

[BLAST®](#) » [blastn suite](#) » RID-YXKSP7WN014

BLAST Results

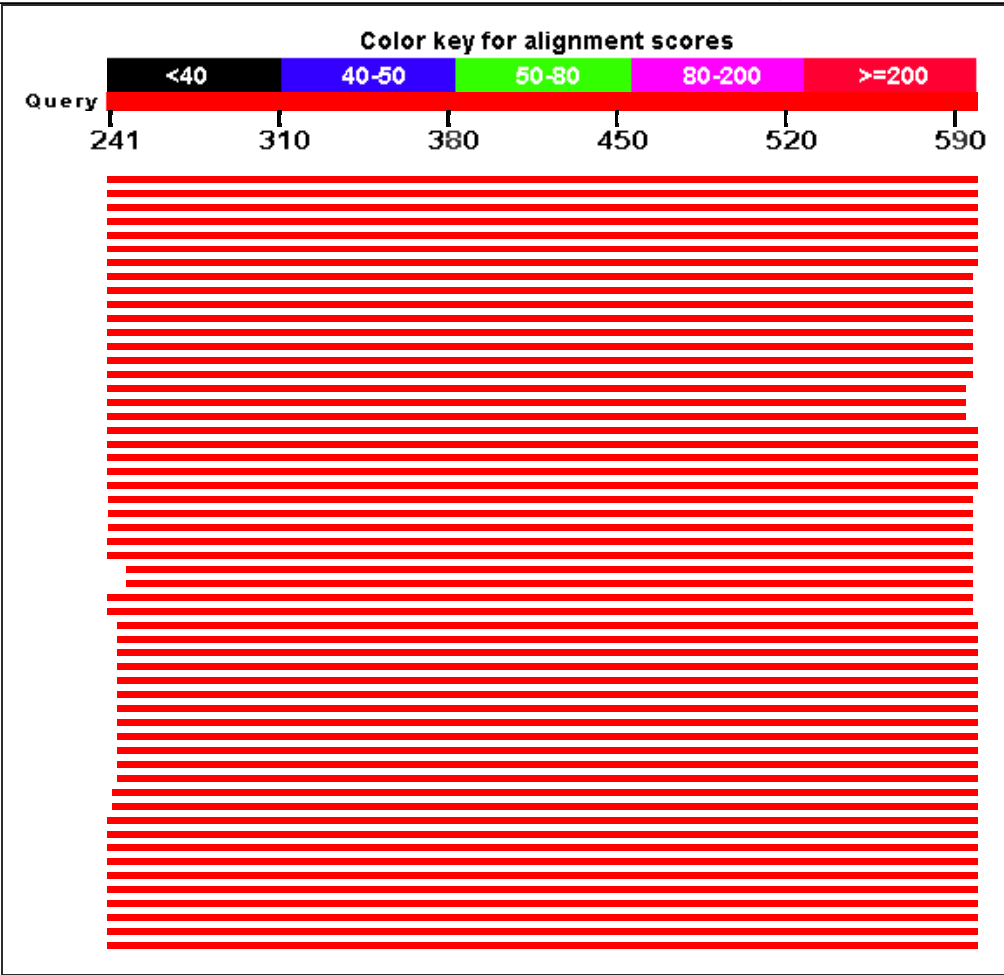
X79493:D.melanogaster ey mRNA (exons 2-9)

RID	YXKSP7WN014 (Expires on 10-02 04:46 am)	Database Name	nr
Query ID	X79493.1	Description	Nucleotide collection (nt)
Description	D.melanogaster ey mRNA (exons 2-9)	Program	BLASTN 2.5.0+
Molecule type	nucleic acid		
Query Length	2848		

Graphic Summary

Distribution of 112 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Description	Max score	Total score	Query cover	E value	Ident	Accession
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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

