
95)	3e-151()	500/594(84%)	34/594(5%)	Plus/Minus		
2	ACTCGGACTCG	AAAATATATTCTT	-TGCTTGTGAACTTG	ATTGAGAAAGTGA	TGTTGAT	59
2754	ACTCGGACTCG	SAAAATATATTATTCO	STG-TT-TGAACTTA	ATTGAAAAAGTGA	TGTTGAT	2697
50	AGTGTCCATGG	CACTTCTGTCATTT	SATTTTCTTCTGCAC	TGGATTCTTGAAA	TGAACTG	119
2	754	3e-151() ACTCGGACTCG	ACTCGGACTCGAAAATATATTCTT	ACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTG	ACTCGGACTCGAAAATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGA	ACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGAT

Sbjct	2696	ATTGTCCATGGCACTTCTGTAATTGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTG	2637
Query	120	CTCTCTTCTGTTGATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCT	179
Sbjct	2636	CTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCCTCTTGCTTT	2577
Query	180	GTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	239
Sbjct	2576	GTTTGATCTTCTGCACTCAAATCTGTAAGTAAACTATTTGTTGTTGTTTTTTGATTG	2521
Query	240	ACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGA	299
Sbjct	2520	AGAAATTGATACCGTCCTTGTATCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGA	2463
Query	300	CTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCAT	359
Sbjct	2462	CTCT-GACT-CTT-TGTT-CTTGAA-CTTGATTGTGTCCAA	2427
Query	360	GGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCT	419
Sbjct	2426	GGCACTTCTGTCATTTGATTTTCCTCTGCACTGGATTCTTGAAATGAACTGCTTTCTTCT	2367
Query	420	GTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCT	479
Sbjct	2366	GTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCCTCTCGAATTGTTTGATCT	2307
Query	480	TCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	539
Sbjct	2306	TCTGCACTCGAATATGTAAGTAAACTATGTGCTGCTGTACTTGATTGTGGGAAGGAA	2247
Query	540	GATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTC 593	
Sbjct	2246	GATAGTGTCCTTGTGTCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGACTC 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	s:					
Query	88	TTTCTTCTGCA	ACTG-GA-TTCTTGA	AATGAACTGCTCTCT	TCTGTTGTTAATT	GAGGTAA 145
Sbjct	2959	†††¢††¢†G	-TTGTGAGTTCTTGA	AATGAACTTATTTC1	cctcttgtagatt	GAGGTAG 2902
Query	146	GGATTTTGAAT	GTTCCGATGTCTCC	CTTGAGCTGTTTGC	TCTTCTGCACTCG	BAACCTGT 205
Sbjct	2901	agcttttgaaz	\drtderdatdteter:	tcttgaartgtatgd	chchhchdchchrd	SAAACTGT 2842
Query	206	AAGTAAACTAT	TTGGCTGTTGCAATT	GATTGTGGGACAGAA	ATTGATAGTGTCC	TTGTATC 265
Sbjct	2841	AAGTAAACTA1	rtrdctdttdtActt	SATTGTGAGAAAGAA	ırttgatagtgtcc	र्मिर्पर्वेपर्वे २७८२
Query	266	TTCTTGAGAA	ATGTTGTCTTCATTT	AAACTCGGACTCGAA	AATATATTCTT	TGCTTGT 323
Sbjct	2781	ttcttgagaaa	Atgttgtcttcattt	ACACTCGGACTCGAA	AATATATTATTCG	std-tt-t 2724
Query	324	GAACTTGATTC	GAGAAAGTGATGTTGA	ATAGTGTCCATGGCA	CTTCTGTCATTTG	ATTTTCT 383
Sbjct	2723	daacttaattd	saaaaagtgatgttg	AtArtGtccAtGGcA	cttctctgtaattgc	र्भितर्मित्रे २६६४
Query	384	TCTGCACTGG <i>A</i>	ATTCTTGAAATGAAC	rgctctcttctgttg	TTAATTGAGGTAA	GGATTTT 443
Sbjct	2663	tccccacactcc	Attettegaateaae	ŀĠĊŦŦŦĊŦŦĊŦĠŦŦĊ	rthaattgaggtaa	agatttt 2604
Query	444	GAATGTTCCGA	ATGTCTCCTCTTGAG(CTGTTTGCTCTTCTC	CACTCGAACCTGT	AAGTAAA 503
Sbjct	2603	GAAAGTTCCGA	vtgtitcctcttgci.	rtgtttgatcttct	cactcaaatctgt	'AAGTAAA 2544
Query	504	CTATTGGCTGT	TTGCAATTGATTGTG(GGACAGAAATTGATA	GTGTCCTTGTATC	TTCTTGA 563
Sbjct	2543	ctattrertet	rtgrrrttgattg	AGAAATTGATA	ccetecttetate	ttcttdA 2490
Query	564	GAAATGTTGTC	CTTCATTTAAACTCG	GACTC 593		
Sbjct	2489	gargtrttgtd	cttcatttacactcro	GACTC 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	S :						
Query	7	GACTCGAAAATA	TATTCTTTGCTTG	TGAACTTGATTGAG	AAAGTGATGTTGAT	AGTGT	64
Sbjct	604	GACTCGAAAATA	ATATTATTCGTG-TT-	tgaacttaattgaa	AAAGTGATGTTGAT	ATTGT	547

Query	65	CCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTC	124
Sbjct	546	CCATGGCACTTCTGTAATTGGATTTTCTTCCGCACTGGATTCTTGGAATGAACTGCTTTC	487
Query	125	TTCTGTTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTG	184
Sbjct	486	TTCTGTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGTTGTTTCCTCTTGCTTTGTTTG	427
Query	185	CTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	244
Sbjct	426	ATCTTCTGCACTCAAATCGGTAAGTAAACTATTTGTTGTTGTTCTTGATTGAGA	373
Query	245	AATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTCGA	304
Sbjct	372	AATTGATACCGTCCTTGTATCTTCTTGAGATGTTTTGTCTTCATTTACACTCTGACTC	315
Query	305	AAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGTGATGTTGATAGTGTCCATGGCAC	364
Sbjct	314		277
Query	365	TTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT	424
Sbjct	276	TTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATGAACTGCTTTCTTCTTGTTGT	217
Query	425	TAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGC	484
Sbjct	216	TAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCCTCGAATTGTTTGATCTTCTGC	157
Query	485	ACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATTG	544
Sbjct	156	ACTCGAATATGTAAGTAAACTATGTGCTGCTGCTTACTTGATTGTGGGAAGGAA	97
Query	545	TGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAACTCGGACTC 593	
Sbjct	96	tgtccttgtgtcttcttgagargtrttgtcttcatttacactctgactc 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	s:						
Query	104	TTCTTGAAATG	AACTGCTCTCTTCT	GTTGTTAATTGAGGT	PAAGGATTTTGAAT	GTTCCGA	163
Sbjct	2091	ttcttgaaatd	AACTTTTTCTCCT	cttgtagattgaggt	ragadcttttdaac	GTTCTGA	2032
Query	164	TGTCTCCTCTT	GAGCTGTTTGCTCT	rctgcactcgaacct	GTAAGTAAACTAT	TGGCTGT	223
Sbjct	2031	td t d	'daartdtatdctct'	rctgcactrgaaact	rgtaagtaaactat	ттĠĊтĠт	1972
Query	224	TGCAATTGATT	GTGGGACAGAAATT(GATAGTGTCCTTGTA	TCTTCTTGAGAAA	TGTTGTC	283
Sbjct	1971	trracttgatt	rgtgggaaggaagtt	ĠAŦĀĠŦĠŦĊĊŦŦĠŦĀ	\rchtchtgagaaa	ተĠተተĠተĊ	1912
Query	284	TTCATTTAAAC	TCGGACTCGAAAAT 	ATATTCTTTGCTT 	GTGAACTTGATTG	AGAAAGT	341
Sbjct	1911	††ca†††acac	trcccakatatr	ATATTATTCGTG-T1	r–tgaacttaattg	AAAAAGT	1854
Query	342	GATGTTGATAG	TGTCCATGGCACTT(CTGTCATTTGATTTT 	CTTCTGCACTGGA	TTCTTGA	401
Sbjct	1853	ĠĀŢĠŢŢĠĀŢĀĠ	stĠtĊĊAAĠĠĊAĊtt	ĊŢĠŢĸĀŢĸĠĠĀŢŢŢ	rcttcccccactcc	ttcttg	1794
Query	402	AATGAACTGCT	CTCTTCTGTTGTTA?	ATTGAGGTAAGGATT 	TTGAATGTTCCGA	TGTCTCC	461
Sbjct	1793	AATĠAAĊTĠĊŢ	rrtcttctctcttat	AttĠAĠĠtAAAĠAtt	rttgaaagttccga	tgtttcc	1734
Query	462	TCTTGAGCTGT	TTGCTCTTCTGCACT	ICGAACCTGTAAGTA 	AACTATTGGCTGT 	TGCAATT	521
Sbjct	1733	†¢††ĠCTT†Ġ†	'TTGATCTTCTGCAC'	rcaaarctgtaagta	\AACTATTGTTGT	TGTTTTT	1674
Query	522	GATTGTGGGAC	CAGAAATTGATAGTG' 	ICCTTGTATCTTCTT 	GAGAAATGTTGTC 	TTCATTT	581
Sbjct	1673		-ÀĠÀÀÀTCĠÀTÀCCĠ	rccttgtatcttct	ŗĠĀĠĀŢĠŤŢŤŤĠŤĊ	ŤŤĊÁŤŤŤ	1620
Query	582	AAACTCGGACT					
Sbjct	1619	ACACTCTGACT	rĊ 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	3:						
Query	104	TTCTTGAAATG	GAACTGCTCTCTTCTC	TTGTTAATTGAGGT	AAGGATTTTGAATC	GTTCCGA 1	L63

Sbjct	1509	TTCTTGAAATGAACTTATTTCTCCTCTTGTAGATTGAGGTAGAGCTTTTGAAAGTTCTGA	1450
Query	164	TGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAA	223
Sbjct	1449	TGTCTCTCTCGAATTGTATGCTCTTCTGCACTTGAAACTGTAAGTAA	1390
Query	224	TGCAATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTC	283
Sbjct	1389	TGTACTTGATTGTGGGAAAGAAGTTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTC	1330
Query	284	TTCATTTAAACTCGGACTCGAAAATATATTCTTTGCTTGTGAACTTGATTGAGAAAGT	341
Sbjct	1329	ttcatttacactcggactcgaaaatatattattcgtg-tt-tgaacttaattgaaaaagt	1272
Query	342	GATGTTGATAGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGA	401
Sbjct	1271	GATGTTGATAGTGTCCATGGCACTTCTGTAATTGGATTTTCTTCCGCACTGGATTCTTGG	1212
Query	402	AATGAACTGCTCTCTTCTGTTGATTGAGTTAAGGATTTTGAATGTTCCGATGTCTCC	461
Sbjct	1211	AATGAACTGCTTTCTTCTGTTGTTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCC	1152
Query	462	TCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAA	521
Sbjct	1151	tcttgctttgtttgatcttctgcactcaaatctgtaagtaa	1092
Query	522	GATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGT-CTTCATT	580
Sbjct	1091	GATTGAGAAATCAAAACTGCCCTTGTATCTTCTTGAGAAGTTTTGTTCTT-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	
Feature	s:					
Query	2	ACTCGGACTC	GAAAATATATTCTT	-TGCTTGTGAACTT(GATTGAGAAAGTGA'	TGTTGAT 59
Sbjct	1902	ACTCGGACTC	GAAAATATATTATTCO	GTG-TT-TGAACTT	AATTGAAAAAGTGA'	TGTTGAT 1845
Query	60	AGTGTCCATGO	GCACTTCTGTCATTT(GATTTTCTTCTGCA(CTGGATTCTTGAAA'	TGAACTG 119
Sbjct	1844	AGTGTCCAAG	scacttctgtaatago	gattttcttccccc	ctggattcttggaa	rgaactg 1785
Query	120	CTCTCTTCTGT	TTGTTAATTGAGGTA <i>I</i>	AGGATTTTGAATGT7	CCGATGTCTCCTC'	TTGAGCT 179
Sbjct	1784	ctrtcttctg	rtgttaattgaggtaz	Aagatttttgaaagtt	rccgatgtrtcctc	rtgctt 1725
Query	180	GTTTGCTCTTC	CTGCACTCGAACCTGT	TAAGTAAACTATTGO	GCTGTTGCAATTGA'	TTGTGGG 239
Sbjct	1724	ĠŦŦŦĠAŦĊŦŦĊ	ctdcactcaaatctd	taagtaaactattc	srtgttgrrrttga	rtg 1669
Query	240	ACAGAAATTGA	ATAGTGTCCTTGTAT(CTTCTTGAGAAATGT	TTGTCTTCATTTAA	ACTCGGA 299
Sbjct	1668	AGAAATCGA	Ataccetecteetate	cttcttgagargtr	rtgtcttcatttac	ActcrdA 1611
Query	300	CTC-GAAAATA	ATATTCTTTG-CTTG-	-TGAACTTGATTG- <i>I</i>	A-GAAAGTGATGTT(GATAGT- 353
Sbjct	1610	ctctgactct1	rtgttċttgaaċttĠ	ATTGTGTCCATGGC <i>I</i>	ACTTCTGTCAT-TT	GATTTTC 1552
Query	354	GTCCA-TGC	GCACTTCTGTCATTT(G-ATTTTCTTCTGC <i>I</i> 	ACTGGATTCTTGAA	ATGAACT 409
Sbjct	1551	TTCTGCACTGC	G-A-TTCT-TGAAAT(ĠAACϮϮϮĊϮϮͲϮĠͲႤ	rG†ĠTG††Ċ††ĠÀÀ	ÁTGÁÁCT 1495
Query	410	GCTCTCTTCTC	GTTGTTAATTGAGGTA	AAGGATTTTGAATGT 	TTCCGATGTCTCCT(CTTGAGC 469
Sbjct	1494	татттстсстс	CTTGTAGATTGAGGT	AGAĠCϮϮϮϮĠAAAĠſ	rtcrgatgtctctt	ĊĊCĠĀAT 1435
Query	470		CTGCACTCGAACCT(
Sbjct	1434	†g†a†g¢†¢††	rctgcactrgaaactc	STAAGTAAACTATT1	rĠĊŦĠŦŦĠŦĀCŦŦĠ	
Query	530	GACAGAAATTO	GATAGTGTCCTTGTAT	rcttcttgagaaat(GTTGTCTTCATTTA 	
Sbjct	1374	ĠÀAÀĠÀÅGŤŤĊ	SATAGTGTCCTTGTAT	tcttcttdagaaatc	Strgtcttcktrk(CÁCTCGG 1315
Query	590	ACTCGAAAATA				
Sbjct	1314	ActcGAAAAtz	ATATT 1300			

