

Resource Summary Report

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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 (transmembrane alpha helices, beta barrels) * predictions for membrane-anchored proteins (GPI-attachment, prenylation, myristoylation) * prediction of the subcellular location * consensus predictions (transmembrane alpha helices, subcellular location) * isospecific homologs ("paralogs") * heterospecific homologs ("orthologs")

Synonyms: ARAMEMNON

Resource Type: data or information resource, database

Keywords: arabidopsis, cdna, heterospecific homologs, isospecific homologs, membrane-anchored proteins, membrane protein, oryza, transmembrane 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: 20260905T133140+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 63 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Hou X, et al. (2026) Evolutionary analysis of MOCA1 gene in Arabidopsis thaliana and functional comparison with PGSIP7 and PGSIP8 genes. Frontiers in plant science, 17, 1734646.

Wehler R, et al. (2025) Identification of 1,6-hexadecanediol and its wax diesters in chloroplasts of Nicotiana benthamiana. Planta, 262(5), 117.

Robe K, et al. (2025) Four ZIPs contribute to Zn, Fe, Cu and Mn acquisition at the outer root domain. PLoS genetics, 21(7), e1011796.

Shaikh KM, et al. (2025) The thylakoid- and pyrenoid-localized phosphate transporter PHT4-9 is essential for photosynthesis in Chlamydomonas. Plant physiology, 198(1).

Wang Y, et al. (2025) The endoplasmic reticulum-associated degradation machinery selectively degrades stress-induced TIN1 during stress recovery. Plant physiology, 199(2).

Tania SS, et al. (2025) Amino Acid Substitutions in Loop C of Arabidopsis PIP2 Aquaporins Alters the Permeability of CO₂. Plant, cell & environment, 48(9), 6835.

Khadgi A, et al. (2025) Mutations in the SWEET15 Sugar Transporter Gene Affect Response of Citrus to Huanglongbing Disease and Citrus Canker. Molecular plant

pathology, 26(5), e70094.

Castanedo L, et al. (2025) Cis-regulatory elements co-opting core circadian clock regulator CCA1 underlie enhanced expression of HMA4 for metal hyperaccumulation in *Arabidopsis halleri*. *Plant communications*, 6(12), 101540.

Linnenbrügger L, et al. (2025) Evidence for peroxisomal redundancy among the glucose-6-phosphate dehydrogenase isoforms of *Arabidopsis thaliana*. *Plant & cell physiology*, 66(5), 722.

Doering LN, et al. (2024) Evidence for dual targeting control of *Arabidopsis* 6-phosphogluconate dehydrogenase isoforms by N-terminal phosphorylation. *Journal of experimental botany*, 75(10), 2848.

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).

Sun Y, et al. (2022) Ubiquitin-based pathway acts inside chloroplasts to regulate photosynthesis. *Science advances*, 8(46), eabq7352.

Talukdar P, et al. (2022) Identification of genomic loci regulating grain iron content in aus rice under two irrigation management systems. *Food and energy security*, 11(1), e329.

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

Berger N, et al. (2022) Root Membrane Ubiquitinome under Short-Term Osmotic Stress. *International journal of molecular sciences*, 23(4).

Huang SH, et al. (2021) Genome-wide identification and expression analysis of the GSK gene family in *Solanum tuberosum* L. under abiotic stress and phytohormone treatments and functional characterization of StSK21 involvement in salt stress. *Gene*, 766, 145156.

Gratz R, et al. (2021) Organic nitrogen nutrition: LHT1.2 protein from hybrid aspen (*Populus tremula* L. x *tremuloides* Michx) is a functional amino acid transporter and a homolog of *Arabidopsis* LHT1. *Tree physiology*, 41(8), 1479.

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.