BLAST® » blastn suite » RID-YXKSP7WN014

BLAST Results

X79493:D.melanogaster ey mRNA (exons 2-9)

RID <u>YXKSP7WN014</u> (Expires on 10-02 04:46 am)

Query ID X79493.1 Database Name nr

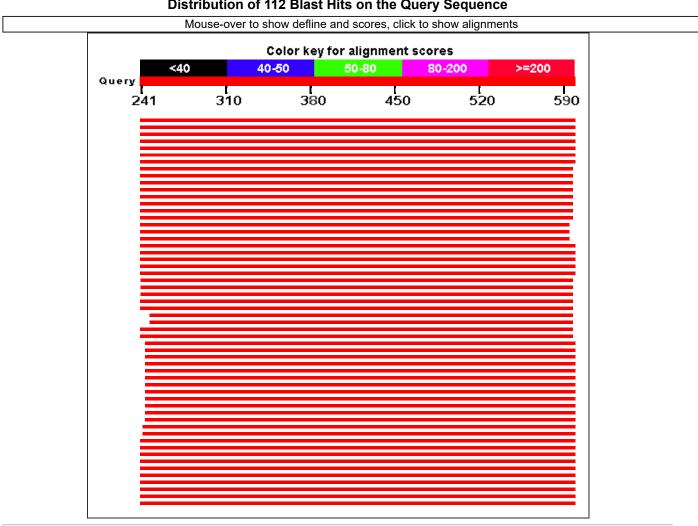
Description D.melanogaster ey mRNA (exons 2-9) **Description** Nucleotide collection (nt)

Molecule type nucleic acid Query Length 2848

Program BLASTN 2.5.0+

Graphic Summary

Distribution of 112 Blast Hits on the Query Sequence



Description	Max	Total	Query	E	Ident	Accession
i.	score	score	cover	value		

Sequences producing significant alignments.

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila melanogaster eyeless (ey), transcript variant D, mRNA	648	648	100%	0.0	100%	NM_001014693.2
Drosophila melanogaster eyeless (ey), transcript variant C, mRNA	648	648	100%	0.0	100%	NM_001014694.2
Drosophila melanogaster eyeless (ey), transcript variant A, mRNA	648	648	100%	0.0	100%	NM 079889.3
Drosophila melanogaster eyeless (ey), transcript variant B, mRNA	648	648	100%	0.0	100%	NM 166789.2
Drosophila melanogaster IP14880 full insert cDNA	648	648	100%	0.0	100%	BT025949.2
Drosophila melanogaster GH01157 full insert cDNA	648	648	100%	0.0	100%	BT011390.1
D.melanogaster ey mRNA (exons 2-9)	648	648	100%	0.0	100%	X79493.1
Drosophila simulans eyeless (Dsim\ey), transcript variant E, mRNA	618	618	99%	4e-173	98%	XM_016180677.1
Drosophila simulans eyeless (Dsim\ey), transcript variant D, mRNA	618	618	99%	4e-173	98%	XM_016180676.1
Drosophila simulans eyeless (Dsim\ey), transcript variant C, mRNA	618	618	99%	4e-173	98%	XM_016180675.1
Drosophila simulans eyeless (Dsim\ey), transcript variant B, mRNA	618	618	99%	4e-173	98%	XM_016180674.1
Drosophila sechellia ey (Dsec∖ey), mRNA	612	612	99%	2e-171	98%	XM_002043659.1
Drosophila yakuba uncharacterized protein (Dyak\GE14559), mRNA	576	576	99%	1e-160	96%	XM_002099582.2
Drosophila erecta uncharacterized protein, transcript variant B (Dere\GG16399), mRNA	563	563	99%	7e-157	95%	XM_015153159.1
Drosophila erecta uncharacterized protein, transcript variant A (Dere\GG16399), mRNA	563	563	99%	7e-157	95%	XM 001982674.2
PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102386), transcript variant X3, mRNA	459	459	98%	2e-125	89%	XM_017207327.1
PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102386), transcript variant X2, mRNA	459	459	98%	2e-125	89%	XM_017207325.1
PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102386), transcript variant X1, mRNA	459	459	98%	2e-125	89%	XM 017207324.1
PREDICTED: Drosophila biarmipes paired box protein Pax-6 (LOC108036028), transcript variant X4, mRNA	453	453	100%	9e-124	88%	XM_017111967.1
PREDICTED: Drosophila biarmipes paired box protein Pax-6 (LOC108036028), transcript variant X3, mRNA	453	453	100%	9e-124	88%	XM 017111966.1

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
	PREDICTED: Drosophila biarmipes paired box protein Pax-6 (LOC108036028), transcript variant X2, mRNA	453	453	100%	9e-124	88%	XM_017111965.1
	PREDICTED: Drosophila biarmipes paired box protein Pax-6 (LOC108036028), transcript variant X1, mRNA	453	453	100%	9e-124	88%	XM_017111962.1
	PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020368), mRNA	453	453	100%	9e-124	88%	XM_017088589.1
	PREDICTED: Drosophila rhopaloa paired box protein Pax-6 (LOC108043626), transcript variant X3, mRNA	448	448	99%	4e-122	88%	XM_017122410.1
	PREDICTED: Drosophila rhopaloa paired box protein Pax-6 (LOC108043626), transcript variant X2, mRNA	448	448	99%	4e-122	88%	XM_017122408.1
	PREDICTED: Drosophila rhopaloa paired box protein Pax-6 (LOC108043626), transcript variant X1, mRNA	448	448	99%	4e-122	88%	XM_017122407.1
	PREDICTED: Drosophila takahashii paired box protein Pax-6 (LOC108058374), transcript variant X2, mRNA	437	437	99%	7e-119	87%	XM 017143069.1
	PREDICTED: Drosophila takahashii paired box protein Pax-6 (LOC108058374), transcript variant X1, mRNA	437	437	99%	7e-119	87%	XM_017143068.1
	PREDICTED: Drosophila elegans paired box protein Pax-6 (LOC108145319), transcript variant X2, mRNA	435	435	97%	2e-118	88%	XM_017270691.1
	PREDICTED: Drosophila elegans paired box protein Pax-6 (LOC108145319), transcript variant X1, mRNA	435	435	97%	2e-118	88%	XM_017270690.1
	PREDICTED: Drosophila ficusphila paired box protein Pax-6 (LOC108095041), transcript variant X2, mRNA	428	428	99%	4e-116	87%	XM_017195935.1
	PREDICTED: Drosophila ficusphila paired box protein Pax-6 (LOC108095041), transcript variant X1, mRNA	428	428	99%	4e-116	87%	XM 017195934.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164499), transcript variant X4, mRNA	419	419	98%	2e-113	86%	XM 017300273.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164499), transcript variant X3, mRNA	419	419	98%	2e-113	86%	XM_017300272.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164499), transcript variant X2, mRNA	419	419	98%	2e-113	86%	XM_017300271.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164499), transcript variant X1, mRNA	419	419	98%	2e-113	86%	XM_017300270.1