Range 7: 1882 to 2440

464 bits	(251)	9e-127()	463/564(82%)	19/564(3%)	Plus/Minus	
Features	s:					
Query	55	TTGATAGTGTC	CATGGCACTTCTGTC	ATTTGATTTTCTTC	TGCACTGGATTCTTGAAATG	114
Sbjct	2440	TTGATTGTGTC	CAAGGCACTTCTGTC	ATTTGATTTTCCTC	TGCACTGGATTCTTGAAATG	2381
Query	115	AACTGCTCTCT	TCTGTTGTTAATTGA	GGTAAGGATTTTGA	ATGTTCCGATGTCTCCTCTI	174
Sbjct	2380	AACTGCTTTCT	rtctgttgttaattga	.ddtaaadatttdaa	AAGTTCCGATGTTTCCTCTC	2321
Query	175	GAGCTGTTTGC	TCTTCTGCACTCGAA	CCTGTAAGTAAACT	ATTGGCTGTTGCAATTGATT	234
Sbjct	2320	ĠĀĀŢĠŢŢĠĀ	tcttctcckk	ratgtaagtaaact	Atgrectecteractteatt	2261
Query	235	GTGGGACAGAA	ATTGATAGTGTCCTT	GTATCTTCTTGAGA	AATGTTGTCTTCATTTAAAC 	294
Sbjct	2260	ĠŦĠĠĠĀAGĠĀĀ	ſĠŢŢĠŖŢŖĠŢĠŢĠŢĠŢ	ĠŦĠŦĊŦŦĊŦŦĠĀĠĀſ	rgttttgtcttcatttacac	2201
Query	295				ATTG-A-GAAAGTGATGTTG 	
Sbjct	2200	TĊTĠAĊTĊTĠA	\CTCTTTGTTĊTT-ĠA	ATTTĠATTGTĠTCC	ÅTGĠCÄCTTCTĠTCÄT-TTĠ	
Query	349				CTTCTGCACTGGATTCTTG	
Sbjct	2142	ATTTTCTTCTG	GCACTGG-A-TTCT-T	'GÀAATĠAÀCTGCTT'	†Ċ††T†ĠTTG†ĠTG††Ċ††Ġ	
Query	401	AAATGAACTGC	TCTCTTCTGTTGTTA	ATTGAGGTAAGGAT' 	ITTGAATGTTCCGATGTCTC 	
Sbjct	2085	ÄÄÄTĠÄÄĊŤTT	'TTTĊTCĊTCTTĠTAG	ATTĠAĠĠTAGAĠCT'	ŗŗŗĠĄĄCĠŢŢĊŢĠĄŢĠŢĊŢĊ	
Query	461	CTCTTGAGCTG	TTTGCTCTTCTGCAC;	TCGAACCTGTAAGTA	AAACTATTGGCTGTTGCAAT 	
Sbjct	2025	ттсттсалтс	;TATĠĊTĊTTĊTĠĊAĊ	rtrgaaactgtaagt	AAACTATTTGCTGTTTTACT	
Query	521	TGATTGTGGGA	CAGAAATTGATAGTG	TCCTTGTATCTTCT"	IGAGAAATGTTGTCTTCATI 	
Sbjct	1965	†gattgtggga	AGGAAGTTGATAGTG	rtccttgtatcttct	rgagaaatgrrgrctrcart	1906
Query	581	TAAACTCGGAC	TCGAAAATATATT	604		
Sbjct	1905	TÁCÁCTCGGÁC	ctcchhahatatatt	1882		

Range 8: 315 to 712

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
453 bits	(245)	2e-123()	354/406(87%)	10/406(2%)	Plus/Minus		
Features	s:						
Query	190	CTGCACTCGAAC	CTGTAAGTAAACTA	TTGGCTGTTGCAATT	: GATTGTGGGACAG	AAATTG	249
Sbjct	712	CTGCACTCGAAT	atgtaagtaaacta	ttrectetteracti	GATTGTGGGAAAG	AAGTTG	653
Query	250	ATAGTGTCCTTG	TATCTTCTTGAGAA	ATGTTGTCTTCATTT	AAACTCGGACTCG	AAAATA	309
Sbjct	652	ATAGTGTCCTTG	TATCTTCTTGAGAA	ATGTTGTCTTCATT	rACAGTCTGACTCG	AAAATA	593
Query	310	TATTCTTTGC	TTGTGAACTTGATT	GAGAAAGTGATGTTG	ATAGTGTCCATGG	CACTTC	367
Sbjct	592	tattattcgtg-	tt-tgaacttaatt	GAAAAAGTGATGTT	atarteteeatee	cacttc	535
Query	368	TGTCATTTGATT	TTCTTCTGCACTGG	ATTCTTGAAATGAAC	CTGCTCTCTTCTGT	TGTTAA	427
Sbjct	534	tgtaattggatt	ttcttcccccactcc	Attcttggaatgaac	ctdctrtcttctdt	tgttaa	475
Query	428	TTGAGGTAAGGA	TTTTGAATGTTCCG	ATGTCTCCTCTTGAG	CTGTTTGCTCTTC	TGCACT	487
Sbjct	474	ttgaggtaaaga	ttttgaaagttccg	ττͼϮττϲϲτϲττͼϲτ	rtdttdatcttc	tgcact	415
Query	488	CGAACCTGTAAG	TAAACTATTGGCTG	TTGCAATTGATTGTG	GGACAGAAATTGA	TAGTGT	547
Sbjct	414	CAAATCGGTAAG	taaactatttgttg	ttgttcttgattg	AGAAATTGA	taccgt	361
Query	548	CCTTGTATCTTC	TTGAGAAATGTTGT	CTTCATTTAAACTCG	GACTC 593		
Sbjct	360	ccttgtatcttc	ttgagargtrttgt	cttcatttacactci	GACTC 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	S :					
Query	55	TTGATAGTGTCC	ATGGCACTTCTGTC	ATTTGATTTTCTTCT	GCACTGGATTCT	GAAATG 114

Sbjct	295	TTGATTGTGTCCATGGCACTTCTGTCATTTGATTTTCTTCTGCACTGGATTCTTGAAATG	236
Query	115	AACTGCTCTCTTCTGTTAATTGAGGTAAGGATTTTGAATGTTCCGATGTCTCCTCTT	174
Sbjct	235	AACTGCTTTCTTCTGTTGATTAATTGAGGTAAAGATTTTGAAAGTTCCGATGTTTCCTCTC	176
Query	175	GAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAAACTATTGGCTGTTGCAATTGATT	234
Sbjct	175	GAATTGTTTGATCTTCTGCACTCGAATATGTAAGTAAACTATGTGCTGCTGTACTTGATT	116
Query	235	GTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTCATTTAAAC	294
Sbjct	115	GTGGGAAGGAAGTTGATAGTGTCCTTGTGTCTTCTTGAGATGTTTTGTCTTCATTTACAC	56
Query	295	TCGGACTC 302	
Shict	55	ተረሞሬልረተረ 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	s:						
Query	2	ACTCGGACTC	CGAAAATATATTCTT-	-TGCTTGTGAACTT(GATTGAGAAAGTGA	TGTTGAT	59
Sbjct	1320	ACTCGGACTC	CGAAAATATATTATTC	GTG-TT-TGAACTT	aattgaaaaagtga	ATGTTGAT	1263
Query	60	AGTGTCCATC	GCACTTCTGTCATTT	GATTTTCTTCTGCAC	CTGGATTCTTGAAA	TGAACTG	119
Sbjct	1262	AGTGTCCATO	scacttctctaattg	GATTTTCTTCCGCA	ctggattcttggaz	rgaactg	1203
Query	120	CTCTCTTCTC	GTTGTTAATTGAGGTA	AGGATTTTGAATGT	CCGATGTCTCCTC	CTTGAGCT	179
Sbjct	1202	ctrtcttctc	strgttaattgaggta	AAGATTTTGAAAGT	rccgatgtrtcctd	cttgcttt	1143
Query	180	GTTTGCTCTT	CTGCACTCGAACCTG	TAAGTAAACTATTG(GCTGTTGCAATTG <i>A</i>	TTGTGGG	239
Sbjct	1142	gtttgatctt	cctdcactcaaatctd	taagtaaactattro	Ġ┰ϮĠϮϮĠ┰┰┰ϮϮĠ₽	лтф	1087
Query	240	ACAGAAATTG	ATAGTGTCCTTGTAT	CTTCTTGAGAAATG	TTGT-CTTCATTT <i>F</i>	291	
Sbjct	1086	AGAAATCA	AAACTGCCCTTGTAT	ĊŦŦĊŦŦĠĀĠĀĀĠŦŦŢ	ŀ ተĠተτĊተተ–ልተተተ <i>ጾ</i>	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	TTTCTTCTGC	ACTG-GA-TTCTTGA	AATGAACTGCTCTC	TTCTGTTGTTA	TTGAGGTAA	436
Sbjct	2959	TTTCTTCTG-	-TTGTGAGTTCTTGA	AATGAACTTATTTC	tcctcttgtag	TTGAGGTAG	2902
Query	437	GGATTTTGAA'	TGTTCCGATGTCTCC'	POTTGAGCTGTTTG	CTCTTCTGCACT	CGAACCTGT	496
Sbjct	2901	AGCTTTTGAA	AGTTCTGATGTCTCT'	rcttgaartgtatg	ctcttctgcact	TGAAACTGT	2842
Query	497	AAGTAAACTA'	TTGGCTGTTGCAATT	GATTGTGGGACAGA	AATTGATAGTGT	CCTTGTATC	556
Sbjct	2841	AAGTAAACTA	ttrgctgttgtactt	GATTGTGAGAAAGA	Arttgatagtgt	ccttgtatc	2782
Query	557	TTCTTGAGAA	ATGTTGTCTTCATTT	AAACTCGGACTCGA	AAATATATT 6	504	
Sbjct	2781	ttcttgagaa.	AtgttgtcttcAttt	Acactcggactcga	AAATATATT 2	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		
Feature	s:						
Query	481	CTGCACTCGA	ACCTGTAAGTAAACTA	\TTGGCTGTTGCAAT	TGATTGTGGGACA	GAAATTG	540
Sbjct	712	CTGCACTCGA	ATATGTAAGTAAACTA	ATTGCTGTTGTACT	TGATTGTGGGAAA	GAAGTTG	653
Query	541	ATAGTGTCCT	rgtatcttcttgaga <i>r</i>	ATGTTGTCTTCATT	TAAACTCGGACTC	GAAAATA	600
Sbjct	652	ATAGTGTCCT	tgtatcttcttgagaz	አልተ <mark></mark> Ġተተ <mark></mark> Ġተ <mark></mark> ĊተተĊልተተ	rtacagtergaete	GAAAATA	593
Query	601	TATT 604					

Range 13: 2095 to 2173

Score		Expect	Identities		Gaps	Strand	Frame	
130 bits	(70)	4e-26()	76/79(96%	6)	0/79(0%)	Plus/Minus		
Features	S:							
Query	55	TTGATAGTGTC	CATGGCACT	TCTGTCA	TTTGATTTTC	CTTCTGCACTGGATT	CTTGAAATG	114
Sbjct	2173	ttgattgtgtc	CATGGCACT	4646464	·tttGAttttd	cttctgcactggatt	CTTGAAATG	2114
Query	115	AACTGCTCTCT	TCTGTTGT	133				
Sbjct	2113	AACTGCTTTCT	TTTGTTGT	2095				

