

# Resource Summary Report

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

## 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 [Kravitz](#) .

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).

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).

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).

- 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.
- Hochmuth A, et al. (2025) Distinct effects of PTST2b and MRC on starch granule morphogenesis in potato tubers. *Plant biotechnology journal*, 23(2), 412.
- Jin F, et al. (2025) Suppression of Nodule Formation by RNAi Knock-Down of Bax inhibitor-1a in *Lotus japonicus*. *Genes*, 16(1).
- Gou C, et al. (2025) Genome wide identification of Dof transcription factors in Carmine radish reveals RsDof33 role in cadmium stress and anthocyanin biosynthesis. *Scientific reports*, 15(1), 4766.
- Le TT, et al. (2025) Cas9-mediated gene-editing frequency in microalgae is doubled by harnessing the interaction between importin  $\alpha$  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.
- 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.
- 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.
- Hoh D, et al. (2025) From quantitative trait loci towards mechanisms: Linkage Integration Hypothesis Testing (LIgHT) sheds light on the mechanisms of genetically modulated stress tolerance. *Journal of experimental botany*, 76(20), 5964.
- Hanba YT, et al. (2025) First contact with greater gravity: Moss plants adapted via enhanced photosynthesis mediated by AP2/ERF transcription factors. *Science advances*, 11(29), eado8664.
- Torres I, et al. (2025) MINE: maximally informative next experiment-toward a new GWAS experimental design and methodology. *G3 (Bethesda, Md.)*, 15(9).
- 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.