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
	Drosophila pseudoobscura pseudoobscura ey, transcript variant F (Dpse\ey), mRNA	419	419	98%	2e-113	86%	XM_015188708.1
	Drosophila pseudoobscura pseudoobscura ey, transcript variant E (Dpse\ey), mRNA	419	419	98%	2e-113	86%	XM_015188707.1
	Drosophila pseudoobscura pseudoobscura ey, transcript variant D (Dpse\ey), mRNA	419	419	98%	2e-113	86%	XM_015188706.1
	Drosophila pseudoobscura pseudoobscura ey, transcript variant C (Dpse\ey), mRNA	419	419	98%	2e-113	86%	XM_015188705.1
	Drosophila pseudoobscura pseudoobscura ey, transcript variant B (Dpse\ey), mRNA	419	419	98%	2e-113	86%	XM_015188704.1
	Drosophila pseudoobscura pseudoobscura ey, transcript variant A (Dpse\ey), mRNA	419	419	98%	2e-113	86%	XM_001352335.3
	Drosophila persimilis ey (Dper\ey), mRNA	419	419	98%	2e-113	86%	XM_002027037.1
	Drosophila ananassae uncharacterized protein (Dana\GF22818), mRNA	407	407	98%	1e-109	85%	XM_001966210.2
	PREDICTED: Drosophila kikkawai paired box protein Pax-6 (LOC108079510), transcript variant X2, mRNA	401	401	99%	5e-108	85%	XM_017173859.1
	PREDICTED: Drosophila kikkawai paired box protein Pax-6 (LOC108079510), transcript variant X1, mRNA	401	401	99%	5e-108	85%	XM 017173853.1
	PREDICTED: Drosophila arizonae paired box protein Pax-6 (LOC108617808), transcript variant X3, mRNA	372	372	100%	2e-99	83%	XM_018013598.1
	PREDICTED: Drosophila arizonae paired box protein Pax-6 (LOC108617808), transcript variant X2, mRNA	372	372	100%	2e-99	83%	XM 018013597.1
	PREDICTED: Drosophila arizonae paired box protein Pax-6 (LOC108617808), transcript variant X1, mRNA	372	372	100%	2e-99	83%	XM_018013596.1
	Drosophila mojavensis uncharacterized protein, transcript variant A (Dmoj\G114081), mRNA	369	369	100%	3e-98	83%	XM_002011366.2
	Drosophila mojavensis uncharacterized protein, transcript variant E (Dmoj\G114081), mRNA	369	369	100%	3e-98	83%	XM_015160694.1
	Drosophila mojavensis uncharacterized protein, transcript variant D (Dmoj\GI14081), mRNA	369	369	100%	3e-98	83%	XM_015160693.1
	Drosophila mojavensis uncharacterized protein, transcript variant C (Dmoj\GI14081), mRNA	369	369	100%	3e-98	83%	XM_015160692.1
	Drosophila mojavensis uncharacterized protein, transcript variant B (Dmoj\GI14081), mRNA	369	369	100%	3e-98	83%	XM_015160691.1
	Drosophila virilis eyeless (Dvir\ey), transcript variant A, mRNA	342	342	100%	4e-90	81%	XM_002059708.2

