

Gene Cluster ID	Atp6v0e
Drosophila melanogaster gene	VhaM9.7-b (CG7625)
FlyBase ID	FBgn0028663
Predicted function	ATPase, H+ transporting, V0 subunit e

Atp6v0e CLEAR element conservation:

	<u>5' / 5' UTR</u>	<u>5' / 5' UTR</u>
Dmel\	GGGACATGTCCGTCATGTGATATTCGTTGCTC	
Mdom\	cattatatttaaTCATGTGAcacacgacgaca	
Ccap\	tcccatgggtgaTCATGTGAcatttgcgtagc	
Gmor\	gctctttacgcaTCATGTGAtaattagtaatt	
Llon\	aacgatttcgggGCACATGAcgtgtgacgtca	
Ppap\	gaaacaaaatagTCATATGAttaatcgaccga	
Agam\	-----	CCTGTACGCCTGTCATGTGATATTTTCTCAT
Aara\	-----	CCTGTACGCCTGTCATGTGATATTTTCTCAT
Aqan\	-----	CCTGTACGCCTGTCATGTGATATTTTCTCAT
Achr\	-----	TGCTTGTGACTGTCATGTGATATTTTCTCTT
Aepi\	-----	TGTTCTGCTCTGTCATGTGATATTTTCTCTT
Amin\	-----	TGTTCTGGTCTGTCATGTGATATTTTCTCTT
Afun\	-----	TGTTCTGGTCTGTCATGTGATATTTTCTCTT
Aste\	-----	GTCCGTGTCTGTCATGTGATATTTTCTCTT
Adir\	-----	TGTTCTTGTCTGTCATGTGATATTTTCTGCC
Anil\	-----	TGGTACAAGCTGTCATGTGATGTTTTCTCTG
Aalb\	-----	ACGTCACTGCTGTCATGTGATGTTTTCTCTC
Adar\	-----	ACGTCACGGCTGTCATGTGATGTTTTCTCTC
Cqui\	GCGTTTGAACGTCACATGATGAGTGACGCGT	CACCCGAACCTGTCATGTGATATTTTCTCAC
Aaeg\	CCACCAAGGACGTCACATGATGACTCACTCA	CACCGAGACCTGTCATGTGATTAATTATTCT
Mdes\	-----	GCGCGCTCACTGTCATGTGATGTCATGAGAA
Bmor\	TATCTATGACAGTCATATGACTCTCGGTGACA	
Msex\	-----	
Hmel\	ATCCGATAATGTCATATGACTACGACATTCA	
Dple\	CCGATTCTCATGTCATATGACTGCCAATGTC	
Pxyl\	ATTCTACGAATGTCATATGACTTAAACAGTG	
Tcas\	GTCCTGTGCGCATCATATGACTTTGACACTTC	
Dpon\	TCCCCTACCTAGTCATATGATTTGACGTCTA	
Amel\	AAATCGAAATATTCACGTGATTCACATTTACT	-----
Aflo\	AAATCGAGATATTCACGTGATTCACGATTTACT	-----
Bter\	AAATCGAGATATTCACGTGACTCTCATTTACA	-----
Bimp\	AAATCGAGATATTCACGTGACTCCCATTTACA	-----

intron2

GTTCAATCGGAA**TCACATGA**CAACAAACACTA
TTCTGTTACTAG**TCATGTGA**TTAAATTATGGG

Mrot\ GAACTGAGCGCTTCACGTGATCTGTTTGTGTC -----
Aech\ CAATCGATGTG-TCACGTGAATAGTACAAAGA ACAAAGAATCTCTCATGTGATCCTTTCGATAC
Acep\ CAATCGATGTG-TCACGTGAATAGTACAAAGA ACAAAGAATCTCTCATGTGATCCTTTCATAC
Cflo\ TAATCGATGTA-TCACGTGACAATACGAAGA ACGAAGATTCTCTCATGTGATCCTCCCAGTTT
Pbar\ AGATCAATGTG-TCACGTGACAGTACGAAGA ACGAAGATTCTCTCATGTGATCCTTCCAGTTT
Sin\ TGATCGATGTG-TCACGTGAATGGTACGAGGA ACGAGGAGTCTCTCATGTGATTCCTTTCGTTAT
Lhum\ GAATCGATATG-TCACGTGAATCAGGCGAAGG GCGAAGGTACTCTCATGTGATCCTCCCAGTTT
Hsal\ GAATCGATATA-TCACGTGAGATCTCTCATG CGTGAAGATCTCTCATGTGATCCTTCCCAGTTT

