Gene Cluster ID	Atp6v1G
Drosophila melanogaster gene	**Vha13 (CG6213)**
FlyBase ID	FBgn0026753
Predicted function	**V-type ATPase, H+ transporting, V1 subunit G**

Atp6v1G CLEAR element conservation:

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                       5'/5'UTR                          intron1_

Dmel\Vha13        TGTGTGACTTCGTCATATGACATTTTTACAGT  GTTGTGTGTGGGTCACATGATGTGGTGGAAAA
Mdom\Atp6v1G      TCCAAAGCAATGTCATATGACATTTTTCGTTT  GCTATGGTGGGGTCACATGATAACCGAGCTTA
Ccap\Atp6v1G-1    TAGGTGGTTTTTTCATGTGACTGCGTTTGTCA  CAACCCATCGGGTCATGTGATAAGCAAAAATT
Gmor\Atp6v1G      TTTCTGTCTATGTCATATGACATTTACAATCC  AGTCCACAAGAGTCACATGATAAGATTATAGT
Llon\Atp6v1G      CGAAGTTGGGAGTCACATGATTTCTCTTATCG  AAATACTGTGAGTCACATGACGATTGTAATAA
Ppap\Atp6v1G-1    TTCAACGGTTGATCACATGATTTCTGTTATCG  GGGAATACTGAGTCACATGACGATGGTGATGA

Agam\Atp6v1G-1    ACCCGGGGGTTGTCATATGATCAGCGAAGAAA  ACACCACTCCGGTCACATGACCCACCTGTTTG
Aara\Atp6v1G-1    ACCCGGGGGTTGTCATATGATCAGCGAAGAAA  ACACCACTCCGGTCACATGACCCACCTGTTTG
Aqan\Atp6v1G-1    ACCCGGGGGTTGTCATATGATCAGCGAAGAAA  ACACCACTCCGGTCACATGACCCACCTGTTTG
Achr\Atp6v1G-1    AGTGGAGGGTTGTCATATGATCAACGATGAAA  ACTGACGGACGGTCACATGACCCACCTGTTGT
Aepi\Atp6v1G-1    GGAAGGGGATTGTCATATGATCAACGAAAAAA  ACGCAGCTCCGGTCACATGACCAACCTGTTGT
Amin\Atp6v1G-1    AAAGGGGGGTTGTCATATGATCAAAGAAAAAA  ACGTAACCCTGGTCACATGACCAACCTGTTGT
Afun\Atp6v1G-1    AAAAGGGGGTTGTCATATGATCAAAGAAAAAA  ACGTAACCCTGGTCACATGACCAACCTGTTGT
Aste\Atp6v1G-1    CAAAGTGGGTTGTCATATGATCAATGAAAAAA  CGTAACTTTGGGTCACATGACCCACCTGTTGT
Adir\Atp6v1G-1    AACGAGGGGTGGTCATATGATCTCGGAAAGAA  CGTAACGCACGGTCACATGACCCACCTGTTGT
Anil\Atp6v1G-1    TTGCAGGGTTTGTCATATGATCAAATTTGAAA  GTAACCACGGGGTCACATGACCCGCTGATGTG
Aalb\Atp6v1G-1    GAAACATCGTAGTCATATGATTGAGGGGTCGG  GACTGTGGCTGGTCACATGACCCTCCTCTGCT
Adar\Atp6v1G-1    TACGAGCGTAGGTCATATGATTGTGGGGTCGG  ACTGTGAATGGGTCACATGACCCTCTTCTTCG
Aaeg\Atp6v1G-1    CAACGATTTCAGTCATATGATCCGTCCTATAT  AGTGTACGGTAGTCACATGACCCATTGGACTA
Cqui\Atp6v1G-1    CAAGTGTCAGAGTCATATGATGCTCGCGCACA  CGCGCACGGTAGTCACATGACTACCTGCTGCT