Range 14: 1513 to 1588

Score		Expect	Identities	Gap	S	Strand	Frame	
115 bits(62)		1e-21()	74/79(94%	(a) 3/79	(3%)	Plus/Minus		
Feature	s:							
Query	55	TTGATAGTGT	CCATGGCACT	TCTGTCATTTG	ATTTTCT'	TCTGCACTGGAT	TCTTGAAATG	114
Sbjct	1588	ttgattgtgt	ccatggcact	tctgtcattg	ልተተተተ <mark>ረ</mark> ተי	rctgcactggat	TCTTGAAATG	1529
Query	115	AACTGCTCTC	ТТСТСТТСТ	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	
Feature	s:					
Query	7	GACTCGAAAATA	TATTCTTTGCTTG	TGAACTTGATTGAC	GAAAGTGATGTTGA	ATAGTGT 64
Sbjct	682	GACTTG-AAA-A	tattettteagrite	rtgracttgatggaz	AGAAGCTTTGTTGA	tAGTGT 625
Query	65	CCATGGCACTTC	TGTCATTTGATTTTC	TTCTGCACTGGATT	CTTGAAATGAACT	GCTCTC 124
Sbjct	624	ccatggcacttc	tgtcatttgatttc	ttctrcactggat	rctttaagtgaact	rdctrtc 565
Query	125	TTCTGTTGTTAA	TTGAGGTAA-GGATT	TTGAATGTTCCGAT	rgtctcctcttgac	CTGTTT 183
Sbjct	564	ttctctttctaga	ttgaggtaaaggagt	rtaadda-ttccgri	ŀĠϮͲϮĊĊϮĊϮϮͲĂ₽	ATTGTTT 506
Query	184	GCTCTTCTGCAC	TCGAACCTGTAAGTA	AACTATTGGCTGTT	rgcaartgattgte	GGACAG 243
Sbjct	505	ĠatċttċtĠċaċ	tcgaaactgtgggaa	AACTATTTGCCATT	tgracttgattgaz	AATTÅG 446
Query	244	AAATTGATAGTG	TCCTTGTATCTTCTT 	GAGAAATGTTGTCT	TTCATTTAAACTCG	GACTCG 303
Sbjct	445	ATATCGATAGTG	tccttgtatcttctt	cagargtretatet	rtcatctacactri	rgactrd 386
Query	304	AAAATATATTCT 	$\mathtt{TTGCTTGTGAACTTG}$	GATTGAGAAAGTGAT 	rgttgatagtgtcc 	CATGGCA 363
Sbjct	385	AAAATATACTTT	CAGTTTGTGTACTTG	SATTGAGGAAGCTTT	tĠttĠAtAĠtĠtĊĊ	cÁtĠĠĊC 326
Query	364	CTTCTGTCATTT	GATTTTCTTCTGCAC 	TGGATTCTTGAAAT	rgaactgetetett 	CTGTTG 423
Sbjct	325	ĊŢŢĊŢĠŢĊĀŢŢŢ	ĠĂŢŢŢŢĊŢŢĊŢŢĊĀĊ	rtggattcttgaaar	rgaactgetttett	टर्टर्मर्द्धर्मर्पे 266
Query	424	TTAATTGAGGTA	A-GGATTTTGAATGT 	TCCGATGTCTCCTC	CTTGAGCTGTTTGC	TCTTCT 482
Sbjct	265	†GGÁ††GÁGG†Á	AAGGATTTAAAAA-1	rtcccrtctrtcctc	ĊŦŦĠĂAŦŦĠŦŦŦĠ₽	ATTTCT 207
Query	483	GCACTCGAACCT	GTAAGTAAACTATTG 	GCTGTTGCAATTG <i>I</i>	ATTGTGGGACAGAA 	ATTGAT 542
Sbjct	206	ĠĊĀĊŦĊĠĠĀĀĊĀ	gtaggtaaactatti	rdccattdtacttda	Attgaaaaggagat	rAtcGAt 147
Query	543	AGTGTCCTTGTA	TCTTCTTGAGAAATG	TTGTCTTCATTTA <i>I</i>	AACTCGGACTCGAA	AATAT 601
Sbjct	146	AGTGTCCTTGTA	tcttcttcagatgtt	ctatctttattac	cactttgacttgaa	AAATAT 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	s:						
Query	7	GACTCGAAAAT	'ATATTCTTTGCTTG	TGAACTTGATTGAGA	AAGTGATGTTGATA	GTGTCC	66
Sbjct	391	GACTTGAAAAT	'ATACTTTCAGTTTG	tgracttgattgagg	AAGCTTTGTTGATA	gtgtcc	332
Query	67	ATGGCACTTCT	GTCATTTGATTTTC	TTCTGCACTGGATTC	TTGAAATGAACTGC	TCTCTT	126
Sbjct	331	ATGGCCCTTCT	ĠŦĊĀŦŦŦĠĀŦŦŦĊ	TTCTTCACTGGATTC	rtgaaatgaactgc	$\pm \tau \pm c \pm \pm$	272
Query	127	CTGTTGTTAAT	TGAGGTAA-GGATT	TTGAATGTTCCGATG	CTCCTCTTGAGCT	GTTTGC	185
Sbjct	271	ctcttctcat	tgaggtaaagga-t	ttaddaattcccttc	trtcctcttdaart	gtttga	213
Query	186	TCTTCTGCACT	CGAACCTGTAAGTA	AACTATTGGCTGTTG(CAATTGATTGTGGG	ACAGAA	245
Sbjct	212	arttctccc	'cdgaacadtagdta	AACTATTTGCCATTG	racttgattgaaaa	.GGAGAT	153
Query	246	ATTGATAGTGT	CCTTGTATCTTCTT	GAGAAATG-T-TGTC	TTCATTTAAACTCG	GACTCG	303
Sbjct	152	ATCGATAGTGT	ĊĊŦŦĠŦĀŦĊŦŦĊŦŦ	CAGATGTTCTATC	rttatttacactrr	GACTTG	95
Query	304	AAAATATATTC	TTTGCTTGTGAA	CTTGATTGAGAAAGTO	GATGTTGATAGTGT	CCATGG	361
Sbjct	94	AAAATATTC	tttcagtttgtgta	CTTGATGGAAGAAGC:	rrtgttgatagtgt	CCATGG	37
Query	362	CACTTCTGTCA	TTTGATTTTCTTCT	GCACTGGATTC 397	7		
Sbjct	36	cacttctctca	tttgattttcttct	TCACTGGATTC 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	s:						
Query	204	GTAAGTAAACT	'ATTGGCTGTTGCAA'	TTGATTGTGGGACAG.	AAATTGATAGTGTC	CCTTGTA	263
Sbjct	776	GTAGGTAAACT	'ATTCGCCATTGTAC'	TTGATTGAAAATTAG.	ATATCGATAGTGTC	ccttgta	717
Query	264	TCTTCTTGAGA	AATG-T-TGTCTTC	ATTTAAACTCGGACT	CGAAAATATATTC	TTTGC	319
Sbjct	716	TCTTCTTCAGA	tgrtctatcttt	ATTTACACTTTGACT	TGAAAATAT——TC	TTTCAGT	661
Query	320	TTGTGAACTTG	ATTGAGAAAGTGAT	GTTGATAGTGTCCAT	GGCACTTCTGTCAT	TTTGATT	379
Sbjct	660	ttgtgtacttg	ATGGAAGAAGCTTT	gttgatagtgtccat	ggcacttctgtca	rttgatt	601
Query	380	TTCTTCTGCAC	TGGATTCTTGAAAT	GAACTGCTCTCTTCT	GTTGTTAATTGAGO	GTAA-GG	438
Sbjct	600	ttcttcttcAc	tggattctttaagt	GAACTGCTTTCTTCT	GttGtagattGAG	STAAAGG	541
Query	439	ATTTTGAATGT	TCCGATGTCTCCTC	TTGAGCTGTTTGCTC	TTCTGCACTCGAAC	CCTGTAA	498
Sbjct	540	AGTTAAAAA-T	ϮϲϲͼϮϯͼϮϮϯϲϲϯϲ·	rtraartettteate	ttctgcactcgaaz	ACTGTGG	482
Query	499	GTAAACTATTG	GCTGTTGCAATTGA	TTGTGGGACAGAAAT	TGATAGTGTCCTTC	TATCTT	558
Sbjct	481	GAAAACTATT	'dccattdtacttda	rtgaaaattagatat	cgatagtgtccttc	STATCTT	422
Query	559	CTTGAGAAATG	TTGTCTTCATTTAA	ACTCGGACTCGAAAA	TATA 602		
Sbjct	421	cttcagargtr	ctatcttcatctac	ACTTTGACTTGAAAA	TATA 378		

Range 4: 1 to 100

Score 108 bits(58)		Expect	Identities	Gaps	Strand	Frame	
		2e-19()	88/102(86%)	4/102(3%)	Plus/Minus		
Feature	s:						
Query	7	GACTCGAAAA'	PATATTCTTTGCT	TGTGAACTTGATTG	AGAAAGTGATGTTO	GATAGTGT	64
Sbjct	100	GACTTG-AAA	-ATATTCTTTCAGTT	tgtgtacttgatgg	AAGAAGCTTTGTTC	GATAGTGT	43
Query	65	CCATGGCACT'	rctgtcatttgattt 	TCTTCTGCACTGGA	TTC 106		

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	s:						
Query	40	ATTGAGAAAGT	GATGTTGATAGTGTC	CATGGCACTTCTGT	CATTTGATTTTC	TTCTGCAC	99
Sbjct	4513	ATTGAGGAAGT	GATGTTGATAATGTC	CCTGGCACTTCTGA	ACATTTGATTTC	TTCTGCAC	4454
Query	100	TGGATTCTTGA	AATGAACTGCTCTCT	TCTGTTGTTAATTO	GAGGTAAGGATTT	TGAATGTT	159
Sbjct	4453	tggattcttgg	AATGAAATGCTTTCT	tctgttgtggattc	SAGGTAAAGATTT	TGAAATTT	4394
Query	160	CCGATGTCTCC	TCTTGAGCTGTTTGC	TCTTCTGCACTCGA	ACCTGTAAGTAA	ACTATTGG	219
Sbjct	4393	cccaccaccaccaccaccaccaccaccaccaccaccacc	trttgaartgttga	tcctctgcactcg	Aactgtaagtaa	ACTATTTT	4334
Query	220	CTGTTGCAATT	GATTGTGGGACAGAA	ATTGATAGTGTCCT	TTGTATCTTCTTG	AGAAATGT	279
Sbjct	4333	CTGTTGCATAT	GATTGAGGGAACGAG.	ATTGATAGTGTCC	rtgtatcttcttg	AGATGTTT	4274
Query	280	TGTCTTCATTT	AAACTCGGACTCGAA	AATATATTCTTTG-	-CTT-GTGAACTT	GATTGAGA	337
Sbjct	4273	tatcttcttct	ACACTTTGACTGGAA	AATGTACTTTTAG	rcttcgt-A-ctt	AGTTGATG	4216
Query	338	AAGTGATGTTG	ATAGTGTCCATGGCA	CTTCTGTCATTTG <i>I</i>	ATTTTCTTCTGCA	CTGGATTC	397
Sbjct	4215	grgtgatgttg	AtAAtGtccAtGGcA	attcagacatttg	Attttcttttck	ctggattc	4156
Query	398	TTGAAATGAAC	TGCTCTCTTCTGTTG	TTAATTGAGGTAAC	GATTTTGAATGT	TCCGATG-	456
Sbjct	4155	ttggaatgaaa	tgctttcatctgttg	taaattgaggtaaz	AGATTTTGAAATT	TCCG-TGA	4097
Query	457	TCTCCTCTTGA	GCTGTTTGCTCTTCT	GCACTCGAACCTGT	TAAGTAAACTATT	GGCTGTTG	516
Sbjct	4096	trtcctrttcc	artettteatetart	gcactcgaaactg	radtaaactatt	TTCTATTG	4037
Query	517	CAATTGATTGT	GGGACAGAAATTG-A	TA 543			
Sbjct	4036	catatgattga	.dddaacdagattdta	TA 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	S:						
Query	40	ATTGAGAAAG:	rgatgttgatagtgtcc	ATGGCACTTCTGTC	CATTTGATTTTCTTC	CTGCAC 99	
Sbjct	2938	AttGAGGAAGG	cgatgttgatagtgtcc	AtGGCATTTCTGTC	catttgattttcttc	ctgcac 28	79
Query	100	TGGATTCTTG	AAATGAACTGCTCTCTT	CTGTTGT-TAAT	TGAGGTAAGGATT	TTGA-A 15	5
Sbjct	2878	†ggat†¢††g	AAGTGAACTCCTTTCTT	cggttgtatatarrgt	rtgrgggacagaaar	rCGATA 28	19
Query	156	TGTTCCGATG	PCTCCTCTTGAGCTGTT	TGCTCTTCTGCACT	CGAACCTGTAAGT	AAACTA 21	5
Sbjct	2818	ccgtcc-rtg:	ratettettgagatett	$ ext{tt-atctrcart}$	ccdaaactgtaagt <i>i</i>	AAACTA 27	63
Query	216	TTGGCTGTTG	CAATTGATTGTGGGACA	GAAATTGATAGTGT	CCTTGTATCTTCT	rgagaa 27	5
Sbjct	2762	ተተተተረተፈተተራ	CATATGATTGAGGGAAC	gagattgatagtgt	cected that control is a second	rgagat 27	03
Query	276	ATGTTGTCTT	CATTTAAACTCGGACTC	GAAAATATATTCTT	TG-CTT-GTGAACT	TTGATT 33	3
Sbjct	2702	GtTttatctt	crtctacactrrgactg	GAAAATGTACTTT	ragrettegt-A-er	rtagtt 26	45
Query	334	GAGAAAGTGA	rgttgatagtgtccatg	GCACTTCTGTCATT	TGATTTTCTTCTG(CACTGG 39	3
Sbjct	2644	GATGGTGTGA:	rgttgataatgtccatg	GCAATTCAGACATT	rtgattttcttrtrc	CACTGG 25	85
Query	394	ATTCTTGAAA	rgaactgctctcttctg	TTGTTAATTGAGGT	AAGGATTTTGAAT(GTTCCG 45	3
Sbjct	2584	AttcttdgAA	rgaaatgettteatetg	ttgtadattgaggt	daagattttgaaa	rttccg 25	25
Query	454	ATG-TCTCCT	CTTGAGCTGTTTGCTCT	TCTGCACTCGAACC	TGTAAGTAAACTA	TTGGCT 51	2
Sbjct	2524	-tGATTTCCT	rttgcartgtttgatct	artddadtddaad	chdtradtaaacta	rtttct 24	66

