

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

Arabidopsis thaliana Protein Interactome Database

RRID:SCR_001896

Type: Tool

Proper Citation

Arabidopsis thaliana Protein Interactome Database (RRID:SCR_001896)

Resource Information

URL: <http://www.megabionet.org/atpid/webfile/>

Proper Citation: Arabidopsis thaliana Protein Interactome Database (RRID:SCR_001896)

Description: Centralized platform to depict and integrate the information pertaining to protein-protein interaction networks, domain architecture, ortholog information and GO annotation in the Arabidopsis thaliana proteome. The Protein-protein interaction pairs are predicted by integrating several methods with the Naive Bayesian Classifier. All other related information curated is manually extracted from published literature and other resources from some expert biologists. You are welcomed to upload your PPI or subcellular localization information or report data errors. Arabidopsis proteins is annotated with information (e.g. functional annotation, subcellular localization, tissue-specific expression, phosphorylation information, SNP phenotype and mutant phenotype, etc.) and interaction qualifications (e.g. transcriptional regulation, complex assembly, functional collaboration, etc.) via further literature text mining and integration of other resources. Meanwhile, the related information is vividly displayed to users through a comprehensive and newly developed display and analytical tools. The system allows the construction of tissue-specific interaction networks with display of canonical pathways.

Abbreviations: AtPID

Synonyms: AtPID Database

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:21036873](#), [PMID:17962307](#)

Keywords: gene, gene expression, domain, annotation, interactome, metabolic pathway, phylogenetic, protein, protein-protein interaction, signaling pathway, proteome, protein subcellular location, ortholog, gene regulation, pathway, phenotype

Funding: National Basic Research Program of China 2010CB945400;
National Basic Research Program of China 2007CB108800;
National High Technology Research and Development Program of China 2006AA02Z313;
National High Technology Research and Development Program of China 2006AA10Z129;
National Natural Science Foundation of China 30870575;
National Natural Science Foundation of China 30730078;
Science and Technology Commission of Shanghai Municipality 06DZ22923

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Arabidopsis thaliana Protein Interactome Database

Resource ID: SCR_001896

Alternate IDs: OMICS_01898, nif-0000-02585

Old URLs: <http://atpid.biosino.org/>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260919T194951+0000

Ratings and Alerts

No rating or validation information has been found for Arabidopsis thaliana Protein Interactome Database.

No alerts have been found for Arabidopsis thaliana Protein Interactome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Vandereyken K, et al. (2018) Hub Protein Controversy: Taking a Closer Look at Plant Stress Response Hubs. Frontiers in plant science, 9, 694.

Balan B, et al. (2018) Transcriptomic responses to biotic stresses in Malus x domestica: a meta-analysis study. Scientific reports, 8(1), 1970.

Mele G, et al. (2016) Arabidopsis Motif Scanner. BMC bioinformatics, 17, 50.

Lu T, et al. (2013) Fuzzy clustering of CPP family in plants with evolution and interaction analyses. BMC bioinformatics, 14 Suppl 13(Suppl 13), S10.

Mochida K, et al. (2011) Advances in omics and bioinformatics tools for systems analyses of plant functions. *Plant & cell physiology*, 52(12), 2017.

Fernandez-Calvino L, et al. (2011) Arabidopsis plasmodesmal proteome. *PloS one*, 6(4), e18880.

Cui J, et al. (2011) Integrative identification of Arabidopsis mitochondrial proteome and its function exploitation through protein interaction network. *PloS one*, 6(1), e16022.

Mochida K, et al. (2010) Genomics and bioinformatics resources for crop improvement. *Plant & cell physiology*, 51(4), 497.