Ngir\ ----- TGGCGATGTTCA TCATGTGA CAGAAAGCAGAC
Nlon\ ----- TGGCGATGTTCA TCATGTGA CAGAAAGCAGAC
Nvit\ ----- TGGCGATGTTCA TCATGTGA CAGAAAGCAGAC

Lful\ ----- tttctagtaata TCATGTGA tccgttcgcaga tgtaattatcgt TCATATGA aagttttaatta

Phum\ aaatattttgaa TCACATGA atttcgtctgctt
Dpul\ caaagtttagctg TCACATGA cacaagatatct

Atp6v0e gene structure comparisons:

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

Key: UTR region, CDS region

Order	Species	Atp6v0e orthologs	Atp6v0e structure					Extended CLEAR region		Position	bps from TSS	
			5'exon	intron	exon	intron	exon3'	Sequence	Position			
Diptera (Drosophilidae)	<i>Drosophila_melanogaster</i>	Dmel\VhaM9.7-b	142	95	70	48	68	127	303	gggacatgccgTCATGTGAtattcgttgctc	5'UTR	38
Diptera (Muscidae)	<i>Musca_domestica</i>	Mdom\Atp6v0e		95	96	48	74	130		cattatatttaaTCATGTGAcacacgacgaca	5'UTR?	>-144
Diptera (Tephritidae)	<i>Ceratitis_capitata</i>	Ccap\Atp6v0e	134	95	81	48	61	130	363	tcccatgggtgaTCATGTGAcatttcgctagc	5'UTR?	-24
Diptera (Glossinidae)	<i>Glossina_morsitans</i>	Gmor\Atp6v0e TMP002992		95	57	48	77	145		gcttcttacgcaTCATGTGAtaattagtaatt	5'UTR?	>-83
Diptera (Psychodidae)	<i>Lutzomyia_longipalpis</i>	Llon\Atp6v0e	116	98	90	48	66	148		aacgatttcgggGCACATGAcgtgtgacgtca	5'UTR	22
	<i>Phlebotomus_papatasi</i>	Ppap\Atp6v0e	26	98	71	48	59	145		gaaacaaaatagTCATATGAtaatcgaccga aattctcacctTCACGTGAttttcttacag	5' intron1	>-32 >176
Diptera (Culicidae)	<i>Anopheles_gambiae</i>	Agam\Atp6v0e AGAP003588	129	98	91	48	76	142	440	cctgtacgcctgTCATGTGAtattttctcat	5'UTR	6
	<i>Anopheles_arabiensis</i>	Aara\Atp6v0e		98	85	48	77	142		cctgtacgcctgTCATGTGAtattttctcat	5'UTR?	>-123
	<i>Anopheles_quadriannulatus</i>	Aqan\Atp6v0e		98	86	48	76	142		cctgtacgcctgTCATGTGAtattttctcat	5'UTR?	>-124

