

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: 20260729T044102+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 7421 mentions in open access literature.

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

Zavala-Paez M, et al. (2026) Climate and hybridization shape stomatal trait evolution in *Populus*. *The New phytologist*, 249(2), 792.

Liu RX, et al. (2026) MdHMGB15-MdXERICO-MdNRP module mediates salt tolerance of apple by regulating the expression of salt stress-related genes. *Journal of advanced research*, 79, 61.

Li L, et al. (2025) Identification and functional analysis of Wall-Associated Kinase genes in *Nicotiana tabacum*. *Frontiers in plant science*, 16, 1543437.

Deng X, et al. (2025) The unconventional TPX2 family protein TPXL3 regulates ? Aurora kinase function in spindle morphogenesis in *Arabidopsis*. *The Plant cell*, 37(4).

Ranade SS, et al. (2025) Metabolomic profiling of shade response and in silico analysis of PAL homologs imply the potential presence of bifunctional ammonia lyases in conifers. *Physiologia plantarum*, 177(2), e70175.

Yu H, et al. (2025) Ecotype-specific phenolic acid accumulation and root softness in *Salvia miltiorrhiza* are driven by environmental and genetic factors. *Plant biotechnology journal*, 23(6), 2224.

Zhang L, et al. (2025) Genome-Wide Identification of ?-Ketoacyl CoA Synthase Gene Family in Melon (*Cucumis melo* L.) and Its Expression Analysis in Autotoxicity, Saline-

Alkali, and Microplastic Exposure Environments. Current issues in molecular biology, 47(3).

Guo P, et al. (2025) Salt stress activates the CDK8-AHL10-SUVH2/9 module to dynamically regulate salt tolerance in Arabidopsis. Nature communications, 16(1), 2454.

Zhang D, et al. (2025) Identification of the Valine-Glutamine gene family in Chenopodium quinoa Willd and analysis of its expression pattern and subcellular localization under drought stress. BMC genomics, 26(1), 252.

Xiang T, et al. (2025) The dynamic regulatory network of stamens and pistils in papaya. BMC plant biology, 25(1), 254.

Krüger T, et al. (2025) DOG1 controls dormancy independently of ABA core signaling kinases regulation by preventing AFP dephosphorylation through AHG1. Science advances, 11(9), eadr8502.

Yang X, et al. (2025) MADS31 supports female germline development by repressing the post-fertilization programme in cereal ovules. Nature plants, 11(3), 543.

Yamaguchi M, et al. (2025) LIPID RICH 1 modulates allocation of carbon between starch and triacylglycerol in Arabidopsis leaves. Journal of experimental botany, 76(8), 2144.

Lan L, et al. (2025) A novel mode of WRKY1 regulating PR1-mediated immune balance to defend against powdery mildew in apple. Molecular horticulture, 5(1), 17.

Li J, et al. (2025) Genome-wide identification and analysis of the UBA2 gene family in wheat (Triticum aestivum L.). BMC genomics, 26(1), 180.

Qin L, et al. (2025) Evolution of Plant Conserved microRNAs After Whole-Genome Duplications. Genome biology and evolution, 17(3).

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.

Omondi E, et al. (2025) Association analyses reveal both anthropic and environmental selective events during eggplant domestication. The Plant journal : for cell and molecular biology, 121(3), e17229.

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.

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).