

Species	Length (a.a.)	Isoelectric Point (pI)	Pairwise BLASTP bit score and e-value with Dmel	Note(s)
<i>D. melanogaster</i>	172	10.7	347, 3e-129	
<i>D. simulans</i>	172	10.6	281, 1e-103	
<i>D. sechellia</i>	172	10.6	293, 7e-108	
<i>D. yakuba</i>	178	11.4	219, 9e-79	
<i>D. erecta</i>	174	11.0	210, 2e-75	
<i>D. ananassae</i>	170	10.3	78, 2e-23	
<i>D. bipectinata</i>	233	10.3	62, 9e-11	Likely contains an ortholog, given significant BLAST hit and RNAseq evidence of male-specific expression, but gene boundaries are unclear. The 5' end of the ORF contains either ~100 extra codons or an intron, neither of which matches the <i>atlas</i> gene structure. Statistics reported at left are for the gene model that includes an intron, GenBank accession XP_017110044.1.
<i>D. elegans</i>	171	10.4	142, 2e-48	
<i>D. ficusphila</i>	180	10.6	147, 2e-50	
<i>D. eugracilis</i>	176	10.9	138, 8e-47	
<i>D. kikkawai</i>	No ortholog detected at mel or ana syntenic region			
<i>D. serrata</i>	No ortholog detected at mel or ana syntenic region			
<i>D. rhopaloa</i>	176	10.7	149, 4e-51	
<i>D. biarmipes</i>	185	10.4	158, 1e-54	
<i>D. sukukii</i>	179	10.6	182, 5e-64	
<i>D. takahashii</i>	198	10.6	165, 4e-57	
<i>D. obscura</i>	No ortholog detected			
<i>D. miranda</i>	No ortholog detected			
<i>D. persimilis</i>	>198	~10.3	n.s.	Found in syntenic region to <i>D. virilis</i> ortholog, but BLAST results do not support orthology; gap in <i>D. persimilis</i> assembly cuts off 3' end of predicted ORF, so length and pI values are estimates
<i>D. pseudoobscura</i>	232	10.1	n.s.	
<i>D. willistoni</i>	No ortholog detected			
<i>D. busckii</i>	88	5.1	34.3, 4e-8	Found in syntenic region to <i>D. virilis</i> ortholog, but low pI does not support homologous function
<i>D. hydei</i>	No ortholog detected			
<i>D. arizonae</i>	No ortholog detected			
<i>D. mojavensis</i>	No ortholog detected			
<i>D. navojoa</i>	No ortholog detected			
<i>D. virilis</i>	116	10.1	40, 1e-9	
<i>D. grimshawi</i>	No ortholog detected			