

Gene Cluster ID	Atp6v1A
Drosophila melanogaster gene	Vha68-2 (CG3762)
FlyBase ID	FBgn0263598
Predicted function	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A

Atp6v1A CLEAR element conservation:

Dmel\	5'/intron1	5'/intron1	intron1	intron1
Mdom\	5'/intron1	5'/intron1	intron1	intron1
Ccap\	5'/intron1	5'/intron1	intron1	intron1
Gmor\	5'/5'UTR	intron		
Llon\	5'/5'UTR	intron		
Ppap\	5'/5'UTR	intron		
Agam\	intron1	intron1	intron2	intron2
Aara\	intron1	intron1	intron2	intron2
Aqan\	intron1	intron1	intron2	intron2
Achr\	intron1	intron1	intron2	intron2
Aepi\	intron1	intron1	intron2	intron2
Amin\	intron1	intron1	intron2	intron2
Afun\	intron1	intron1	intron2	intron2
Aste\	intron1	intron1	intron2	intron2
Adir\	intron1	intron1	intron2	intron2
Anil\	intron1	intron1	intron2	intron2
Aalb\	intron1	intron1	intron2	intron2
Adar\	intron1	intron1	intron2	intron2
Cqui\	intron1	intron1	intron2	intron2
Aaeg\	intron1	intron1	intron2	intron2
Mdes\	5'/5'UTR	intron1	intron1	
Mdes\	5'/5'UTR	intron1	intron1	
Mdes\	5'/5'UTR	intron1	intron1	
Bmor\	5'/5'UTR	intron1	intron1	
Msex\	5'/5'UTR	intron1	intron1	
Dple\	5'/5'UTR	intron1	intron1	
Hmel\	5'/5'UTR	intron1	intron1	
Pxyl\	5'/5'UTR	intron1	intron1	
Tcas\	5'/5'UTR	intron1	intron1	
Dpon\	5'/5'UTR	intron1	intron1	
Amel\	5'/5'UTR	intron1	intron1	
Aflo\	5'/5'UTR	intron1	intron1	
Bter\	5'/5'UTR	intron1	intron1	
Bimp\	5'/5'UTR	intron1	intron1	
Mrot\	5'/5'UTR	intron1	intron1	
Cflo\	5'/5'UTR	intron1	intron1	
Aech\	5'/5'UTR	intron1	intron1	
Acep\	5'/5'UTR	intron1	intron1	
Sinv\	5'/5'UTR	intron1	intron1	
Lhum\	5'/5'UTR	intron1	intron1	
Pbar\	5'/5'UTR	intron1	intron1	
Hsal\	5'/5'UTR	intron1	intron1	
Ngir\	5'/5'UTR	intron1	intron1	
Nvit\	5'/5'UTR	intron1	intron1	
Nlon\	5'/5'UTR	intron1	intron1	
Lful\	5'/5'UTR	intron1	intron1	
Apis\	5'/5'UTR?/intron1?	5'/5'UTR?/intron1	5'/5'UTR?/intron1	
Dpul\	5'/5'UTR?/intron1?	5'/5'UTR?/intron1	5'/5'UTR?/intron1	
Isca\	5'/5'UTR?/intron1?	5'/5'UTR?/intron1	5'/5'UTR?/intron1	
Phum\	5'/5'UTR?/intron1?	5'/5'UTR?/intron1	5'/5'UTR?/intron1	
Hsap\	5'/5'UTR?/intron1?	5'/5'UTR?/intron1	5'/5'UTR?/intron1	

Atp6v1A gene structure comparison:

Order	Species	Atp6v1A orthologs	5'exon	intron	exon	intron	exon	intron	exon	intron	exon3'	Extended CLEAR region	Position	bps from TSS
Diptera (Drosophilidae)	Drosophila_melanogaster	DmelVha68.2	124	1170	23	76	413	698	108	978	67	93	546	470
Diptera (Muscidae)	Musca_domestica	MdomVatp6v1A.1			ND	76	74	698	83	978	70	93		470