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

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila pseudoobscura pseudoobscura ey, transcript variant F (Dpseley), mRNA	419	419	98%	2e-113	86%	XM_015188708.1
Drosophila pseudoobscura pseudoobscura ey, transcript variant E (Dpseley), mRNA	419	419	98%	2e-113	86%	XM_015188707.1
Drosophila pseudoobscura pseudoobscura ey, transcript variant D (Dpseley), mRNA	419	419	98%	2e-113	86%	XM_015188706.1
Drosophila pseudoobscura pseudoobscura ey, transcript variant C (Dpseley), mRNA	419	419	98%	2e-113	86%	XM_015188705.1
Drosophila pseudoobscura pseudoobscura ey, transcript variant B (Dpseley), mRNA	419	419	98%	2e-113	86%	XM_015188704.1
Drosophila pseudoobscura pseudoobscura ey, transcript variant A (Dpseley), mRNA	419	419	98%	2e-113	86%	XM_001352335.3
Drosophila persimilis ey (Dperley), 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\GI14081), mRNA	369	369	100%	3e-98	83%	XM_002011366.2
Drosophila mojavensis uncharacterized protein, transcript variant E (Dmoj\GI14081), 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 (Dvirley), transcript variant A, mRNA	342	342	100%	4e-90	81%	XM_002059708.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
<i>Drosophila virilis</i> eyeless (Dvirley), transcript variant B, mRNA	342	342	100%	4e-90	81%	XM_015168533.1
PREDICTED: <i>Drosophila busckii</i> paired box protein Pax-6 (LOC108607418), transcript variant X2, mRNA	334	334	99%	6e-88	81%	XM_017998214.1
PREDICTED: <i>Drosophila busckii</i> paired box protein Pax-6 (LOC108607418), transcript variant X1, mRNA	334	334	99%	6e-88	81%	XM_017998213.1
<i>Drosophila melanogaster</i> chromosome 4	334	884	100%	6e-88	100%	AE014135.4
<i>Drosophila melanogaster</i> clone BACR06K04, complete sequence	334	663	100%	6e-88	100%	AC150557.1
<i>Drosophila melanogaster</i> eyeless (ey) gene, exons 2, 3 and partial cds; and transposon jockey, partial sequence	334	563	85%	6e-88	100%	DQ091189.1
<i>Drosophila melanogaster</i> , chromosome 4, region 101C-101D, BAC clone BACR16H06, complete sequence	334	663	100%	6e-88	100%	AC099309.1
<i>Drosophila melanogaster</i> , chromosome 4, region 101F-102F, BAC clone BACR30L15, complete sequence	334	663	100%	6e-88	100%	AC010576.16
<i>Drosophila willistoni</i> uncharacterized protein (Dwil\GK13702), mRNA	320	320	98%	1e-83	80%	XM_002072588.2
<i>Drosophila simulans</i> eyeless (ey) gene, exons 2, 3 and partial cds; and transposon jockey, partial sequence	316	539	85%	2e-82	98%	DQ091188.1
PREDICTED: <i>Drosophila eugracilis</i> paired box protein Pax-6 (LOC108102386), transcript variant X4, mRNA	313	313	64%	2e-81	90%	XM_017207328.1
PREDICTED: <i>Drosophila navojoa</i> paired box protein Pax-6-like (LOC108657902), partial mRNA	309	309	85%	2e-80	82%	XM_018110557.1
PREDICTED: <i>Bactrocera dorsalis</i> paired box protein Pax-6-like (LOC105228660), mRNA	288	288	98%	8e-74	78%	XM_011208561.1
<i>Drosophila ananassae</i> uncharacterized protein, transcript variant B (Dana\GF21877), mRNA	280	280	99%	1e-71	78%	XM_014903679.1
<i>Drosophila ananassae</i> uncharacterized protein, transcript variant A (Dana\GF21877), mRNA	280	280	99%	1e-71	78%	XM_001967394.2
PREDICTED: <i>Ceratosolen solmsi</i> marchali paired box protein Pax-6 (LOC105363389), mRNA	275	275	99%	5e-70	77%	XM_011501059.1
PREDICTED: <i>Stomoxys calcitrans</i> paired box protein Pax-6-like (LOC106094139), mRNA	269	269	98%	2e-68	77%	XM_013261329.1
PREDICTED: <i>Stomoxys calcitrans</i> paired box protein Pax-6-like (LOC106093015), mRNA	269	269	98%	2e-68	77%	XM_013259984.1
PREDICTED: <i>Drosophila bipectinata</i> paired box protein Pax-6-like (LOC108131200), partial mRNA	260	260	98%	1e-65	76%	XM_017249961.1
PREDICTED: <i>Bactrocera cucurbitae</i> paired box protein Pax-6 (LOC105219314), mRNA	260	260	96%	1e-65	77%	XM_011195357.1
PREDICTED: <i>Drosophila bipectinata</i> paired box protein Pax-6-like (LOC108133768), partial mRNA	259	259	65%	4e-65	84%	XM_017253833.1

