Gene Cluster ID	Atp6ap2
Drosophila melanogaster gene	**VhaM8.9 (CG8444)**
FlyBase ID	FBgn0037671
Predicted function	**ATPase, H+ transporting, lysosomal accessory protein 2**

Atp6v1H CLEAR element conservation:

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            ___5'/5'UTR___                    ___5'/5'UTR___
Dmel\  CAACCCTGTTCATCACATGATAGTCAGGGTGA   TGCAGTCGTTCGTCATATGATTAAAAGTCCAG
Mdom\  TCTCTCTTTACATCATGTGACCAAATGCAACC   GTTTGTCGATTGTCATATGATCACGAACAAAA
            ___5'/5'UTR___
Ccap\  CCGTCGCAGTTGTCATATGATCAATTTTCATT
Gmor\  TCTAGCCGTTGTCATATGATCAATTTTTGAT
Llon\  AGACACCTTTGGTCATATGATTTTAGTGTGAG
Ppap\  CTTGGGCGATTGTCATATGATTTTACTGTGAA


            ___5'/5'UTR___                    ___5'/5'UTR___                              ___intron1___
Agam\  CTGCGCAAAGTGTCACGTGAGGAACGGGACGG   ACCACAATAACGTCATATGATCACAAGTGCAA   TCTCATCG-CTGTTCACATGACATGAAGTATC
Aara\  CTGCGCAAAGTGTCACGTGAGGAACGGGACGG   ACCACAATAACGTCATATGATCACAAGTGCAA   TCTCATCG-CTTTTCACATGACATGAAGTATC
Aqan\  CTGCGCAAAGTGTCACGTGAGGAACGGGACGG   ACCACAATAACGTCATATGATCACAAGTGCAA   TCTCATCG-CTGTTCACATGACATGAAGTATC
Achr\  CTGCGCAAAGTGTCACGTGAGGAACGGAGTCG   ACCACAATAACGTCATATGATCACAAGTGCAA   TCCTGTG-CAGTTCACATGACATAAAAATAC
Amin\  CTGCGCAAAGTGTCACGTGAGGAACGGAATGG   AACACAATAACGTCATATGATCACAAGTGCAA   TCTCATCGTCTGTTCACATGACAACGAAAGG
Afun\  CTGCACAAAGTGTCACGTGAGGAACGGAATGG   AACACAATAACGTCATATGATCACAAGTGCAA   --------------------------------
Aste\  CTGCGCAAAGTGTCACGTGAGGAACGCAGTGG   AACACAATAACGTCATATGATCACAAGTGCAA   --------------------------------
Aepi\  CTGCAGTAAGTGTCACGTGAGGAACAAGGTGG   ACCACAATAACGTCATATGATCACAAGTGCAA   --------------------------------
Adir\  -------------------------------    AACAGAAAAAGTCATATGACCAACTCGGTCA   --------------------------------
Anil\  -------------------------------    ACGACAAAACGTCATATGATCACAAGTGCAA   --------------------------------
Aalb\  CCCGTCCAAACGTCACGTGAGGCGCTCCAAAC   GCGCTCCAAACGTCATATGATCAAAATTCAGA   --------------------------------
Adar\  CCCGTTCAAACGTCACGTGAGGCGCTCCAAAC   GCGCTCCAAACGTCATATGATCAAAAATCAGA   --------------------------------
Aaeg\  AAACTCGAAAGTCACGTGAGGGACCATATCG   AAATCGGGAACGTCATATGATCACTGGTGCAA   --------------------------------
Cqui\  -------------------------------    AAAGTGAAAACGTCATATGATCACTGGGTGCA   --------------------------------