		Mdom\Atp6v1A-2			ND	76	66	698										75	978										61	93		ND														
		Mdom\Atp6v1A-3			ND	1932																										ND														
Diptera (Tephritidae)	Ceratitis_capitata	Ccap\Atp6v1A-1	81	621	22	76	69	698										77	978										70	93		tpagcaaacatgTCAGCTGAaccggaatgct tgtaacacgcgTCAGCTGAacctagcagat ctaagctgtggTCACGTGAataaaagcttt gagataagccgTCAGCTGAacttaaccgtt	5' 5' intron1 intron1	-284 -63 230 594												
		Ccap\Atp6v1A-2			ND	76	222	698										61	978										174	93		ND														
Diptera (Glossinidae)	Glossina_morsitans	Gmor\Atp6v1A-1 TMP01178	133	274	55	76	93	698										60	978										73	93	144	caattccaaatgTCACGTGAataaaagcttt ggaaaggaaaagTCAGCTGAcaagtgaaaaa	5'UTR? intron1	-35 254												
		Gmor\Atp6v1A-2 TMP02752			ND	73	70	698										59	978										73	93		ND														
		Gmor\Atp6v1A-3 TMP007159			ND	1932																										ND														
Diptera (Psychodidae)	Lutzomyia_longipalpis	Llon\Atp6v1A	93	490	23	76	71	195	2085	1084										65	397										87	93	76	tcacaagatcgtTCAGCTGAgtgtgtgtgat atgtaactcaagTCATGTGAatcgaaaaaat	5'UTR intron1	8 412										
	Phlebotomus_papatasi	Ppap\Atp6v1A	38	559	23	76	67	195	ND	578										ND	506										ND	397										66	93		tcacaagcgtgTCAGCTGAgaagctgtgtgat catcggggagTCATGTGAacagtgaatt	5'UTR? intron1
Diptera (Culicidae)	Anopheles_gambiae	Agam\Atp6v1A AGAP003153	30	574	67	76	735	195	75	1084										74	397										100	93		gaaccaaacaggTCACATGAaccgcagacct ttgcaacctgaTCAGCTGAacctttttgag gggtcgccagaagTCACATGAagtggaatgg ttatgaatcggTCATGTGAaccactgtgcc tggtggaaaggTCAGATGAgtgtgtaccga	intron1 intron1 intron2 intron2	405 514 927 1020 1248										
	Anopheles_arabiensis	Ara\Atp6v1A			ND	76	724	195	75	1084										75	397										122	93		gaaccaaacaggTCACATGAaccgcagacct ttgcaacctgaTCAGCTGAacctttttgag gggtcgccagaagTCACATGAagtggaatgg ttatgaatcggTCATGTGAaccactgtgcc tggtggaaaggTCAGATGAgtgtgtaccga	intron1? intron1? intron2? intron2?	> -262 > -149 > 256 > 351 > 579										
	Anopheles_quadrannulatus	Aqan\Atp6v1A			ND	76	731	195	75	1084										90	397										121	93		gaaccaaacaggTCACATGAaccgcagacct ttgcaacctgaTCAGCTGAacctttttgag gggtcgccagaagTCACATGAagtggaatgg ttatgaatcggTCATGTGAaccactgtgcc tggtggaaaggTCAGATGAgtgtgtaccga	intron1? intron1? intron2? intron2?	> -262 > -149 > 261 > 354 > 576										
	Anopheles_christyi	Achr\Atp6v1A			ND	76	693	195	70	1084*										90	397										75	93		gaaccaaacaggTCACATGAactgcagacca tttcaacctgaTCAGCTGAacctttttgag gggtcgccagagTCACATGAagtggaatgg ttatgaatcggTCATGTGAaccactctc atctggaatggTCAGATGAgtgggtgtgat	intron1? intron1? intron2? intron2?	> -252 > -161 > 246 > 321 > 530										
	Anopheles_epiroticus	Aepi\Atp6v1A			ND	76	674	195	68	1084										93	397										97	93		aaaccaaacaggTCACATGAactgcagacca tcttcaaccggaTCAGCTGAacctttttgag cgctgtgtcgagTCACATGAagtggaatgg ttatgaatcggTCATGTGAaccactgttgg atctagaatggTCAGATGAgtgggtgtgtt	intron1? intron1? intron2? intron2?	> -244 > -153 > 228 > 309 > 511										