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(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Features:					
Query 241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	300			
Sbjct 847	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	906			
Query 301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG	360			
Sbjct 907	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG	966			
Query 361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420			
Sbjct 967	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	1026			
Query 421	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT	480			
Sbjct 1027	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT	1086			
Query 481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC	540			
Sbjct 1087	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC	1146			
Query 541	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA	599			
Sbjct 1147	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA	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(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	
Features:					
Query 241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	300			

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Sbjct  287  AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG  346
Query   301  GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG  360
Sbjct  347  GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG  406
Query   361  GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT  420
Sbjct  407  GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT  466
Query   421  GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT  480
Sbjct  467  GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT  526
Query   481  TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC  540
Sbjct  527  TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC  586
Query   541  AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA  599
Sbjct  587  AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA  645

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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	

Features:

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Query   241  AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG  300
Sbjct   667  AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG  726
Query   301  GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG  360
Sbjct   727  GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG  786
Query   361  GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT  420
Sbjct   787  GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT  846
Query   421  GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT  480
Sbjct   847  GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT  906
Query   481  TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC  540
Sbjct   907  TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC  966
Query   541  AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA  599
Sbjct   967  AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA  1025

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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(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	

Features:

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Query   241  AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG  300
Sbjct   239  AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG  298
Query   301  GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG  360
Sbjct   299  GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG  358
Query   361  GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT  420
Sbjct   359  GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT  418
Query   421  GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT  480
Sbjct   419  GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT  478
Query   481  TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC  540
Sbjct   479  TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC  538
Query   541  AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA  599
Sbjct   539  AAGTGTGTCCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA  597

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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(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAAC	TGGCACATTCTGGAGCTCG	300
Sbjct	813	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAAC	TGGCACATTCTGGAGCTCG	872
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG		360
Sbjct	873	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG		932
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT		420
Sbjct	933	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT		992
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGCAGTACAAACGCGAGTGTCTAGCATATT		480
Sbjct	993	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGCAGTACAAACGCGAGTGTCTAGCATATT		1052
Query	481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC		540
Sbjct	1053	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC		1112
Query	541	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA		599
Sbjct	1113	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA		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	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAAC	TGGCACATTCTGGAGCTCG	300
Sbjct	239	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAAC	TGGCACATTCTGGAGCTCG	298
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG		360
Sbjct	299	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG		358
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT		420
Sbjct	359	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT		418
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGCAGTACAAACGCGAGTGTCTAGCATATT		480
Sbjct	419	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGCAGTACAAACGCGAGTGTCTAGCATATT		478
Query	481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC		540
Sbjct	479	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC		538
Query	541	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA		599
Sbjct	539	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA		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(718)	0.0()	359/359(100%)	0/359(0%)	Plus/Plus	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAAC	TGGCACATTCTGGAGCTCG	300
Sbjct	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAAC	TGGCACATTCTGGAGCTCG	300

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Query 301 GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG 360
Sbjct 301 GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG 360
Query 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Sbjct 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Query 421 GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT 480
Sbjct 421 GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT 480
Query 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Sbjct 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Query 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA 599
Sbjct 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCAAA 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(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	

Features:

