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.

Abbreviations: Phytozome

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

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Resource Name: Phytozome

Resource ID: SCR_006507

Alternate IDs: biotools:phytozome, nlx_151490

Alternate URLs: https://bio.tools/phytozome

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250519T203439+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 2979 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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.

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).

Wang Y, et al. (2025) Identification of the CaCRT gene family and function of CaCRT1 under low-temperature stress in pepper (Capsicum annuum L.). Scientific reports, 15(1), 90.

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton

antiporter (CPA) gene family in rice (Oryza sativa L.) and their expression profiles in response to phytohormones. PloS one, 20(1), e0317008.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (Eleusine indica). Scientific data, 12(1), 156.

Horn A, et al. (2025) Transcriptional and functional characterization in the terpenoid precursor pathway of the early land plant Physcomitrium patens. Plant biology (Stuttgart, Germany), 27(1), 29.

Lai G, et al. (2025) CRISPR/Cas9-mediated CHS2 mutation provides a new insight into resveratrol biosynthesis by causing a metabolic pathway shift from flavonoids to stilbenoids in Vitis davidii cells. Horticulture research, 12(1), uhae268.

Li S, et al. (2025) Genome-Wide Identification and Expression Analysis Under Abiotic Stress of the Lipoxygenase Gene Family in Maize (Zea mays). Genes, 16(1).

Liang X, et al. (2025) Genome-Wide Identification of GmPIF Family and Regulatory Pathway Analysis of GmPIF3g in Different Temperature Environments. International journal of molecular sciences, 26(2).

Anwar A, et al. (2025) Genome-wide identification of MGT gene family in soybean (Glycine max) and their expression analyses under magnesium stress conditions. BMC plant biology, 25(1), 83.

Mohammed SB, et al. (2025) Quantitative Trait Loci for Phenology, Yield, and Phosphorus Use Efficiency in Cowpea. Genes, 16(1).

Santhoshi Y, et al. (2025) Comprehensive Analysis of the NHX Gene Family and Its Regulation Under Salt and Drought Stress in Quinoa (Chenopodium quinoa Willd.). Genes, 16(1).

Rizwan HM, et al. (2025) The members of zinc finger-homeodomain (ZF-HD) transcription factors are associated with abiotic stresses in soybean: insights from genomics and expression analysis. BMC plant biology, 25(1), 56.

Zou Y, et al. (2025) ATG8 delipidation is not universally critical for autophagy in plants. Nature communications, 16(1), 403.

López CM, et al. (2025) CRISPR/Cas9 editing of two adenine phosphoribosyl transferase coding genes reveals the functional specialization of adenine salvage proteins in common bean. Journal of experimental botany, 76(2), 346.

Enyew M, et al. (2025) Genome-wide association study and genomic prediction of root system architecture traits in Sorghum (Sorghum bicolor (L.) Moench) at the seedling stage. BMC plant biology, 25(1), 69.

Wang Y, et al. (2025) ZmNF-YB10, a maize NF-Y transcription factor, positively regulates drought and salt stress response in Arabidopsis thaliana. GM crops & food, 16(1), 28.

Mukuze C, et al. (2025) Genome-wide association mapping of bruchid resistance loci in soybean. PloS one, 20(1), e0292481.