

Gene Cluster ID	Atp6v0d		
Drosophila melanogaster gene	VhaAC39-1 (CG2934)		
FlyBase ID	FBgn0028665		
Predicted function	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d		
Atp6v0d CLEAR element conservation:			
	5' / 5' UTR	intron1	intron1
Dmel\	AAGAGTTAAAAA TCATATGA CTTGTGATCGA	CACGCCCTGG TCA CATGA CC AGCGATAACA	
Mdom\	CAACTGCTATA GTC ATATGA CA CTCGATAAAAG	TACAGGGCAAG TCA TGTGA CAT TTGTATGTG	
Ccap\	TACCAATGACAG TC AT GT GA TG ACTTATGACA	GGGTGGTGTGG TCA TGTGA CA CACCATAAA	
Gmor\	ACTCTGAGAGA GTC ATATGA CA GTAAAGATGA	ACAAGGGCCTGG TCA TGTGA TG CGTACTATGT	TAGTAATAATT TCA TATGA AT GTATGTATGA
Ppap\	CTCAACTACGG GTC ATATGA CA TTTGATAAT	TTGAGAAAATT TCA CGTGA TCT TGATTAACC	-----
Llon\	-----	TTTTGATTTAT TCA CATGA TT TCACAGGTTTC	AAACTCTGGAA TCA TATGA CC ACGGAAATT
Agam\	AAA ACTAGGTAGTCATATGA TG CGTTTTGCC	GTGTAAGGC GG TATATGACC AG CCTTCAGC	
Aara\	AAA ACTAGGTAGTCATATGA TG CGTTTTGCC	GTGTAAGGC GG TATATGACC AG CCATCAGC	
Aqan\	AAA CTAGGCAGTCATATGA TG CGTTTTGCC	GTGTAAGGC GG TATATGACC AG CCATCAGC	
Achr\	AAA AAATTG TAG TATATGA TG CGTTTTGCC	AGTAAGGCC GG TATATGACC TG CCTTCAA	
Aepi\	GC AAA ATTG TAG TATATGA TG CGTTTTGCC	GGTATTG AC GG GG TATATGACC TG CCTTCGGT	
Amin\	ACACAAATTG TAG TATATGA TG CGTTTTAGCT	ACGGCAGGC GG TATATGACC TG CTAACATAC	
Afun\	CAAAAATTG TAG TATATGA TG CGTTTTACCT	ACGGCAGGC GG TATATGACC TG CTAACAC	
Aste\	ACAAAATTG TAG TATATGA TAC TTTGCCC	CGGGTAGGC GG TATATGACC TAC TCAACCG	
Adir\		ACATAAGGCAG TCA TGTGACC CCT TTGCA TG	
Aalb\	AAGACTGAG TAG TATATGA TG CACATTCTGC	TCACCCAC GG TATATGACC GAT TTTCA	
Adar\	AGTCAGGGGTAGTCATATGA TG CGCTTTCAGC	TCACATACT GG TATATGACC CG TCTTTCA	
Aaeg\	TCCGAGT GCG AGTCATATGA CA CTTTTCAGAG	CATCTTGGTT GAT CATATGACC TAT TCACACG	
Cqui\	CCC AT GC GC AGTCATATGA CA CTTTTCAGAG	CGATTGGTT GAT CATATGACC TAT CATATA	
Mdes\	TT CG CATTGTTA TCA CATGA ATT GTCAATGTT	TGTTGTTGTTAT TCA TATGA TG AAAAGTGAC	
Bmor\	TCT ATGTT CAC A TCA TATGA TCA ATT TTT CTTT		
Msex\	TCT ATGAT CG C A TCA AT ATGA TCA AT G CAACTC		
Dple\	TCT ATG GG G CT A TCA TATGA TCA AT G ATCTAC		
Hmell\	TCT ATG GG G GT T A TCA AT ATGA TCA AT G ATCTAT		
Pxyl\	TCT ATG GT CAA A TCA AT ATGA TCA AT G AATGAT		
Tcas\	ctg TCACATGA ttgtcaactaa TC ATATGA <aa></aa>		
Dpon\	caa TCACATGA ..gtcaaaa TC ATATGA <gc></gc>		
Amel\	CTC ACAAGA TAG T C ATATGA TG ACACGAAAA		
Aflo\	CTC CAT AAGA TAG T C ATATGA TG ACACGAAAA		
Bter\	CTC G CT AGAT TG T CATATGA TG ACACGAAAA		
Bimp\	CTC G CT AGAT TG T CATATGA TG ACACGAAAA		
Mrot\	CTC ACT GT AC GG T C ATATGA TG ACACGAAAA		
Ngir\	GTT AGACT TT TAG T C ATATGA TG CA T C CT GAC		
Nvit\	GTT AGACT TT TAG T C ATATGA TG CA T C CT GAC		
Nlon\	GTT AGACT TT TAG T C ATATGA TG CA T C CT GAC		
Aech\	ATGACAT GAC A TG CATATGA TTT TAGAAGAGG		
Acep\	GTGACAT GAC A TG CATATGA TTT TAGAAGAGG		
Sinv\	CGG CT AG CT CG GT CATATGA TTT TGTG G AAAA		