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Query 241 AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTTGTCGAACGGCACATTCTGGAGCTCG 300
Sbjct 243 AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTTGTCGAACGGCACATTCTGGAGCTCG 302
Query 301 GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG 360
Sbjct 303 GCCATGTGATATTTCTCGAATTTCTACAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG 362
Query 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Sbjct 363 GAGATATTATGAAACAGGAAGCATACGACCTCGTGTATCGGAGGATCCAAGCCACGTGT 422
Query 421 GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT 480
Sbjct 423 GGCCACAGCCGAAGTGGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT 482
Query 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Sbjct 483 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATCCC 542
Query 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 597
Sbjct 543 AAGTGTGTCTCTCATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 599

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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	

Features:

```

Query 241 AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTTGTCGAACGGCACATTCTGGAGCTCG 300
Sbjct 682 AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTTGTCGAACGGCACATTCTGGAGCTCG 741
Query 301 GCCATGTGATATTTCTCGAATTTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG 360
Sbjct 742 GCCATGTGATATTTCTCGAATTTCTACAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG 801
Query 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Sbjct 802 GAGATATTATGAAACAGGAAGCATACGACCTCGTGTATCGGAGGATCCAAGCCACGTGT 861
Query 421 GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT 480
Sbjct 862 GGCCACAGCCGAAGTGGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTAGCATATT 921
Query 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Sbjct 922 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATCCC 981
Query 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 597
Sbjct 982 AAGTGTGTCTCTCATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 1038

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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(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	300
Sbjct	404	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	463
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	360
Sbjct	464	GCCATGTGATATTTCTCGAATTCTACAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	523
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420
Sbjct	524	GAGATATTATGAAACAGGAAGCATACGACCTCGTGCTATCGGAGGATCCAAGCCACGTGT	583
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTTAGCATATT	480
Sbjct	584	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTTAGCATATT	643
Query	481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC	540
Sbjct	644	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATCCC	703
Query	541	AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA	597
Sbjct	704	AAGTGTGTCTCTCCATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA	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(684)	4e-173()	351/357(98%)	0/357(0%)	Plus/Plus	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	300
Sbjct	863	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	922
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	360
Sbjct	923	GCCATGTGATATTTCTCGAATTCTACAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	982
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420
Sbjct	983	GAGATATTATGAAACAGGAAGCATACGACCTCGTGCTATCGGAGGATCCAAGCCACGTGT	1042
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTTAGCATATT	480
Sbjct	1043	GGCCACAGCCGAAGTCGTTAGCAAAATTTTCGAGTACAAACGCGAGTGTCTTAGCATATT	1102
Query	481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC	540
Sbjct	1103	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATCCC	1162
Query	541	AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA	597
Sbjct	1163	AAGTGTGTCTCTCCATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA	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(678)	2e-171()	350/357(98%)	0/357(0%)	Plus/Plus	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	300
Sbjct	333	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	392
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	360
Sbjct	393	GCCATGTGATATTTCTCGAATTCTACAAGTATCAAATGGATGTGTGAGCAAAATCTCGG	452

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Query 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Sbjct 453 GAGATATTATGAAACAGGAAGCATACGTCTCGTGTATCGGAGGATCCAAGCCACGTGT 512
Query 421 GGCCACAGCCGAAGTCGTTAGCAAAATTCGCAGTACAAACGCGAGTGTCTAGCATATT 480
Sbjct 513 GGCCACAGCCGAAGTGGTTAGCAAAATTCGCAGTACAAACGCGAGTGTCTAGCATATT 572
Query 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Sbjct 573 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATCCC 632
Query 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 597
Sbjct 633 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 689

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Drosophila yakuba uncharacterized protein (Dyak\GE14559), mRNA

Sequence ID: **XM_00209582.2** Length: 3908 Number of Matches: 1

Range 1: 1301 to 1657

Score	Expect	Identities	Gaps	Strand	Frame
576 bits(638)	1e-160()	342/357(96%)	0/357(0%)	Plus/Plus	

Features:

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Query 241 AAGGCCTTTGCCAGATTCAACACGGCAAAAAATGTCGAACTGGCACATTCTGGAGCTCG 300
Sbjct 1301 AAGGCCTTTGCCAGATTCAACACGACAAAAAATGTCGAGCTGGCACATTCTGGAGCTCG 1360
Query 301 GCCATGTGATATTTCTCGAATTCGCAAGTATCAAATGGATGTGTGAGCAAAATTCGCG 360
Sbjct 1361 TCCATGTGATATTTCCCGAATTCACAAGTTTCAAATGGATGTGTGAGCAAAATTCGCG 1420
Query 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Sbjct 1421 GAGGTACTATGAAACAGGAAGCATACGTCCCGTGTATCGGAGGATCCAAGCCACGTGT 1480
Query 421 GGCCACAGCCGAAGTCGTTAGCAAAATTCGCAGTACAAACGCGAGTGTCTAGCATATT 480
Sbjct 1481 GGCCACAGCCGAAGTTGTTAGCAAAATTCGCAGTACAAGCGCGAGTGTCTAGCATATT 1540
Query 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Sbjct 1541 CGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATCC 1600
Query 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 597
Sbjct 1601 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCAGCGCAAAAGGAGCAGCA 1657

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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(624)	7e-157()	339/357(95%)	0/357(0%)	Plus/Plus	

Features:

