

Gene Cluster ID	Atp6v1H
Drosophila melanogaster gene	VhaSFD (CG17332)
FlyBase ID	FBgn0027779
Predicted function	V-type ATPase, H ⁺ transporting, V1 subunit H
Cytogenetic map	2L:6A12-36A12
Gene sequence location	2L:16723138..16727825[-]
Dmel CLEAR sequence	TCACAAGAccagTCAGCTGA
CLEAR sequence location	2L:16727801..16727782

FlyBase VhaSFD (CG17332) gene model & CLEAR element (red) positions:



Atp6v1H (VhaSFD) gene structure comparison:

Key: UTR region, CDS region, intron, alternatively spliced exon

Species	VhaSFD Atp6v1H orthologs	5'exon	intron	exon	intron	exon3'	Extended CLEAR region	Position	bps from TSS										
<i>Drosophila_melanogaster</i>	Dmel\VhaSFD	159	37	141	479	896	222	898	135	64	563	60	114	160	79	681	gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR	36
<i>Drosophila_simulans</i>	Dsim\GD21903	37	145	479	919	231	882	135	64	563	57	114	158	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_sechellia</i>	Dsec\GM17165	37	145	479	905	231	869	135	64	563	55	114	160	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_yakuba</i>	Dyak\GE13171	37	145	479	900	231	891	135	64	563	65	114	160	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_erecta</i>	Dere\GG20115	37	147	479	901	231	885	135	64	563	65	114	160	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila.biarmipes</i>	Dbia\VhaSFD	37	160	479	1075	231	741	135	64	563	103	114	153	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_suzukii</i>	Dsuz\VhaSFD	37	158	479	1098	222	845	135	64	563	109	114	153	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_takahashii</i>	Dtak\VhaSFD	37	169	479	1500	231	795	135	64	563	61	114	151	79		aaaaagTCACAAGAccaagTCAGCTGAattcteg	5'UTR?		
<i>Drosophila_eugracilis</i>	Deug\VhaSFD	37	154	479	983	231	845	135	64	563	95	114	162	79		agaaaaTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_elegans</i>	Dele\VhaSFD	37	157	479	1057	231	767	135	64	563	181	114	160	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_rhopaloa</i>	Drho\VhaSFD	37	156	479	1071	231	779	135	64	563	215	114	159	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_ficusphila</i>	Dfic\VhaSFD	37	150	479	1022	231	830	135	64	563	67	114	160	79		gaaaagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_kikkawai</i>	Dkik\VhaSFD	37	146	479	1199	222	767	135	64	563	65	114	158	79		aaaaagTCACAAGAccaagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_bipectinata</i>	Dbip\VhaSFD	37	154	479	854	222	524	135	64	563	68	114	142	79		aaaaagTCACAAGAccagTCAGCTGAattct	5'UTR?		
<i>Drosophila_ananassae</i>	Dana\GF24362	37	156	479	821	231	557	135	64	563	60	114	138	79		aaaaagTCACAAGAccagTCAGCTGAattct	5'UTR?		
<i>Drosophila_pseudoobscura</i>	Dpse\GA14464	37	125	479	1063	240	1088	135	64	563	60	114	146	79		gcacagTCACAAGAccaaagTCAGCTGAatttc	5'UTR?		
<i>Drosophila_persimilis</i>	Dper\GL19340	37	130	479	1066	240	1081	135	64	563	60	114	146	79		gcacagTCACAAGAccaaagTCAGCTGAatttc	5'UTR?		
<i>Drosophila_miranda</i>	Dmir\VhaSFD	37	130	479	1037	240	1112	135	64	563	60	114	146	79		gcacagTCACAAGAccaaagTCAGCTGAatttc	5'UTR?		
<i>Drosophila_willistoni</i>	Dwil\GK15126	37	173	479	1595	219	1052	135	66	563	98	114	194	79		aagaagTCACAAGAccagTCAGCTGAatttc	5'UTR?		
<i>Drosophila_albomicans</i>	Dalb\VhaSFD	37	121	479	ND	ND	135	66	563	63	114	196	79		aataagTCACAAGAccagTCAGCTGAattcg	5'UTR?			
<i>Drosophila_mojavensis</i>	Dmoj\GI21354	37	136	479	1823	231	1150	135	64	563	63	114	200	79		aataagTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_virilis</i>	Dvir\GJ11146	37	129	479	2101	219	1227	135	64	563	61	114	174	79		gaataaTCACAAGAccagTCAGCTGAattcg	5'UTR?		
<i>Drosophila_grimshawi</i>	Dgri\GH10362	37	122	479	1351	234	911	135	64	563	62	114	185	79		aataagTCACAAGAccagTCAGCTGAattcg	5'UTR?		

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