

Resource Summary Report

Generated by T1D on Jul 29, 2026

AthaMap

RRID:SCR_006717

Type: Tool

Proper Citation

AthaMap (RRID:SCR_006717)

Resource Information

URL: <http://www.athamap.de/>

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Description: Genome wide map of putative transcription factor binding sites in Arabidopsis thaliana genome. Data in AthaMap is based on published transcription factor (TF) binding specificities available as alignment matrices or experimentally determined single binding sites. Integrated transcriptional and post transcriptional data. Provides web tools for analysis and identification of co-regulated genes. Provides web tools for database assisted identification of combinatorial cis-regulatory elements and the display of highly conserved transcription factor binding sites in Arabidopsis thaliana.

Synonyms: Arabidopsis thaliana Map

Resource Type: data or information resource, database

Defining Citation: [PMID:22800758](#), [PMID:21177332](#), [PMID:18842622](#), [PMID:17148485](#), [PMID:16922688](#), [PMID:15980498](#), [PMID:14681436](#)

Keywords: gene, arabidopsis thaliana, binding site, genome, transcription factor, small rna binding site, small rna, rna, microrna, cis-regulatory element, post-transcriptional regulation, FASEB list

Availability: Free, Freely available

Resource Name: AthaMap

Resource ID: SCR_006717

Alternate IDs: nif-0000-02583, biotools:athamap, OMICS_00549, nif-0000-20814, SCR_013106

Alternate URLs: <https://bio.tools/athamap>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260729T044137+0000

Ratings and Alerts

No rating or validation information has been found for AthaMap.

No alerts have been found for AthaMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 48 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Cui H, et al. (2025) CANTAC-seq analysis reveals E2f1 and Otx1 coordinate zygotic genome activation in *Xenopus tropicalis*. *Nature communications*, 16(1), 10101.

Córdoba SC, et al. (2023) Identification of gene function based on models capturing natural variability of *Arabidopsis thaliana* lipid metabolism. *Nature communications*, 14(1), 4897.

Vaseva II, et al. (2021) The Diverse Salt-Stress Response of *Arabidopsis* ctr1-1 and ein2-1 Ethylene Signaling Mutants Is Linked to Altered Root Auxin Homeostasis. *Plants* (Basel, Switzerland), 10(3).

Dergilev AI, et al. (2021) Statistical estimates of multiple transcription factors binding in the model plant genomes based on ChIP-seq data. *Journal of integrative bioinformatics*, 19(1).

Serrano-Ron L, et al. (2021) Reconstruction of lateral root formation through single-cell RNA sequencing reveals order of tissue initiation. *Molecular plant*, 14(8), 1362.

Castillo MC, et al. (2021) NIN-like protein7 and PROTEOLYSIS6 functional interaction enhances tolerance to sucrose, ABA, and submergence. *Plant physiology*, 187(4), 2731.

Fan T, et al. (2021) Accessible chromatin reveals regulatory mechanisms underlying cell fate decisions during early embryogenesis. *Scientific reports*, 11(1), 7896.

Savadel SD, et al. (2021) The native cistrome and sequence motif families of the maize ear. *PLoS genetics*, 17(8), e1009689.

Hishinuma-Silva SM, et al. (2020) The soybean gene GmHsp22.4 is involved in the resistance response to *Meloidogyne javanica* in *Arabidopsis thaliana*. *BMC plant biology*, 20(1), 535.

Ramos RS, et al. (2020) Ribosomal Protein RPL10A Contributes to Early Plant Development and Absciscic Acid-Dependent Responses in Arabidopsis. *Frontiers in plant science*, 11, 582353.

Andreeva AA, et al. (2020) Cytokinin-Regulated Expression of Arabidopsis thaliana PAP Genes and Its Implication for the Expression of Chloroplast-Encoded Genes. *Biomolecules*, 10(12).

Andrási N, et al. (2019) The mitogen-activated protein kinase 4-phosphorylated heat shock factor A4A regulates responses to combined salt and heat stresses. *Journal of experimental botany*, 70(18), 4903.

Da L, et al. (2019) AppleMDO: A Multi-Dimensional Omics Database for Apple Co-Expression Networks and Chromatin States. *Frontiers in plant science*, 10, 1333.

Tsitsekian D, et al. (2019) Comprehensive analysis of Lon proteases in plants highlights independent gene duplication events. *Journal of experimental botany*, 70(7), 2185.

Penning BW, et al. (2019) Expression profiles of cell-wall related genes vary broadly between two common maize inbreds during stem development. *BMC genomics*, 20(1), 785.

Kovács H, et al. (2019) Light Control of Salt-Induced Proline Accumulation Is Mediated by ELONGATED HYPOCOTYL 5 in Arabidopsis. *Frontiers in plant science*, 10, 1584.

Kulkarni SR, et al. (2018) TF2Network: predicting transcription factor regulators and gene regulatory networks in Arabidopsis using publicly available binding site information. *Nucleic acids research*, 46(6), e31.

Liu Y, et al. (2018) PCSD: a plant chromatin state database. *Nucleic acids research*, 46(D1), D1157.

Qi H, et al. (2018) PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. *Genomics, proteomics & bioinformatics*, 16(4), 283.

Ahmed MB, et al. (2018) A rust fungal effector binds plant DNA and modulates transcription. *Scientific reports*, 8(1), 14718.