

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## Arabidopsis Hormone Database

RRID:SCR\_001792

Type: Tool

### Proper Citation

Arabidopsis Hormone Database (RRID:SCR\_001792)

### Resource Information

**URL:** <http://ahd.cbi.pku.edu.cn>

**Proper Citation:** Arabidopsis Hormone Database (RRID:SCR\_001792)

**Description:** Database providing a systematic and comprehensive view of morphological phenotypes regulated by plant hormones, as well as regulatory genes participating in numerous plant hormone responses. By integrating the data from mutant studies, transgenic analysis and gene ontology annotation, genes related to the stimulus of eight plant hormones were identified, including abscisic acid, auxin, brassinosteroid, cytokinin, ethylene, gibberellin, jasmonic acid and salicylic acid. Another pronounced characteristics of this database is that a phenotype ontology was developed to precisely describe all kinds of morphological processes regulated by plant hormones with standardized vocabularies. To increase the coverage of phytohormone related genes, the database has been updated from AHD to AHD2.0 adding and integrating several pronounced features: (1) added 291 newly published Arabidopsis hormone related genes as well as corrected information (e.g. the arguable ABA receptors) based on the recent 2-year literature; (2) integrated orthologues of sequenced plants in OrthoMCLDB into each gene in the database; (3) integrated predicted miRNA splicing site in each gene in the database; (4) provided genetic relationship of these phytohormone related genes mining from literature, which represents the first effort to construct a relatively comprehensive and complex network of hormone related genes as shown in the home page of our database; (5) In convenience to in-time bioinformatics analysis, they also provided links to a powerful online analysis platform Weblab that they have recently developed, which will allow users to readily perform various sequence analysis with these phytohormone related genes retrieved from AHD2.0; (6) provided links to other protein databases as well as more expression profiling information that would facilitate users for a more systematic analysis related to phytohormone research. Please help to improve the database with your contributions.

**Abbreviations:** AHD, AHD2.0

**Synonyms:** Arabidopsis Hormone Database 2.0

**Resource Type:** controlled vocabulary, data or information resource, data repository, database, ontology, service resource, storage service resource

**Defining Citation:** [PMID:21045062](#), [PMID:19015126](#)

**Keywords:** arabidopsis thaliana, hormone, hormone function, hormone gene, phytohormone, abscisic acid, auxin, brassinosteroid, cytokinin, ethylene, gibberellin, jasmonic acid, salicylic acid, microarray, phenotype, gene, mirna prediction, expression, mutant, blast, orthologue, mirna splicing site, root, cotyledon, leaf, hypocotyl, stem, flower, silique, seed, embryo, stress, morphology, plant, hormone, regulatory gene, mutant, transgenic, annotation, data analysis service

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National Natural Science Foundation of China 30730011;  
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**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Arabidopsis Hormone Database

**Resource ID:** SCR\_001792

**Alternate IDs:** nif-0000-02559

**Record Creation Time:** 20220129T080209+0000

**Record Last Update:** 20260905T132439+0000

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## Ratings and Alerts

No rating or validation information has been found for Arabidopsis Hormone Database.

No alerts have been found for Arabidopsis Hormone Database.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Ai Y, et al. (2023) Uncovering early transcriptional regulation during adventitious root formation in *Medicago sativa*. *BMC plant biology*, 23(1), 176.

Lei L, et al. (2022) Transcriptome Analysis of Early Senescence in the Post-Anthesis Flag Leaf of Wheat (*Triticum aestivum* L.). *Plants* (Basel, Switzerland), 11(19).

- Song M, et al. (2022) Genome-wide analysis of JAZ family genes expression patterns during fig (*Ficus carica* L.) fruit development and in response to hormone treatment. *BMC genomics*, 23(1), 170.
- Zhang Y, et al. (2019) Comprehensive analysis of dynamic gene expression and investigation of the roles of hydrogen peroxide during adventitious rooting in poplar. *BMC plant biology*, 19(1), 99.
- Huang J, et al. (2018) Transcriptome analysis of nitric oxide-responsive genes in upland cotton (*Gossypium hirsutum*). *PloS one*, 13(3), e0192367.
- Zhang H, et al. (2018) Transcriptome characterization of moso bamboo (*Phyllostachys edulis*) seedlings in response to exogenous gibberellin applications. *BMC plant biology*, 18(1), 125.
- Jian H, et al. (2018) Integrated mRNA, sRNA, and degradome sequencing reveal oilseed rape complex responses to *Sclerotinia sclerotiorum* (Lib.) infection. *Scientific reports*, 8(1), 10987.
- Prasad KVSK, et al. (2018) Vascular Plant One-Zinc-Finger (VOZ) Transcription Factors Are Positive Regulators of Salt Tolerance in Arabidopsis. *International journal of molecular sciences*, 19(12).
- Hande AS, et al. (2017) Transcript profiling of genes expressed during fibre development in diploid cotton (*Gossypium arboreum* L.). *BMC genomics*, 18(1), 675.
- Gupta A, et al. (2017) Global profiling of phytohormone dynamics during combined drought and pathogen stress in *Arabidopsis thaliana* reveals ABA and JA as major regulators. *Scientific reports*, 7(1), 4017.
- Jian H, et al. (2017) Screening of Candidate Leaf Morphology Genes by Integration of QTL Mapping and RNA Sequencing Technologies in Oilseed Rape (*Brassica napus* L.). *PloS one*, 12(1), e0169641.
- Dai X, et al. (2016) HRGRN: A Graph Search-Empowered Integrative Database of Arabidopsis Signaling Transduction, Metabolism and Gene Regulation Networks. *Plant & cell physiology*, 57(1), e12.
- Shah JN, et al. (2016) Depletion of Key Meiotic Genes and Transcriptome-Wide Abiotic Stress Reprogramming Mark Early Preparatory Events Ahead of Apomeiotic Transition. *Frontiers in plant science*, 7, 1539.
- Kumar S, et al. (2016) Genome-wide transcriptomic and proteomic analyses of bollworm-infested developing cotton bolls revealed the genes and pathways involved in the insect pest defence mechanism. *Plant biotechnology journal*, 14(6), 1438.
- Li D, et al. (2016) Gene expression analysis and SNP/InDel discovery to investigate yield heterosis of two rubber tree F1 hybrids. *Scientific reports*, 6, 24984.
- Simm S, et al. (2016) Survey of Genes Involved in Biosynthesis, Transport, and Signaling of Phytohormones with Focus on *Solanum lycopersicum*. *Bioinformatics and biology insights*, 10, 185.

Yue X, et al. (2016) The Arabidopsis phytohormone crosstalk network involves a consecutive metabolic route and circular control units of transcription factors that regulate enzyme-encoding genes. *BMC systems biology*, 10(1), 87.

Hung CY, et al. (2016) Gibberellin deficiency is responsible for shy-flowering nature of *Epipremnum aureum*. *Scientific reports*, 6, 28598.

Sun P, et al. (2015) Dynamic transcriptional profiling provides insights into tuberous root development in *Rehmannia glutinosa*. *Frontiers in plant science*, 6, 396.

Lin M, et al. (2015) Global analysis of the *Gossypium hirsutum* L. Transcriptome during leaf senescence by RNA-Seq. *BMC plant biology*, 15, 43.