Phytozome
RRID:SCR_006507
Type: Tool

Proper Citation

Phytozome (RRID:SCR_006507)

Resource Information

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

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

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 Agency: Gordon and Betty Moore Foundation, DOE

Resource Name: Phytozome
Resource ID: SCR_006507
Alternate IDs: nlx_151490, biotools:phytozome
Alternate URLs: https://bio.tools/phytozome

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 2649 mentions in open access literature.

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


Weits DA, et al. (2023) Acquisition of hypoxia inducibility by oxygen sensing N-terminal cysteine oxidase in spermatophytes. Plant, cell & environment, 46(1), 322.


Ma G, et al. (2023) Molecular characterization of a flavanone 3-hydroxylase gene from citrus fruit reveals its crucial roles in anthocyanin accumulation. BMC plant biology, 23(1), 233.


Su SH, et al. (2023) Brachypodium distachyon Seedlings Display Accession-Specific Morphological and Transcriptomic Responses to the Microgravity Environment of the International Space Station. Life (Basel, Switzerland), 13(3).
Craig RJ, et al. (2023) The Chlamydomonas Genome Project, version 6: Reference assemblies for mating-type plus and minus strains reveal extensive structural mutation in the laboratory. The Plant cell, 35(2), 644.


Zhang L, et al. (2023) GWAS of grain color and tannin content in Chinese sorghum based on whole-genome sequencing. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 136(4), 77.


Nazipova A, et al. (2023) The In Silico Characterization of Monocotyledonous ?-l-Arabinofuranosidases on the Example of Maize. Life (Basel, Switzerland), 13(2).

Kim CY, et al. (2023) Emergence of a proton exchange-based isomerization and lactonization mechanism in the plant coumarin synthase COSY. Nature communications, 14(1), 597.

Cao Y, et al. (2023) Large-scale analysis of putative Euphorbiaceae R2R3-MYB transcription factors identifies a MYB involved in seed oil biosynthesis. BMC plant biology, 23(1), 145.