

Gene Cluster ID	Atp6v1H	
Drosophila melanogaster gene	VhaSFD (CG17332)	
FlyBase ID	FBgn0027779	
Predicted function	V-type ATPase, H+ transporting, V1 subunit H	
Atp6v1H CLEAR element(s) conservation:		
	<div>5' / 5' UTR</div>	<div>intron1</div>
Dmel\	GCTGCAGAAAAGTCACAAGACCA---GTCAGCTGAATTCGGTGTCTG	
Gmor\	GAAGCGAAAAGTCACAAGACTC---GTCAGCTGAATCTTCCATTA	
Mdom\	TTACATCACAAGTCACAAGACCTTCTGTCAGCTGAATTCAGAGTAAA	
Ccap\	TTTCTGGGTCTTTGTGAC-TTTTGTCACTGAATTTGTTTCATCG	GGTAAGTGTGTGTACATGACACATTTTGTGCG
Llon\	CAATCGTATTGTTCAGCTGAAGTCAGAAACT	
Ppap\	CCCTCCATTCTGTCACTGAATTCGAAGGAGC	
Agam\	GTTCACTTCAGGTCATATGATCACAATATTT	GAGCAAATTCATCACGTGATGTTGTTTCTTT
Aara\	GTTCACTTCAGGTCATATGATCACAATATTT	AGCTAAATTCATCACGTGATGTTGTTTCTTT
Aqan\	GTTCACTTCAGGTCATATGATCACAATATTT	AGCTAAATTCATCACGTGATGTTGTTTCTTT
Achr\	ATTCACCTTTGGTCATATGATCACAATATTT	AGTTGAATTTAATCACGTGATGTTGTTTCTTT
Aepi\	ATTCACCTTTGGTCATATGATCACAATATTT	AGTTAAATATCATCACGTGATGTTGTTTCTTT
Amin\	ATGCACCTTTGGTCATATGATCACAATATTT	ATTTAATTTCCATCACGTGATGGTATTCTTT
Afun\	CTACACCTTTAGGTCATATGATCACAATATTT	ATTTAATTTTCATCACGTGATGATGTTTCTTT
Aste\	CACCCCTTTAGGTCATATGATCACAATATTT	CTTTACTTTTCATCACGTGATGGTATTTCGTT
Adir\	AAGAAGAAGAGGTCATATGATCACAATTTT	CCATCACTTCTATCACGTGATGAGTTTCGTT
Anil\	AAGAAGAAGAGGTCATATGATCACAATATTT	AATCTACTTCCATCACGTGACTTACTTTT
Aalb\	TTATCAGCGCAGTCATATGATTTGATTTTCA	CTTCTTCGTTCTCACGTGACGTTCTACGCTT
Adar\	TATTCAGCGCAGTCATATGATGCCGAGAGT	GTTCCTCGCTCATCACGTGACGTTCTACGTT
Cqui\	CTTTACCCCAAGTCATATGACATTCAGCTGAG	GAAATTTTGGAAATCACGTGACCTTTTCTCTC
Aaeg\	ACCCCATGCAAGTCATATGACATTCAGCTGCG	AGAAATTTGGAATCACGTGATGCTTTTGTGTC
Mdes\	CCGATGGAAAAGTCACAAGAC-TCTCAGCTGAGGTTTTTCTTC	
Bmor\	CATTTCTTACAGTCACAAGACCTCTCAGCTGAGCAGTGTGCGAT	
Msex\	CACCTTTTCATAGTCACAAGACCACTCAGCTGAGGCTGTGTTCTGA	
Dple\	CACGTCGAGTAGTCACAAGACCTCTCAGCTGAGTTCACGTCTGC	
Hmel\	CACATCGAATAGTCACAAGACCTCTCAGCTGAGGTATCTGTCTA	
Pxyl\	CACCTTCAATAGTCACAAGACCTCTCAGCTGAGGTTGTGTTGGT	
Tcas\	GCGTGTCAATAATCACAAGACTTGTGAGGTGT	GGCTGAGCACACTCACGTGACACTTGAGTATC
Dpon\	tcaaaagattggTCATATGAtcaatctgccag	taatgaaactatTCACGTGAcattggtcaagt
Dpon	aatctgccagtgTCAGCTGAttgagactacgt	
Aflo\	GTTATACATCGATCTTGTGATCCAACATATGA	
Amel\	GTTATACATCGATCTTGTGATCCAACATATGA	
Bimp\	GTAATATATCAGTCTTGTGATCCAAGTGTGA	
Bter\	GTAATATATCAGTCTTGTGATCCAAGTGTGA	
Mrot\	TATGTACATTGGTCTTGTGATTTTAAACAGCTG	
Aech\	ATATTCGTGTGGTCTTGTGATCGAACAGCTGA	
Acep\	GTATTCGCGTGATCTTGTGATCGAAGAAGCTG	
Sinv\	GTATTCGCATGGTCTTGTGATCGAACAGCTGA	
Pbar\	GTATTTGCGTGGTCTTGTGATCGAACAGCTGA	
Cflo\	GTATCTGCACGGTCTTGTGATCGAACAGCTGA	
Lhum\	GTAGTTGATTGGTCTTGTGATCGAACAGCTGA	