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
	Drosophila virilis eyeless (Dvir\ey), transcript variant B, mRNA	342	342	100%	4e-90	81%	XM_015168533.1
	PREDICTED: Drosophila busckii paired box protein Pax-6 (LOC108607418), transcript variant X2, mRNA	334	334	99%	6e-88	81%	XM_017998214.1
	PREDICTED: Drosophila busckii paired box protein Pax-6 (LOC108607418), transcript variant X1, mRNA	334	334	99%	6e-88	81%	XM_017998213.1
	Drosophila melanogaster chromosome 4	334	884	100%	6e-88	100%	AE014135.4
	Drosophila melanogaster clone BACR06K04, complete sequence	334	663	100%	6e-88	100%	AC150557.1
	Drosophila melanogaster eyeless (ey) gene, exons 2, 3 and partial cds; and transposon jockey, partial sequence	334	563	85%	6e-88	100%	DQ091189.1
	Drosophila melanogaster, chromosome 4, region 101C-101D, BAC clone BACR16H06, complete sequence	334	663	100%	6e-88	100%	AC099309.1
	Drosophila melanogaster, chromosome 4, region 101F-102F, BAC clone BACR30L15, complete sequence	334	663	100%	6e-88	100%	AC010576.16
	Drosophila willistoni uncharacterized protein (Dwil\GK13702), mRNA	320	320	98%	1e-83	80%	XM_002072588.2
	Drosophila simulans eyeless (ey) gene, exons 2, 3 and partial cds; and transposon jockey, partial sequence	316	539	85%	2e-82	98%	DQ091188.1
	PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102386), transcript variant X4, mRNA	313	313	64%	2e-81	90%	XM_017207328.1
	PREDICTED: Drosophila navojoa paired box protein Pax-6-like (LOC108657902), partial mRNA	309	309	85%	2e-80	82%	XM_018110557.1
	PREDICTED: Bactrocera dorsalis paired box protein Pax-6-like (LOC105228660), mRNA	288	288	98%	8e-74	78%	XM_011208561.1
	Drosophila ananassae uncharacterized protein, transcript variant B (Dana\GF21877), mRNA	280	280	99%	1e-71	78%	XM_014903679.1
	Drosophila ananassae uncharacterized protein, transcript variant A (Dana\GF21877), mRNA	280	280	99%	1e-71	78%	XM_001967394.2
	PREDICTED: Ceratosolen solmsi marchali paired box protein Pax-6 (LOC105363389), mRNA	275	275	99%	5e-70	77%	XM_011501059.1
	PREDICTED: Stomoxys calcitrans paired box protein Pax-6-like (LOC106094139), mRNA	269	269	98%	2e-68	77%	XM 013261329.1
	PREDICTED: Stomoxys calcitrans paired box protein Pax-6-like (LOC106093015), mRNA	269	269	98%	2e-68	77%	XM_013259984.1
	PREDICTED: Drosophila bipectinata paired box protein Pax-6-like (LOC108131200), partial mRNA	260	260	98%	1e-65	76%	XM_017249961.1
	PREDICTED: Bactrocera cucurbitae paired box protein Pax-6 (LOC105219314), mRNA	260	260	96%	1e-65	77%	XM_011195357.1
	PREDICTED: Drosophila bipectinata paired box protein Pax-6-like (LOC108133768), partial mRNA	259	259	65%	4e-65	84%	XM_017253833.1
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	Description	Max score	Total score	Query cover	E value	Ident	Accession
	PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102342), transcript variant X6, mRNA	257	257	97%	1e-64	76%	XM 017207183.1
	PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102342), transcript variant X4, mRNA	257	257	97%	1e-64	76%	XM_017207181.1
	PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102342), transcript variant X3, mRNA	257	257	97%	1e-64	76%	XM 017207180.1
	PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102342), transcript variant X2, mRNA	257	257	97%	1e-64	76%	XM 017207179.1
	PREDICTED: Drosophila eugracilis paired box protein Pax-6 (LOC108102342), transcript variant X1, mRNA	257	257	97%	1e-64	76%	XM_017207178.1
	PREDICTED: Bactrocera oleae paired box protein Pax-6 (LOC106622499), mRNA	257	257	96%	1e-64	76%	XM_014241693.1
	Drosophila pseudoobscura pseudoobscura GA27636 (Dpse\GA27636), miscRNA	255	255	97%	5e-64	76%	XR_001453414.1
	Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant B (Dpse\GA27636), mRNA	255	255	97%	5e-64	76%	XM_015188732.1
	Drosophila pseudoobscura pseudoobscura uncharacterized protein, transcript variant A (Dpse\GA27636), mRNA	255	255	97%	5e-64	76%	XM 002135628.2
	Drosophila persimilis GL17563 (Dper\GL17563), mRNA	255	255	97%	5e-64	76%	XM_002028436.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164475), transcript variant X4, mRNA	253	253	97%	2e-63	76%	XM_017300230.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164475), transcript variant X2, mRNA	253	253	97%	2e-63	76%	XM_017300228.1
	PREDICTED: Drosophila miranda paired box protein Pax-6 (LOC108164475), transcript variant X1, mRNA	253	253	97%	2e-63	76%	XM_017300227.1
	Drosophila willistoni uncharacterized protein (Dwil\GK13683), mRNA	253	253	97%	2e-63	76%	XM_002072557.2
	PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X8, mRNA	250	250	99%	2e-62	76%	XM_017088673.1
	PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X7, mRNA	250	250	99%	2e-62	76%	XM_017088672.1
	PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X6, mRNA	250	250	99%	2e-62	76%	XM_017088670.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X5, mRNA	250	250	99%	2e-62	76%	XM_017088669.1
PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X4, mRNA	250	250	99%	2e-62	76%	XM_017088668.1
PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X2, mRNA	250	250	99%	2e-62	76%	XM_017088666.1
PREDICTED: Drosophila suzukii paired box protein Pax-6 (LOC108020394), transcript variant X1, mRNA	250	250	99%	2e-62	76%	XM_017088665.1
Drosophila simulans uncharacterized protein, transcript variant C (Dsim\GD24416), mRNA	250	250	99%	2e-62	76%	XM_016180731.1
Drosophila simulans uncharacterized protein, transcript variant B (Dsim\GD24416), mRNA	250	250	99%	2e-62	76%	XM_016180730.1
PREDICTED: Bactrocera cucurbitae paired box protein Pax-6 (LOC105219702), mRNA	250	250	97%	2e-62	76%	XM_011195998.1

Alignments

Drosophila melanogaster eyeless (ey), transcript variant D, mRNA

Sequence ID: NM_001014693.2 Length: 3462 Number of Matches: 1

Range 1: 847 to 1205

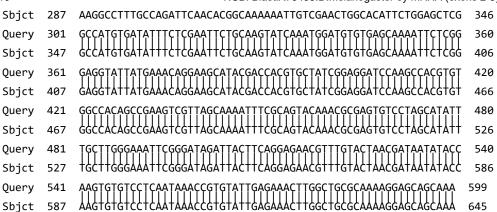
Score		Expect	Identities	Gaps	Strand	Frame
648 bits	s(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCC	AGATTCAACACGGCAA	ι ΑΑΑΤΤΘΤΕΘΑΑΕΤΘΘ	- - - - - - - - - - - - - - - - - - -	CG 300
Sbjct	847	YYGGC5+++GC5	<u></u> AGA++¢AA¢A¢GG¢AA	ͿϪϪϪϯϯͼϯϲͼϪϪϲϯͼͼͼ	-	CG 906
Query	301	GCCATGTGATAT	TTCTCGAATTCTGCAAG	϶ͳΑΤϚΑΑΑΤ <mark>Θ</mark> ΘΑΤΘΤΘ	ΓGAGCAAAATTCTC	GG 360
Sbjct	907	gccytgtgytyt.	ttctcgAAttctgcAA	₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	tgygcyyyy	GG 966
Query	361	GAGGTATTATGA	AACAGGAAGCATACGA(CACGTGCTATCGGAGG	GATCCAAGCCACGT	GT 420
Sbjct	967	GAGGTATTATGA	ΑΑ ĊΑĠĠΑΑĠĊΑ†ΑĊĠΑα	ccycetecty	gytççyygççyçet	dt 1026
Query	421	GGCCACAGCCGA	AGTCGTTAGCAAAATT	rcgcagtacaaacgcg <i>i</i>	\GTGTCCTAGCATA	TT 480
Sbjct	1027	ęęccycyecegy.	AĠ†ċĠ††AĠċAAAA††	tcgcygtycyy	detetectaecata	†† 1086
Query	481	TGCTTGGGAAAT	TCGGGATAGATTACTT	AGGAGAACGTTTGTA	TAACGATAATATA	CC 540
Sbjct	1087	tĠĊ††ĠĠĠAAA†	tċĠĠĠAtAĠAttAċtto	taggagaacgtttgtac	ttaacgataatata	CC 1146
Query	541	AAGTGTGTCCTC	AATAAACCGTGTATTGA	\GAAACTTGGCTGCGCA	AAAAGGAGCAGCAA 	A 599 I
Sbjct	1147	AAGTGTGTCCTC	AATAAACCGTGTATTGA	\dAAActtddctdcdc <i>i</i>	\AAAĠĠAĠĊAĠĊAA	Å 1205

Drosophila melanogaster eyeless (ey), transcript variant C, mRNA

Sequence ID: NM_001014694.2 Length: 2902 Number of Matches: 1

Range 1: 287 to 645

Score		Expect	Identities	Gaps	Strand	Frame
648 bits	s(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCA	GATTCAACACGGCAAAAA 	ATTGTCGAACTGGCA	ACATTCTGGAGCTCG	300