Mdes\  TGTGCTGTGATGTCACGTGAATGTTTCGAAAC   AATCATAGTACATCATATGATCTGGCTTTAGT

Bmor\  GTATGAATTTAATCATATGACATTGTGATTGT
Dple\  GTAACACTTTAATCATATGACAGTAAGCCACC
Hmel\  GCAATACTTTAATCATATGACAGTCAGCTACT
Msex\  GTAAGACTTTAATCATATGACAGTCAGTCATT
Pxyl\  GCAACACTGAAATCATATGACAGTCTGCCATT
            ___5'/5'UTR___                    ___5'/5'UTR___
Tcas\  GTCACAAGACTGTCATATGATTATGACATTTG   GTTAGTTTAATGTCATATGACTTCAAATTTCC
            ___5'/5'UTR___
Amel\  ATTACATTAATGTCATATGATCAGTTTGTGAA
Aflo\  ATTACGTTAATGTCATATGATCAGTTTGTGAA
Bter\  ACTCCTTTGTGGTCATATGATCAGTTTGTGAA
Bimp\  ACTCCTTTGTGGTCATATGATCAGTTTGTGAA
Mrot\  TGGATTAGCGTGTCATATGATAAACTTATAGA
Nvit\  GTGCAAAGGTGTCATATGATCGGACGAAAAA
Nlon\  GTGCAAAGGTGTCATATGATCGGACGAAAAA
Ngir\  GTGCAAAGGTGTCATATGATCGGACGAAAAA
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Aech\   CATCTGACATGATCACATGATCACGTCCGAAA
Lhum\   CATCTGATGTGATCACATGATCGCGTCCGAAA
Sinv\   TACCTGACATGATCATATGATCGCGTCTGAAA
Pbar\   TGTCTGACATAATCACATGATCGCGTCTGAAA
Cflo\   GATCTGAAGTTATCACATGATCATGTCCGAAA
Hsal\   GACCACAGGTGATCACATGATCATGTCCGAAT
Acep\   TATCTGACATGATCACATGATCCGAAATTGAT

Lful\   catatcgtctggTCATATGAttcttaagcgaa
Dpul\   agcacgaacacaTCACCTGActtttagctgtca
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Atp6ap2 gene structure comparisons:

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

Key: UTR region, CDS region

Order	Species	Atp6ap2 orthologs	5'exon	intron	exon	intron			exon3'				Extended CLEAR region	Position	bps from TSS
Diptera (Drosophilidae)	*Drosophila_melanogaster*	Dmel\VhaM8.9	84 43	223	353	262		567				421	caaccctgttcaTCACATGAtagtcagggtga tgcagtcgttcgTCATATGAttaaaagtccag	5' 5'UTR	-1 52
Diptera (Muscidae)	*Musca_domestica*	Mdom\Atp6ap2	43	260	731				747	183			tctctctttacaTCATGTGAccaaatgcaacc gtttgtcgattgTCATATGAtcacgaacaaaa	5' 5'	>-93 >-13
Diptera (Tephritidae)	*Ceratitis_capitata*	Ccap\Atp6ap2	43	218	353	64	-	-	249	56	186	285	ccgtcgcagttgTCATATGAtcaattttcatt	5'UTR?	>-37
Diptera (Glossinidae)	*Glossina_morsitans*	Gmor\Atp6ap2	60 43	149	356	1905		378		60	186	236	tctagccgtttgTCATATGAtcaattttgat	5'	-3
Diptera (Psychodidae)	*Lutzomyia_longipalpis*	Llon\Atp6ap2	52 43	141	341	58	138	59	246	433	189	246	agacacctttggTCATATGAttttagtgtgag	5'UTR	3
	Phlebotomus_papatasi	Ppap\Atp6ap2	56 43[-]?	ND	344	58	138	55	246	ND	189	226	cttgggcgattgTCATATGAttttactgtgaa	5'UTR	14
Diptera (Culicidae)	*Anopheles_gambiae*	Agam\Atp6ap2 AGAP003430	43	214	224	81		519		80	189	584	ctgcgcaaagtgTCACGTGAggaacgggacgg accacaataacgTCATATGAtcacaagtgcaa tctcatcgctgtTCACATGAcatgaagtatcg	5' 5'UTR? intron1	-35 18 278
	Anopheles_arabiensis	Aara\Atp6ap2	43	214	224	87		519		80	189		ctgcgcaaagtgTCACGTGAggaacgggacgg accacaataacgTCATATGAtcacaagtgcaa tctcatcgctttTCACATGAcatgaagtatcg	5' 5'UTR? intron1	>-108 >-47 >206
	Anopheles_quadriannulatus	Aqan\Atp6ap2	43	214	224	81		519		80	189		ctgcgcaaagtgTCACGTGAggaacgggacgg accacaataacgTCATATGAtcacaagtgcaa tctcatcgctgtTCACATGAcatgaagtatcg	5' 5'UTR? intron1	>-108 >-47 >206
	Anopheles_christyi	Achr\Atp6ap2	43	217	224	83		513		76	189		ctgcgcaaagtgTCACGTGAggaacggagtcg accacaataacgTCATATGAtcacaagtgcaa tccctgtgcagtTCACATGAcataaaaatacg	5' 5'UTR? intron1	>-109 >-47 >211
	Anopheles_epiroticus	Aepi\Atp6ap2	43	234	224	75		516		64	189		ctgcagtaagtgTCACGTGAggaacaaggtgg accacaataacgTCATATGAtcacaagtgcaa ctcatcgtctgtTCACATGAcaacgaaaagga	5' 5'UTR? intron1	>-108 >-47 >218
	Anopheles_minimus	Amin\Atp6ap2	43	196	224	59		513		74	189		ctgcgcaaagtgTCACGTGAggaacggaatgg aacacaataacgTCATATGAtcacaagtgcaa	5' 5'UTR?	>-108 >-47