Mdes\Atp6v1G-1    ATTTTTATTGGATCATATGATCCGAAATGAAA  TATACAAAGCGGTCACATGACTACATGATTGG
Bmor\Atp6v1G      TAACTAATTAAATCATATGACTTTCGTCACGA  AATCCATGGTCGTCACATGATTTAATTCAAAT
Msex\Atp6v1G      GAACTAATGTAATCATATGACTTTCGTCACGA  GGTCTTTTATCATCACATGATTGCTTTCATAT
Dple\Atp6v1G      GAACTAAACCAATCATATGACTATTTTCGTCA  --------------------------------
Hmel\Atp6v1G      GAACTAAACCAATCATATGACTTACTTTTCGT  TTACTTTTCTTATCACATGATATATCTTAAGA
Pxyl\Atp6v1G      GAGATAAACTAATCATATGACTTTCGTCACAT
Tcas\Atp6v1G-1    CCCAACTAGCGATCATATGACATTTGCCTCAA
Dpon\Atp6v1G-1    ATCGATTGGAAGTCATATGACTGTCACTGGGT

Amel\Atp6v1G      GAAACTCTAAAGTCATATGATCGATTTGCGAT
Aflo\Atp6v1G      GAAACTCTAAAGTCATATGATCGATTTGCGAT
Bter\Atp6v1G      AAAGTCATATGATCATATGATCGATTTGCGAT
Bimp\Atp6v1G      AAAGTCATATGATCATATGATCGATTTGCGAT
Mrot\Atp6v1G      GAAACTCCAAAGTCATATGATCGATTTGTAAT
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Aech\Atp6v1G    GAAGCTCCAAAGTCATATGATCGATTCGTGAC
Acep\Atp6v1G    GAAGCTCCAAAGTCATATGATCGATTCGTGAC
Pbar\Atp6v1G    GAAGCTCCAAAGTCATATGATCGATTCGTGAC
Hsal\Atp6v1G    GAAGCTCCAAAGTCATATGATCGATTCGTGAT
Cflo\Atp6v1G    GAAGCTCCAAAGTCATATGATCGATTCGTGAT
Sinv\Atp6v1G    GAAGCTCTAAAGTCATATGATCGATTCGTGAC
Lhum\Atp6v1G    GAAGCGCCAAAGTCATATGATCGATTCATGAT
Ngir\Atp6v1G    GAGGTGCCTTGATCATATGATCGACTTTTCAG
Nlon\Atp6v1G    GAGGTGCCTTGATCATATGATCGATTTTTCAG
Nvit\Atp6v1G    GAGGTGCCTTGATCATATGATCGATTTTTCAG

Phum\Atp6v1G    TGCTTGTTACTGTCACGAGATCGATAAGAATT
Lful\Atp6v1G    TCCTGTGTCTTGTCATGTGATCGATCTGTAAC
Dpul\Atp6v1G    TGGCTCCAGCAGTCATATGACAGGAAGTCACA
Isca\Atp6v1G    GTAGGTCGCCGATCACCTGACTGCGGCAGTGT
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Atp6v1G gene structure comparison:

Key: UTR region, CDS region

Order	Species	Atp6v1G orthologs	5'exon		intron	exon	intron	exon	intron	exon3'	Extended CLEAR region	Position	bps from TSS
Diptera (Drosophilidae)	*Drosophila_melanogaster*	Dmel\Vha13	117	82	367	101	59	171		250	tgtgtgacttcgTCATATGAcatttttacagt gttgtgtgtgggTCACATGAtgtggtggaaaa	5'UTR intron1	9 317
Diptera (Muscidae)	*Musca_domestica*	Mdom\Atp6v1G		82	259	101	3128	174			tccaaagcaatgTCATATGAcatttttcgttt gctatggtggggTCACATGAtaaccgagctta	5'UTR intron1	>-133 >259
Diptera (Tephritidae)	*Ceratitis_capitata*	Ccap\Atp6v1G-1		82	173	101	110	171			taggtggtttttTCATGTGActgcgtttgtca caacccatcgggTCATGTGAtaagcaaaaatt	5'UTR? intron1	>-133 >166
		Ccap\Atp6v1G-2		82	105	101	62	171			ND		
Diptera (Glossinidae)	*Glossina_morsitans*	Gmor\Atp6v1G TMP007097	94	82	121	101	70	171		341	tttctgtctatgTCATATGAcatttacaatcc agtccacaagagTCACATGAtaagattatagt	5'UTR intron1	63 220
Diptera (Psychodidae)	*Lutzomyia_longipalpis*	Llon\Atp6v1G		82	113	278					cgaagttgggagTCACATGAtttctcttatcg aaatactgtgagTCACATGAcgattgtaataa	5'UTR intron1	>-118 >155
	Phlebotomus_papatasi	Ppap\Atp6v1G-1		82	109	278					ttcaacggttgaTCACATGAtttctgttatcg gggaatactgagTCACATGAcgatggtgatga	5'UTR intron1	
		Ppap\Atp6v1G-2		82	67	101	3682	171 (strand[-])			ND		
Diptera (Culicidae)	*Anopheles_gambiae*	Agam\Atp6v1G-1 AGAP001823	132	82	204	101	82	168		457	gcgctcttgcaaTCACGTGAaccaccgtgggg acccgggggttgTCATATGAtcagcgaagaaa acaccactccggTCACATGAcccacctgtttg	5' 5' intron1	-73 -19 294
	Anopheles_arabiensis	Aara\Atp6v1G-1		82	204	101	82	168			gcgctcttgcaaTCACGTGAaccaccgtgggg acccgggggttgTCATATGAtcagcgaagaaa acaccactccggTCACATGAcccacctgtttg	5' 5' intron1	>-205 >-152 >163

