

GEPHE SUMMARY

Gephebase Gene		GepheID
Na/K-ATPase alpha-subunit (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Na/K-ATPase alpha-subunit"#gephebase-summary-title)	GP00001738	
Entry Status	Courtier	Main curator
Published		

PHENOTYPIC CHANGE

Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)	
Trait	
Xenobiotic resistance (cardiac glycosides) (<a (cardiac="" glycosides)"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=" resistance="" xenobiotic="">https://www.gephebase.org/search-criteria?/and+Trait="Xenobiotic resistance (cardiac glycosides)"#gephebase-summary-title)	
Trait State in Taxon A	
sensitive	
Trait State in Taxon B	
resistant	
Ancestral State	
Taxon A	
Taxonomic Status	
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intergeneric or Higher"#gephebase-summary-title)	
Taxon A	
Taxon B	
Latin Name	
Eumetazoa (<a eumetazoa"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Eumetazoa"#gephebase-summary-title)	Hydra vulgaris (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Hydra vulgaris"#gephebase-summary-title)
Common Name	
-	-
Synonyms	
-	Hydra attenuata; Hydra magnipapillata; Hydra magnipapillata Ito, 1947; Hydra vulgaris Pallas, 1766
Rank	
no rank	
Lineage	
cellular organisms; Eukaryota; Opisthokonta; Metazoa	species
Parent	
Metazoa (metazoans) - (Rank: kingdom) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33208)	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Cnidaria; Hydrozoa; Hydroidolina; Anthoathecata; Aplanulata; Hydridae; Hydra
NCBI Taxonomy ID	
6072 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6072)	Hydra () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6083)
is Taxon A an Intraspecies?	
No	6087 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6087)
is Taxon B an Intraspecies?	
No	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Mus musculus
Atp1a1	Q8VDN2 (http://www.uniprot.org/uniprot/Q8VDN2)	
Synonyms		GenebankID or UniProtKB
Atpa-1; BC010319	()	
String		
10090.ENSMUSP000000039657 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP000000039657)		
Sequence Similarities		
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIC subfamily.		
GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0043531 : ADP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043531)		
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)		
GO:0043548 : phosphatidylinositol 3-kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043548)		
GO:0005391 : sodium:potassium-exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005391)		
GO:0051087 : chaperone binding (https://www.ebi.ac.uk/QuickGO/term/GO:0051087)		

GO:0019904 : protein domain specific binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019904>)
GO:0030506 : ankyrin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0030506>)
GO:0016791 : phosphatase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0016791>)
GO:0030955 : potassium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0030955>)
GO:0031402 : sodium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0031402>)
GO:1990239 : steroid hormone binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990239>)

GO - Biological Process

GO:0071383 : cellular response to steroid hormone stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071383>)
GO:0006813 : potassium ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)
GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)
GO:0071260 : cellular response to mechanical stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071260>)
GO:0042493 : response to drug (<https://www.ebi.ac.uk/QuickGO/term/GO:0042493>)
GO:0008217 : regulation of blood pressure
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008217>)
GO:0015991 : ATP hydrolysis coupled proton transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015991>)
GO:0030007 : cellular potassium ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030007>)
GO:0006883 : cellular sodium ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006883>)
GO:1990573 : potassium ion import across plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990573>)
GO:0036376 : sodium ion export across plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0036376>)
GO:0090662 : ATP hydrolysis coupled transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090662>)
GO:0060081 : membrane hyperpolarization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060081>)
GO:0086009 : membrane repolarization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0086009>)
GO:0031947 : negative regulation of glucocorticoid biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031947>)
GO:0045822 : negative regulation of heart contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045822>)
GO:0045823 : positive regulation of heart contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045823>)
GO:0045989 : positive regulation of striated muscle contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045989>)
GO:0086004 : regulation of cardiac muscle cell contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0086004>)
GO:0002028 : regulation of sodium ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002028>)
GO:0002026 : regulation of the force of heart contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002026>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0016324 : apical plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016324>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0045121 : membrane raft (<https://www.ebi.ac.uk/QuickGO/term/GO:0045121>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0032991 : protein-containing complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032991>)
GO:0005783 : endoplasmic reticulum
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005783>)
GO:0005768 : endosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005768>)
GO:0016323 : basolateral plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016323>)
GO:0005901 : caveola (<https://www.ebi.ac.uk/QuickGO/term/GO:0005901>)
GO:0030315 : T-tubule (<https://www.ebi.ac.uk/QuickGO/term/GO:0030315>)
GO:0014069 : postsynaptic density (<https://www.ebi.ac.uk/QuickGO/term/GO:0014069>)
GO:0014704 : intercalated disc (<https://www.ebi.ac.uk/QuickGO/term/GO:0014704>)
GO:0043209 : myelin sheath (<https://www.ebi.ac.uk/QuickGO/term/GO:0043209>)
GO:0042383 : sarcolemma (<https://www.ebi.ac.uk/QuickGO/term/GO:0042383>)
GO:0005890 : sodium:potassium-exchanging ATPase complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005890>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title>)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Unknown~#gephebase-summary-title)	Molecular Details of the Mutation
-	
	Experimental Evidence
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene~#gephebase-summary-title)	Main Reference
Molecular cloning and characterization of Na,K-ATPase from Hydra vulgaris: implications for enzyme evolution and ouabain sensitivity. (1992) (https://pubmed.ncbi.nlm.nih.gov/1320398)	Authors
Canfield VA; Xu KY; D'Aquila T; Shyjan AW; Levenson R	Abstract
We have used molecular and biochemical techniques to analyze Na,K-ATPase from a simple metazoan, Hydra vulgaris. First we isolated and characterized cDNA clones encoding the Na,K-ATPase alpha subunit from a Hydra lambda gt11 cDNA library. The open reading frame predicts a protein of 1031 amino acids that bears a high degree of primary sequence and secondary structure similarity to mammalian, avian, and arthropod alpha subunits. The predicted Hydra alpha subunit contains charged residues at the termini of the H1-H2 extracellular domain, suggesting that the Hydra alpha subunit may be resistant to cardiac glycoside inhibition. Biochemical analysis of partially purified Hydra Na,K-ATPase reveals both high- and low-affinity components of ouabain-inhibitable ATPase activity. Our results suggest that the evolutionary ancestor of all metazoans possessed a Na,K-ATPase alpha subunit that was highly conserved with respect to its vertebrate counterparts. Further, expression of a ouabain-resistant Na,K-ATPase activity in Hydra suggests that cardiac glycoside resistance arose randomly during evolution of the Na,K-ATPase.	
	Additional References