Drosophila melanogaster eyeless (ey), transcript variant A, mRNA Sequence ID: **NM_079889.3** Length: 3282 Number of Matches: 1 Range 1: 667 to 1025

Score		Expect	Identities	Gaps	Strand	Frame
648 bits	(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	s:					
Query	241	AAGGCCTTTGCC	ĄĠĄŢŢĊĄĄĊĄĊĠĠĊĄĄ	 AAAATTGT CGAACTGGG	ACATTCTGGAGC	ГСG 300
Sbjct	667	YYGGCC+++GCC	ϟͼϗϯϯϲϗϗϲϗϲϗͼϲϗϗ	ልልልልተተ <u></u> ፈተና <mark></mark> ያልል	;ϥϛϥϯϯϛϯͼͼϥͼϲ·	rcg 726
Query	301	GCCATGTGATAT	TTCTCGAATTCTGCAA	GTATCAAATGGATGTG1	GAGCAAAATTCT	CGG 360
Sbjct	727	<u></u> 	Ͱϯϲϯϲͼϭϭϯϯϲϯͼϲϭϭ	ĠŦĂŦĊĂĂĂŦĠĠĂŦĠŦĠŦ	-gygcyyyyttet	GG 786
Query	361	GAGGTATTATGA	AACAGGAAGCATACGA	CCACGTGCTATCGGAGG	GATCCAAGCCACG ⁻	[GT 420
Sbjct	787	GAGGTATTATGA	λΑĊΑĠĠΑΑĠĊΑ†ΑĊĠΑ	ccycetecty+ceeye	ġĄţĊĊĄĄĠĊĊĄĊĠ <u>-</u>	tgt 846
Query	421	GGCCACAGCCGA	AGTCGTTAGCAAAATT	TCGCAGTACAAACGCGA	\GTGTCCTAGCATA	ATT 480
Sbjct	847	ggccycygccgy	deteettaeeddad	tcgcyetycyyy	λ <u>Ġ</u> ϯĠϯċċϯλĠċλϯ	\tt 906
Query	481	TGCTTGGGAAAT	TÇĞĞĞATAĞATTAÇTT	CAGGAGAACGTTTGTAG	TAACGATAATAT	ACC 540
Sbjct	907	tgcttgggyyyt.	tcgggatagattactt	çyeqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	taacgataatat	7CC 966
Query	541	AAGTGTGTCCTC/	^	AGAAACTTGGCTGCGCA	AAAAGGAGCAGCA/	AA 599
Sbjct	967	<u> </u> አለ <u></u> ተ	<u></u>	AGAAAC++GGC+GCGCA	γγγγβεγβεγβεγγ	A 1025

Drosophila melanogaster eyeless (ey), transcript variant B, mRNA Sequence ID: **NM_166789.2** Length: 2854 Number of Matches: 1 Range 1: 239 to 597

Score		Expect	Identities	Gaps	Strand	Frame
648 bits	s(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCA	GATTCAACACGGCAAA	AAATTGTCGAACTGGCAC	ĄŢŢĊŢĠĠĄĠĊŢĊĠ	300
Sbjct	239	AAGGCC+++GCCA	 βΑΤΤĊΑΑĊΑĊĠĠĊΑΑΑ	ϪϪϪϯϯϗϯϲϗϪϪϲϯϗϗϲϪϲ	Attctggygctcg	298
Query	301	GCCATGTGATATT	Τςτςφρρττςτοςρρο	TATCAAATGGATGTGTGA	GCAAAATTCTCGG	360
Sbjct	299	gccytgtgytytt.	ϯ⋵ϯ⋵Ġልልϯϯ⋵ϯĠ⋵ልልĠ	tatcaaatggatgtgtga	ĠĊĂĂĂĂŦŦĊŦĊĠĠ	358
Query	361	GAGGTATTATGAA	ACAGGAAGCATACGAC	CACGTGCTATCGGAGGAT	CCAAGCCACGTGT	420
Sbjct	359	GAGGTATTATGAA	ACAGGAAGCATACGAC	cycetecty	ccyyeccycetet	418
Query	421	GGCCACAGCCGAA	GTCGTTAGCAAAATTT	CGCAGTACAAACGCGAGT	GTCCTAGCATATT	480
Sbjct	419	ggccycygccgyy	ĠŦĊĠŦŦĀĠĊĀĀĀĀŦŦŦ	cgcygtycy	ĠŦĊĊŦĀĠĊĀŦĀŦŦ	478
Query	481	TGCTTGGGAAATT	CGGGATAGATTACTTC	AGGAGAACGTTTGTACTA	ACGATAATATACC	540
Sbjct	479	tĠĊttĠĠĠAAAtt	ĊĠĠĠĂŦĂĠĂŦŦĂĊŦŦĊ	AGGAGAACGTTTGTACTA	AĊĠĂŦĂĂŦĂŦĂĊĊ	538
Query	541	AAGTGTGTCCTCA	<u>ATAAACCGTGTATTGA</u>	GAAACTTGGCTGCGCAAA	AGGAGCAGCAAA	599
Sbjct	539	AAGTGTGTCCTCA	ልተልልል ċċ ĠተĠተልተተĠል	ĠĂĂĂĊŦŦĠĠĊŦĠĊĠĊĂĂĀ	AGGAGCAGCAAA	597