Anopheles_quadriannulatus	Aqan\Atp6v1G-1		82	215	101	87	168			acccgggggttgTCATATGAtcagcgaagaaa acaccactccggTCACATGAcccacctgtttg	5' intron1	>-152 >163
Anopheles_christyi	Achr\Atp6v1G-1		82	214	101	82	168			aaccgagtgcaaTCACGTGAacgctgcggacg agtggagggttgTCATATGAtcaacgatgaaa actgacggacggTCACATGAcccacctgttgt	5' 5' intron1	>-196 >-141 >173
Anopheles_epiroticus	Aepi\Atp6v1G-1		82	191	101	87	168			cgatgtttgcaaTCACGTGAacccgtcggttg ggaaggggattgTCATATGAtcaacgaaaaaa acgcagctccggTCACATGAccaacctgttgt	5' 5' intron1	>-213 >-141 >158
Anopheles_minimus	Amin\Atp6v1G-1		82	199	101	69	168			cactgtatgctaTCACGTGAaccaacctaccg aaaggggggttgTCATATGAtcaaagaaaaaa acgtaaccctggTCACATGAccaacctgttgt	5' 5' intron1	>-196 >-139 >145
Anopheles_funestus	Afun\Atp6v1G-1		82	222	101	68	168			aaaaggggggttgTCATATGAtcaaagaaaaaa acgtaaccctggTCACATGAccaacctgttgt	5' intron1	>-176 >151
Anopheles_stephensi	Aste\Atp6v1G-1		82	207	101	77	171			caaagtgggttgTCATATGAtcaatgaaaaaa cgtaactttgggTCACATGAcccacctgttgt	5' intron1	>-145 >170
Anopheles_dirus	Adir\Atp6v1G-1		82	213	101	71	168			cgccgaacgctaTCACGTGAgagtgggggttg aacgaggggtggTCATATGAtctcggaaagaa cgtaacgcacggTCACATGAcccacctgttgt	5' 5' intron1	>-213 >-162 >169
Anopheles_nili	Anil\Atp6v1G-1		82	>126	ND	ND	ND			ctctcgcacgagTCACGTGAgcaagtgttttt ttgcagggtttgTCATATGAtcaaatttgaaa gtaaccacggggTCACATGAcccgctgatgtg	5' 5' intron1	>-160 >-130 >150
Anopheles_albimanus	Aalb\Atp6v1G-1		82	228	101	107	168			gaaacatcgtagTCATATGAttgaggggtcgg gactgtggctggTCACATGAccctcctctgct	5' intron1	>-170 >146
Anopheles_darlingi	Adar\Atp6v1G-1		82	253	101	113	168			tacgagcgtaggTCATATGAttgtggggtcgg actgtgaatgggTCACATGAccctcttcttcg	5' intron1	>-176 >151
Aedes_aegypti	Aaeg\Atp6v1G-1 AAEL012819	140	82	191	101	7661	168	381		gcgctcttgcaaTCACGTGAaccaccgtgggg caacgatttcagTCATATGAtccgtcctatat agtgtacggtagTCACATGAcccattggacta	5' 5' intron1	-73 -20 295
Culex_pipiens_qui.	Cqui\Atp6v1G-1 CPIJ006975		82	171	101	5527	168			caagtgtcagagTCATATGAtgctcgcgcaca cgcgcacggtagTCACATGActacctgctgct	5' intron1	>-253 >123
Anopheles_gambiae	Agam\Atp6v1G-2 AGAP004867	126	82	239	101	75	174	1151		ND		
Anopheles_arabiensis	Aara\Atp6v1G-2		82	238	101	75	174			ND		
Anopheles_quadriannulatus	Aqan\Atp6v1G-2		82	238	101	75	174			ND		
Anopheles_christyi	Achr\Atp6v1G-2		82	212	101	74	174			ND		
Anopheles_epiroticus	Aepi\Atp6v1G-2		82	223	101	73	174			ND		
Anopheles_minimus	Amin\Atp6v1G-2		82	203	101	85	174			ND		
Anopheles_funestus	Afun\Atp6v1G-2		82	219	101	81	174			ND		
Anopheles_stephensi	Aste\Atp6v1G-2		82	208	101	89	174			ND		