RELATED GEPHE

	Related Genes
102 (ABCA2, Aminopeptidase N (APN), cadherin, CYP337B3, Ha_BtR, para (kdr), tetraspanin, ABCC2, ABCB1, ABCB4, CYP9J26, CYP9M6, resistance to dieldrin, Acetylcholinesterase (Ace-1), Chitin synthase 1 (CHS1), CYP6BG1, FMO2, glutamate-gated chloride channel (GluCl), MAP4K4, nAChR, RYR, CYP321A8, CYP9A186, GSTe, CYP9A, acetyl-CoA carboxylase (ACC), Acetylcholinesterase (Ace-2), CYP6CM1, CYP6CY3, CYP6CY3-CYP6CY4, esterase E4, esterase FE4, beta-tubulin (ben-1), GLC-1, str-217, SAP-2, Cpm1, esterase A8 and B8, esterase B4, esterase B5, esterase B1, CPR, CYP392A16, CYP392E8, cytochrome b, PSST, CYP6AY1, CYP6ER1, esterase NI-EST1, GST, CYP6FU1, Acetylcholinesterase (Ace), CYP6D1, esterase isozyme E7 = E3, alcohol dehydrogenase (Adh), Aldehyde dehydrogenase (Aldh), CG11699, Cyp12d1, Cyp28d1, Cyp28d1-Cyp28d2, cyp6d2, cyp6g1, GSS (glutathione synthetase), GSTE1-E10 cluster, kin of irre (kire), PHGPx, RnrS, SOD1, Ugt86Dd, esterase isozyme E3, AHR, Vkorc1, SCN9A (Nav1.7), AHR2, AIP, ARNT-1c, ARNT-L2a, alcohol dehydrogenase (ADH1B), CYP2C9, CYP4F2, MDR1, beta-tubulin, CHRNA1, esterase B1 + esterase A, esterase B1 = esterase beta1, CYP6AB3, CYP6P9 cluster (CYP6P9a and CYP6P9b), CYP6P9; CYP6P4 cluster, esterase type I, Nav1 sodium channel, Nav1.6 sodium channel, Nav1.7 sodium channel, SCN4A (Nav1.4), β^2 -adrenergic octopamine receptor gene (AOR), SCN8A (Nav1.6), SCN4A (Nav1.4a gene copy), SCN4A (Nav1.4b gene copy), Sulfotransferase-OXA-Resistance (SULT-OR), CHKov1, CYP6B1, CYP6B4, FMO1) (https://www.gephebase.org/search-criteria?/or+Taxon+ID=~6072~/and+Trait=Xenobiotic+resistance/or+Taxon+ID=~6087~/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title)	
	Related Haplotypes
22 (https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~Na/K-ATPase+alpha-subunit~/and+Taxon+ID=~6072~/or+Gene+Gephebase=~Na/K-ATPase+alpha-subunit~/and+Taxon+ID=~6087~#gephebase-summary-title)	

EXTERNAL LINKS

COMMENTS