```

Query 241 AAGGCCTTTGCCAGATTCAACACGGCAAAAAATGTCGAACTGGCACATTCTGGAGCTCG 300
Sbjct 747 AAGGCCTTTGCTTGATTCAACACGGCAAAAAATGTCGAACTGGCACATTCTGGAGCTCG 806
Query 301 GCCATGTGATATTTCTCGAATTCGCAAGTATCAAATGGATGTGTGAGCAAAATTCGCG 360
Sbjct 807 GCCATGTGATATTTCCCGAATTCACAAGTTTCAAATGGATGCGTGAGCAAAATTCGCG 866
Query 361 GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 420
Sbjct 867 GAGGTACTATGAAACGGGGAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT 926
Query 421 GGCCACAGCCGAAGTCGTTAGCAAAATTCGCAGTACAAACGCGAGTGTCTAGCATATT 480
Sbjct 927 GGCCACTGCTGAAGTTGTTAGCAAAATTCGCAGTACAAGCGCGAGTGTCTAGCATATT 986
Query 481 TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC 540
Sbjct 987 TGCTTGGGAAATTCGAGATAGATTACTTCAGGAGAACGTTTGTACTAATGATAATATCCC 1046
Query 541 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 597
Sbjct 1047 AAGTGTGTCTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA 1103

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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(624)	7e-157()	339/357(95%)	0/357(0%)	Plus/Plus	

Features:

Query	241	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	300
Sbjct	927	AAGGCCTTTGCCAGATTCAACACGGCAAAAAATTGTCGAACTGGCACATTCTGGAGCTCG	986
Query	301	GCCATGTGATATTTCTCGAATTCTGCAAGTATCAAATGGATGTGTGAGCAAAATTCCTCGG	360
Sbjct	987	GCCATGTGATATTTCCCGAATTCTACAAGTTTCAAATGGATGCGTGAGCAAAATTCCTCGG	1046
Query	361	GAGGTATTATGAAACAGGAAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	420
Sbjct	1047	GAGGTACTATGAAACGGGGAGCATACGACCACGTGCTATCGGAGGATCCAAGCCACGTGT	1106
Query	421	GGCCACAGCCGAAGTCGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT	480
Sbjct	1107	GGCCACTGCTGAAGTTGTTAGCAAAATTTGCGAGTACAAACGCGAGTGTCTAGCATATT	1166
Query	481	TGCTTGGGAAATTCGGGATAGATTACTTCAGGAGAACGTTTGTACTAACGATAATATACC	540
Sbjct	1167	TGCTTGGGAAATTCGAGATAGATTACTTCAGGAGAACGTTTGTACTAATGATAATATCCC	1226
Query	541	AAGTGTGTCTCAATAAACCGTGTATTGAGAAACTTGGCTGCGCAAAAGGAGCAGCA	597
Sbjct	1227	AAGTGTGTCTCAATAAACCGCGTATTGAGAAACTTGGCTGCGCAAAAGAACAGCA	1283

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