GEPHE SUMMARY

Gephebase Gene
Na/K-ATPase alpha-subunit (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Na/K-ATPase alpha-subunit^#gephebase-summary-title)

GepheID
GP00001738

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Xenobiotic resistance (cardiac glycosides) (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

Latin Name
Eumetazoa (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Eumetazoa^#gephebase-summary-title)

Common Name
-

Synonyms
-

Rank
no rank

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa

Parent
Metazoa (metazoans) - (Rank: kingdom) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33208)

NCBI Taxonomy ID
6072 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6072)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
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
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Cnidaria; Hydrozoa; Hydroidolina; Anthoathecata; Aplanulata; Hydridae; Hydra

Parent
Hydra () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6083)

NCBI Taxonomy ID
6087 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6087)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Atp1a1

Synonyms
Atpa-1; BC010319

String
10090.ENSMUSP00000039657 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 10090.ENSMUSP00000039657)

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)

UniProtKB Mus musculus
Q8VDN2 (http://www.uniprot.org/uniprot/Q8VDN2)

GenebankID or UniProtKB
()

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), Î²-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