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	S :						
Query	40	ATTGAGAAAG	TGATGTTGATAGTG7	TCCATGGCACTTCTG	CATTTGATTTTC:	TTCTGCAC	99
Sbjct	6115	ATTGAGGAAG	TGATGTTGATAATG	rccatggcaattcag:	rcatttgattttc:	TTTTGCAC	6056
Query	100	TGGATTCTTG	AAATGAACTGCTCTC	CTTCTGTTGTTAATT(GAGGTAAGGATTT	FGAATGTT	159
Sbjct	6055	TGGATTCTTT	GAGGGAAATGCTTTC	cttctgttgtggatt	GAGGTAAAGATTT:	rgaaartt	5996
Query	160	CCGATGTCTC	CTCTTGAGCTGT7	TTGCTCTTCTGCACTO	CGAACCTGTAAGT	AAACTATT	217
Sbjct	5995	CCGTGGATTC	CT-TT-CGCATTTT	rtgatectetgeacte	CGAAACTGTAAGTZ	AAACTATT	5938
Query	218	GGCTGTTGCA	ATTGATTGTGGGAC <i>I</i>	AGAAATTGATAGTGT(CCTTGTATCTTCTT	ГGAGAAAT 	277
Sbjct	5937	TTCTGTTGCA	TATGATTGAGGGAAC	CGAGATTGATAGTGT	CCTTAGATATTCT		5878
Query	278	GTTGTCTTCA	TTTAAACTCGGACTC	CGAAAATATATTCTT	TGCTTGTGAACTT(GATTGAGA	337
Sbjct	5877	тттатсттст	tctAcActtTGACto	GAAAGTATACTT:	htaghtrth	AATTGAGG	5824
Query	338	AAGTGATGTT	GATAGTGTCCATGGC	CACTTCTGTCATTTG	ATTTTCTTCTGCAC	CTGGATTC	397
Sbjct	5823	AAGTGTAGTT	GATAGTGCCCATGG	CACTTCTGTCATTTG	AtttcttctAccAc	CTGGATTG	5764
Query	398	TTGAAATGAA	СТБСТСТСТТСТБТТ	TGT 424			
Sbjct	5763	TTGAAGTGAA	CTGCTTTTTTCTGTT	rGT 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		
Feature	s:						
Query	37	TTGATTGAGAA	AGTGATGTTGATAGT(GTCCATGGCACTTC'	TGTCATTTGATTTT	CTTCTG	96
Sbjct	337	TTGATTGAGGA	AGTGATGTTGATAAT	GTCCATGGCACTTC'	rgtcatttgattt	cttctc	278
Query	97	CACTGGATTCT	rgaaatgaactgctc'	rcttctgttgttaa'	TTGAGGTAAGGATT	TTGAAT	156
Sbjct	277	cactgaattct:	rgaagtgaactgctr	tcttttdttdtaga	ttgaggtaaagact	rttgaaa	218
Query	157	GTTCCGATGTC	rcctcttgagctgtt	rgctcttctgcact	CGAACCTGTAAGTA	AACTAT	216
Sbjct	217	TTTCCGTGGTT	tcctrttgcactgtt	rgatcctctgcact	cgaaactgtaagta	AACTAT	158
Query	217	TGGCTGTTGCA	ATTGATTGTGGGACA	GAAATTGATAGTGT(CCTTGTATCTTCTT	GAGAAA	276
Sbjct	157	trégtéttéak	cctagttgaggtaaa	gaaatcgatattgt:	ccttgtatcttrtt	'GAGA	100
Query	277	TGTTGTCT	TCATTTAAACTCGGA(CTCGAAAATATATT 	CTTTGCTTGTGAAC	TTGATT	333
Sbjct	99	tgtt-tcarrt	tcatctacactrrda	ctggaaaatatact [,]	rtcagrtttagrac	CTTAACT	41
Query	334	GAGAAAGTGAT(GTTGATAGTGTCCAT(GGCACTTCTGTCAT	373		
Sbjct	40	TAGTAAGAGAT	gttgatagtgtccat	ĠĠĊĀĊŦŦĊŦĠŦĊĀŦ	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		
Feature	s:						
Query	331	ATTGAGAAAG	TGATGTTGATAGTGTC	CCATGGCACTTCTG	TCATTTGATTTTC	TTCTGCAC	390
Sbjct	4513	ATTGAGGAAG	TGATGTTGATAATGTC	cctggcacttctg	acatttgattttc	rtctgcac	4454
Query	391	TGGATTCTTG	AAATGAACTGCTCTCT	TTCTGTTGTTAATT	GAGGTAAGGATTT'	TGAATGTT 	450

Sbjct	4453	TGGATTCTTGGAATGAAATGCTTTCTTCTGTTGTGGATTGAGGTAAAGATTTTGAAATTT	4394
Query	451	CCGATGTCTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAA	510
Sbjct	4393	CCGTGGTTTCCTTTTGAATTGTTTGATCCTCTGCACTCGAAACTGTAAGTAA	4334
Query	511	CTGTTGCAATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGT	570
Sbjct	4333	CTGTTGCATATGATTGAGGGAACGAGATTGATAGTGTCCTTGTATCTTCTTGAGATGTTT	4274
Query	571	TGTCTTCATTTAAACTCGGACTCGAAAAT 599	
Sbjct	4273	TATCTTCTACACTTTGACTGGAAAAT 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		
Feature	s:						
Query	49	GTGATGTTGA	TAGTGTCCATGG	GCACTTCTGTCATTTGA'	TTTTCTTCTGCACT	GGATTCTT	108
Sbjct	2638	GTGATGTTGA	TAATGTCCATGG	CAATTCAGACATTTGA	TTTTCTTTTCACT	GGATTCTT	2579
Query	109	GAAATGAACT	GCTCTCTTCTGT	TGTTAATTGAGGTAAG	GATTTTGAATGTTC	CGATG-TC	167
Sbjct	2578	GGAATGAAAT	GCTTTCATCTGT	rtgtaaattgaggtaaa	GATTTTGAAATTTC	CG-TGATT	2520
Query	168	TCCTCTTGAG	CTGTTTGCTCTT	CTGCACTCGAACCTGT	AAGTAAACTATTGG(CTGTTGCA	227
Sbjct	2519	tcctrttgca	rtdtttdatcta	rtgcactcgaaactgt	TAGTAAACTATTT	ctattgca	2460
Query	228	ATTGATTGTG	GGACAGAAATTG	ATAGTGTCCTTGTATC'	TTCTTGAGAAATGT'	TGTCTTCA	287
Sbjct	2459	TATGATTG-A	.ddd-AA-cd	AGATTGTATA'	TTCCTGAGATGCTT'	ratcttca	2412
Query	288	TTTAAACTCG	GACTCGAAAATA	TATTCTTTGCTTGTGA	ACTTGATTGAGAAA	GTGATGTT	347
Sbjct	2411	tctAcActtr	GACTGGAAAATA	\trctrtttgrttragr	acttgattgaggaa	GAGATGTT	2352
Query	348	GATAGTGTCC	ATGGCACTTCTG	TCATTTGATTTTCTTC'	TGCACTGGATTCTT	GAAATGAA	407
Sbjct	2351	aatagtgtcc	AtGGCACTTCTG	;+cA++tGA++++r++c	tgcactggattgtt	GAAGTGAA	2292
Query	408	CTGCTCTCTT	CTGTTGT 424	•			
Sbjct	2291	CTGCTTTTTT	टर्मर्दर्मर्पदर्म 227	'5			

Range 7: 3850 to 4213

Score		Expect	Identities	Gaps	Strand	Frame	
279 bits	(151)	3e-71()	304/377(81%	5) 14/377(3%)	Plus/Minus		
Features	S :						
Query	49	GTGATGTTGA	TAGTGTCCATG	GCACTTCTGTCATTTGAT	TTTCTTCTGCACTO	GGATTCTT	108
Sbjct	4213	GTGATGTTGA	TAATGTCCATG	GCAATTCAGACATTTGAT	TTTCTTTTCACT	GATTCTT	4154
Query	109	GAAATGAACT	GCTCTCTTCTG'	TTGTTAATTGAGGTAAGG	ATTTTGAATGTTC	CGATG-TC	167
Sbjct	4153	GGAATGAAAT	GCTTTCATCTG	rtgtaaartgaggtaaa	SATTTTGAAATTTC	CG-TGATT	4095
Query	168	TCCTCTTGAG	CTGTTTGCTCT'	TCTGCACTCGAACCTGTA	AGTAAACTATTGG	CTGTTGCA	227
Sbjct	4094	TCCTTTTGCA	TTGTTTGATCT	attgcactcgaaactgti	ragtaaactattri	CTATTGCA	4035
Query	228	ATTGATTGTG	GGACAGAAATT	GATAGTGTCCTTGTATCT	TCTTGAGAAATGT	TGTCTTCA	287
Sbjct	4034	TATGATTG-A	GGG-AA-C	GAGATTGTATA1	TCCTGAGATGCTT	TATCTTCA	3987
Query	288	TTTAAACTCG	GACTCGAAAAT	ATATTCTTTGCTTGTGA	CTTGATTGAGAAAG	GTGATGTT	347
Sbjct	3986	TCTACACTTT	GACTGGAAAAT	ATTCTTTTTGTTTTAGT	\cttgattgaggaa	GAGATGTT	3927
Query	348	GATAGTGTCC	ATGGCACTTCT(GTCATTTGATTTTCTTCT	GCACTGGATTCTT	GAAATGAA	407
Sbjct	3926	AATAGTGTCC	Atggcacttct	GTCATTTGATTTTTCT	rgcactggattgtt	GAAGTGAA	3867
Query	408	СТССТСТТ	CTGTTGT 42	4			
Sbjct	3866	CTGCTTTTT	CTGTTGT 38	50			

Score		Expect	Identities	Gaps	Strand	Frame	
270 bits	(146)	2e-68()	278/343(81%)	4/343(1%)	Plus/Minus		
Feature	s:						
Query	220	CTGTTGCA-A	TTGATTGTGGGACAGA	AATTGATAGTGTC	CTTGTATCTTCTT	GAGAAATG	278
Sbjct	3856	CTGTTGTAGA	TTG-TTGTGGGAGAGA	AATCGATAGTGTC	CTTGTATCTTCTT!	TAGATGTT	3798
Query	279	TTGTCTTCAT	TTAAACTCGGACTCGA	AAATATATTCTTT	GCTTGTGAACTTG	ATTGAGAA	338
Sbjct	3797	TTATCTTCTT	CTACACTTTGACTGGA	AAATATACTTTCA	GCTTTAGTACTTA	ATTTAGGA	3738
Query	339	AGTGATGTTG.	ATAGTGTCCATGGCAC	TTCTGTCATTTGA	TTTTCTTCTGCAC	TGGATTCT	398
Sbjct	3737	AGTGATGTAG.	Ataatgcccatrgraa	.ttcagtartttga	ttttcttctgcac	rggattet	3678
Query	399	TGAAATGAAC	TGCTCTCTTCTGTTGT	TAATTGAGGTAAG	GATTTTGAATGTT(CCGATGTC	458
Sbjct	3677	TGAAGTGAAC	ϮĠĊϮͲϮĊϮϮͲϮĠϮϮĠϮ	'agattgaggtaaa	GACTTTGAAATTT	CCGTGGTT	3618
Query	459	TCCTCTTGAG	CTGTTTGCTCTTCTGC	ACTCGAACCTGTA	AGTAAACTATTGG(CTGTTGCA	518
Sbjct	3617	TCCTCTTGCA	ctgtttgatcctctgc	ACTCGAAACTGTA	AGTAAACTATTTG	CTGTTGAA	3558
Query	519	ATTGATTGTG	GGACAGAAATTGATAG	TGTCC-TTGTATC	TTCT 560		
Sbjct	3557	cttaattgag	GAAAAGATGTTGATGG	;tdtccattdca-c'	ttct 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		
Feature	s:						
Query	328	TTGATTGAGAA	AGTGATGTTGATAGTO	TCCATGGCACTTC	TGTCATTTGATTTT	СТТСТС	387
Sbjct	337	TTGATTGAGGA	AGTGATGTTGATAATC	TCCATGGCACTTC	TGTCATTTGATTT	CTTCTG	278
Query	388	CACTGGATTCT	TGAAATGAACTGCTC7	CTTCTGTTGTTAA	TTGAGGTAAGGATT	TTGAAT	447
Sbjct	277	cactgaattct	rgaagtgaactgctri	rcttrtgttgtaga	ttgaggtaaagact	rttgaaa	218
Query	448	GTTCCGATGTC'	TCCTCTTGAGCTGTT7	GCTCTTCTGCACT	CGAACCTGTAAGTA	AACTAT	507
Sbjct	217	тттссств	tcctrttgcactgtt	rgatectetgeact	cgaaactgtaagta	AACTAT	158
Query	508	TGGCTGTTGCA	ATTGATTGTGGGACAC	SAAATTGATAGTGT	CCTTGTATCTTCTT	GAGAAA	567
Sbjct	157	TTGGTGTTGAA	CCTAGTTGAGGTAAAG	SAAATCGATATTGT	ccttgtatcttrtd	GAGA	100
Query	568	TGTTGTCT	TCATTTAAACTCGGAC	CTCGAAAATATA	602		
Sbjct	99	tgtt-tcattt	tcatctacactrigad	ctggaaaatata	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	3 :						
Query	51	GATGTTGATA	GTGTCCATGGCACTT	'CTGTCATTTGATTT'	TCTTCTGCACTGGA	TTCTTGA	110
Sbjct	3215	GATATTGATG	gtgtccatrgcacti	·chghcahhhgahhh	tettetgeaetgga	ttcttgg	3156
Query	111	AATGAACTGC	TCTCTTCTGTTGTTA	ATTG-AG-GTAAG-0	GATTTTGAATGT-T	CCGATGT	166
Sbjct	3155	AATGAAATGC	trtcctrtgttgtag	ATTGTTGTGGGAGA	gaaatcgatggtgt	cc-Atgt	3097
Query	167	CTCCTCTTGA	GCTGTTTGCTCTTCT	GCACTCGAACCT	GTAAGTAAACTATT	GGCTGTT	224
Sbjct	3096	ATCTTCTTGA	GATGTTTTATCTTCT	TTGTA-tTCTT	g-aagtgaactgct	ттстттт	3042
Query	225	GCAATTGATT	GTGGGACAGAAATTG	ATAGTGTCCTTGTA'	TCTTCTTGAGAAAT 	GTTGTCT	284
Sbjct	3041	GTTGTAGATT	GAGGTAAAGACTTTG	sa–aatttccgtggt	t-tcctttrtgcact	gtt-tga	2985
Query	285	TCATTTAAAC	TCG-GACTCGAAAAT	ATATTCT-TTGCTT	GTGAAC-TTGATTG	AGAAAGT	341
Sbjct	2984	tctctgcAc	tcgaaact-gtgagt	'A-A-ACTATTGTTT	rtagrċrttaattĠ	AGGAAGC	2928
Query	342	GATGTTGATA	GTGTCCATGGCACTT	'CTGTCATTTGATTT' 	TCTTCTGCACTGGA	TTCTTGA	401
Sbjct	2927	ĠAŦĠŦŦĠAŦĀ	ĠŦĠŦĊĊĀŦĠĠĊĀŦŦŦ	'ctgtcatttgattt	tcttctccactcda	ttcttda	2868