Pbar\ CTGCTCGTT**TAGTCATATGA**TTTGAGA**AAGG**
 Cflo\ AGTCCATATTG**GTCA**TATGA**TTTCACCGA**GG
 Lhum\ GGTCAATGCT**GTCA**TATGA**TCTTCGTGAAA**
 Hsal\ CCGTGCCTCG**GTCA**TATGA**TCTCGGTGAAA**
 Lful\ CACATCCTCGA**GTCA**TATGA**TCTGCTATCCCT**

Rpro\ cagactgaattg**TCATATGA**atacaccctgcc
 Phum\ tcattaatgtat**TCATATGA**atcattaaaaat
 Phum\ cactttctctg**TCATATGA**caacagatggg
 Dpul\ ccgtcccaagtgc**TCA**TGTGA**ttctgatccgtc**
 Isca\ taactgcccggag**TCATATGA**tcaatacgcccc
 Hsap\ gcccccttatgg**TCACGTGAgggcgcttgcgcg**
 Nvec\ ttccctgcgggg**TCATGTGAttcttacatgt**a
 Tadh\ gtatctcggtgc**TCACATGA**tcctcttgtag

Atp6v0d gene structure comparisons:

(Click on orthologs for genomic, mRNA and protein sequence informations)

Key: UTR region, CDS region

Order	Species	Atp6v0d orthologs	5'exon	intron	exon	intron	exon3'		Extended CLEAR region	Position	bps from TSS			
Diptera (Drosophilidae)	<i>Drosophila_melanogaster</i>	Dmel\Vha39-1	249	127	338	509	90	417	502	aagagttaaaaTCATATGActtgtcgatcgacacggccctggTCACATGAccaggcgaaaca	5'UTR intron1	47 437		
Diptera (Muscidae)	<i>Musca_domestica</i>	Mdom\Vha39-1		127	357	509	948	417		caactgctatagTCATATGAcagtcgataaag tacaggggcaagTCATGTGAcattgtatgt	5'UTR? intron1	>213 >223		
Diptera (Tephritidae)	<i>Ceratitis_capitata</i>	Ccap\Vha39-1	197	124	292	509	70	417	138	taccaatgacagTCATGTGAtgacttatgaca gggtgtgttggTCATGTGAcacaccattaaa	5'UTR? intron1	-33 425		
Diptera (Glossinidae)	<i>Glossina_morsitans</i>	Gmor\Vha39-1	199	127	213	509	58	417	158	actctgagagTCATATGAcagataagaatgaca acaaggccctggTCATGTGAtgcgtactatgt tagtaataattTCATATGAtgtatgtatgtatg	5'UTR intron1 intron1	39 382 419		
Diptera (Psychodidae)	<i>Lutzomyia_longipalpis</i>	Llon\Atp6v0d	94	121	418	764 (509+255)			67	162	333	ttttgattatTCACATGAttcacaggtttc aaacttggaaTCATATGAccacggaaaatt	5' 5'UTR	-617 12
	<i>Phlebotomus_papatasi</i>	Ppat\Atp6v0d		121	3295	764 (509+255)			ND	162		ctcaaacacggTCATATGAcatttgataat ttgagaaattatTCACGTGAtcttgattaaacc	5' intron1	>93 >552
Diptera (Culicidae)	<i>Anopheles_gambiae</i>	Agam\Atp6v0d AGAP000721	370	121	517	509	1037	417	219	aaaacttagtagTCATATGAtgcgttttgcgtgtaaaggcgTCATATGAccgccttcagegcaaaatgTCATGTGAA TCACGTGAtagtccacc	5'UTR intron1 intron2	5 799 2033		
	<i>Anopheles_arabiensis</i>	Aara\Atp6v0d-1		121	500	509	1314	417		aaaacttagtagTCATATGAtgcgttttgcgtgtaaaggcgTCATATGAccgccttcagegcaaaatgTCATGTGAA TCACGTGAtaatcacc	5'UTR? intron1 intron2	>368 >438 >1603		
	<i>Anopheles_quadriannulatus</i>	Aqan\Atp6v0d-1		121	511	509	1305	417		aaaacttaggcagTCATATGAtgcgttttgcgtgtaaaggcgTCATATGAccgccttcagegcaaaatgTCATGTGAA TCACGTGAtaatcacc	5'UTR intron1 intron2	>368 >451 >1617		
	<i>Anopheles_christyi</i>	Achr\Atp6v0d-1		121	495	509	450	417		aaaaatagtagTCATATGAtgcgttttgcgtgtaaaggcgTCATATGAccgccttcagea	5'UTR intron1	>317 >421		
	<i>Anopheles_epiroticus</i>	Aepi\Atp6v0d-1		121	1287	509	792	417		gcaaaatttagTCATATGAtgcgttttgcgtgttgcggTCATATGAccgccttcgg	5'UTR intron1	>326 >445		

