

Resource Summary Report

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Phytozome

RRID:SCR_006507

Type: Tool

Proper Citation

Phytozome (RRID:SCR_006507)

Resource Information

URL: <http://www.phytozome.net/>

Proper Citation: Phytozome (RRID:SCR_006507)

Description: A comparative platform for green plant genomics. Families of orthologous and paralogous genes that represent the modern descendents of ancestral gene sets are constructed at key phylogenetic nodes. These families allow easy access to clade specific orthology / paralogy relationships as well as clade specific genes and gene expansions. As of release v9.1, Phytozome provides access to forty-one sequenced and annotated green plant genomes which have been clustered into gene families at 20 evolutionarily significant nodes. Where possible, each gene has been annotated with PFAM, KOG, KEGG, and PANTHER assignments, and publicly available annotations from RefSeq, UniProt, TAIR, JGI are hyper-linked and searchable., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Phytozome

Resource Type: service resource, data analysis service, database, analysis service resource, production service resource, data or information resource

Defining Citation: [PMID:22110026](#)

Keywords: genome, genomics, plant, green plant, cluster sequence, alignment, gene, node, cluster, blast, blat, biomart, peptide homolog, gene ancestry, sequence, annotation, gene structure, gene family, genome organization, comparative genomics, physiology, comparative, bio.tools, FASEB list

Funding: Gordon and Betty Moore Foundation ;
DOE DE-AC02-05CH11231

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Phytozome

Resource ID: SCR_006507

Alternate IDs: biotools:phytozome, nlx_151490, r3d100010850

Alternate URLs: <https://bio.tools/phytozome>, <https://doi.org/10.17616/R38021>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260728T043234+0000

Ratings and Alerts

No rating or validation information has been found for Phytozome.

No alerts have been found for Phytozome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3108 mentions in open access literature.

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

Dramé D, et al. (2026) Genetic architecture of cowpea domestication: QTL mapping and comparison shed new light on the dual domestication events. *G3* (Bethesda, Md.), 16(1).

Hata Y, et al. (2025) snRNA-seq analysis of the moss *Physcomitrium patens* identifies a conserved cytokinin-ESR module promoting pluripotent stem cell identity. *Developmental cell*, 60(13), 1884.

Lang J, et al. (2025) Complexome profiling of the *Chlamydomonas* psb28 mutant reveals TEF5 as an early PSII assembly factor. *The Plant cell*, 37(6).

Gu H, et al. (2025) Genome-wide analysis and functional validation of the cotton FAH gene family for salt stress. *BMC genomics*, 26(1), 271.

Shu J, et al. (2025) The chromosome-level genome assembly of Broad-Leaf Fern (*Dipteris shenzhenensis*). *Scientific data*, 12(1), 475.

Li X, et al. (2025) Characterization of fatty acid desaturase gene family in *Glycine max* and their expression patterns in seeds after *Fusarium fujikuroi* infection. *Frontiers in plant science*, 16, 1540003.

Wang M, et al. (2025) Genome-wide characterization and expression profiling of the TGA gene family in sweet orange (*Citrus sinensis*) reveal CsTGA7 responses to multiple phytohormones and abiotic stresses. *Frontiers in plant science*, 16, 1530242.

Wu N, et al. (2025) Genome-wide identification and expression analysis of soybean bHLH transcription factor and its molecular mechanism on grain protein synthesis. *Frontiers in plant science*, 16, 1481565.

Jin F, et al. (2025) Suppression of Nodule Formation by RNAi Knock-Down of Bax inhibitor-1a in *Lotus japonicus*. *Genes*, 16(1).

Qian X, et al. (2025) The Potassium Utilization Gene Network in *Brassica napus* and Functional Validation of BnaZSHAK5.2 Gene in Response to Potassium Deficiency. *International journal of molecular sciences*, 26(2).

Luo Y, et al. (2025) Characterization and functional analysis of conserved non-coding sequences among poaceae: insights into gene regulation and phenotypic variation in maize. *BMC genomics*, 26(1), 46.

Hochmuth A, et al. (2025) Distinct effects of PTST2b and MRC on starch granule morphogenesis in potato tubers. *Plant biotechnology journal*, 23(2), 412.

Tian Y, et al. (2025) Genome-wide identification, phylogeny, and expression analysis of PEBP gene family in *Castanea mollissima*. *Frontiers in genetics*, 16, 1530910.

Yolcu S, et al. (2025) Deciphering melatonin biosynthesis pathway in *Chenopodium quinoa*: genome-wide analysis and expression levels of the genes under salt and drought. *Planta*, 262(1), 23.

Contreras E, et al. (2025) Regulation of HvASN1 expression by bZIP transcription factors during barley embryo development and germination. *Planta*, 262(1), 20.

Garg V, et al. (2025) An Australian chickpea pan-genome provides insights into genome organization and offers opportunities for enhancing drought adaptation for crop improvement. *Plant biotechnology journal*, 23(9), 3967.

Fang J, et al. (2025) Integrated multi-omics analysis unravels the floral scent characteristics and regulation in "Hutou" multi-petal jasmine. *Communications biology*, 8(1), 256.

Khaskhali S, et al. (2025) Expression profile and characterization of respiratory burst oxidase homolog genes in rice under MeJA, SA and Xoo treatments. *Scientific reports*, 15(1), 5936.

Le TT, et al. (2025) Cas9-mediated gene-editing frequency in microalgae is doubled by harnessing the interaction between importin α and phytopathogenic NLSs. *Proceedings of the National Academy of Sciences of the United States of America*, 122(10), e2415072122.

Bertolini E, et al. (2025) Regulatory variation controlling architectural pleiotropy in maize. *Nature communications*, 16(1), 2140.