Hsal\	GTACCCCAAGTGGTCTTGTGATCGAACAGCTGA	
Ngir\	ACGCTACTCCAACTCTGTGACCTGACTTGTGA	
Nlon\	ACGCTACTCCAACTCTGTGACCTGACTTGTGA	
Nvit\	ACGCTACACCAA TCTCTGTGACCTGACTTGTGA	
Phum\	CCCCATAGTTAATCACGTGAAAAATCGTAGGA	
Lful\	gatcatggaatgTCACGAGAcaggcgagacgg	
Dpul\	TTGGAGGGCCAGTCACATGACACAACCTGACAA	
Isca\	GTGTCCTCTCACTCACGTGACGTCTGCTGCTG	
Atp6v1H gene structure comparison:		

Key: UTR region		CDS region	INTRON																						
Order	Species	Atp6v1H orthologs	5'ex	int	exon				int	ex	int	exon				int	ex	int	exon3'	Extended CLEAR region	Position	bps from TSS			
Diptera (Drosophilidae)	<i>Drosophila_melanogaster</i>	Dmel\VhaSFD-RA (CG17332)	159	37	141	479				2016	135	64	563 (126+437)				60	114	160	79 681	gaaaagTCACAAGAccagTCAGCTGAatttcg	5'UTR	36		
Diptera (Muscidae)	<i>Musca_domestica</i>	Mdom\Atp6v1H		46	136	479				1191	135	58	126	64	437				66	114	69	79	ttacatcacagTCACAAGAccttcgTCAGCTGAattcagagtaaa	5'UTR?	>-100
Diptera (Tephritidae)	<i>Ceratitis_capitata</i>	Ccap\Atp6v1H		46	106	479				3452	135	86	126	72	437				56	114	249	85	ttgtgactttgTCAGCTGAattgttcacg ggtaagtgtgtgTCACATGAacattttgtgcg	5'UTR? intron	>-117 >58
Diptera (Glossinidae)	<i>Glossina_morsitans</i>	Gmor\Atp6v1H	149	46	85	479				2729	135	84	126	62	437				57	114	171	79 115	aaaagTCACAAGActcgTCAGCTGAattctccaata	5'UTR	9
Diptera (Psychodidae)	<i>Lutzomyia_longipalpis</i>	Llon\Atp6v1H	130	52	104	82	75	400				2509	698 (135+126+437)				72	205			caatcgtattgtTCACGTGAatcgagaaaa	5'UTR	33		
	<i>Phlebotomus_papatasi</i>	Ppap\Atp6v1H		52	127	82	64	400				ND	698 (135+126+437)				364	202			ccctccattctgTCACGTGAattcgaaggagc	5'UTR?	>-86		
Diptera (Culicidae)	<i>Anopheles_gambiae</i>	Agam\Atp6v1H AGAP009486*		49	299	82	106	406				1237	135	78	563				69	114	89	79 99	gttcacttcaggTCATATGAtcacaaatatt gagcaaatccaTCACGTGAgtgtgtttcttt	5'UTR? intron1	6 433
	<i>Anopheles_arabiensis</i>	Aara\Atp6v1H		49	308	82	100	406				1208	135	78	563				69	114	85	79	gttcacttcaggTCATATGAtcacaaatatt agctaaattccaTCACGTGAgtgtgtttcttt	5' intron1	>-121 >327
	<i>Anopheles_quadriannulatus</i>	Aqan\Atp6v1H		49	315	82	100	406				1221	135	75	563				68	114	88	79	gttcacttcaggTCATATGAtcacaaatatt agctaaattccaTCACGTGAgtgtgtttcttt	5' intron1	>-121 >334
	<i>Anopheles_christyi</i>	Achr\Atp6v1H		49	316	82	64	406				1087	135	78	563				63	114	76	79	attcactttggTCATATGAtcacaaatatt agttgaatttaaTCACGTGAgtgtgttttttc caagggaatcTCACGTGAacctaacggttag	5' intron1 intron3	>-117 >336 >1651
	<i>Anopheles_epiroticus</i>	Aepi\Atp6v1H		49	294	82	95	406				1121	135	62	563				69	114	64	79	attcactttggTCATATGAtcacaaatatt agttaaatccaTCACGTGAgtgtgtttcttt	5' intron1	>-129 >313
