

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: analysis service resource, data analysis service, data or information resource, database, production service resource, service 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: 20260905T132555+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 3189 mentions in open access literature.

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

Tian X, et al. (2026) A GLUTAMATE CYSTEINE LIGASE Gene StGSH1 Regulated by StERF10 Enhanced Glutathione Accumulation and Adaptation to Low Phosphorus Stress in Potato. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(8), e09143.

Gandhadmath SS, et al. (2026) Genome-wide exploration of bacterial leaf blight resistance and fine mapping of major resistance gene (Bb13) in upland cotton (*Gossypium hirsutum* L.). *The plant genome*, 19(1), e70214.

Ren J, et al. (2026) Comparative analysis of seven types of phosphate transporters in forty species from the phylogenetic and transcriptomic perspective. *PLoS one*, 21(5), e0349574.

Li Z, et al. (2026) Comparative proteomics analysis of wild and cultivated accessions reveals key candidate proteins associated with seed weight variations in peanut. *BMC plant biology*, 26(1).

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).

de Souza SCR, et al. (2026) Urease-null soybean (eu3-a) under salt and copper stress: nitrogen metabolism, antioxidant defense, and arginine pathway genes. *Planta*, 263(5).

Li Y, et al. (2026) Genome-wide identification and functional analysis of the SAMS gene family in peanut reveal the role of Ah6Q1KS5 in resistance to bacterial wilt. *BMC plant biology*, 26(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.

Shen Y, et al. (2025) Genome-wide identification and analysis of phosphate utilization related genes (PURs) reveal their roles involved in low phosphate responses in *Brassica napus* L. *BMC plant biology*, 25(1), 326.

Liu Z, et al. (2025) Genome-wide identification of GmEDS1 gene family members in soybean and expression analysis in response to biotic and abiotic stresses. *Frontiers in plant science*, 16, 1554399.

Huang S, et al. (2025) Genome-wide identification and characterization of Ethylene-Insensitive 3 (EIN3/EIL) gene family in *Camellia oleifera*. *PloS one*, 20(5), e0324651.

Pan M, et al. (2025) Study on physiological changes and response mechanism of *Cerasus humilis* under alkali stress. *Frontiers in plant science*, 16, 1586093.

Liu J, et al. (2025) Genomic and biochemical comparison of allelic triple-mutant lines derived from conventional breeding and multiplex gene editing. *The plant genome*, 18(2), e70056.

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.

Chen Z, et al. (2025) Genome-wide identification and expression analysis of ACS and ACO gene family in *Ziziphus jujuba* mill during fruit ripening. *Scientific reports*, 15(1), 18106.

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.

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.

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.