Order/Family	Species	Gene																	Promoter	5'UTR	Position
	Anopheles_funestus	Afun\Atp6ap2	■	43	216	224	65	516				79	189	■					ctgcacaaagtgTCACGTGAggaacggaatgg aacacaataacgTCATATGAtcacaagtgcaa	5' 5UTR?	>-107 >-47
	Anopheles_stephensi	Aste\Atp6ap2	■	43	217	224	62	516				71	189	■					ctgcgcaaagtgTCACGTGAggaacgcagtgg aacacaataacgTCATATGAtcacaagtgcaa	5' 5UTR?	>-107 >-47
	Anopheles_dirus A	Adir\Atp6ap2	■	43	237	224	73	516				78	180	■					aacagaaaaagTCATATGAccaactcggtca tgaccaactcggTCATATGAcaagtgcaaaaa	5' 5UTR?	>-67 >-50
	Anopheles_nili	Anil\Atp6ap2	■	43	212	224	65	513				82	189	■					acgacaaaacgTCATATGAtcacaagtgcaa	5UTR?	>-50
	Anopheles_albimanus	Aalb\Atp6ap2	■	43	185	224	67	513				74	180	■					cccgtccaaacgTCACGTGAggcgctccaaac gcgctccaaacgTCATATGAtcaaaattcaga	5' 5UTR?	>-63 >-42
	Anopheles_darlingi	Adar\Atp6ap2	■	43	189	224	60	513?				72	180	■					cccgttcaaacgTCACGTGAggcgctccaaac gcgctccaaacgTCATATGAtcaaaatcaga	5' 5UTR?	
	Aedes_aegypti	Aaeg\Atp6ap2 AAEL002411	■	43	197	224	74	114	16650	399		63	180	421					aaactcgaaaagTCACGTGAgggaccatatcg aaatcgggaacgTCATATGAtcactggtgcaa	5' 5UTR	-73 15
	Culex_pipiens_qui.	Cqui\Atp6ap2 CPIJ009739	■	43	205	224	80	519				66	180	■					aaagtgaaaacgTCATATGAtcactgggtgca	5UTR?	-30
Diptera (Cecidomyiidae)	*Mayetiola_destructor*	Mdes\Atp6ap2	54 ■	43	170	350		95	363			104	207	■					tgtgctgtgatgtgTCACGTGAatgtttcgaaac aatcatagtacaTCATATGAtctggctttagt	5' 5UTR	24 -64
Lepidoptera	*Bombyx_mori*	Bmor\Atp6ap2	■	52	77	131	96	99	165	144	91	141	827	130	422	140	1453	177	275	gtatgaatttaaTCATATGAcattgtgattgt	5UTR?	-15
	Manduca_sexta	Msex\Atp6ap2	■	52	80	131	142	99	321	144	248	141	78	130	360	140	216	174		gtaagactttaaTCATATGAcagtcagtcatt	5UTR?	>-27
	Danaus_plexippus	Dple\Atp6ap2	■	52	70	131	126	99	178	144	88	141	174	130	353	137	441	174		gtaacactttaaTCATATGAcagtaagccacc	5UTR?	>-26
	Heliconius_melpomene	Hmel\Atp6ap2	■	52	71	131	83	99	60	144	77	144	105	130	2632	137	705	174		gcaatactttaaTCATATGAcagtcagctact	5UTR?	>-37
	Plutella _xylostella	Pxyl\Atp6ap2	15	52	94	131	126	99	334	144	387	135	511	130	378	131	1417	180	497	gcaacactgaaaTCATATGAcagtctgccatt	5UTR?	>-11
Coleoptera	*Tribolium_castaneum*	LOC662403	■	43	43	365		46	135	1537	285			50	180	273			gtcacaagactgtCATATGAttatgacatttg gttagtttaatgTCATATGActtcaaatttcc	5' 5UTR	-20 14
Hymenoptera	*Apis_mellifera*	GB17311	■	43	117	128	175	231	380	315	100	93	7467	103	82	80	■			attacattaatgTCATATGAtcagtttgtgaa	5UTR?	1
	Apis_florea	Aflo\Atp6ap2	■	43	108	128	180	231	253	315	111	93	7469	103	82	80	■			attacgttaatgTCATATGAtcagtttgtgaa	5UTR?	>-78
	Bombus_terrestris	Bter\Atp6ap2	■	43	101	128	180	231	117	315	111	93	4720	112	90	80	■			actcctttgtggTCATATGAtcagtttgtgaa	5UTR?	-7
	Bombus_impatiens	Bimp\Atp6ap2	■	43	101	128	178	231	117	315	111	93	4731	112	90	80	■			actcctttgtggTCATATGAtcagtttgtgaa	5UTR?	>-69
	Megachile_rotundata	Mrot\Atp6ap2	■	43	111	128	128	231	135	315	71	105	3446	106	74	80	■			tggattagcgtgTCATATGAtaaacttataga	5UTR?	
	Acromyrmex_echinatior	AECH19445*	■	43	280	131	346	240	119	309	1285	87	6402	109	2353	80	■			catctgacatgaTCACATGAtcacgtccgaaa	5'	>-65
	Atta_cephalotes	ACEP24633*	■	43	280	134	352	240	120	309	1336	87	5463	109	ND	80	■			tatctgacatgaTCACATGAtccgaaattgat	5UTR?	>-60
	Solenopsis_invicta	Sinv\Atp6ap2	■	43	284	128	394	240	297	309	799	84	5699	109	1056	80	14			tacctgacatgaTCATATGAtcgcgtctgaaa	5UTR?	-81
	Camponotus_floridanus	CFLO15335*	■	43	282	128	263	237	356	309	155	87	2862	109	433	80	■			gatctgaagttaTCACATGAtcatgtccgaaa	5UTR?	>-65
	Harpegnathos_saltator	Hsal\Atp6ap2	■	43	427	128	177	240	116	309	177	93	3736	109	648	80	■			gaccacaggtgaTCACATGAtcatgtccgaat	5UTR?	>-70