Drosophila melanogaster IP14880 full insert cDNA

Sequence ID: BT025949.2 Length: 1604 Number of Matches: 1

Range 1: 813 to 1171

Score		Expect	Identities	Gaps	Strand	Frame
648 bits	s(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	es:					
Query	241	A AGGCCTTTGCC	AGATTCAACACGGCAAA	<i></i>	- - - - - - - - - - - - - - - - - - -	TCG 300
Sbjct	813	YYGGCC+++GCC	 Α <mark>ΘΑΤΤΕΑΑΕΑΕΘΕΕΑΑΑΑ</mark>	ϪϪͰϯϗϯϲϗϪϪϲϯϗϗϭ	₽₩₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	tcG 872
Query	301	ĢÇÇATĢTĢATAT	TTCTCGAATTCTGCAAG	ΤΑΤϹΑΑΑΤΘΘΑΤΘΤΘ	ΓGAGCAAAATTCT	CGG 360
Sbjct	873	<u></u>	++6+6999+46496999	tatcaaatggatgtg	ͰĠਖ਼ĠĊਖ਼ਖ਼ਖ਼ਖ਼ႵႵĊႵ	CGG 932
Query	361	ĢĄĢĢŢĄŢŢĄŢĢĄ	AACAGGAAGCATACGAC	CACGTGCTATCGGAGG	GATCCAAGCCACG [*]	TGT 420
Sbjct	933	<u> </u>	ΑΑĊΑĠĠΑΑĠĊΑϯΑĊĠΑĊ	ckkcgtgctktcggkg	β Υ4ςςΥΥΘςςΥςΘ.	tgt 992
Query	421	GGCCACAGCCGA	AGTCGTTAGCAAAATTT	CGCAGTACAAACGCGA	AGTGTCCTAGCAT	ATT 480
Sbjct	993		AGTCGTTAGCAAAATTT	ŗċĠċਖ਼ĠႵਖ਼ċਖ਼ਖ਼ਖ਼ċĠċĠ	ϟͼϯͼϯϲϲϯϫͼϲϫϯ	Att 1052
Query	481	TGCTTGGGAAAT	TCGGGATAGATTACTTC	AGGAGAACGTTTGTAG	TAACGATAATAT	ACC 540
Sbjct	1053	†ĠĊ††ĠĠĠĂĂÆ	tcgggytygytyg	addadaacdtttdta	ttaacgataatat.	ACC 1112
Query	541	AAGTGTGTCCTC	AATAAACCGTGTATTGA	GAAACTTGGCTGCGC/	AAAAGGAGCAGCA	AA 599 II
Sbjct	1113	AAGTGTGTCCTC	AATAAACCGTGTATTGA	ĠĂĂĂĊŦŦĠĠĊŦĠĊĠĊ	\AAAĠĠAĠĊAĠĊĀ	ÅÅ 1171

Drosophila melanogaster GH01157 full insert cDNA

Sequence ID: BT011390.1 Length: 2891 Number of Matches: 1

Range 1: 239 to 597

Score		Expect	Identities	Gaps	Strand	Frame
648 bits	(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	s:					
Query	241	AAGGCCTTTGCCA	GATTCAACACGGCAAAA	AATTGTCGAACTGGCA	\CATTCTGGAGCTG	.G 300
Sbjct	239	AAGGCC+++GCCA	Ġ ĂŦŦĊĂĂĊĂĊĠĠĊĂĂĂĀ	ለልተተ <mark></mark> ፈተራ <mark>ይ</mark> ልልረተ	ζζΑΤΤζΤĠĠΑĠζΤζ	G 298
Query	301	GCCATGTGATATT	TCTCGAATTCTGCAAGT	ʹϟͳϹϟϟϟͳϬϴϟͳϬͳϬͳ	GAGCAAAATTCTCG	iG 360
Sbjct	299	gccyteteytyt.	tctcgaattctgcaagt	-4+6444+664+6+6+6	sagcaaaattctcd	id 358
Query	361	GAGGTATTATGAA	ACAGGAAGCATACGACC	ACGTGCTATCGGAGGA	^λ ΤΕΓΑΑΘΕΕΑΕΘΤΘ	T 420
Sbjct	359	ĠĀĠĠŦĀŦŦĀŦĠĀĀ	Acaddaddcatacdacd	:AċĠ†Ġċ†A†ċĠĠAĠĠA	\tċċAAĠċċAċĠtċ	i† 418
Query	421	GGCCACAGCCGAA	GTCGTTAGCAAAATTTC	GCAGTACAAACGCGAG	TGTCCTAGCATAT	T 480
Sbjct	419	ĠĠĊĊĂĊĂĠĊĊĠĂĂ	ĠŦĊĠŦŦĂĠĊĂĂĂĂŦŦŦĊ	cdcadtacaaacdcdad	stgtcctagcatat	† 478
Query	481	TGCTTGGGAAATT	CGGGATAGATTACTTCA 	GGAGAACGTTTGTAC1	TAACGATAATATAC	C 540
Sbjct	479	tĠĊŦŦĠĠĠĀĀĀŦŦ	ĊĠĠĠĀŦĀĠĀŦŦĀĊŦŦĊĀ	ıddadakcetttetacı	taacgataatatad	.c 538
Query	541	AAGTGTGTCCTCA	ATAAACCGTGTATTGAG	GAAACTTGGCTGCGCAA	\AAGGAGCAGCAAA	599
Sbjct	539	AAGTGTGTCCTCA	ATAAACCGTGTATTGAG	iAAActtĠĠĊtĠĊĠĊĀA	\AAĠĠAĠĊAĠĊAA	597

D.melanogaster ey mRNA (exons 2-9)

Sequence ID: X79493.1 Length: 2848 Number of Matches: 1

Range 1: 241 to 599

Score		Expect	Identities	Gaps	Strand	Frame
648 bits	s(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Feature	es:					
Query	241	 AAGGCCTTTGCCAG	9 ATTCAACACGGCAAAAA	 АТТ ӨТСӨААСТӨӨСА	САТТСТӨӨАӨСТСӨ	300
Sbjct	241	AAGGCCTTTGCCA	GATTCAACACGGCAAAAA 	ϟϯϯϗϯϲϗϫϪϲϯϗϗϲϫ	54445466465456	300

		3 , (- /
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCTCGG	360
Sbjct	301	GCCA+G+GA+A+++C+CGAA+++C+GCAAG+A+CAAA+GGA+G+G+GAGCAAAAA++C+CGG	360
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420
Sbjct	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTCGCAGTACAAACGCGAGTGTCCTAGCATATT	480
Sbjct	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTCGCAGTACAAACGCGAGTGTCCTAGCATATT	480
Query	481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC	540
Sbjct	481	tĠĊŦŦĠĠĠAAAŦŦĊĠĠĠAŦAĠAŦŦAĊŦŦĊAĠĠAĠAAĊĠŦŦŦĠŦAĊŦAAĊĠAŦAAŦAŦAĊĊ	540
Query	541	AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA	599
Sbjct	541	AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA	599

Drosophila simulans eyeless (Dsim\ey), transcript variant E, mRNA Sequence ID: **XM_016180677.1** Length: 2731 Number of Matches: 1 Range 1: 243 to 599

