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 analysis service, database, analysis service resource, production service resource, data or information resource, data repository, storage service resource, service resource

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

Availability: GNU Lesser General Public License, (source code), Acknowledgement required, The community can contribute to this resource, Non-commercial, Account required, (To access some portions of the service), Paid subscription, (To access some portions of the service)

Resource Name: TAIR

Resource ID: SCR_004618

Alternate IDs: nlx_61477, OMICS_01662

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250505T053600+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 7029 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG.

García-Hernández S, et al. (2025) Functional and Structural Analysis Reveals Distinct Biological Roles of Plant Synaptotagmins in Response to Environmental Stress. Plant, cell & environment, 48(1), 260.

McGuire ST, et al. (2025) The first intron and promoter of Arabidopsis DIACYLGLYCEROL ACYLTRANSFERASE 1 exert synergistic effects on pollen and embryo lipid accumulation. The New phytologist, 245(1), 263.

Wang HW, et al. (2025) Identification, characterization, and expression of Oryza sativa tryptophan decarboxylase genes associated with fluroxypyr-meptyl metabolism. The plant genome, 18(1), e20547.

Jin J, et al. (2025) Violet LED light-activated MdHY5 positively regulates phenolic accumulation to inhibit fresh-cut apple fruit browning. Horticulture research, 12(1), uhae276.

Kolesnikova A, et al. (2025) Drought Response in the Transcriptome and Ionome of Wild and Domesticated Lablab purpureus L. Sweet, an Underutilized Legume. Plant-environment interactions (Hoboken, N.J.), 6(1), e70027.

Zheng S, et al. (2025) Pupylation-based proximity labeling reveals regulatory factors in cellulose biosynthesis in Arabidopsis. Nature communications, 16(1), 872.

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (Oryza sativa L.) and their expression profiles in response to phytohormones. PloS one, 20(1), e0317008.

Tian Z, et al. (2025) Genome-wide identification and analysis of the NF-Y transcription factor family reveal its potential roles in tobacco (Nicotiana tabacum L.). Plant signaling & behavior, 20(1), 2451700.

Ming R, et al. (2025) The GRAS transcription factor PtrPAT1 of Poncirus trifoliata functions in cold tolerance and modulates glycine betaine content by regulating the BADH-like gene. Horticulture research, 12(1), uhae296.

Kuang X, et al. (2025) HDC1 Promotes Primary Root Elongation by Regulating Auxin and K+ Homeostasis in Response to Low-K+ Stress. Biology, 14(1).

Yang X, et al. (2025) Genome-wide characterization of the MADS-box gene family in Paeonia ostii and expression analysis of genes related to floral organ development. BMC genomics, 26(1), 49.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Zhao X, et al. (2025) Genome-Wide Identification and Expression Analysis of PkNRT Gene Family in Korean Pine (Pinus koraiensis). Plants (Basel, Switzerland), 14(2).

Yu L, et al. (2025) Unraveling TEOSINTE BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTOR Transcription Factors in Safflower: A Blueprint for Stress Resilience and Metabolic Regulation. Molecules (Basel, Switzerland), 30(2).

Liu J, et al. (2025) A plant mutant screen CURE integrated with core biology concepts showed effectiveness in course design and students' perceived learning gains. Biochemistry and molecular biology education : a bimonthly publication of the International Union of Biochemistry and Molecular Biology, 53(1), 57.

Zluhan-Martínez E, et al. (2025) The MADS-box gene XAANTAL1 participates in Arabidopsis thaliana primary root growth and columella stem cell patterns in response to ROS, via direct regulation of PEROXIDASE 28 and RETINOBLASTOMA-RELATED genes. Journal of experimental botany, 76(2), 411.

Kong X, et al. (2025) Transcriptional regulation of miR528-PPO module by miR156 targeted SPLs orchestrates chilling response in banana. Molecular horticulture, 5(1), 2.

Wang X, et al. (2025) Genome-wide identification and functional roles relating to anthocyanin biosynthesis analysis in maize. BMC plant biology, 25(1), 57.

Liu Q, et al. (2025) Identification of EXPA4 as a key gene in cotton salt stress adaptation through transcriptomic and coexpression network analysis of root tip protoplasts. BMC plant biology, 25(1), 65.

Wang L, et al. (2025) Identification and Candidate Gene Analysis of Brcl1, a Novel Gene Confers a Leaf Curled Phenotype in Brassica rapa L. International journal of molecular sciences, 26(2).