Generated by <u>dkNET</u> on Apr 29, 2025

ARAMEMNON, a Novel Database for Arabidopsis Integral Membrane Proteins

RRID:SCR_007552 Type: Tool

Proper Citation

ARAMEMNON, a Novel Database for Arabidopsis Integral Membrane Proteins (RRID:SCR_007552)

Resource Information

URL: http://aramemnon.botanik.uni-koeln.de

Proper Citation: ARAMEMNON, a Novel Database for Arabidopsis Integral Membrane Proteins (RRID:SCR_007552)

Description: A database of putative membrane proteins of Thale Cress (Arabidopsis thaliana), Rice (Oryza sativa) and about some 6700 putative membrane proteins of ~300 other seed plants. The database stores data about: * protein, cDNA and genomic sequences * exon predictions (A.thaliana and O.sativa) * different cDNA/protein models of genes (A.thaliana and O.sativa) * ontology terms according to the Gene Ontology (GO) Consortium * protein sequence motifs as predictable by using the PFAM database * transporter classification as predictable by using the TC-system * bibliographic references * predictions for transmembrane spanning proteins (GPI-attachment, prenylation, myristoylation) * prediction of the subcellular location * consensus predictions (transmembrane alpha helices, subcellular location) * isospecic homologs ("paralogs") * heterospecic homologs ("orthologs")

Synonyms: ARAMEMNON

Resource Type: data or information resource, database

Keywords: arabidopsis, cdna, heterospecic homologs, isospecic homologs, membraneanchored proteins, membrane protein, oryza, transmemebrane spanning proteins, FASEB list Funding: GABI program ; BMBF

Resource Name: ARAMEMNON, a Novel Database for Arabidopsis Integral Membrane Proteins

Resource ID: SCR_007552

Alternate IDs: nif-0000-02563

Record Creation Time: 20220129T080242+0000

Record Last Update: 20250429T055146+0000

Ratings and Alerts

No rating or validation information has been found for ARAMEMNON, a Novel Database for Arabidopsis Integral Membrane Proteins.

No alerts have been found for ARAMEMNON, a Novel Database for Arabidopsis Integral Membrane Proteins.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Chen K, et al. (2024) OsSRF8 interacts with OsINP1 and OsDAF1 to regulate pollen aperture formation in rice. Nature communications, 15(1), 4512.

Deng CH, et al. (2023) Genotype and phenotype data standardization, utilization and integration in the big data era for agricultural sciences. Database : the journal of biological databases and curation, 2023.

Yáñez-Domínguez C, et al. (2023) A cornichon protein controls polar localization of the PINA auxin transporter in Physcomitrium patens. Development (Cambridge, England), 150(9).

Lin Y, et al. (2022) Characterization and expression analysis of the glycosyltransferase 64 family in rice (Oryza sativa). Gene, 838, 146708.

Zhang W, et al. (2021) Cytokinin oxidase/dehydrogenase OsCKX11 coordinates source and

sink relationship in rice by simultaneous regulation of leaf senescence and grain number. Plant biotechnology journal, 19(2), 335.

Begam RA, et al. (2020) The Arabidopsis L-Type Amino Acid Transporter 5 (LAT5/PUT5) Is Expressed in the Phloem and Alters Seed Nitrogen Content When Knocked Out. Plants (Basel, Switzerland), 9(11).

Jin X, et al. (2018) TaAAP6-3B, a regulator of grain protein content selected during wheat improvement. BMC plant biology, 18(1), 71.

Zhang M, et al. (2017) Identification of a rice metal tolerance protein OsMTP11 as a manganese transporter. PloS one, 12(4), e0174987.

Winkler AJ, et al. (2017) Short-Chain Chitin Oligomers: Promoters of Plant Growth. Marine drugs, 15(2).

Ruge H, et al. (2016) The calmodulin-like proteins AtCML4 and AtCML5 are single-pass membrane proteins targeted to the endomembrane system by an N-terminal signal anchor sequence. Journal of experimental botany, 67(13), 3985.

Atkinson N, et al. (2016) Introducing an algal carbon-concentrating mechanism into higher plants: location and incorporation of key components. Plant biotechnology journal, 14(5), 1302.

Herdean A, et al. (2016) A voltage-dependent chloride channel fine-tunes photosynthesis in plants. Nature communications, 7, 11654.

Voiniciuc C, et al. (2016) Extensive Natural Variation in Arabidopsis Seed Mucilage Structure. Frontiers in plant science, 7, 803.

Zhu G, et al. (2015) Molecular Characterization and Expression Profiling of NAC Transcription Factors in Brachypodium distachyon L. PloS one, 10(10), e0139794.

San Clemente H, et al. (2015) WallProtDB, a database resource for plant cell wall proteomics. Plant methods, 11(1), 2.

Pertl-Obermeyer H, et al. (2014) In vivo cross-linking combined with mass spectrometry analysis reveals receptor-like kinases and Ca(2+) signalling proteins as putative interaction partners of pollen plasma membrane H(+) ATPases. Journal of proteomics, 108, 17.

Jung HI, et al. (2014) Brachypodium distachyon as a model system for studies of copper transport in cereal crops. Frontiers in plant science, 5, 236.

Zhang Z, et al. (2014) Salicylic acid signaling controls the maturation and localization of the arabidopsis defense protein ACCELERATED CELL DEATH6. Molecular plant, 7(8), 1365.

Häusler RE, et al. (2014) How sugars might coordinate chloroplast and nuclear gene expression during acclimation to high light intensities. Molecular plant, 7(7), 1121.

Saier MH, et al. (2014) The transporter classification database. Nucleic acids research,

42(Database issue), D251.