	Anopheles_minimus	Amin\Atp6v1A			ND	76	606	195	65	1084										76	397										72	93		gaaccgaactgtTCACATGAactgcgtttcgg agcttctctgaTCAGCTGAacctttttgag gtcgtgtgcagTCACATGAagtggaatgg atatgaatcggTCATGTGAactgtttgaaga ttctggaatggTCAGATGAgtgaagaagtg	intron1? intron1? intron2? intron2?	> -217 > -144 > 238 > 312 > 509										
	Anopheles_funestus	Afun\Atp6v1A			ND	76	616	195	67	1084										83	397										78	93		gaacctaacaggTCACATGAactgcgtttcgg agcttctttgaTCAGCTGAacctttttgag gtgggtcagcagTCACATGAagtggaatgg ttatgaatcggTCATGTGAactgtttgaaga tttgaatggTCAGATGAgtgatggaag	intron1? intron1? intron2? intron2?	> -219 > -146 > 233 > 307 > 506										
	Anopheles_stephensi	Aste\Atp6v1A			ND	76	628	195	69	1084										75	397										82	93		gtaccgaacaggTCACATGAaccgcgtttcgg cttcaacctgaTCAGCTGAacctcttccat gggtcgtgcagTCACATGAagtggaatgg acatgaatcggTCATGTGAactgtttgtgag atctgaatcggTCAGATGAgtgggagactc	intron1? intron1? intron2? intron2?	> -231 > -152 > 244 > 319 > 521										
	Anopheles_dirus	Adir\Atp6v1A			ND	76	603	195	73	1084										78	397										111	93		gtacctaacaggTCACATGAactgcgtgtgatg ggctgttttgaTCAGCTGAacctttttgag gtgcgcagccagTCACATGAagtggaatgg agatgaatcggTCATGTGAaccggtgtgtt atctgtgtgggTCAGATGAgtcgtttactt	intron1? intron1? intron2? intron2?	> -231 > -142 > 213 > 296 > 485										
	Anopheles_nili	Anil\Atp6v1A			ND	76	645	195	80	1084										83	397										88			aatcaaacgggTCACATGAaccaagactca ccatcctttgaTCAGCTGAactttttga tcttcaagaagTCACATGAagtggaatg tttgatgttaTCATGTGAactcctcagc atgtgtttggTCAGATGAcatgatgattt	intron1? intron1? intron2? intron2?	> -210 > -140 > 241 > 373 > 570										
	Anopheles_albimanus	Aalb\Atp6v1A			ND	76	644	1279												77	397										83	93		gaaacccpgggTCACATGAaccacactccc ttgtgtggaagTCACATGAacaggtgtggaac gtctcgggggTCAGATGAaccacaggtgtg	intron1? intron2?	> -228 > 191 > 521										
	Anopheles_darlingi	Adar\Atp6v1A			ND	76	646	1279												75	397										82	93		gaaacccpgggTCACATGAaccacactccc ttgtgtggaagTCACATGAacaggtgtggaat gcggtgtggggTCAGATGAccccctcgtg	intron1? intron2?	> -237 > 187 > 512										
	Aedes_aegypti	Aaep\Atp6v1A AAEL008782	127	523	48	76	9638	195	67	1084										68	397										98	93	1088	attagatttggTCACATGAacctctaccact caagaacaggTCACATGAactgtatgtga agtaacatactTCAGCTGAgtcgtttggaat	intron1 intron2	479 905 1004										
Culex_pipiens_qui.	Cqui\Atp6v1A CP0007722			ND	76	5977	1279												61	397										3297	93		ttctgattgtgTCACATGAaccagaccact acagagagtcagTCACATGAactgtgtgtga	intron1? intron2?	> -209 > 207											
Diptera (Cecidomyiidae)	Mayetiola_destructor	Mdes\Atp6v1A			ND	76	91	663										71	616										109	93		gtgaataacaggTCATGTGAactgttcacag agcaggtgtgagTCATGTGAaccagactctc gtcaattaaatTCATGTGAactgcagaaatt	5' 5' intron1?	> -709 > -480 > -256												
Lepidoptera	Bombyx_mori	Bmor\Atp6v1A	90	2217	34	85	368	113	371	228	371	138	931	152	760	125	847	147	215	216	694	160	694	70	1031	137	939	190	353	93	285	aatcaatgatTCAGCTGAatcatgacaag gtatgattgggTCAGCTGAactcttaaat	5' 5'	-117 -81												

[illegible]