	<i>Anopheles_minimus</i>	Amin\Atp6v0d-1		121	365	509	72	417		acacaattgttagTCATATGAtgcgttttagct acggcaggcggtTCATATGAccgtcaatac	5'UTR intron1	>370 >309
	<i>Anopheles_funestus</i>	Afun\Atp6v0d-1		121	418	509	77	417		caaaaattgttagTCATATGAtgcgttttaect acggcaggcaggTCATATGAccgtcaacac	5'UTR intron1	>378 >304
	<i>Anopheles_stephensi</i>	Aste\Atp6v0d-1		121	413	509	79	>392		acaaaattgttagTCATATGAtacatttgcc cggtaggggTCATATGAcctaactcaaccg	5'UTR intron1	>436 >372
	<i>Anopheles_dirus</i>	Adir\Atp6v0d-1		121	314	509	62	417		acataaggcaggTCATGTGAcccatttgcag	5'UTR? intron1	>293
	<i>Anopheles_nili</i>	Anil\Atp6v0d-1										
	<i>Anopheles_albimanus</i>	Aalb\Atp6v0d-1		121	467	509	73	417		aagactgagtagTCATATGAtgcacattctgc tcaccacccgggTCATATGAccgtctttca	5'UTR? intron1	>254 >385
	<i>Anopheles_darlingi</i>	Adar\Atp6v0d-1		121	633	509	92	417	421	agtcaaaaaatggtagTCATATGAtgcgtttcagc tcacatactgggTCATATGAccgtctttca	5'UTR? intron1	>244 >450
	<i>Aedes_aegypti</i>	Aaeg\Atp6v0d AAEL011025*	143	121	ND	509	337	417 (255 + 162)	445	tccgagtgccggTCATATGAcactttcagag catcttgggtgaTCATATGAccttatcacacg	5' intron1	-20 409
	<i>Culex_pipiens_qui.</i>	Cqui\Atp6v0d CPJU009947		121	ND	926 (509+417)			110	ccccatgcgcgagTCATATGAcactttcagag cgatttgggtgaTCATATGAccttatcatata	5' intron1	>154 >255
	<i>Anopheles_gambiae</i>	Agam\Atp6v0d-2 AGAP013199				1044				ND		
	<i>Anopheles_arabiensis</i>	Aara\Atp6v0d-2				1044				ND		
	<i>Anopheles_quadriannulatus</i>	Aqan\Atp6v0d-2				1044				ND		
	<i>Anopheles_christyi</i>	Achr\Atp6v0d-2				1044				ND		
	<i>Anopheles_epiroticus</i>	Aepi\Atp6v0d-2				1044				ND		
	<i>Anopheles_minimus</i>	Amin\Atp6v0d-2				1044				ND		
	<i>Anopheles_funestus</i>	Afun\Atp6v0d-2				1044				ND		
	<i>Anopheles_stephensi</i>	Aste\Atp6v0d-2				1044				ND		
	<i>Anopheles_dirus</i>	Adir\Atp6v0d-2				1044				ND		
	<i>Anopheles_nili</i>	Anil\Atp6v0d-2				1044				ND		
	<i>Anopheles_albimanus</i>	Aalb\Atp6v0d-2				1068				ND		
	<i>Anopheles_darlingi</i>	Adar\Atp6v0d-2				1071				ND		

Diptera (Cecidomyiidae)	<i>Mayetiola_destructor</i>	Mdes\Atp6v0d		121	332	509	76	255	81	162	tttcgttttgttaTCACATGAattgtcaatgtt tgttgttgttatTCATATGAtcaaaaggatgac	5' intron1	>171 >310	
Lepidoptera	<i>Bombyx_mori</i>	Bmor\Atp6v0d		121	786	509	213	255	262	162	tctatgttcacaTCATATGAtcaatttctt	5'	>-117	
	<i>Manduca_sexta</i>	Msex\Atp6v0d		121	272	509	75	255	335	162	tctatgtatcgcaTCATATGAtcaatgtcaactc	5'	>-126	
	<i>Danaus_plexippus</i>	Dple\Atp6v0d	110	121	176	509	86	255	82	162	59	tctatggagetaTCATATGAtcaatgtatctac	5'UTR	5
	<i>Heliconius_melpomene</i>	Hmel\Atp6v0d		121	157	509	408	255	332	162		tctatggagitaTCATATGAtcaatgtatctat	5'	>-97