	<i>Anopheles_minimus</i>	Amin\Atp6v1H		49	294	82	70	406				974	135	68	563				65	114	67	79	atgcactttggTCATATGAtcacaaatatt atttaattccaTCACGTGAgtgtattctttt	5' intron1	>-115 >316
	<i>Anopheles_funestus</i>	Afun\Atp6v1H		49	285	82	70	406				988	135	70	563				83	114	67	79	ctacactttaggTCATATGAtcacaaatatt atttaattccaTCACGTGAgtgatgtctttt	5' intron1	>-115 >307
	<i>Anopheles_stephensi</i>	Aste\Atp6v1H		49	302	82	76	406				1045	135	80	563				ND	114	72	79	caccctttaggTCATATGAtcacaaatatt ctttactttccaTCACGTGAgtgtattcgtt	5' intron1	>-117 >323
	<i>Anopheles_dirus</i>	Adir\Atp6v1H		49	273	82	62	406				1013	135	68	563				67	114	71	79	aagaagaaggTCATATGAtcacaaattttt ccatcactictaTCACGTGAgtgatgtcgttt gaagggaatcTCACGTGAaccttacggttag	5' intron1 intron3	>-133 >286 >1538
	<i>Anopheles_nili</i>	Anil\Atp6v1H		49	273	82	59	406				ND	135	70	563				78	114	69	79	aagaagaaggTCATATGAtcacaaatatt aatcacttccaTCACGTGAacttatttttt	5' intron1	>-118 >289
	<i>Anopheles_albimanus</i>	Aalb\Atp6v1H		49	270	82	72	394				1032	135	71	563				70	114	69	79	ttatcagcgagTCACCTGAgttgattttcca cttcttcgttcTCACGTGAacttctacgctt	5' intron1	>-106 >284
	<i>Anopheles_darlingi</i>	Adar\Atp6v1H		49	261	82	74	394				1026	135	87	563				70	114	67	79	tattcagcgagTCACCTGAgttcccagagat gttctcgtctcaTCACGTGAacttctacggtt	5' intron1	>-115 >274
	<i>Culex_pipiens_qui.</i>	Cqui\Atp6v1H CPJ002428		46	232	82	64	406				936	135	2950	563				56	114	59	79	ctttaccccaagTCATATGAacatTCAGCTGA gaaatttggaaTCACGTGAaccttttcttc	5'UTR? intron1	>-135 >245
	<i>Aedes_aegypti</i>	Aaeg\Atp6v1H AAEL006516	169	49	246	488 (82+406)				4353	135	59	563 (374+189)				404	114	76	79	acctcatcagTCATATGAacttacetgag agaaatttggaaTCACGTGAgtttttgtgc	5'UTR intron1	5 435		
Diptera (Cecidomyiidae)	<i>Mayetiola_destructor</i>	Mdes\Atp6v1H		52	414	482 (82+400)				1809	135	86	374 (186+188)			68	189	68	114	76	94	gaaaagTCACAAGActcTCAGCTGAgttttttcttc gcgataaagtTCATTGAacttggttgta	5' 5'	>-153 >-61	
Lepidoptera	<i>Bombyx_mori</i>	Bmor\Atp6v1H LOC733031	116	64	76	82	69	181	636	213	2275	135	321	186	480	188	440	189	256	114	352	76 143	catttctcatagTCACAAGAcctcTCACCTGAgcagtgctggat	5'UTR	16
	<i>Manduca sexta</i>	Msex\Atp6v1H		64	74	82	81	181	1136	213	2509	135	495	186	115	188	501	189	691	114	557	76	cactttcatagTCACAAGAccaTCAGCTGAgtcgtgtgtcga	5'	>-95
	<i>Danaus_plexippus</i>	Dple\Atp6v1H		52	94	82	67	181	358	210	2006?	135	303	186	108	188	256	189	486	114	361	79	cacgtcgagtagTCACAAGAcctcTCAGCTGAgttcactgtcgc	5'	>-98