Score		Expect	Identities	Gaps	Strand	Frame
618 bits	s(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCAGA	TTCAACACGGCAAAA	AATTGTCGAACTGGCA	CATTCTGGAGCTCG	300
Sbjct	243	YYGGCC+++GCCYGY-	ttçyyçyçgeçyyyy	ል	ϛϫϯϯϲϯͼͼϫͼϲϯϲͼ	302
Query	301	GCCATGTGATATTTC	ŢĊĠĄĄŢŢĊŢĠĊĄĄĠŢ	ATCAAATGGATGTGTG	AGCAAAATTCTCGG	360
Sbjct	303	gccyteteyteyt	tcgaattctacaagt	AtcAAAtGGAtGtGtG	AGCAAAATTCTCGC	362
Query	361	GAGGTATTATGAAAC	AGGAAGCATACGACC	ACGTGCTATCGGAGGA	TCCAAGCCACGTGT	420
Sbjct	363	ĠAĠAŦAŦŦĀŦĠĀĀĀĊ	dddaddda ac ddddddddddddddddddddddddddd	TĊĠŦĠĊŦĂŦĊĠĠĀĠĠĀ	tccaagccacgtg1	422
Query	421	GGCCACAGCCGAAGT	CGTTAGCAAAATTTC	GCAGTACAAACGCGAG	TGTCCTAGCATATT	480
Sbjct	423	ĠĠĊĊĀĊĀĠĊĊĠĀĀĠŤ	GĠŦŦĀĠĊĀĀĀĀŦŦŦĊ	ĠĊĀĠŦĀĊĀĀĀĊĠĊĠĀĠ	tĠtċċtAĠċAtAt1	482
Query	481	TGCTTGGGAAATTCG	GGATAGATTACTTCA 	.GGAGAACGTTTGTACT	AACGATAATATACC	540
Sbjct	483	TĠĊŦŦĠĠĠAAAŦŦĊĠ	ĠĠAŦAĠAŦŦAĊŦŦĊA	ĠĠĀĠĀĀĊĠŦŦŦĠŦĀĊŦ	AAĊĠAŤAAŤAŤĊĊĊ	542
Query	541	AAGTGTGTCCTCAAT	AAACCGTGTATTGAG 	AAACTTGGCTGCGCAA		597
Sbjct	543	AAGTGTGTCCTCCATA	4AACCGTGTATTGAG	AAACTTĠĠĊŦĠĊĠĊAA	AAĠĠAĠĊAĠĊA 5	599

Drosophila simulans eyeless (Dsim\ey), transcript variant D, mRNA Sequence ID: **XM_016180676.1** Length: 3170 Number of Matches: 1 Range 1: 682 to 1038

Score		Expect	Identities	Gaps	Strand	Frame
618 bits	(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	
Feature	s:					
Query	241	AAGGCCTTTGCCAG	GATTCAACACGGCAAAA	ͱϙͱϯϯϭϯϲϭ	ACATTCTGGAGC	TCG 300
Sbjct	682	AAGGCC+++GCCAG	PYTEPYFER	ϪϪϯϯϗϯϲϗϪϪϲϯϗϗϭ	ϝϒϚϒϯϯϚϯϐϾϒϾϚ·	tc6 741
Query	301	GCCATGTGATATTT	rctcgaattctgcaagt	ATCAAATGGATGTG1	rgagcaaaattct	CGG 360
Sbjct	742	<u></u> <u></u>	tctcgyyttctvcyyq	₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	ͰĠĂĠĊĂĂĂĂŦŦĊŦŧ	CGG 801
Query	361	GAGGTATTATGAAA	ACAGGAAGCATACGACC	ACGTGCTATCGGAGG	GATCCAAGCCACG	TGT 420
Sbjct	802	ĠAĠAŦAŦŦAŦĠAAA	\c\qquad \qquad \qqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	trcgtgctytcggygg	β ΑϯϲϲΫΫΫ	tĠ† 861
Query	421	GGCCACAGCCGAAG	TCGTTAGCAAAATTTG	GCAGTACAAACGCGA	ŊĠŢĠŢĊĊŢĄĠĊĄŢ	ATT 480
Sbjct	862	ĠĠĊĊĂĊĂĠĊĊĠĂĂĠ	stgáttáácááááátttá	cĠĊĀĠŦĀĊĀĀĀĊĠĊĠĀ	deteteetaeedt.	ņ† 921
Query	481	TGCTTGGGAAATTG	GGGATAGATTACTTCA	AGGAGAACGTTTGTAC	TAACGATAATAT	ACC 540
Sbjct	922	tĠĊŦŦĠĠĠĀĀĀŦŦĊ	tgggatagattacttc	ĸĠĠĀĠĀĀĊĠŦŦŦĠŦĀĊ	ttaacgataatat	ccc 981
Query	541	AAGTGTGTCCTCAA	\TAAACCGTGTATTGAG	GAAACTTGGCTGCGCA	AAAGGAGCAGCA	597
Sbjct	982	AAGTGTGTCCTCCA	\tAAAĊĊĠŦĠŦAŦŦĠAĠ	sAAAĊ††ĠĠĊ†ĠĊĠĊA	AAAAGGAGCAGCA	1038

Drosophila simulans eyeless (Dsim\ey), transcript variant C, mRNA Sequence ID: XM_016180675.1 Length: 2892 Number of Matches: 1 Range 1: 404 to 760

Score		Expect	Identities	Gaps	Strand	Frame
618 bits	s(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCAGA	rtcaacacggcaaaa	^	ÇATTÇTGGAGÇTÇ	300
Sbjct	404	AAGGCC+++GCCAGA-	ŀႵ¢ਖ਼ਖ਼çਖ਼çêçਖ਼ਖ਼ਖ਼ਖ਼	AATTGTEGAAETGGEA	ϛϫϯϯϛϯĠĠĂĠϛϯϛϭ	463
Query	301	GCCATGTGATATTTC	rcgaattetgeaagt	ATCAAATGGATGTGTG	AGCAAAATTCTCGG	360
Sbjct	464	gccatgtgatatttc	tcgaattctacaagt	AtcAAAtGGAtGtGtG	<u></u> ልፍርልልልልተተረተረፅ	523
Query	361	GAGGTATTATGAAACA	\GGAAGCATACGACC	ACGTGCTATCGGAGGA	TCCAAGCCACGTG	420
Sbjct	524	GAGATATTATGAAACA	γ α της συστημές της συστή της	τϲͼϯͼϲϯϫϯϲͼͼϫͼͼϫ	ϯϲϲϥϥͼϲϲϥϲͼϯͼ·	583
Query	421	GGCCACAGCCGAAGT	CGTTAGCAAAATTTC	GCAGTACAAACGCGAG	TGTCCTAGCATAT	T 480
Sbjct	584	ggccycyggggg	sgttygcygygygygygygygygygygygygygygygygyg	ĠĊĀĠŦĀĊĀĀĀĊĠĊĠĀĠ	tĠtċċtAĠċAtAt [.]	643
Query	481	TGCTTGGGAAATTCGG	GATAGATTACTTCA	GGAGAACGTTTGTACT	AACGATAATATAC	540
Sbjct	644	tĠĊŦŦĠĠĠĀĀĀŦŦĊĠĠ	sgatagattacttca	ĠĠĀĠĀĀĊĠŦŦŦĠŦĀĊŦ	AACGATAATATCC	703
Query	541	AAGTGTGTCCTCAATA	\AACCGTGTATTGAG	AAACTTGGCTGCGCAA	AAGGAGCAGCA !	597
Sbjct	704	AAGTGTGTCCTCCATA	\AAċċĠ†Ġ†A††ĠAĠ.	AAACTTĠĠĊTĠĊĠĊAA	AAGGAGCAGCA :	760