	<i>Plutella_xylostella</i>	Pxyl\Atp6v0d	129	121	102	509			78	255	141	162	334	tctatggtcaaaTCATATGAtcaatgaatgat	5'UTR	26		
Strepsiptera	<i>Mengenilla_moldrzyki</i>	Mmol\Atp6v0d		121	ND	509?			ND	408				ND				
Coleoptera	<i>Tribolium_castaneum</i>	Tcas\Atp6v0d LOC663777	73	121	50	509 (351+158)			43	255(177+178)	54	162	192	TCACATGAtttactaaTCATATGAcattttgttg	5'/5'UTR	-4/6		
	<i>Dendroctonus_ponderosae</i>	Dpon\Atp6v0d	73	121	801	926 (351+158+177+78+162)				267	tgtcacatgacaaTCACATGAtctgccaaggat ggatttgtaaaaTCATATGAcgcctcgggag			5' 5'UTR	-9 13			
Hymenoptera	<i>Apis_mellifera</i>	Amel\Atp6v0d GB12698	112	121	121	351			125	158	94	177	155	78	102	162	411	
	<i>Apis_florea</i>	Aflo\Atp6v0d		121	126	351			119	158	115	177	133	78	97	162		
	<i>Bombus_terrestris</i>	Bter\Atp6v0d		121	126	351			129	158	209	177	118	78	76	162		
	<i>Bombus_impatiens</i>	Bimp\Atp6v0d		121	126	351			142	158	209	177	118	78	77	162		
	<i>Megachile_rotundata</i>	Mrot\Atp6v0d		121	90	351			123	158	77	177	79	78	77	162		
	<i>Acromyrmex_echinatior</i>	Aech\Atp6v0d		121	258	351			145	158	76	177	1075	78	190	162		
	<i>Atta_cephalotes</i>	Acep\Atp6v0d		121	249	351			132	158	73	177	1121	78	ND	162		
	<i>Solenopsis_invicta</i>	Sinv\Atp6v0d	76	121	389	351			2226	158	281	177	ND	78	136	162		
	<i>Camponotus_floridanus</i>	Cflo\Atp6v0d		121	789	351			524	158	86	177	141	78	140	162		
	<i>Harpegnathos_saltator</i>	Hsal\Atp6v0d		121	242	351			310	158	76	177	119	78	110	162		
	<i>Pogonomyrmex_barbatus</i>	Pbar\Atp6v0d		121	263	351			117	158	67	177	135	78	163	162		
	<i>Linepithema_humile</i>	Lhum\Atp6v0d		121	239	351			102	158	102	255(177+178)	110	162		ggtcatatgtTCATATGAttttcgtaaaa	5' ->81	
	<i>Nasonia_vitripennis</i>	Nvit\Atp6v0d NV13431		121	82	351			90	158	80	177	89	78	89	162	433	
	<i>Nasonia_giraulti</i>	Ngir\Atp6v0d		121	82	351			90	158	88	177	88	78	89	162		
	<i>Nasonia_longicornis</i>	Nlon\Atp6v0d		121	82	351(172+179)			90	158	80	177	88	78	89	162		
Hemiptera	<i>Acyrthosiphon_pisum</i>	Apis\Atp6v0d ACYP1003170	197+16	786						85	270			ND				
	<i>Rhodnius_prolixus</i>	Rpro\Atp6v0d		121	116	172	1506	179	81	158	143	177	520	78	233	162		
	<i>Pediculus_humanus</i>	Phum\Atp6v0d PHUM410380		121	100	172	67	179	177	158	90	177	80	78	86	>144		
	<i>Odonata</i>	Lful\Atp6v0d		121	72	172	79	179	111	158	477	177	1429	78	84	162		
	<i>Crustacea</i>	Daphnia_pulex		121	64	172	76	337 (179 + 158)			65	177	59	78	60	162	167	
	<i>Ixodida</i>	Ixodes_scapularis	53	121	ND	172	3991	179	127	158(80+78)	814	177	74	78	1886	162		
																taactgccggagTCATATGAtcaatacgcccc	5'UTR	29

	<i>Homo_sapiens</i>	ATP6V0D1	100	130	27241	172	8837	179	1349	80	3747	78	126	177	100	78	103	162	1	gcgccctatggTCACGTGAggcgttgcgcg	5'	-23	
Cnidaria	<i>Nematostella_vectensis</i>	v1g128006	1	130	2206	172	456	179	880	80	357	78	513	177	1100	78	385	162	1	ttcctgtgcggTCATGTGAttttacatgtta	5'	>-81	
Placozoa	<i>Trichoplax_adhaerens</i>	TRIADDRAFT_37067	1	127	287	172	126	179	122	80	211	78	144	177	79	78	79	162	712	1	atctcggtgcTCACATGAtccttgtgagtc	5'	>-324