Query	402	AATGAACTGCTCTCTCTGTTGT-TAATTGAGGTAAGGATTTTGA-ATGTTCCGATGT	457
Sbjct	2867	AGTGAACTCCTTTCTTCGGTTGTATATTGTTGTGGGACAGAAATCGATACCGTCC-TTGT	2809
Query	458	CTCCTCTTGAGCTGTTTGCTCTTCTGCACTCGAACCTGTAAGTAA	517
Sbjct	2808	ATCTTCTTGAGATGTTTT-ATCTTCATTCGAAACTGTAAGTAAACTATTTTCTGTTGC	2752
Query	518	AATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCTTCTTGAGAAATGTTGTCTTC	577
Sbjct	2751	ATATGATTGAGGGAACGAGATTGATAGTGTCCTTGTATCTTCTTGAGATGTTTTATCTTC	2692
Query	578	ATTTAAACTCGGACTCGAAAAT 599	
Sbjct	2691	TTCTACACTTTGACTGGAAAAT 2670	

Range 11: 5050 to 5469

Score		Expec	t Identities	Gaps	Strand	Frame	
230 bits	(124)	3e-56() 329/426(77%)	21/426(4%)	Plus/Minus		
Features	S :						
Query	35	ACTTGAT'	rgagaaagtgatgtt(GATAGTGTCCATGGCAC	TTCTGTCATTTGA	TTTTCTTC	94
Sbjct	5469	ACTTAAT:	TTAGGAAGTGATGTC	GATAATGCCCATTGTAA	TTCAGTCTTTTGA	rtttctt	5410
Query	95	TGCACTG	GATTCTTGAAATGAA	CTGCTCTCTTCTGTTGT	TAATTGAGGTAAGG	GATTTTGA	154
Sbjct	5409	tgcactgo	GATTCTTGGAAGGAA	atggtrtcttctgttgt	ggattgaggtaaa	GATTTTGA	5350
Query	155	ATGTTCC	GATGTCTCCTCTTGA(GCTGTTTGCTCTTCTGC	ACTCGAACCTGTAA	AGTAAACT	214
Sbjct	5349	AATTTCC	gragarteetrttge	artgtttgatectetge	ActcGAAActGtA	AGTAAACT	5290
Query	215	ATTGG	CT-GTT-GCAATT	GATTGTGGGACAGAAAT	TGATAGTGTCCTT(GTATCTTC	268
Sbjct	5289	ATTTTTT	rtagtttagtactt	GATTGAGGAAGTGATGT	tgatagtgtccato	GTCACTTC	5230
Query	269	TTGAGAA	ATGTTG-TCTTCATT	TAAACTCGGACTCGA	AAATATATTC-TT	rgcttgt-	323
Sbjct	5229	-tGTC	At-ttgattttctc	tgcact-ggattcttga	AGTGAAATGCTTT	trrttrta	5175
Query	324	GAACTTG	ATTGAGAAAGTGATG'	TTGATAGTGTCCATGGC	ACTTCTGTCATTT(GATTTTCT	383
Sbjct	5174	GTTTTTA	AttGAGGAAGtGAtG'	ttgataatgtccctggc	ActtctctctcAtttc	SATTTTCT	5115
Query	384	TCTGCAC'	rggattettgaaatg	AACTGCTCTCTTCT	GTTGTTAATTGAG	GTAAG-GA	439
Sbjct	5114	TCTGCAC'	rddattcttdaagtd	AACTGCTTTCTTTTTA	ĠŦŦŦŦŦĠĂŦŦĠĀĠ	G-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		
Feature	s:						
Query	129	GTTGTTAAT:	rgaggtaag-gattt	GAATGTTCCGAT	GTCTCCTCT-TGA	GCTGTTTG	184
Sbjct	1718	GTTTTTAAT:	rgagg-aagtgatgt	GATAATG-TCC-AT	GTCACTTCTGTCA	TTTGATTT	1662
Query	185	CTCTTCTGC	ACTCGA-ACCTGTAAC	GT-AAACTATTGG	CTGTTGCA-ATTG	ATTGTGGG	239
Sbjct	1661	-tcttctgc	ACTGGATTCCTG-AAC	STGAACTGCTTTTTT	CTGTTGAAGATTG	-ttgtagc	1605
Query	240	ACAGAAATT(GATAGTGTCCTTGTAT	CTTCTTGAGAAATG'	TTGTCTTCATTTA	AACTCGGA	299
Sbjct	1604	AGAAAAATC	GATAGTGTCCTTGTA	rcttcttgagatgtt'	TTATCTTCATCTA	CACTTTGA	1545
Query	300	CTCGAAAAT	ATATTCTTT-GCTTGT	GAACTTGATTGAGA	AAGTGATGTTGAT	AGTGTCCA	358
Sbjct	1544	CTGGAAAAT	AtA-cctttagtttr	AGTACTTGATTGAGG.	AAGCGATGTTGAT	AGTGTCCA	1486
Query	359	TGGCACTTC	rgrcatttgattttc	TTCTGCACTGGATTC	TTGAAATGAACTG	CTCTCTTC	418
Sbjct	1485	CGGCATTTC	rgtcatttgatttc	rtctgcactggattc	ctgaagtgaactg	ctrtcttc	1426
Query	419	TGTTGT 42	24				
Sbjct	1425	TGTTGT 1	120				

Score		Expect	Identities	Gaps	Strand	Frame
211 bits	(114)	1e-50()	362/476(76%)	40/476(8%)	Plus/Minus	
Features	s:					
Query	129	GTTGTTAATTG	GAGGTAAG-GATTT	rgaatgttccgatg	TCTCCTCT-TGAGG	CTGTTTG 184
Sbjct	794	GttrttAAttd	ad-adagtgatgt:	rgataatg-tcc-atg	tcacttctgtcat	rtgattt 738
Query	185	CTCTTCTGCAC	TCGA-ACCTGTAA(GTAAACTATT-GGC	TGTTGCA-ATTGA:	TTGTGGG 239
Sbjct	737	-tcttctgcac	tggattcctg-aac	GTGAACTGCTTTCTTC	rgtrgtagattg-:	rtgtggg 681
Query	240	ACAGAAATTGA	TAGTGTCCTTGTAT	rcttcttgagaaatgt 	TGTCTTCATTTAA <i>I</i>	ACTCGGA 299
Sbjct	680	AGAGAAATCGA	taccetecteeta	tcttcttdadargtrt	tatetteacetac	Actrigi 621
Query	300	CTCGAAAATAT	ATTCTTTGCTTGT(GAACTTGATTGAGAAA	GTGATGTTGATAG	rgrccar 359
Sbjct	620	ctggaaaatat	'Acttttagt-	cttaattgaggaa	gcgytgttgyty?	rgtccat 567
Query	360	GGCACTTCTGT	CATTTGATTTTCTT	rctgcactggattctt 	GAAATGAACTGCT(CTCTTCT 419
Sbjct	566	ddcarttctdt	ckatttgattttct	tctgcactggattctt	gaagtgaactgct:	гттттта 507
Query	420	GTTGTTA	-A-TTGAGGTAAG-	-GATTTTGAATGT-TC	CGATGTCTCCTCT-	-TGAGCT 470
Sbjct	506	GTTGTAGTACT	raattgagg-aag	AGATGTTGATGGTGTC	c-attgcacttctc	GTCATTT 449
Query	471	GTTTGCTCTTC	TGCACTCGAACCT(GTAAGTAAACTA-TTG	GCTGTTGCA-A	TTGATTG 526
Sbjct	448	GATTT-TCTTC	tgcycteratect	rgaagtgaactgettt	cttctcttttctac	rtd-ttd 391
Query	527	TGGGACAGAAA	TTGATAGTGTCCT	rgtatcttcttgagaa	-ATGTTGTCTTCAT	TTT 581
Sbjct	390	tdddagrdraa	tcgytygtgtgt	rgtatcttcttgagar	gat-ttatetter:	rtt 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	s:						
Query	196	TCGAACCTGT	AAGTAAACTATTGGC'	TGTTGCAATTGATT	GTGGGACAGAAA	TGATAGTG	255
Sbjct	1840	tcgaaactgt	AAGTAAACTATTTC'	tgttgcatatgatt	GAGGGAACGAGA1	rtgatagtg	1781
Query	256	TCCTTGTATC	TTCTTGAGAAATGTT	GTCTTCATTTAAAC'	TCGGACTCGAAA <i>I</i>	ATATATTCT	315
Sbjct	1780	TCCTTGTATT	TTCTTGAGATGTTTT	atcttcttctacac	TGTGACTGGAAAA	ATATACT	1723
Query	316	TTGCTTGTGA	ACTTGATTGAGAAAG'	TGATGTTGATAGTG'	TCCATGGCACTTC	TGTCATTT	375
Sbjct	1722	TTTAGT	TTTTAATTGAGGAAG	tgatgttgataatg	tccatgrcacttd	ctgtcattt	1667
Query	376	GATTTTCTTC	TGCACTGGATTCTTG	AAATGAACTGCTCT(CTTCTGTTG 42	23	
Sbjct	1666	ĠĂŦŦŦŦĊŦŦĊ	tgcactggattcctg	AAGTGAACTGCTTT'	${ m r}$ ttctgttg 1 ϵ	519	

Range 15: 1909 to 2201

Score		Expect	Identities	Gaps	Strand	Frame	
211 bits	(114)	1e-50()	240/300(80%)	11/300(3%)	Plus/Minus		
Feature	s:						
Query	150	TTTGAATGT	TCCGATGTCTCCTCTT	GAGCTGTTTGCTCT	TCTGCACTCGAAC	CTGTAAGT	209
Sbjct	2201	TTTGAAATT	rccgrggtrtcctct	GCACTGTTTGATCC	tctgcactcgaaa	CTGTAAGT	2142
Query	210	AAACTATTG(GCTGTTGCAATTGATT	GTGGGACAGAAATT	GATAGTGTCCTTG	TATCTTCT	269
Sbjct	2141	AAAATATTT	Schohrdaacchagh	rdgddtaaadaaatc	ĠĀŦĀŦŦĠŦĊĊŦŦĠ	tatcttrt	2082
Query	270	TGAGAAATG	TTGTCTTCATTTAAAC	TCGGACTCGAAAAT	ATATTCTTTGCTT	GTGAACTT	329
Sbjct	2081	TGAGATATT	rcattttcatctacac	CTTTGACTGGAAAAT	ATACTTT-C-A	GTCTTT	2028
Query	330	GATTGAGAA	AGTGATGTTGATAGTG	GTCCATGGCACTTCT	GTCATTTGATTTT	CTTCTGCA	389
Sbjct	2027	AATTGAGGAZ	AGCGATGTTGATAGTG	stecatereacted	ĠተĊ₳ተተተĠ₳ተተተ	cttctcca	1968
Query	390	CTGGATTCT	TGAAATGAACTGCTCT	CTTCTGTTGT-T	AATTGAGGTAAG-	GATTTTGA	445