	<i>Anopheles_christyi</i>	Achr\Atp6v0e		98	64	48	77	142				tgcttgactgTCATGTGAtattttctctt	5'UTR?	>-123
	<i>Anopheles_epiroticus</i>	Aepi\Atp6v0e		98	74	48	78	142				tggtctgctctgTCATGTGAtattttctctt	5'UTR?	>-105
	<i>Anopheles_minimus</i>	Amin\Atp6v0e		98	78	48	90	142				tggtctgctctgTCATGTGAtattttctctt	5'UTR?	>-112
	<i>Anopheles_funestus</i>	Afun\Atp6v0e		98	74	48	87	142				tggtctgctctgTCATGTGAtattttctctt	5'UTR?	>-110
	<i>Anopheles_stephensi</i>	Aste\Atp6v0e		98	79	48	75	142				gtccgtggctgTCATGTGAtattttctctt	5'UTR?	>-119
	<i>Anopheles_dirus</i>	Adir\Atp6v0e		98	70	48	80	145				tggtctgctctgTCATGTGAtattttctgcc	5'UTR?	>-120
	<i>Anopheles_nili</i>	Anil\Atp6v0e		98	74	48	74	142				tggtacaagctgTCATGTGAtgttttctctg	5'UTR?	>-119
	<i>Anopheles_albimanus</i>	Aalb\Atp6v0e		98	91	48	91	136				acgtcactgctgTCATGTGAtgttttctctc	5'UTR?	>-116
	<i>Anopheles_darlingi</i>	Adar\Atp6v0e		98	86	48	85	133				acgtcacggctgTCATGTGAtgttttctctc	5'UTR?	>-122
	<i>Aedes_aegypti</i>	Aaeg\Atp6v0e AAEL010819	48+82+5	98	70	48	4734	151	674			ccaccaaggacgTCACATGAgtgactcactca caccgagacctgTCATGTGAtattttctctt	5' 5'UTR	-26 4
	<i>Culex_pipiens_qui.</i>	Cqui\Atp6v0e CPI013144		98	91	48	71	148	422			gcgtttgaacgTCACATGAtgagtgacgcgt caccgaaacctgTCATGTGAtattttctcac	5' 5'	>-129 >-173
Diptera (Cecidomyiidae)	<i>Mayetiola_destructor</i>	Mdes\Atp6v0e		92	82	48	90	145				gcgcgctcactgTCATGTGAttgcatgagaa	5'UTR?	>-164
Lepidoptera	<i>Bombyx_mori</i>	Bmor\Atp6v0e	84	98	83	48	1579	88	ND	30	449	tatctatgacagTCATATGActctcggtgaca	5'	>-26
	<i>Manduca sexta</i>	Msex\Atp6v0e		ND	ND	ND	ND	88	7377	33	351	ND		
	<i>Danaus_plexippus</i>	Dple\Atp6v0e		98	68	48	476	88	ND	ND		ccgattctcatgTCATATGActgccaattg	5'	>-109
	<i>Heliconius_melpomene</i>	Hmel\Atp6v0e		98	74	48	873	88	ND	ND		atccgataattgTCATATGActacgacattca	5'	>-102
	<i>Plutella_xylostella</i>	Pxy\Atp6v0e	35	98	88	48	965	88	3949	24		attctacgaatgTCATATGActtaaaacagtg tagttaatgtgcTCATATGAtggtcataagtc	5' intron2	-67 447
Strepsiptera	<i>Mengenilla_moldrzyki</i>	Mmo\Atp6v0e		98	45	48	49	88	57	21		ND		
Coleoptera	<i>Tribolium_castaneum</i>	Tcas\Atp6v0e LOC662403	79	98	61	48	46	88	53	18	140	gtcctgtgcgcaTCATATGActttgacacttc gttcaatcgaaTCATATGAcacaacaactca	5' intron2	-17 322
	<i>Dendroctonus_ponderosae</i>	Dpon\Atp6v0e	81	98	61	48	678	88	133	27	272	tegtgaatgcaTCACGTGAatgacaactccc tcccctacctagTCATATGAttttgactctca ttctgttactagTCATGTGAttaaattatggg	5' 5' intron2	-27 -6 326
Hymenoptera	<i>Apis_mellifera</i>	Amel\Atp6v0e GB18948	103	98	154	48	86	88	105	36	585	aaatcgaaatTCACGTGAttcacatttact	5'UTR	20
	<i>Apis_florea</i>	Aflo\Atp6v0e		98	151	48	77	88	101	42		aaatcgagatafTCACGTGAttcacgattact	5'	>-74

