

Gene Cluster ID	Tmem199
Drosophila melanogaster dicistronic gene	CG7071
FlyBase ID	FBgn0260467
Predicted function	ATPase, H+ transporting, vacuolar ER assembly factor, Vma12
Protein size	302 amino acids
Cytogenetic map	3R:94A6-94A6
Gene sequence location	3R:18188619..18190306 [+]
Dmel CLEAR sequence	TCATGTGA
CLEAR sequence location	3R:18188617..18188624

NOTE: Dicistronic gene with dicistronic transcript.

FlyBase gene model & CLEAR element (red) position:



muted/Tmem199 (CG7071) gene structure comparison:

Key: UTR region, CDS region

Species	CG7071 Tmem199 orthologs	muted (CG34131)					CG7071				Extended CLEAR region	Position	bps from TSS		
		5'exon	intron	exon	intron	exon3'	5'exon	intron	exon3'						
<i>Drosophila_melanogaster</i>	Dmel\CG7071	28	22	60	281	66	171	5	598	69	311	77	cgtcagatttcTCATGTGAcagctgtggcg	5'UTR	6
<i>Drosophila_simulans</i>	Dsim\GD20938		22	60	281	66	171	5	598	68	311		tgtcagatttcTCATGTGAcagctgtggcg	5'UTR?	
<i>Drosophila_sechellia</i>	Dsec\GM26419		22	60	281	66	171	5	598	58	311		cgtcagatttcTCATGTGAcagctgtggcg	5'UTR?	

<i>Drosophila_yakuba</i>	Dyak\GE10288	22	60	281	66	171	5	604	60	323		cgatggcatttcTCATGTGAcagctgtaggcg	5'UTR?	
<i>Drosophila_erecta</i>	Dere\GG11121	22	60	287	66	171	5	568	61	320		cgatggcatttcTCATGTGAcagctgtggcg	5'UTR?	
<i>Drosophila_biarmipes</i>	Dbia\CG7071	22	63	272	69	171	5	601	60	323		cggteggatttcTCATGTGAcagctgtggcca	5'UTR?	
<i>Drosophila_suzukii</i>	Dsuz\CG7071	22	65	272	69	171	5	598	60	323		tggtgtgatttcTCATGTGAcagctgtgtca	5'UTR?	
<i>Drosophila_takahashii</i>	Dtak\CG7071	22	63	272	66	171	5	583	60	326		cactgggatttcTCATGTGAcagctgtaggcg	5'UTR?	
<i>Drosophila_eugracilis</i>	Deug\CG7071	22	60	272	64	171	5	592	60	323		tgccaggatttcTCATGTGAcagctgtagacg	5'UTR?	
<i>Drosophila_elegans</i>	Dele\CG7071	22	59	272	64	171	5	589	63	323		ccaacactgcccTCATGTGAcagctgtcgttg	5'UTR?	
<i>Drosophila_rhopaloea</i>	Drho\CG7071	22	61	272	65	171	4	592	68	323		ccaacactgtgcTCATGTGAcagctgtcgttg	5'UTR?	
<i>Drosophila_ficusphila</i>	Dfie\CG7071	22	61	272	62	165	5	592	57	323		acaacactagccTCATGTGAcagctgaacgga	5'UTR?	
<i>Drosophila_kikkawai</i>	Dkik\CG7071	22	61	272	65	171	8	604	68	317		gcaacgccgcacTCATGTGAcagctgtaggtg	5'UTR?	
<i>Drosophila_bipectinata</i>	Dbip\CG7071	22	63	272	60	171	6	583	63	314		acaacctacacTCATGTGAcagctgtaggaa	5'UTR?	
<i>Drosophila_ananassae</i>	Dana\GF18081	22	63	272	72	171	6	583	60	314		acaacctacacTCATGTGAcagctgtaggaa	5'UTR?	
<i>Drosophila_pseudoobscura</i>	Dpse\GA20078	22	61	272	72	171	13	625	63	317		taatcgataagTCATGTGAcagctgtgggtg	5'UTR?	
<i>Drosophila_persimilis</i>	Dper\GL23377	22	61	272	72	171	13	625	63	317		taatcgataagTCATGTGAcagctgtgggtg	5'UTR?	
<i>Drosophila_miranda</i>	Dmir\CG7071	22	61	272	72	171	14	625	63	317		taagccgataagTCATGTGAcagctgtgggtg	5'UTR?	
<i>Drosophila_willistoni</i>	Dwil\GK12992	22	61	272	58	171	14	613	61	299		gagcatcactgcTCATGTGAtgtgccgtgact	5'UTR?	
<i>Drosophila_albomicans</i>	Dalb\CG7071	22	177	ND	ND	171	27	589	62	290		tcgttgaccacTCACATGAcggtaaagaaaa	5'UTR?	
<i>Drosophila_mojavensis</i>	Dmoj\GI10478	22	60	272	59	171	13	586	73	290		tcgttgactacTCATGTGAcagatgtaaaaa	5'UTR?	
<i>Drosophila_virilis</i>	Dvir\GJ23158	22	58	272	68	171	13	577	64	287		tcgtgcgccacTCATGTGAcagaagcaaaaa	5'UTR?	
<i>Drosophila_grimshawi</i>	Dgrn\GH21152	22	62	272	69	171	23	589	54	287		cgttaacttacTCATGTGAcaggagcagaaa	5'UTR?	