	<i>Heliconius_melpomene</i>	Hmel\Atp6v1H		64	89	82	81	181	119	210	2506	135	675	186	524	188	595	189	252	114	241	79	cacatcgaaagTCACAAGAcctcTCAGCTGAgttatctgtcta	5'	>-95
	<i>Plutella_xylostella</i>	Pxyi\Atp6v1H		64	93	82	255	181	728	204	2035	135	437	186	596	188	716	189	1043	114	474	76	cactttcaatagTCACAAGAcctcTCAGCTGAgttgtgtgtgt	5'	>-93
Strepsiptera	<i>Mengenilla_moldrzyki</i>	Mmol\Atp6v1H		ND	ND	82	58	190	237	219	ND	360			ND	335	59	184?				ND			

Coleoptera	<i>Tribolium_castaneum</i>	Tcas\Atp6v1H LOC657235*	83	79	232	82	49	190	4486	219	4351	695 (135+186+188+186)						48	199					gcgtgtcaataaTCACAAGAcctgtcagggtg ggctgagcacTCACGTGAacctgtgagtc	5'UTR? intron1	1 291						
	<i>Dendroctonus_ponderosae</i>	Dpon\Atp6v1H	101	73	2654	82	59	190	4486	219	4351	135	55	225	60	135	ND		200	150	198	63	55	40+125	tcaaaagattggTCATATGAtcaatgtccag aatgtccaggtTCAGCTGAttgagactagt taatgaactatTCACGTGAacctgttcaagt	5'UTR? 5'UTR intron1	-21 2 365					
Hymenoptera	<i>Apis_florea</i>	Aflo\Atp6v1H		58	440	82	94	190	616	219	1125	206	78	85	107	407				63	114	111	94		gttatcatcgaTCTTGTGAtccaactatga	5'UTR?	>-99					
	<i>Apis_mellifera</i>	Ame\Atp6v1H GB17480	119	58	452	82	102	190	583	219	1023	206	87	85	99	407				63	114	122	94	439	gttatcatcgaTCTTGTGAtccaactatga	5'UTR	14					
	<i>Bombus_impatiens</i>	Bimp\Atp6v1H		58	491	82	838	190	378	219	1203	206	85	85	875	407				73	114	102	91		gtaatatcacgTCTTGTGAtccaagtgtga	5'UTR?	>-102					
	<i>Bombus_terrestris</i>	Bter\Atp6v1H LOC100648051		58	506	82	936	190	372	219	1204	206	85	85	856	407				73	114	102	91		gtaatatcacgTCTTGTGAtccaagtgtga	5'UTR?	>-102					
	<i>Megachile_rotundata</i>	Mrot\Atp6v1H		58	603	82	78	190	78	219	991	206	78	85	67	407				80	114	78	94		tatgtacattggTCTTGTGAtttaacagctg	5'UTR?	>-104					
	<i>Acromyrmex_echinator</i>	Aech\Atp6v1H AECH24129*		61	200	82	196	190	455	219	ND	206	95	85	87	407				79	114	164	94		afattcgtgtggTCTTGTGAtcgaacagctga	5'	>-99					
	<i>Atta_cephalotes</i>	Acep\Atp6v1H ACEP26838*		61	196	82	176	190	487	219	19366	206	97	85	77	407				75	114	163	94		gtattcgcgtgaTCTTGTGAtcgaagaagctg	5'	>-102					
	<i>Solenopsis_invicta</i>	Sinv\Atp6v1H SINV11121*		58	195	82	168	190	775	219	ND	206	84	85	82	407				77	114	171	94		gtattcgcagtgTCTTGTGAtcgaacagctga	5'	>-102					
	<i>Pogonomyrmex_barbatus</i>	Pbar\Atp6v1H PB18819*		58	191	82	73	190	112	219	ND	206	91	85	92	407				119	114	188	88		gtatttgcgtggTCTTGTGAtcgaacagctga	5'						
	<i>Harpegnathos_saltator</i>	Hsal\Atp6v1H HSAL13159*		58	189	82	225	190	164	219	1499	206	69	85	82	407				82	114	137	94		gtaccaagtgTCTTGTGAtcgaacagctga	5'	>-102					