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	S :						
Query	35	ACTTGATTGA	GAAAGTGATGTTGA	PAGTGTCCATGGCAC	TTCTGTCATTTGA	TTTTCTTC	94
Sbjct	5271	ACTTGATTGA	dgaagtgatgttga	ragtgtccatgtcac;	rtctgtcatttga	րդդդբրդ Ի	5212
Query	95	TGCACTGGAT	TCTTGAAATGAACT	GCTCTCTTCTGT	rgttaattgaggt	AAG-GATT	150
Sbjct	5211	TGCACTGGAT	rtcttgaagtgaaat	GCTTTTTTTTTTAGT:	rrttaattgagg-2	AAGTGATG	5153
Query	151	TTGA-A-TGT	TCCGATGTCTCCTC	r-tgagctgtttgct(CTTCTGCACTCGA	ACCTGTAA	207
Sbjct	5152	TTGATAATGT	ccctggcacttc	rgtcatttgattt-to	CTTCTGCACTGGA:	TTCTTGAA	5096
Query	208	GTAAACTATT	GGCTGTTGCAA	TTGATTGTGGGACAG	AAATTGATAGTGT(CCTTGTAT	264
Sbjct	5095	GTGAACTGCT	rtctttttagtt	rtgattgaggaagtg	ATGTTGATAGTGC	CCATGGCA	5036
Query	265	CTTCTTGAGA	AATG-TTGTCTTCA	TTTAAACTCGGACTC	GAAAATATATT(CTTTGCTT	321
Sbjct	5035	cttct-grc	\rrtgattrtctac-	rgcact-ggartc	rtgaagtgaaatg	ԵተተተĠተተተ	4981
Query	322	GTGAA-CTTG	G-ATTGAGAAAGTGA	rgttgatagtgtcca:	rggcacttctgtc	ATTTGATT	379
Sbjct	4980	TTTAGTCTTT	raattgaggaagcga:	rgttgatagtgtcca	rggcarttctgtc	ATTTGATT	4921
Query	380	TTCTTCTGCA	CTGGATTCTTGAAA!	rgaactgctctcttc:	IGTTGT 424		
Sbjct	4920	++<++<+	ctggattcttgaag:	rgaactcctrrtcttc	GGTTGT 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	S :						
Query	7	GACTCGAAAA'	PATATTCTTTGCTTG	TGAACTTGATTGAG	AAAGTGATGTTGA	TAGTGTCC	66
Sbjct	3778	GACTGGAAAA'	tatactrtcaccttr	agracttaattrag	gaagtgatgtaga	taatgccc	3719
Query	67	ATGGCACTTC'	IGTCATTTGATTTTC	TTCTGCACTGGATT	CTTGAAATGAACT	GCTCTCTT	126
Sbjct	3718	ATTGTAATTC	agtartttgattttc	ttctccactccatt	cttgaagtgaact	GCTTTCTT	3659
Query	127	CTGTTGTTAA'	TTGAGGTAAGGATTT 	TGAATGTTCCGATG	TCTCCTCTTGAGC	TGTTTGCT	186
Sbjct	3658	TTGTTGTAGA'	rtgaggtaaagactt	tgaaarttccgrgg	trtcctcttgcac	TGTTTGAT	3599
Query	187	CTTCTGCACT(CGAACCTGTAAGTAA 	ACTATTGGCTGTTG	CAATTGATTGTGG	GACAGAAA 	246
Sbjct	3598	cctctcckch	cdaaactdtaadtaa	ActAttrGctGttG.	aacttaattgagg.	AAAAGATG	3539
Query	247	TTGATAGTGT(CC-TTGTATCTTCT	269			
Sbjct	3538	ttdatgdtdt(ccattgca-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	S :						
Query	220	CTGTTGCA-A	TTGATTGTGGGACAG	AAATTGATAGTGTC	CTTGTATCTTCTT	TGAGA-AAT	277
Sbjct	3466	CTGTTGTAGA	.ttg-ttgtgggagtg	raatcgatagtgtc	chharatchhar	rGAGATGAT	3408
Query	278	GTTGTCTTCA	TTTAAACTCGGACTC	GAAAATATATTCTT	rgcttgtgaact	TGATTGAGA	337
Sbjct	3407	-ttatcttct	tctacactrrgagtg	:GAAAATATACTT:	rtagtctt	raattgagg	3355
Query	338	AAGTGATGTT	GATAGTGTCCATGGC	ACTTCTGTCATTTG	ATTTTCTTCTGC <i>I</i>	ACTGGATTC	397
Sbjct	3354	AAGTGATGTT	datadtdtccatddc	arttctgtcattg	Attttcttctctcc	Actggattc	3295

Range 19: 400 to 787

Score		Expect	Identities	Gaps	Strand	Frame	_
193 bits	(104)	4e-45()	305/399(76%)	25/399(6%)	Plus/Minus		
Feature	s:						
Query	40	ATTGAGAAAGT	GATGTTGATAGTGT	CCATGGCACTTCTGT	CATTTGATTTTCTTC'	IGCAC 99	
Sbjct	787	AttGAGAAAGt	GATGTTGATAATGT	ccatgrcacttctgt	CATTTGATTTTCTTC	rgcac 728	8
Query	100	TGGATTCTTGA	AATGAACTGCTCTC	TTCTGTTGTTAATTG	AGGTAAG-GATTT	TGA-A 15	5
Sbjct	727	tggattcctga	AGTGAACTGCTTTC	ttctgttgtagattg:	rtgtgggagagaaat	CGATA 668	8
Query	156	TGTTCCGATGT	CTCCTCTTGAGCTG	TTTGCTCTTCTGCAC	rcgaacctgtaagta	AACTA 21	5
Sbjct	667	ccgtccr-tgt	atcttcttgagatg	tttratcttca-c-c	racacttreftctega	AAATA 613	1
Query	216	TTGGCTGTT-G	CAATTGATTGTGGG.	ACAGAAATTGATAGT(GTCCTTGT-ATCTTC	TTGAG 27	3
Sbjct	610	tactrttad	TCTTTAATTGAGGA	AGCGATGTTGATAGT	Gtccatggcat-ttc:	r-GTC 55	5
Query	274	AAATG-TTGTC	TTCATTTAAACTCG	GACTCGAAAA-	-TATATTCTTTGCTT(GT-GA 325	5
Sbjct	554	ATTTGATTTTC	tttc-tgchct-d	GATTCTTGAAGTGAAG	ctgctttttttagtt	GTAGT 499	9
Query	326	ACTTGATTGAG	AAAGTGATGTTGAT.	AGTGTCCATGGCACT	CTGTCATTTGATTT	CTTC 385	5
Sbjct	498	Acttaattgag	GAAGAGATGTTGAT	gĠŦĠŦĊĊĀŦŦĠĊĀĊŦŢ	tctgtcatttgattt	tette 439	9
Query	386	TGCACTGGATT	CTTGAAATGAACTG	CTCTCTTCTGTTGT	424		
Sbjct	438	tgcactgratt	cttgaagtgaactg	ctrtcttctgttgt	400		

Range 20: 1228 to 1463

Score		Exp	ect	Identities	Gaps	Strand	Frame	
189 bits	(102)	6e-4	14()	199/244(82%)	13/244(5%)	Plus/Minus		
Features	s:							
Query	186	TCTTC	TGCAC'	rcga-acctgtaag	TAAACTATT-GGC	TGTTGCA-ATTGA	TTGTGGGA	240
Sbjct	1463	TCTTC!	rgcac	rggattcctg-aag	TGAACTGCTTTCTTC	der	TTGTGGGA	1406
Query	241	CAGAA	ATTGA:	PAGTGTCCTTGTAT	CTTCTTGAGAAATGT	TGTCTTCATTTAA.	ACTCGGAC	300
Sbjct	1405	GAGAA	AtcGA	taccdtccttdtat	cttcttgagargtrt	rtatcttcacctac.	ACTTTGTC	1346
Query	301	TCGAA	AATATA 	ATTCTTTGCTTGTG	AACTTGATTGAGAAA	GTGATGTTGATAG	TGTCCATG	360
Sbjct	1345	TGGAA	AATAT	Actttttagt-	-CTTTAATTGAGGAA	.dcdatdttdatad	TGTCCATG	1292
Query	361	GCACT'	CTGTO	CATTTGATTTTCTT 	CTGCACTGGATTCTT	GAAATGAACTGCT	CTCTTCTG	420
Sbjct	1291	ĠĊĀTŤ'	լ Էգգգ	Ե⅄ϮϮϮĠ⅄ϮϮϮϮϲϮϮ	ctgcactggattctt	rgyyddygaethaeth	TTCTTCGG	1232
Query	421	TTGT	424					
Sbjct	1231	ተተĠተ	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	s:						
Query	328	TTGATTGAG	AAAGTGATGTTGATAG	TGTCCATGGCACTT	CTGTCATTTGATT	TTCTTCTG	387
Sbjct	5071	TTGATTGAG	GAAGTGATGTTGATAC	stgcccatggcactt	ctgtcatttgatt	ttctactc	5012
Query	388	CACTGGATT	CTTGAAATGAACTGC	rCTCTTCT-GTTG	TTAATTGAGGTAA	G-GATTTT	443
Sbjct	5011	CACTGGATT	CTTGAAGTGAAATGCT	TTTGTTTTTTAGTCT	TTAATTGAGG-AA	GCGATGTT	4953
Query	444	GAATGT-TC	CGATGTCTCCTCT-TC	GAGCTGTTTGCTCTT	CTGCACTCGAACC	TGTAAGTA	501

Sbjct	4952	GATAGTGTCC-ATGGCATTTCTGTCATTTGATTT-TCTTCTGCACTGGATTCTTGAAGTG	4895
Query	502	AACTATT-GGCTGTTGCA-ATTGATTGTGGGACAGAAATTGATAGTGTCCTTGTATCT	557
Sbjct	4894	AACTCCTTTCTTCGGTTGTATATTG-TTGTGGGACAGAAATCGATACCGTCCTTGTATCT	4836
Query	558	TCTTGAGAAATGTTGTCTTCAT 579	
Shict	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	s:						
Query	37	TTGATTGAG	SAAAGTGATGTTGATA(GTGTCCATGGCACTT	CTGTCATTTGATTT	TTCTTCTG	96
Sbjct	5071	TTGATTGAG	GAAGTGATGTTGATAG	gtgcccatggcactt	ctgtcatttgatt	rtctactG	5012
Query	97	CACTGGATT	CTTGAAATGAACTGC	rctcttct-gttg	TTAATTGAGGTAAC	G-GATTTT	152
Sbjct	5011	CACTGGATT	'CTTGAAGTGAAATGC'	rttgtttttagtct	ttaattgagg-aac	GCGATGTT	4953
Query	153	GAATGT-TC	CGATGTCTCCTCT-T	GAGCTGTTTGCTCTT	CTGCACTCGAACCT	TGTAAGTA	210
Sbjct	4952	GATAGTGTC	:c-Atgccatttctgt	cattdattt-tctt	ctdcactgdarrc	TGAAGTG	4895
Query	211	AACTATT	GGCTGTTGCA-ATT	GATTGTGGGACAGAA 	ATTGATAGTGTCCT	TTGTATCT	266
Sbjct	4894	AACTCCTTT	cttcccttctt	g-ttgtgggacagaa	AtcGAtAccGtcc	rtgtatct	4836
Query	267	TCTTGAGAA	ATGTTGTCTTCAT	288			
Sbjct	4835	тсттбабат	rgttttatcttcat	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	3 :						
Query	230	TGATTGTGG	GACAGAAATTGATAGT	GTCCTTGTATCTTC	CTTGAGAAATGTTG	TCTTCATT	289
Sbjct	4812	TGATTGAGG.	AAACGAAATCGATAGT	gtcattgtatttgc	CTTGAGATGTTTTA	ATCTTCATC	4753
Query	290	TAAACTCGG.	ACTCGAAAATATATTC	-TTT-GCTTGTGAA	CTTGATTGAGAAA	GTGATGTT	347
Sbjct	4752	TACACTTTG.	Act-GgAgA-AtAttc	rttagtttagt	cttgattgaggaa	GTGATGTT	4695
Query	348	GATAGTGTC	CATGGCACTTCTGTCA	TTTGATTTTCTTCT.	GCACTGGATTCTT	GAAATGAA	407
Sbjct	4694	gatagtgtc	catercacttetetca	ͺϮϮϮĠΑϮϮϮϮϲϮϮϲϯ	rdcactddattctt	daggtgaa	4635
Query	408	CTGCTCTCT	TCTGTTGT-TAATT	GAGGTAAG-GATTT	TGA 445		
Sbjct	4634	ĊĠĠAŤŦŤĊŤ	TTTTAGTCTTTAATT	ĠĠĠĠĸĠĠĸĠĠĠĠĠĠ	TTGA 4594		