Order	Species	Gene		1		2		3		4		5		6		7			Motif	5'UTR	Dist
	Pogonomyrmex_barbatus	Pbar\Atp6ap2	▮	43	320	128	208	240	126	309	485	87	2782	109	ND	80	▮		tgtctgacataaTCACATGAtcgcgtctgaaa	5UTR?	>-66
	Linepithema_humile	Lhum\Atp6ap2	▮	43	303	128	288	234	430	306	102	84	2685	112	307	80	▮		catctgatgtgaTCACATGAtcgcgtccgaaa	5UTR?	>-60
	Nasonia_vitripennis	NV14085	▮	46	108	128	82	231	81	315	72	108	1095	103	88	80	▮		gtgcaaaaggtgTCATATGAtcggacgaaaaa	5UTR?	>-84
	Nasonia_giraulti	Ngir\Atp6ap2	▮	46	139	128	82	231	81	315	72	108	1102	103	88	80	▮		gtgcaaaaggtgTCATATGAtcggacgaaaaa	5UTR?	>-84
	Nasonia_longicornis	Nlon\Atp6ap2	▮	46	139	128	82	231	81	315	72	108	ND	103	88	80	▮		gtgcaaaaggtgTCATATGAtcggacgaaaaa	5UTR?	>-84
Odonata	*Ladona_fulva*	Lful\Atp6ap2	▮	43	108	128	166	241	1031	152	83	108	289	109	73	80	▮		catatcgtctggTCATATGAttcttaagcgaa	5UTR?	>-40
Hemiptera	*Acyrthosiphon_pisum*	ACYPI007940	176	52	148	137	441	240	62	132	224	180	694	75	82	103	1872	80	1224	ND		
Phthiraptera	*Pediculus_humanus*	PHUM376100	▮	135	66	423						165	141	105	109	253	80	▮		ND		
Crustacea	*Daphnia_pulex*	Dpul\Atp6ap2	▮	46	59	128	126	309+61+168				62	81	69	115	76	80	▮		agcacgaacacaTCACCTGActttagctgtca	5'	>-80
Ixodida	*Ixodes_scapularis*		▮														▮				