	<i>Linepithema_humile</i>	Lhum\Atp6v1H LH13415*		58	191	82	122	190	118	219	1639	206	97	85	77	407				107	114	86	94		gtagtgattggTCTTGTGAtcgaacagctga	5'	>-101					
	<i>Camponotus_floridanus</i>	Cflo\Atp6v1H CFL015154*		58	190	82	159	190	121	219	1525	206	104	85	96	407				117	114	208	94		gtatctgcacggTCTTGTGAtcgaacagctga	5'						
	<i>Nasonia_giraulti</i>	Ngir\Atp6v1H		58	144	82	76	190	68	219	1032	291			72	407				72	114	81	94		tctgtgggagtaTCAGCTGAtcaatcacgct aacatgcgcgTCATCTGAcgtactgacac acgtactccaaTCTCTGTGAcctgactgtga	5'UTR?	>-222 >-190 >-136					
	<i>Nasonia_longicornis</i>	Nlon\Atp6v1H		58	144	82	82	190	68	219	1020	291			79	407				72	114	81	94		tctgtgggagtaTCAGCTGAtcaatcacgct aacgtcgcgcgTCATCTGAcgtactgacac acgtactccaaTCTCTGTGAcctgactgtga	5'UTR?	>-222 >-190 >-136					
	<i>Nasonia_vitripennis</i>	Nvit\Atp6v1H NV13458	37	58	144	82	82	190	68	219	1053	291 (206+85)			79	407 (179+228)				72	114	81	94		tctgtgggagtaTCAGCTGAtcaatcacgct aacgtcgcgcgTCATCTGAcgtactgacac acgtactaccaaTCTCTGTGAcctgactgtga	5'UTR?	>-186 >-154 >-99					
Hemiptera	<i>Acyrtosiphon_pisum</i>	Apis\Atp6v1H LOC100161058*	122	58	98	82	71	184	104	219	414	206	68	85	58	179	74	228	85	114	2505	79	330		ND							
	<i>Rhodnius_prolixus</i>	Rpro\Atp6v1H		58	76	82	69	190	169	219	73	206	71	85	66	179	87	228	157	114	1010	88			ND							
Phthiraptera	<i>Pediculus_humanus</i>	Phum\Atp6v1H PHUM375970		61	333	82	203	190	89	219	148	206 (98+108)			472	264 (85+179)			132	228	107	114	556	82		ccccatagttaaTCACGTGAaaatcgtagga	5'	>-789				
Odonata	<i>Ladona_fulva</i>	Lful\Atp6v1H		52	228	82	ND	190	1262	219 (114+105)		ND	108+ND+98			655	85	ND	ND	228 (126+102)		ND	114	ND	94		gatcatggaatTCACGAGAcaggcacaggg	5'	>-126			
Crustacea	<i>Daphnia_pulex</i>	Dpul\Atp6v1H	142	61	72	82	190	190	73	354				64	71	67	492 (85+179+126+102)				74	114	68	76	75	ttagaggccagTCACATGAacaaactgacaa	5'UTR	1				
Ixodida	<i>Ixodes_scapularis</i>	Iscs\Atp6v1H ISCW013948*	24	64	ND	82	ND	190	ND	114	444	105	1960	98	1396	108	94	85	939	179	1483	126	642	102	ND	114	ND	73	45	gtgtctctcacTCACGTGAcgtgtgtgtgt	5'	-11
	<i>Homo_sapiens</i>	ATP6V1H	422	113				103	90	114			105		98		193		179		126		102		114		61	atcattcaagTCATATGAaaccattgac ctaaacctTCACGTGAaactcaaaagc	5'	-596 -139		
Cnidaria	<i>Nematostella_vectensis</i>	Nvec\Atp6v1H v1g164874	8	95				100	90	44	70		105		98		111	88	72	48	53	79	47		102	114	34	tgcttcgttaTCACGTGAacagaagtcac	5'	-108		
Placozoa	<i>Trichoplax_adhaerens</i>	Tadh\Atp6v1H TRIADDRAFT_36227	ND	56				106	90	44	73		105		98		108	85	72	48	53	79	47		102	114	64	ND				

