

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: 20260904T000226+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 [kravitz2](#) .

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.

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.

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

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

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

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).

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.

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

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

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

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.