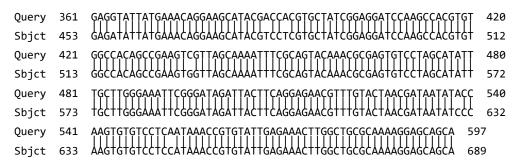
Drosophila simulans eyeless (Dsim\ey), transcript variant B, mRNA Sequence ID: XM_016180674.1 Length: 3351 Number of Matches: 1 Range 1: 863 to 1219

Score		Expect	Identities	Gaps	Strand	Frame
618 bits	s(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCAG	ΑΤΤ ΓΑΑ ΓΑ Γ ΘΘΓΑΑΑ	\ AATTGTCGAACTGGG	- ACATTCTGGAGC	TCG 300
Sbjct	863	YYPPS THE THE TENT OF THE TENT	9444699696999	744446466446466	ϝϒϚϒϯϯϚϯϐϾϒϾϚ	tcg 922
Query	301	GCCATGTGATATT1	rctcgaattctgcaag	ΓΑΤΓΑΑΑΤΘΘΑΤΘΤΘΊ	[GAGCAAAATTCT	CGG 360
Sbjct	923	gccytgtgytytt	tctcgyyttctvcyyg	ͰϪϯϲϪϪϪϯϗϭϪϯϗϯϗϯ	ͰĠ⅄ĠĊ⅄⅄⅄⅄⅄ϯϯĊϯ	CGG 982
Query	361	GAGGTATTATGAAA	ACAGGAAGCATACGAC	CACGTGCTATCGGAGG	GATCCAAGCCACG	TGT 420
Sbjct	983	ĠAĠA†A††A†ĠAAA	ACAGGAAGCATACGACG	trcgtgctatcggag	BATCCAAGCCACG	tĠ† 1042
Query	421	GGCCACAGCCGAAG	TCGTTAGCAAAATTT	GCAGTACAAACGCG/	\GTGTCCTAGCAT	ATT 480
Sbjct	1043	ĠĠĊĊĂĊĂĠĊĊĠĂĂĠ	stgĠttAĠĊAAAAttt	tgcagtacaaacgcg/	AGTGTCCTAGCAT.	ņ† 1102
Query	481	TGCTTGGGAAATTC	CGGGATAGATTACTTCA	AGGAGAACGTTTGTA(TAACGATAATAT	ACC 540
Sbjct	1103	tĠĊŦŦĠĠĠĀĀĀŦŦĊ	tgggatagattacttc	AGGAGAACG†††G†AC	ttaacgataatat	ccc 1162
Query	541	AAGTGTGTCCTCAA	\TAAACCGTGTATTGA(GAAACTTGGCTGCGCA	\AAAGGAGCAGCA	597
Sbjct	1163	AAGTGTGTCCTCC/	\tAAAccdtdtAttGAa	SAAACTTGGCTGCGC/	\AAAĠĠAĠĊAĠĊA	1219

Drosophila sechellia ey (Dsec\ey), mRNA

Sequence ID: **XM_002043659.1** Length: 2700 Number of Matches: 1 Range 1: 333 to 689

Score		Expect	Identities	Gaps	Strand	Frame
612 bits	s(678)	2e-171()	350/357(98%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCAGA ⁻	ŢŢĊĄĄĊĄĊĠĠĊĄĄĄĄĄĄŤ	ΓĠŢĊĠŶŶĊŢĠĠĊŶĊ	ATTCTGGAGCTCG	300
Sbjct	333	AAGGCC+++GCCAGA-	ttçqqçqçqqqqqq	ͰĠႵĊĠĂĂĊϯĠĠĊĂĊ	<u> </u>	392
Query	301	GCCATGTGATATTTC	ΓϚĠϟΑΤΤϚΤĠϚĄĄĠΤΑΤϚΑ	` AATGGATGTGTGA	GCAAAATTCTCGG	360
Sbjct	393	gccytetgytytte	Ͱϲͼϫϫϯϯϲϯϫϲϫϫͼϯϫϯϲ͵	ላ ልተፅፅልተፅተፅተ <mark></mark> ል	ͼϛΫΫΫΫϯͰϚͰϚͼͼ	452



Drosophila yakuba uncharacterized protein (Dyak\GE14559), mRNA Sequence ID: **XM_002099582.2** Length: 3908 Number of Matches: 1 Range 1: 1301 to 1657

Score		Expect	Identities	Gaps	Strand	Frame
576 bits	s(638)	1e-160()	342/357(96%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	ĄĄĢĢÇÇŢŢŢĢÇÇĄĢ	ĄŢŢĊĄĄĊĄĊĠĠĊĄĄĄ	ϙ ϙϙͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺͺ	ÇĄÇĄTŢÇŢĢĢĄĢÇ	ТСӨ 300
Sbjct	1301	YYGGCC+++GCCYG	Υ	AAATTGTCGAGCTGG	ϛϥϛϥϯϯϲϯͼͼϥͼϲ	tcG 1360
Query	301	GCCATGTGATATTT	CTCGAATTCTGCAAG	ΤΑΤϹΑΑΑΤΘΘΑΤΘΤΘ	ΤĢΑĢÇΑΑΑΑΤΤϚΤ	CGG 360
Sbjct	1361	τζζητβηθητή	cccgyy++c+vcyye	Ⴕ ⊤ ႵċልልልႵĠĠልႵĠႵĠ	†ĠAĠĊAAAA††Ċ†	CGG 1420
Query	361	GAGGTATTATGAAA	CAGGAAGCATACGAC	CACGTGCTATCGGAG	GATCCAAGCCACG	TGT 420
Sbjct	1421	GAGGTACTATGAAA	ĊĄĠĠĄĄĠĊĄŢĄĊĠŢĊ	cccgtgctatcggag	 β Α Α Α Α Α Α Α Α Α Α Α Α Α	tgt 1480
Query	421	GGCCACAGCCGAAG	TCGTTAGCAAAATTT	CGCAGTACAAACGCG	ĄĠŢĠŢĊĊŢĄĠĊĄŢ	ATT 480
Sbjct	1481	g gccycygccgyyg	ttgttagcaaaattt	¢ĠċAĠ†AċAAGċĠċĠ,	AGTGTCCTAGCAT	Att 1540
Query	481	TGCTTGGGAAATTC	GGGATAGATTACTTC	AGGAGAACGTTTGTA	CTAACGATAATAT 	ACC 540
Sbjct	1541	cĠċttĠĠĠAAAttċ	ĠĠĠĀŦĀĠĀŦŦĀĊŦŦĊ	AĠĠAĠAAĊĠ†††Ġ†A	ĊŦĀĀĊĠĀŦĀĀŦĀŦ	TCC 1600
Query	541	AAGTGTGTCCTCAA	TAAACCGTGTATTGA	GAAACTTGGCTGCGC/	AAAAGGAGCAGCA IIIIIIIIII	597
Sbjct	1601	AAGTGTGTCTCAA	taaaccgtgtattga	ĠĂĂĂĊŦŦĠĠĊĀĠĊĠĊ	AAAAGGAGCAGCA	1657