	Anopheles_dirus	Adir\Atp6v1G-2		82	198	101	86	174			ND		
	Anopheles_nili	Anil\Atp6v1G-2		82	184	101	73ß	174			ND		
	Anopheles_albimanus	Aalb\Atp6v1G-2		82	187	101	74	180			ND		
	Anopheles_darlingi	Adar\Atp6v1G-2		82	182	101	71	180			ND		
	Aedes_aegypti	Aaeg\Atp6v1G-2 AAEL007184	133	82	152	101	10739	180		755	ND		
		Aaeg\Atp6v1G-3 AAEL013302		363							ND		
	Culex_pipiens_qui.	Cqui\Atp6v1G-2 CPIJ013849		82	207	101	6688	180			ND		
Diptera (Cecidomyiidae)	*Mayetiola_destructor*	Mdes\Atp6v1G-1		82	296	101	76	174			attttattggaTCATATGAtccgaaatgaaa cataatgttcgaTCATGTGAgtttatttgcct tatacaaagcggTCACATGActacatgattgg	5' intron1 intron1	>-146 >170 >209
		Mdes\Atp6v1G-2		82	782	101	95	183			ND		
Lepidoptera	*Bombyx_mori*	Bmor\Atp6v1G LOC692985	93	82	917	101	ND	99	203	72	154	taactaattaaaTCATATGActttcgtcacga aatccatggtcgTCACATGAtttaattcaaat	5' intron1	-2 342
	Manduca_sexta	Msex\Atp6v1G		82	562	101	1005	99	1133	72		gaactaatgtaaTCATATGActttcgtcacga ggtcttttatcaTCACATGAttgctttcatat	5' intron1	>-87 >253
	Danaus_plexippus	Dple\Atp6v1G		82	560	101	503	99	84	72		gaactaaaccaaTCATATGActattttcgtca	5'	>-87
	Heliconius_melpomene	Hmel\Atp6v1G		82	1121	101	585	99	1216	72		gaactaaaccaaTCATATGActtacttttcgt ttacttttcttaTCACATGAtatatcttaaga	5' intron1	>-85 >284
	Plutella_xylostella	Pxyl\Atp6v1G		82	1024	101	1509	99	618	78		gagataaactaaTCATATGActttcgtcacat	5'	>-87
Strepsiptera	*Mengenilla_moldrzyki*	Mmol\Atp6v1G		82	68	287								
Coleoptera	*Tribolium_castaneum*	Tcas\Atp6v1G-1 LOC662804	37	82	86	200		50	69	253		cccaactagcgaTCATATGAcatttgcctcaa	5'	21
		Tcas\Atp6v1G-2 LOC658882		82	157	200		98	90			ND		
	Dendroctonus_ponderosae	Dpon\Atp6v1G-1		82	215	200		945	69			atcgattggaagTCATATGActgtcactgggt tattccgttcagTCATGTGActctctgatcaa gtgctggtttgcTCACATGAtgtacaggtgat	5' intron2 intron2	>-97 >531 >679
		Dpon\Atp6v1G-2		85	206	200 (101+99)		52	90			ND		
Hymenoptera	*Apis_mellifera*	Amel\Atp6v1G GB13499	76	82	412	101	117	99	79	75	741	gaaactctaaagTCATATGAtcgatttgcgat	5'UTR	26

