

Resource Summary Report

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Arabidopsis Gene Regulatory Information Server

RRID:SCR_006928

Type: Tool

Proper Citation

Arabidopsis Gene Regulatory Information Server (RRID:SCR_006928)

Resource Information

URL: <http://arabidopsis.med.ohio-state.edu>

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Description: An information resource of Arabidopsis promoter sequences, transcription factors and their target genes that contains three databases. *AtcisDB consists of approximately 33,000 upstream regions of annotated Arabidopsis genes (TAIR9 release) with a description of experimentally validated and predicted cis-regulatory elements. *AtTFDB contains information on approximately 1,770 transcription factors (TFs). These TFs are grouped into 50 families, based on the presence of conserved domains. *AtRegNet contains 11,355 direct interactions between TFs and target genes. They provide free download of Arabidopsis thaliana cis-regulatory database (AtcisDB) and transcription factor database (AtTFDB).

Abbreviations: AGRIS

Resource Type: data or information resource, database

Defining Citation: [PMID:21059685](#), [PMID:16524982](#), [PMID:12820902](#)

Keywords: gene regulatory, gene, arabidopsis thaliana, promoter sequence, target gene, transcription factor, FASEB list

Funding: NSF

Availability: Free, Acknowledgement requested

Resource Name: Arabidopsis Gene Regulatory Information Server

Resource ID: SCR_006928

Alternate IDs: OMICS_00548, nif-0000-02540

Record Creation Time: 20220129T080238+0000

Ratings and Alerts

No rating or validation information has been found for Arabidopsis Gene Regulatory Information Server.

No alerts have been found for Arabidopsis Gene Regulatory Information Server.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Salvati A, et al. (2025) Berberine bridge enzyme-like oxidases orchestrate homeostasis and signaling of oligogalacturonides in defense and upon mechanical damage. The Plant journal : for cell and molecular biology, 122(1), e70150.

Kababji AM, et al. (2024) Synthetic directed evolution for targeted engineering of plant traits. Frontiers in plant science, 15, 1449579.

Dossa K, et al. (2021) A novel motif in the 5'-UTR of an orphan gene 'Big Root Biomass' modulates root biomass in sesame. Plant biotechnology journal, 19(5), 1065.

Mohanty B, et al. (2021) Promoter Architecture and Transcriptional Regulation of Genes Upregulated in Germination and Coleoptile Elongation of Diverse Rice Genotypes Tolerant to Submergence. Frontiers in genetics, 12, 639654.

Grzybkowska D, et al. (2020) Hypermethylation of Auxin-Responsive Motifs in the Promoters of the Transcription Factor Genes Accompanies the Somatic Embryogenesis Induction in Arabidopsis. International journal of molecular sciences, 21(18).

Gratkowska-Zmuda DM, et al. (2020) The SWI/SNF ATP-Dependent Chromatin Remodeling Complex in Arabidopsis Responds to Environmental Changes in Temperature-Dependent Manner. International journal of molecular sciences, 21(3).

Zhai Y, et al. (2019) Putative Auxin and Light Responsive Promoter Elements From the Tomato spotted wilt tospovirus Genome, When Expressed as cDNA, Are Functional in Arabidopsis. Frontiers in plant science, 10, 804.

Bahrman N, et al. (2019) Identification of Genes Differentially Expressed in Response to Cold in Pisum sativum Using RNA Sequencing Analyses. Plants (Basel, Switzerland), 8(8).

Chang HC, et al. (2019) Regulation of ABI5 expression by ABF3 during salt stress responses in *Arabidopsis thaliana*. *Botanical studies*, 60(1), 16.

Tada Y, et al. (2019) The HKT Transporter Gene from *Arabidopsis*, AtHKT1;1, Is Dominantly Expressed in Shoot Vascular Tissue and Root Tips and Is Mild Salt Stress-Responsive. *Plants* (Basel, Switzerland), 8(7).

Zhang F, et al. (2019) Genome-wide dynamic network analysis reveals a critical transition state of flower development in *Arabidopsis*. *BMC plant biology*, 19(1), 11.

Safavi-Rizi V, et al. (2018) Divergent N Deficiency-Dependent Senescence and Transcriptome Response in Developmentally Old and Young *Brassica napus* Leaves. *Frontiers in plant science*, 9, 48.

Vidya SM, et al. (2018) Transcriptional profiling and genes involved in acquired thermotolerance in Banana: a non-model crop. *Scientific reports*, 8(1), 10683.

Guan X, et al. (2018) FdC1 and Leaf-Type Ferredoxins Channel Electrons From Photosystem I to Different Downstream Electron Acceptors. *Frontiers in plant science*, 9, 410.

Solís-Guzmán MG, et al. (2017) Expression analysis of the *Arabidopsis thaliana* AtSpen2 gene, and its relationship with other plant genes encoding Spen proteins. *Genetics and molecular biology*, 40(3), 643.

Becker MG, et al. (2017) SeqEnrich: A tool to predict transcription factor networks from co-expressed *Arabidopsis* and *Brassica napus* gene sets. *PloS one*, 12(6), e0178256.

Cordovez V, et al. (2017) Plant Phenotypic and Transcriptional Changes Induced by Volatiles from the Fungal Root Pathogen *Rhizoctonia solani*. *Frontiers in plant science*, 8, 1262.

Sheshadri SA, et al. (2016) Stress-Mediated cis-Element Transcription Factor Interactions Interconnecting Primary and Specialized Metabolism in planta. *Frontiers in plant science*, 7, 1725.

Martín G, et al. (2016) Phytochrome and retrograde signalling pathways converge to antagonistically regulate a light-induced transcriptional network. *Nature communications*, 7, 11431.

Kumar G, et al. (2016) Comparative phylogenetic analysis and transcriptional profiling of MADS-box gene family identified DAM and FLC-like genes in apple (*Malus domestica*). *Scientific reports*, 6, 20695.