Drosophila erecta uncharacterized protein, transcript variant B (Dere\GG16399), mRNA Sequence ID: **XM_015153159.1** Length: 3368 Number of Matches: 1 Range 1: 747 to 1103

Score		Expect	Identities	Gaps	Strand	Frame
563 bits	s(624)	7e-157()	339/357(95%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	AAGGCCTTTGCCAG	GATTCAACACGGCAAAA	^	CACATTCTGGAGCT	ÇĢ 300
Sbjct	747	AAGGCC+++GCC+	99445995959999	ል	₽₩₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	CG 806
Query	301	GCCATGTGATATT	Τςτςφρηττςτοςρρότ	ΑΤ <u>Ϲ</u> ΑΑΑΤΘΘΑΤΘΤΘ	ΓĢΑĢÇΑΑΑΑΤΤϚΤϚ	GG 360
Sbjct	807	gççyt@t@ytytt.	tçcçqyyttçtvçyyqt	т фаруудан та	ͰĠ⅄ĠĊ⅄⅄⅄⅄Ϯϯċϯċ	GG 866
Query	361	GAGGTATTATGAA	ACAGGAAGCATACGACC	ĄĊĠŢĠĊŢĄŢĊĠĠĄĠŧ	GATCCAAGCCACGT	GT 420
Sbjct	867	gyggtyctytgyy	yçeqqeyqçytyçqyçç	Acetectytceeye	ϟϥϯϲϲϥϥͼϲϲϥϲͼϯ	dt 926
Query	421	GGCCACAGCCGAA	GTCGTTAGCAAAATTTC	GCAGTACAAACGCG/	^ GTGTCCTAGCATA	TT 480
Sbjct	927	ggccactgctgaa	strgttygcyyyytt	gcyg4ycyydcgcg	qqtqtççtyqçyty	11 986
Query	481	ŢĠĊŢŢĠĠĠĄĄĄŢŢſ	CGGGATAGATTACTTCA	GGAGAACGTTTGTA	;ϯϙϥϲϙϥϯϙϯϯϯͳ	CC 540
Sbjct	987	tgcttgggyyytt	cgagatagattacttca	ĠĠĀĠĀĀĊĠŦŦŦĠŦĀſ	ctaatgataatatc	cc 1046
Query	541	AAGTGTGTCCTCA	ATAAACCGTGTATTGAG.	AAACTTGGCTGCGC/	AAAAGGAGCAGCA	597
Sbjct	1047	AAGTGTGTCCTCA	AtAAAccdcdtAttdAd.	AAACTTGGCTGCGC/	AAAAAGAACAGCA	1103

Drosophila erecta uncharacterized protein, transcript variant A (Dere\GG16399), mRNA Sequence ID: **XM_001982674.2** Length: 3548 Number of Matches: 1 Range 1: 927 to 1283

Score		Expect	Identities	Gaps	Strand	Frame
563 bits	s(624)	7e-157()	339/357(95%)	0/357(0%)	Plus/Plus	
Feature	es:					
Query	241	ĄĄĠĠĊĊŢŢŢĠĊĊĀĠ	ΑΤΤ Ϲ ΑΑ <mark>ϹΑ</mark> ϹΘΘΕΑΑΑΑ	៶ ΑΑΤΤΘΤϚΘΑΑϚΤΘΘ	CACATTCTGGAGC	TCG 300
Sbjct	927	Αλάβςς+++βςς+β	;ϟϯϯϛϥϥϛϥϛϥϛϥϥϥ	₹₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	₽Ÿ₽₽₽₽₽₽₽₽₽₽₽₽	tcg 986
Query	301	ĢÇÇATĢTĢATATTT	CTCGAATTCTGCAAG	ΓΑΤϹΑΑΑΤΘΘΑΤΘΤΘ	ΓĢΑĢĊΑΑΑΑΤΤΟΤ	ÇGG 360
Sbjct	987	gccytgtgytytt	cccepy++c+vcyye.	⊦⊥∔çषष्प्रमृदेष्प्रमृदेष्	tgygcyyyyttçt	CGG 1046
Query	361	GAGGTATTATGAAA	CAGGAAGCATACGAC	CACGTGCTATCGGAGG	GATCCAAGCCACG	TGT 420
Sbjct	1047	GAGGTACTATGAAA	.cegegyecytyce	tacetectatceeae	gytccyygccyce	tgt 1106
Query	421	GGCCACAGCCGAAG	TCGTTAGCAAAATTT	GCAGTACAAACGCG/	AGTGTCCTAGCAT	ATT 480
Sbjct	1107	ggccyctgctgyyg	ttgttygcyyy	tgcygtycyydd g	deteteetaeeat.	Att 1166
Query	481	TGCTTGGGAAATTC	GGGATAGATTACTTC	ŊĠĠŖĠŖŖĊĠŦŦŢĠŢŖſ	ΤΑΑΟΘΑΤΑΑΤΑΤ	ACC 540
Sbjct	1167	tĠĊŦŦĠĠĠAAAŦŦĊ	ĠAĠĀŦĀĠĀŦŦĀĊŦŦĊĀ	\ddaddadddd ddadddddddddddddddddddddddd	ttaatgataatat	ငင်င် 1226
Query	541	AAGTGTGTCCTCAA	TAAACCGTGTATTGAG	GAAACTTGGCTGCGCA	AAAAGGAGCAGCA	597
Sbjct	1227	AAGTGTGTCCTCAA	tAAAccdcdtAttGAa	BAAACTTGGCTGCGCA	\AAAAGAACAGCA	1283

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