	Apis_florea	Aflo\Atp6v1G		82	438	101	114	99	79	75		gaaactctaaagTCATATGAtcgatttgcgat	5'UTR?	>-42
	Bombus_terrestris	Bter\Atp6v1G		82	348	101	123	99	93	75		aaagTCATATGATCATATGAtcgatttgcgat	5'UTR?	>-48
	Bombus_impatiens	Bimp\Atp6v1G		82	348	101	123	99	90	75		aaagTCATATGATCATATGAtcgatttgcgat	5'UTR?	>-48
	Megachile_rotundata	Mrot\Atp6v1G		82	353	101	93	99	77	75		gaaactccaaagTCATATGAtcgatttgtaat	5'UTR?	>-48
	Acromyrmex_echinatior	Aech\Atp6v1G		82	560	101	95	99	86	75		gaagctccaaagTCATATGAtcgattcgtgac	5'UTR?	>-39
	Atta_cephalotes	Acep\Atp6v1G		82	466	101	92	99	84	75		gaagctccaaagTCATATGAtcgattcgtgac	5'UTR?	>-39
	Solenopsis_invicta	Sinv\Atp6v1G		82	820	101	92	99	79	75		gaagctctaaagTCATATGAtcgattcgtgac	5'UTR?	>-39
	Pogonomyrmex_barbatus	Pbar\Atp6v1G*		82	576	101	94	99	81	75		gaagctccaaagTCATATGAtcgattcgtgac	5'UTR?	>-39
	Linepithema_humile	Lhum\Atp6v1G		82	538	101	104	99	84	75		gaagcgccaaagTCATATGAtcgattcatgat	5'UTR?	>-44
	Harpegnathos_saltator	Hsal\Atp6v1G		82	586	101	118	99	85	75		gaagctccaaagTCATATGAtcgattcgtgat	5'UTR?	>-44
	Camponotus_floridanus	Cflo\Atp6v1G		82	561	101	107	99	122	75		gaagctccaaagTCATATGAtcgattcgtgat	5'UTR?	>-66
	Nasonia_giraulti	Ngir\Atp6v1G		360								gaggtgccttgaTCATATGAtcgacttttcag	5'UTR?	>-172
	Nasonia_longicornis	Nlon\Atp6v1G		360								gaggtgccttgaTCATATGAtcgatttttcag	5'UTR?	>-172
	Nasonia_vitripennis	Nvit\Atp6v1G NV17706	23+91+37	360								gaggtgccttgaTCATATGAtcgatttttcag	5'UTR?	-21
Hemiptera	*Acyrthosiphon_pisum*	Apis\Atp6v1G ACYPI000034	68	82	958	101	68	183			405	ND		
Hemiptera	*Rhodnius_prolixus*	Rpro\Atp6v1G	123	82	270	101	76	99	1773	72	187	ND		
Phthiraptera	*Pediculus_humanus*	Phum\Atp6v1G		82	ND	278						ttcttactatTCAAATGAcatttatttg	5'?	> -422
Odonata	*Ladona_fulva*	Lful\Atp6v1G		82	125	101	74	99	79	87		tcctgtgtcttgTCATGTGAtcgatctgtaac	5'UTR?	>-49
Crustacea	*Daphnia_pulex*	Dpul\Atp6v1G	79	82	425	101	62	171			161	tggctccagcagTCATATGAcaggaagtcaca	5'	-34
Ixodida	*Ixodes_scapularis*	Isca\Atp6v1G	86	82	117	101	ND	168			95	gtaggtcgccgaTCACCTGActgcggcagtgt	5'UTR	18
	Homo_sapiens	ATP6V1G1	125	82	4631	101	4917	174			1129	gttcaagagcggTCAGCTGAtgctacgctgtg tacgctgtgcggTCACGTGAcaacgggggcga	5' 5'UTR?	-19 4
		ATP6V1G2	291	82	268	101	527	174			946	ND		
Cnidaria	*Nematostella_vectensis*	v1g191954	28	82	3361?	101	591	171			606	acgTCACGTGAccgagtaccaTCATGTGAtga ttttgttatcttTCATATGAttttgctactac	5' intron1	-12 285
Placozoa	*Trichoplax_adhaerens*	Tadh\Atp6v1G	39	82	287	101	776	171 (99+72)			124	tctgtcaagaggTCATATGAtcgcagatgtca	5'	-638