	<i>Bombus_terrestris</i>	Bter\Atp6v0e	192	98	128	48	81	88	107	24	375	aaatcgagataTCACGTGActctcattaca	5'UTR	100
	<i>Bombus_impatiens</i>	Bimp\Atp6v0e		98	123	48	80	88	103	24		aaatcgagataTCACGTGActcccattaca	5'UTR?	>-84
	<i>Megachile_rotundata</i>	Mrot\Atp6v0e		98	173	48	74	88	94	21		gaactgagcgtTCACGTGAtctgtttgtgtc	5'	>-82
	<i>Acromyrmex_echinator</i>	Aech\Atp6v0e		107	261	48	76	88	181	18		tcaatcgatgtTCACGTGAatagtacaaaga acaagaatctcTCATGTGAtctttcgatac	5' 5'	>-121 >-96
	<i>Atta_cephalotes</i>	Acep\Atp6v0e		107	268	48	82	88	169	21		tcaatcgatgtTCACGTGAatagtacaaaga acaagaatctcTCATGTGAtctttcaatac	5' 5'	>-113 >-88
	<i>Solenopsis_invicta</i>	Sinv\Atp6v0e	122	107	254	48	82	88	285	21	139	gtgatcgatgtTCACGTGAatgtacgagga acgaggagtctcTCATGTGAtcttctggtat	5' 5'UTR	-14 13
	<i>Camponotus_floridanus</i>	Cflo\Atp6v0e		107	244	48	84	88	64	21		ttaatcgatgtTCACGTGAacaatacgaaga acgaagattctcTCATGTGAtctcccagttt	5' 5'	>-132 >-107
	<i>Harpegnathos_saltator</i>	Hsal\Atp6v0e		98	283	48	81	88	161	24		cgaatcgatataTCACGTGAagatctcTCATGTGAtcttcccgttt	5'	>-108
	<i>Pogonomyrmex_barbatus</i>	Pbar\Atp6v0e		107	474	48	83	88	165	21		cagatcaatgtTCACGTGAacagtacgaaga acgaagattctcTCATGTGAtcttcccagttt	5' 5'	>-131 >-106
	<i>Linepithema_humile</i>	Lhum\Atp6v0e		107	261	48	87	88	161	21		cgaatcgatgtTCACGTGAatcagcgaagg gcgaagtactcTCATGTGAtctcccagttt	5' 5'	>-136 >-111
	<i>Nasonia_giraulti</i>	Ngir\Atp6v0e		98	99	48	76	88	222	33		tgcgatgttcaTCATGTGAcagaagcagac	5'	>-83
	<i>Nasonia_longicornis</i>	Nlon\Atp6v0e		98	99	48	76	88	221	33		tgcgatgttcaTCATGTGAcagaagcagac	5'	>-83
	<i>Nasonia_vitripennis</i>	Nvit\Atp6v0e NV10516	25	98	99	48	73	88	223	33		tgcgatgttcaTCATGTGAcagaagcagac	5'	>-59
Hemiptera	<i>Acyrtosiphon_pisum</i>	Apis\Atp6v0e LOC100571036	440	98	67	48	2880	88	65	18		tactaccacgTCATATGAttgccgtcaa	intron 2	2344
	<i>Rhodnius_prolixus</i>	Rpro\Atp6v0e		98	71	48	140	88	1483	30		ND		
Phthiraptera	<i>Pediculus_humanus</i>	Phum1\Atp6v0e PHUM238330		98	70	48	124			94		aaatattttaaTCACATGAtttcgtctgctt	5'	>-99
Odonata	<i>Ladona_fulva</i>	Lful\Atp6v0e		98	69	48	286	88	63	33		tttctagtaataTCATGTGAtccgttcgaga tgtaatatcgtTCATATGAaagtttaatta	5' intron2	>-49 >260
Crustacea	<i>Daphnia_pulex</i>	Dpu1\Atp6v0e	107	98	70	48	210			109	108	caaagttagctgTCACATGAcacaagatatct	5'	-1
Aracnida	<i>Ixodes_scapularis</i>	Isca\Atp6v0e ISCW018653		98	57	48	63			94		ND		
	<i>Homo_sapiens</i>	ATP6V0E1		104	10810	48	24415			94	36			
Cnidaria	<i>Nematostella_vectensis</i>	NEMVEDRAFT_v1g192225	18	113	318	48	1144			106	17			
Placozoa	<i>Trichoplax_adhaerens</i>	TRIADDRAFT_63123	16	98	989	48	148			106	15			

