

Gene Cluster ID	Atp6ap2
Drosophila melanogaster gene	VhaM8.9 (CG8444)
FlyBase ID	FBgn0037671
Predicted function	ATPase, H⁺ transporting, lysosomal accessory protein 2
Protein size	320 amino acids
Cytogenetic map	3R:85D6-85D7
Gene sequence location	3R:5086363..5088315 [+]
Dmel CLEAR sequence	TCACATGA; TCATATGA
CLEAR sequence location(s)	3R:5086356..5086363; 3R:5086414..5086421

FlyBase VhaM8.9 (CG8444) gene model & CLEAR element position:



VhaM8.9 (CG8444) gene structure comparison in Drosophila species:

Key: UTR region, CDS region

Species	VhaM8.9 Atp6ap2 orthologs	5'exon		intron	exon	intron	exon3'		Extended CLEAR region	Position	bps from TSS
<i>Drosophila_melanogaster</i>	Dmel\VhaM8.9	84	43	223	353	262	567	421	caaccctgttcaTCACATGAtagtcagggtga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR	-1 52
<i>Drosophila_simulans</i>	Dsim\GD18602		43	223	353	251	567		caaccctgttcaTCACATGAtagtcagggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_sechellia</i>	Dsec\GM23791		43	223	353	265	567		caaccctgttcaTCACATGAtagtcagggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_yakuba</i>	Dyak\GE25938		43	226	353	359	567		caaccctgtcaTCACATGAtagtcagggaga tgcagtcgttcgTCATATGAttaaaagtccaa	5' 5UTR?	
<i>Drosophila_erecta</i>	Dere\GG15974		43	217	353	230	567		caaccctgtctcaTCACATGAtagtcacgggtga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_biarmipes</i>	Dbia\VhaM8.9		43	224	353	436	567		caaccgtgtcaTCACATGAtagccaggggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_suzukii</i>	Dsuz\VhaM8.9		43	223	353	541	567		caaccctgtctcaTCACATGAtagctagggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_takahashii</i>	Dtak\VhaM8.9		43	218	353	1418	567		caaccctgtcaTCACATGAtagccaggggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_eugracilis</i>	Deug\VhaM8.9		43	187	353	260	567		caaccctgtctcaTCACATGAtagccaggggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_elegans</i>	Dele\VhaM8.9		43	214	353	913	567		caaccctgtctcaTCACATGAtagccagggggag tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_rhopaloea</i>	Drho\VhaM8.9		43	215	353	485	567		caaccctgtctcaTCACATGAtagccaggggaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_ficusphila</i>	Dfic\VhaM8.9		43	222	353	232	570		caactctgtctcaTCACATGAtagccagagagaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_kikkawai</i>	Dkik\VhaM8.9		43	235	353	65	570		caaccctgttcaTCACATGAtagccaggggaga tgcagtcgtttgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_bipectinata</i>	Dbip\VhaM8.9		43	207	353	67	567		caaccctgtctcaTCACATGAtagctagagaga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_ananassae</i>	Dana\GF16587		43	216	353	59	567		caaccctgtctcaTCACATGAtagccagggtga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5UTR?	
<i>Drosophila_pseudoobscura</i>	Dpse\GA21083		43	226	353	71	567	386	caaccctgttcaTCACATGAtagtcagaggtg gcaagtcgttcgTCATATGAttgaaaaagtc	5' 5UTR?	
<i>Drosophila_persimilis</i>	Dper\GL13947		43	226	353	71	567		caaccctgttcaTCACATGAtagtcagaggtg gcaagtcgttcgTCATATGAttgaaaaagtc	5' 5UTR?	
<i>Drosophila_miranda</i>	Dmir\VhaM8.9		43	226	353	71	567		caaccctgttcaTCACATGAtagtcagaggtg gcaagtcgttcgTCATATGAttgaaaaagtc	5' 5UTR?	

<i>Drosophila_willistoni</i>	Dwil\GK14261		43	225	353	63	573		acactgagactgTCACATGAcagatatcatcg ttttcgacgttgTCATATGAttaaaagcagaa	5' 5UTR?	
<i>Drosophila_albomicans</i>	Dalb\VhaM8.9		43	237	353	68	567		aacaactacccaTCACATGAcagtgagagcgt gcagttgttcgTCATATGAttgaaagcctgg	5' 5UTR?	
<i>Drosophila_mojavensis</i>	Dmoj\GI10428		43	237	353	58	564		ttcttcgacccaTCACATGAcagtcagagcgt tgcagttgttcgTCATATGAttaaaagcctgg	5' 5UTR?	
<i>Drosophila_virilis</i>	Dvir\GJ10644		43	245	353	64	564		ttctactatccaTCACATGAcagtcagagcgt tgcagttgttcgTCATATGAttaaaagcctgg	5' 5UTR?	
<i>Drosophila_grimshawi</i>	Dgri\GH14333		43	231	353	57	567		ttcgataaccaTCACATGAcagtaggagcgt tgcagttgttcgTCATATGAttaaaagcctgg	5' 5UTR?	