Range 24: 336 to 595

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
156 bits	(84)	6e-34()	208/265(78%)	19/265(7%)	Plus/Minus		
Features	s:						
Query	40	ATTGAGAAAG	TGATGTTGATAGTGT	CCATGGCACTTCTGT	CATTTGATTTTCT	TCTGCAC	99
Sbjct	595	ATTGAGGAAG	cgatgttgatagtgt	ccateecarttctet	catttgattttct	rctgcac	536
Query	100	TGGATTCTTG	AAATGAACTGCTCTC	TTCTGTTGTTA	-A-TTGAGGTAAG-	-GATTTT	152
Sbjct	535	TGGATTCTTG	AAGTGAACTGCTTTT	TTTAGTTGTAGTACT	TAATTGAGG-AAG	AGATGTT	477
Query	153	GAATGT-TCC	GATGTCTCCTCT-TG	AGCTGTTTGCTCTTC	TGCACTCGAACCT	GTAAGTA	210
Sbjct	476	GATGGTGTCC	-Attgcacttctgtc	arrtgattr-tette	tgcactgrarrct	rgaagtg	419
Query	211	AACTA-TTGG	CTGTTGCA-ATTG	ATTGTGGGACAGAAA	TTGATAGTGTCCT	TGTATCT	266
Sbjct	418	AACTGCTTTC	rrctgttgragattg	-ttgtgggagtgtaa	tcgatagtgtcct	rgtatct	360
Query	267	TCTTGAGAA-	ATGTTGTCTTCATTT	290			

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	s:						
Query	7	GACTCGAAA	ATATATTCTTT-GCTT	TGTGAACTTGATTGA	GAAAGTGATGTT(GATAGTGTC	65
Sbjct	1546	GACTGGAAA	ATATA-CCTTTAGTT1	rtagtacttgattga	dgaadcdatdtt	GATAGTGTC	1488
Query	66	CATGGCACT'	rctgtcatttgattt1	CTTCTGCACTGGAT	TCTTGAAATGAA	CTGCTCTCT	125
Sbjct	1487	CACGGCATT'	tctgtcatttgattt	rcttctgcactggat	rtcctgaagtgaa	ctgctrtct	1428
Query	126	TCTGTTGT	133				
Sbjct	1427	ተ ۈተۈተተۈተ	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		
Feature	s:						
Query	40	ATTGAGAAAG'	rgatgttgatagtg:	rccatggcactt	CTGTCATTTGATTTT	CTTCTGCAC	99
Sbjct	3361	ATTGAGGAAG	TGATGTTGATAGTG:	rccatggcatt1	CTGTCATTTGATTT	CTTCTGCAC	3302
Query	100	TGGATTCTTG	AAATGAACTGCTCT	СТТСТСТТСТ	133		
Sbjct	3301	TGGATTCTTG	AAGTGAACTGCTTT(cttctgttgt	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	s:						
Query	331	ATTGAGAAAGTO	GATGTTGATAGTGT	CCATGGCACTTCT	GTCATTTGATTTTC	CTTCTGCAC	390
Sbjct	787	ATTGAGAAAGT	GATGTTGATAATGT	CCATGTCACTTCT	greathtgathtd	TTCTGCAC	728
Query	391	TGGATTCTTGA	AATGAACTGCTCTC	TTCTGTTGT 42	4		
Sbjct	727	TGGATTCCTGAZ	AGTGAACTGCTTTC	rtctgttgt 69	4		

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	S :						
Query	7	GACTCGAAA	ATATATTCTTTGCTTC	GTGAACTTGATTGAG	SAAAGTGATGTTG	ATAGTGTCC	66
Sbjct	2401	GACTGGAAA	ATATTCTTTTTGTTT	ragtacttgattgac	GAAGAGATGTTA	ATAGTGTCC	2342
Query	67	ATGGCACTT	CTGTCATTTGATTTTC	CTTCTGCACTGGATT	CTTGAAATGAAC	TGCTCTCTT	126
Sbjct	2341	ATGGCACTT	cctgtcatttgatttt	rttctgcactggatt	rgttgaagtgaac	rtgctrrtrrt	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 3917 Query 67 126 Sbjct 3916 3857 Query 127 133 CTGTTGT Sbjct 3856 3850

Range 30: 5149 to 5271

Score		Exp	ect lo	dentities	Gaps	Strand	Frame	
147 bits	(79)	4e-3	1() 1	10/124(89%)	5/124(4%)	Plus/Minus		
Features	s:							
Query	326	ACTTG.	ATTGAGA	AAGTGATGTTGA	ATAGTGTCCATGGCAC	CTTCTGTCATTTG	ATTTTCTTC	385
Sbjct	5271	ACTTG	ATTGAGGZ	AAGTGATGTTG	ATAGTGTCCATGTCAC	cttctgtcatttg	ATTTTCTTC	5212
Query	386	TGCAC	TGGATTC	rtgaaatgaac:	rgctctcttctgi	TTGTTAATTGAGG	TAAG-GATT	441
Sbjct	5211	TGCAC	tggyttç:	rtgaagtgaaar	rgctrtrttttragd	rtrttaattgagg	-AAGTGATG	5153
Query	442	TTGA	445					
Sbjct	5152	ттĠА	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		
Feature	s:						
Query	315	TTTGCTTGTC	GAACTTGATTGAGAA	AGTGATGTTGATAG	TGTCCATGGCACT	TCTGTCATT	374
Sbjct	3569	TTTGCTGTTC	SAACTTAATTGAGGA	AAAGATGTTGATGG	rtgtccattgcact	rtctgtcatt	3510
Query	375	TGATTTTCTT	CTGCACTGGATTCT'	TGAAATGAACTGCT	CTCTTCTGTTGT	424	
Sbjct	3509	TGATTTTCT	CTGCACTGTATTCT	rgaagtgaactgct	TTCTTCTGTTGT	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		
Feature	s:						
Query	24	TTTGCTTGT	GAACTTGATTGAGAA	AGTGATGTTGATAG	TGTCCATGGCACT	TCTGTCATT	83
Sbjct	3569	TTTGCTGTT	JAACTTAATTGAGGA	AAAGATGTTGATGG	TGTCCATTGCACT	TCTGTCATT	3510
Query	84	TGATTTTCTT	TCTGCACTGGATTCT	TGAAATGAACTGCT	CTCTTCTGTTGT	133	
Sbjct	3509	†GATTTCT:	rctgcactgrattct:	rgaagtgaactgct	TTCTTCTGTTGT	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	s:						
Query	40	ATTGAGAAAGT	GATGTTGATAGTG	rccatggcacttc	TGTCATTTGATTTT	'CTTCTGCAC	99
Sbjct	1321	ATTGAGGAAGG	GATGTTGATAGTG:	rccatggcatttc	TGTCATTTGATTT	CTTCTGCAC	1262
Query	100	TGGATTCTTG	AATGAACTGCTCT(CTTCTGTTGT 1	33		
Sbjct	1261	tggattcttg	Agtgaactgctrt	cttcggttgt 1	228		

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	s:						
Query	29	TTGT-GAACTT	GATTGAGAAAGTGA	TGTTGATAGTGTCC	ATGGCACTTCTGT	CATTTGAT	87
Sbjct	505	ttgtagtactt	raattgaggaagaga	tgttgytgtgt	AttGCACTTCTGT	catttgat	446
Query	88	TTTCTTCTGCA	CTGGATTCTTGAAA	TGAACTGCTCTCTT	CTGTTGT 133		
Sbjct	445	TTTCTTCTGCA	CTGTATTCTTGAAG	TGAACTGCTTTCTT	CTGTTGT 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	S :						
Query	331	ATTGAGAAA	GTGATGTTGATAGTGT	CCATGGCACTTCTG	TCATTTGATTTTC	TTCTGCAC	390
Sbjct	4612	ATTGAGGAA	GCGATGTTGATAGTGT	ccateccarttcte	;tcatttgattttc	TTCTGCAC	4553
Query	391	TGGATTCTT	GAAATGAACTGCTCTC	TTCTGTTGTTA	ATTGAGGTAAG-G	ATTTTGA	445
Sbjct	4552	TGGATTCCT	GAAGTGAACTGCTTTC	TTTTTTAGTTTTTA	ATTGAGG-AAGTG	ATGTTGA	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	
Feature	s:					
Query	40	ATTGAGAAA	GTGATGTTGATAGTGT	CCATGGCACTTCT	GTCATTTGATTTTC	CTTCTGCAC 99
Sbjct	4612	ATTGAGGAA	GCGATGTTGATAGTGT	ccarddcarttcto	GTCATTTGATTTC	CTTCTGCAC 4553
Query	100	TGGATTCTT	GAAATGAACTGCTCTC	TTCTGTTGTT	AATTGAGGTAAG-G	GATTTTGA 154
Sbjct	4552	TGGATTCCT	GAAGTGAACTGCTTTC	######################################	AATTGAGG-AAGTG	ATGTTGA 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	s:						
Query	40	ATTGAGAAA	GTGATGTTGATAGTGT	CCATGGCACTTCTC	GTCATTTGATTTTC	TTCTGCAC	99
Sbjct	5167	ATTGAGGAA	 GTGATGTTGATAATGT	ccctggcacttctc	STCATTTGATTTC	TTCTGCAC	5108
Query	100	TGGATTCTT	GAAATGAACTGCTCTC	TTCTGTTGTT	AATTGAGGTAAG-G	ATTTTGA	154
Sbjct	5107	TGGATTCTT	GAAGTGAACTGCTTTC	chtrhrraghhrhho	sattgagg-aagtg	ATGTTGA	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		
Feature	s:						
Query	35	ACTTGATTG	AGAAAGTGATGTTGAT	AGTGTCCATGGCAC	TTCTGTCATTTG <i>I</i>	ATTTTCTTC	94
Sbjct	4716	ACTTGATTG.	AGGAAGTGATGTTGAT	AGTGTCCATGTCAC	cttctctcatttc	ATTTTCTTC	4657
Query	95	TGCACTGGA	TTCTTGAAATGAACTG	CTCTCTTCTGTTGT	-TAATTGAGG1	TAAG-GATT	150
Sbjct	4656	TGCACTGGA	ttcttgaggtgaacgd	atrtcttrtrtagt	ctttaattgagg-	-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	s:						
Query	40	ATTGAGAAAG'	rgatgttgatagtg:	rccatggcactt	CTGTCATTTGATTT	CTTCTGCAC	99
Sbjct	4969	ATTGAGGAAG	CGATGTTGATAGTG:	rccatggcarti	rCTGTCATTTGATTT	CTTCTGCAC	4910
Query	100	TGGATTCTTG	AAATGAACTGCTCT(CTTCTGTTGT	133		
Sbjct	4909	tggattettg	AAGTGAACTCCTTT	cttcgdttgt	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	s:						
Query	331	ATTGAGAAAG	rgatgttgatagtg:	CCATGGCACTT	CTGTCATTTGATTT	CTTCTGCAC	390
Sbjct	5662	ATTGAGGAAG!	rgatgttgataatg	tccctggcactt	cctctcatttcattt	rcttctgcac	5603
Query	391	TGGATTCTTG	AAATGAACTGCTCT(СТТСТСТТСТ	424		
Sbjct	5602	tggattettg	AAGTGAAATGCTTT	rttctgttgt	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		
Feature	s:						
Query	40	ATTGAGAAAG'	TGATGTTGATAGTG	TCCATGGCACTT	CTGTCATTTGATTTT	CTTCTGCAC	99
Sbjct	5662	ATTGAGGAAG	TGATGTTGATAATG:	rccctggcactt	ctgtcatttgattt	CTTCTGCAC	5603
Query	100	TGGATTCTTG	AAATGAACTGCTCT(CTTCTGTTGT	133		
Sbjct	5602	tggattettg	AAGTGAAATGCTTT	rttctgttgt	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	s:						
Query	331	ATTGAGAAAG'	rgatgttgatagtg:	PCCATGGCACTT(CTGTCATTTGATTTT	CTTCTGCAC	390
Sbjct	1153	ATTGAGGAAG'	rgatgttgataatg:	rccatgrcactto	CTGTCATTTGATTT	cttctgcac	1094
Query	391	TGGATTCTTG	AAATGAACTGCTCT	CTTCTGTTG 42	23		
Sbjct	1093	TGGATTCCTG	AAGTGAACTGCTTT	rttctgttg 10	061		

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	S :						
Query	40	ATTGAGAAAG'	TGATGTTGATAGTG	rccatggcactt(CTGTCATTTGATTTT	CTTCTGCAC	99
Sbjct	1153	ATTGAGGAAG	rgatgttgataatg:	rccatgrcacttc	CTGTCATTTGATTT	cttctgcac	1094
Query	100	TGGATTCTTG	AAATGAACTGCTCT	CTTCTGTTG 13	32		

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	s:						
Query	40	ATTGAGAAAGT	rgatgttgatagtg:	rccatggcacttc	CTGTCATTTGATTTT	CTTCTGCAC	99
Sbjct	1711	ATTGAGGAAG	rgatgttgataatg	rccatgrcacttc	ctgtcatttgattt	CTTCTGCAC	1652
Query	100	TGGATTCTTGA	AATGAACTGCTCT(CTTCTGTTG 13	32		
Sbjct	1651	tggattcctg	Agtgaactgctrt:	rttctgttg 16	519		

