

Resource Summary Report

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TAIR

RRID:SCR_004618

Type: Tool

Proper Citation

TAIR (RRID:SCR_004618)

Resource Information

URL: <http://www.arabidopsis.org>

Proper Citation: TAIR (RRID:SCR_004618)

Description: Database of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana*. Data available includes the complete genome sequence along with gene structure, gene product information, metabolism, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every two weeks from the latest published research literature and community data submissions. Gene structures are updated 1-2 times per year using computational and manual methods as well as community submissions of new and updated genes. TAIR also provides extensive linkouts from data pages to other Arabidopsis resources. The data can be searched, viewed and analyzed. Datasets can also be downloaded. Pages on news, job postings, conference announcements, Arabidopsis lab protocols, and useful links are provided.

Abbreviations: TAIR, AGI LocusCode

Synonyms: AGI LocusCode, The Arabidopsis Information Resource

Resource Type: data or information resource, database

Defining Citation: [PMID:22140109](#), [PMID:17986450](#), [PMID:12444417](#), [PMID:12519987](#), [PMID:18287693](#)

Keywords: genetic, molecular biology, gene, genome, structure, product, metabolism, gene expression, dna, seed stock, genome map, genetic marker, physical marker, genome sequence, gene product, blast, experimental protocol, gold standard

Funding: NSF DBI-0850219;
corporate and nonprofit organizations

Resource Name: TAIR

Resource ID: SCR_004618

Alternate IDs: r3d100010185, nlx_61477, OMICS_01662

Alternate URLs: <https://doi.org/10.17616/R3QW21>

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260912T195615+0000

Ratings and Alerts

No rating or validation information has been found for TAIR.

No alerts have been found for TAIR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9170 mentions in open access literature.

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

Li Y, et al. (2026) A MaERF110-MaMYB308 Transcriptional Module Negatively Regulates Lignin-Mediated Defence Against Fusarium Wilt in Banana. *Plant biotechnology journal*, 24(5), 2811.

Shi H, et al. (2026) Genetic Mapping and Functional Characterisation of GhCUP Regulating Leaf Curling in Cotton. *Plant biotechnology journal*, 24(4), 2607.

Xu S, et al. (2026) Comprehensive Investigation of GRF Transcription Factors and Associated Responses to Drought Stress in Oat (*Avena sativa*). *Plants (Basel, Switzerland)*, 15(1).

Tang X, et al. (2026) PfTALE5 Acts as a hub for multi-stress resilience: a genome-wide study of the TALE family in *Paulownia fortunei*. *BMC plant biology*, 26(1), 255.

Meng X, et al. (2026) Genome-wide identification and expression analysis of the GRAS transcription factor family and its expression profiles in *Elymus sibiricus*. *BMC genomics*, 27(1), 156.

Park S, et al. (2026) JULGI coordinates vascular development and leaf patterning through non-cell-autonomous regulation of miR165/166. *Nature communications*, 17(1), 684.

Zhang B, et al. (2026) Pan-NLR gene family analyses decipher evolutionary dynamics, population diversity, and potential disease resistance genes in cucumber. *BMC plant*

biology, 26(1), 345.

Zhang Q, et al. (2026) Identification and characterization of the DREB family in Chinese yam and functional study of DoDREB28 under drought stress. BMC plant biology, 26(1).

Chen J, et al. (2026) Analysis of the TGA gene family and the role of SITGA03 in tomato resistance to *Meloidogyne enterolobii*. BMC genomics, 27(1).

Su M, et al. (2026) Type one protein phosphatases (TOPPs) catalyze EIN2 dephosphorylation to regulate ethylene signaling in Arabidopsis. Science advances, 12(7), eaec5937.

Zhao Q, et al. (2026) Identification of miRNAs Responsive to a Defined Period of Iron Deficiency and Resupply in Arabidopsis thaliana. Plants (Basel, Switzerland), 15(2).

Li J, et al. (2026) Identification, Transcriptome, and Proteome Analysis of Expansin-like Subfamilies in the Storage Root Across *L. trifida* (2x), Wild (4x, 6x) and Cultivated Sweet Potatoes. Plants (Basel, Switzerland), 15(2).

Gitman IFB, et al. (2026) OmicIntegrator: A Simple and Versatile Tool for Meta-Analysis. Plants (Basel, Switzerland), 15(2).

Baral B, et al. (2026) Decoding plant defense signaling using the defenseless mutant. The New phytologist, 250(2), 1141.

He H, et al. (2026) WRKY transcription factors govern selenium metabolism in *Broussonetia papyrifera*: genome-wide identification, expression profiling, and regulatory network analysis. BMC plant biology, 26(1).

Tian Y, et al. (2026) Genome-Wide Identification of the *Medicago ruthenica* FTIP Gene Family and Expression Profiling Under Salt Stresses. International journal of molecular sciences, 27(4).

Khan A, et al. (2026) The Impact of Mitochondrial DNA Depletion on Mitochondrial Ultrastructure, Photosynthesis, and the mTERF Gene Family in *Chlamydomonas reinhardtii*. International journal of molecular sciences, 27(4).

Podio M, et al. (2026) Leaf transcriptome differences between diploid and tetraploid bahiagrass. The plant genome, 19(1), e70212.

Wang D, et al. (2026) Genome-wide identification and expression analysis of Trehalose 6-phosphate (Tre6P) synthase (TPS) and Tre6P phosphatase (TPP) genes under cold stress in winter Rye (*Secale cereals* L.). BMC genomics, 27(1).

Wei H, et al. (2026) Identification, evolutionary diversification, and stress response roles of SmLACSs in *Salix matsudana*. BMC genomics, 27(1).