Range 45: 1841 to 1927

Score		Expect	Identities	Gaps	Strand	Frame	
128 bits	(69)	1e-25()	81/87(93%)	0/87(0%)	Plus/Minus		
Feature	s:						
Query	331	ATTGAGAAAG'	TGATGTTGATAGTG	rccatggcacttc'	TGTCATTTGATTTT	CTTCTGCAC	390
Sbjct	1927	ATTGAGGAAG	CGATGTTGATAGTG:	rccatggcatttc	tgtcatttgattt	CTTCTGCAC	1868
Query	391	TGGATTCTTG	AAATGAACTGCTCT(CTT 417			
Sbjct	1867	TGGATTCCTG	AAGTGAACTGCTTT(CTT 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		
Feature	s:						
Query	40	ATTGAGAAAG'	TGATGTTGATAGTG7	CCATGGCACTTC	TGTCATTTGATTTT	CTTCTGCAC	99
Sbjct	1927	AttGAGGAAG	cdatdttdatadtd1	cccatggcarttc	rgtcatttgattt	cttctgcac	1868
Query	100	TGGATTCTTG	AAATGAACTGCTCTC	CTT 126			
Sbjct	1867	TGGATTCCTG	AAGTGAACTGCTTTC	TT 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	s:						
Query	40	ATTGAGAAAG!	rgatgttgatagtg	ICCATGGCACTT	CTGTCATTTGATTTT	CTTCTGCAC	99
Sbjct	5830	AttGAGGAAG!	tgragttgatagtg	cccateccactt	ct d t c A t t d A t t d	cttctccac	5771
Query	100	TGGATTCTTG	AAATGAACTGCTCT(CTTCTGTTGT	133		
Sbjct	5770	TGGATTGTTG	AAGTGAACTGCTTT	rttctcttt	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	s:						
Query	40	ATTGAGAAA	GTGATGTTGATAGTGT	CCATGGCACTTCT	GTCATTTGATTTTC	TTCTGCAC	99
Sbjct	2026	ATTGAGGAA	 GCGATGTTGATAGTGT	CCATGTCACTTCT		TTCTGCAC	196

Ouery	100	TGGATTCTTGAAATGAACTGCTCTCTTCTGTTGT-TAATTGAGGTAAG-GATTTTGA	154
~ - 1			
Sbjct	1966	ŤĠĠĂŤŤĊŤŤĠĂĠĠŤĠĂĂĊĠĠĂŤŦŤĊŤŤŦŤŤŤAĠŤĊŤŦŦĂĂŤŤĠĂĠĠ–ĂĂĠĊĠĂŤĠŤŤĠĂ	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	S :						
Query	342	GATGTTGATA	GTGTCCATGGCACT	TCTGTCATTTGAT	TTTCTTCTGCACTG	GATTCTTGA	401
Sbjct	3215	GATATTGATG	gtgtccatrgcact	tctgtcatttgat	tttcttctgcactg	GATTCTTGG	3156
Query	402	AATGAACTGC'	TCTCTTCTGTTGT	424			
Sbjct	3155	AATGAAATGC'	rttcctttgttgt	3133			

Range 50: 1 to 76

Score		Expect	Identities	Gaps	Strand	Frame	<u> </u>
63.9 bits	s(34)	4e-06()	64/78(82%)	4/78(5%)	Plus/Minus		
Features	S :						
Query	7	GACTCGAAAATATA	ATTCTTTGC-TTG	r-gaacttgattga	AGAAAGTGATGTTO	SATAGTGT	64
Sbjct	76	GACTGGAAAATATA	ACTTTCAGTTT	ragtacttaactt	AGTAAGAGATGTT	SATAGTGT	19
Query	65	CCATGGCACTTCT	GTCAT 82				
Sbjct	18	ccatggcacttct	GTCAT 1				

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	GACTCGAAAATA	TATTCTTTGCTTGTG	AACTTGATTGAGA	AAGTGATGTTGATA	GTGTCC 6	66
Sbjct	813	GACTTGAAAATA	TACTTTTAGTTTGAG	TACTTGTTTGAGG	AAGCTTTGTTGATA	dfftcc 7	754
Query	67	ATGGCACTTCTG	TCATTTGATTTTCTT	CTGCACTGGATTC	TTGAAATGAACTGC	TCTCTT 1	126
Sbjct	753	Atgccacttctc	ተ ۈልተተተۈልተተተተረተተ	ctrcactagattc	rtgaaatgaactgc	c trtctt ϵ	694
Query	127	CTGTTGTTAATT	GAGGTAA-GGATTTT	GAATGTTCCGATG	CTCCTCTTGAGCT	GTTTGC 1	185
Sbjct	693	ctgttgtagatt	gaggtaaaggagtta	aaaa-ttcccttc	rtgcctctttaatt	dtttca 6	635
Query	186	TCTTCTGCACTC	GAACCTGTAAGTAAA 	CTATTGGCTGTTG	CAATTGATTGTGGG	SACAGAA 2	245
Sbjct	634	arttctgcactc	GAAACTGTAGGTAAA	ctrttrgccattg:	rACCTGATTGAAAA	GGAGAT 5	575
Query	246	ATTGATAGTGTC	CTTGTATCTTCTTGA	GAAATGTTGTCTT(CATTTAAACTCGGA	CTCGAA 3	305
Sbjct	574	AtcGAtAGtGtC	cttgtatcttct	.dargtrctatcttc	catctacactrica	ctrgaa 5	515
Query	306	AATATATTCTTT	GCTTGTGAACTTGAT	TGAGAAAGTGATGT	TTGATAGTGTCCAT	GGCACT 3	365
Sbjct	514	AATATACTTTTA	grttgagtacttgtt	rtgaggaagctttg	rtgatagtgtccat	deckt 4	455
Query	366	TCTGTCATTTGA	TTTTCTTCTGCACTG	GATTCTTGAAATGA	ACTGCTCTCTTCT	GTTGTT 4	425
Sbjct	454	tctgtcatatga	ttttcttcttctcactd	GATTCTTGAAATGA	Akctectrtcttct	dright 3	395
Query	426	AATTGAGGTAA-	GGATTTTGAATGTTC	CGATGTCTCCTCT	rgagctgtttgctc	CTTCTGC 4	484
Sbjct	394	GATTGAGGTAAA	ggagttaaaaa-ttc	cccrtctrtrctctr	тааттсттсаат	rttctgc 3	336
Query	485	ACTCGAACCTGT.	AAGTAAACTATTGGC	TGTTGCAATTGAT	rgtgggacagaaat	TGATAG 5	544
Sbjct	335	ActcGAAAcaGt.	AGGTAAACTATTGC	cattgracttgat	rgaaaaggagatat	cgatag 2	276
Query	545	TGTCCTTGTATC	TTCTTGAGAAATGTT 	GTCTTCATTTAAA(CTCGGACTCGAAAA	ТАТА 602 	2

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	GACTCGAAAATA	TATTCTTTGCTTGTG	AACTTGATTGAGAA	AGTGATGTTGATA	GTGTCC	66
Sbjct	522	GACTTGAAAATA	TACTTTTAGTTTGAG	TACTTGTTTGAGGA	AGCTTTGTTGATA	GTGTCC	463
Query	67	ATGGCACTTCTG	TCATTTGATTTTCTT	CTGCACTGGATTCT	TGAAATGAACTGC	CTCTCTT	126
Sbjct	462	Atgccacttctc	tcatatgattttctt	ctrcactedattc	rtgaaatgaactgc	ctrtctt	403
Query	127	CTGTTGTTAATT	GAGGTAA-GGATTTT	GAATGTTCCGATGT	CTCCTCTTGAGCT	GTTTGC	185
Sbjct	402	ctdttdtggatt	gaggtaaagga-gtt	addaattcccttct	тттстсттатт	GTTTCA	344
Query	186	TCTTCTGCACTC	GAACCTGTAAGTAAA 	CTATTGGCTGTTGC	CAATTGATTGTGGG	SACAGAA 	245
Sbjct	343	arttctgcactc	gaaacagtaggtaaa	ctattrdccattd	racttgattgaaaa	AGGAGAT	284
Query	246	ATTGATAGTGTC	CTTGTATCTTCTTGA 	GAAATGTTGTCTTC	CATTTAAACTCGGA	CTCGAA	305
Sbjct	283	AtcGAtAGtGtC	cttgtatcttctta	ĠĀTĀŢŢĊŢĠŢŢŢŢ	rAtctrcActrrdA	сттĠАА	224
Query	306	AATATATTCTTT	GCTTGTGAACTTGAT 	TGAGAAAGTGATG7	TGATAGTGTCCAT	GGCACT	365
Sbjct	223	AATATACTTTCA	ĠŦŦŦĠŦĠŦĀĊŦŦĠĀŦ	†gaggaagctttg:	rtgatagtgtccat	rĠĠĊĀĊŦ	164
Query	366	TCTGTCATTTGA	TTTTCTTCTGCACTG	GATTCTTGAAATGA	ACTGCTCTCTTCT	GTTGTT	425
Sbjct	163	tctgtcatttga	ttttcttcttckctg	ĠĀŦŦĊŦŦĠĀĀĀŦĠĀ	Actgctrccttct	cĠţţĠţG	104
Query	426	AATTGAGGTAA-	GGATTTTGAATGTTC 	CGATGTCTCCTCT7	GAGCTGTTTGCTC	CTTCTGC	484
Sbjct	103	GATTGGGGTAAA	ĠĠĀGŦŦĀĀĀĀĀ—ŦŦĊ	ĊĠŦŦĠŦŦŦĊĊŦĊŦſ	тааттфтттсаат	rttċtĠċ	45
Query	485	ACTCGAACCTGT	AAGTAAACTATTGGC 	TGTTGCAATTGATT	TG 526		
Sbjct	44	AĊŢĊĠĀĀAĊĀĠŢ.	AGĠ TÀÀÀĊTÀTTGĊ	CATTĠTACTTĠATT	ːĠ 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	Features:						
Query	104	TTCTTGAAAT	GAACTGCTCTCTC	TGTTGTTAATTGAGG	TAA-GGATTTTGA	ATGTTCCG	162
Sbjct	1007	ttcttgaact	GAACTGCTTTCTTC	tgttgtggattgagd	rtaaagga-gtta <i>r</i>	AAATTTCG	949
Query	163	ATGTCTCCTC	TTGAGCTGTTTGCT	CTTCTGCACTCGAAC	CTGTAAGTAAACT	ATTGGCTG	222
Sbjct	948	TTGTTTTCTT	rtgaartgtttgat	CTTCTGCACTCGAAA	cagtaggcaaact	TATTTGCCA	889
Query	223	TTGCAATTGA	TTGTGGGACAGAAA 	TTGATAGTGTCCTTC	TATCTTCTTGAG <i>F</i>	AATG-T-T	280
Sbjct	888	TTGTACTTGA:	rtgaaaaggagata	tcgatagtgtccttc	statettetteag	AtGTtCt	831
Query	281	GTCTTCATTT	AAACTCGGACTCGA	AAATATATTCTTTGC	TTGTGAACTTGAT	TGAGAAAG	340
Sbjct	830	atcttcatct2	Acactrrdactrda	AAATATACTTTTAGT	rttgagtacttgt	Trgaggaag	771
Query	341	TGATGTTGAT	AGTGTCCATGGCAC	TTCTGTCATTTGATT	TTCTTCTGCACTO	GATTCTTG	400
Sbjct	770	ctttgttgyt	AGTGTCCATGGCAC	ttctctchtthtt	rttcttcttckctz	AGATTCTTG	711
Query	401	AAATGAACTG(CTCTCTTCTGTTGT	TAATTGAGGTAA-GG	GATTTTGAATGTTC	CCGATGTCT	459
Sbjct	710	AAATGAACTG	chrhchtchchch	agattgaggtaaagd	sagttaaaaa_ttd	cccrtctrc	652
Query	460	CCTCTTGAGC	rgtttgctcttctg 	CACTCGAACCTGTAA	GTAAACTATTGGC	CTGTTGCAA	519
Sbjct	651	cctctttaar	rgtttcaatttctg	cactcgaaactgtac	schaaachthtec	CCATTGTAC	592
Query	520	TTGATTGTGG	GACAGAAATTGATA	GTGTCCTTGTATCTT	CTTGAGAAATGT7	GTCTTCAT	579
Sbjct	591	CTGATTGAAA	aggagatatcgata	ĠŦĠŦĊĊŦŦĠŦĂŦĊŦŦ	cttcagargtrct	TATCTTCAT	532
Query	580	TTAAACTCGG	ACTCGAAAATATA	602			
Sbjct	531	CTACACTTTG	Actrgaaaatata	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	GACTCGAAAATA	ATATTCTTTGCTTGTC	GAACTTGATTGAGA	AAGTGATGTTGA	TAGTGTCC	66
Sbjct	231	GACTTGAAAAT	ATACTTTCAGTTTGTC	TACTTGATTGAGG.	AAGCTTTGTTGA	TAGTGTCC	172
Query	67	ATGGCACTTCTC	GTCATTTGATTTTCT7	CTGCACTGGATTC	TTGAAATGAACT	GCTCTCTT	126
Sbjct	171	ArggeActtete	steatttgattttet	rctrcactggattc	ttgaaatgaact	GCTTCCTT	112
Query	127	CTGTTGTTAATT	rgaggtaa-ggattti	GAATGTTCCGATG	TCTCCTCTTGAG	CTGTTTGC	185
Sbjct	111	CTGTTGTGGAT	rggggtaaaggagtt <i>i</i>	AAAA-TTCCGTTG	тттсстстть	TTGTTTCA	53
Query	186	TCTTCTGCACTO	CGAACCTGTAAGTAA	ACTATTGGCTGTTG	CAATTGATTG	235	
Sbjct	52	ATTTCTGCACTC	CGAAACAGTAGGTAAA	Actattrdccattd	TACTTGATTG	3	