Resource Summary Report

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PLEXdb - Plant Expression Database

RRID:SCR_006963
Type: Tool

Proper Citation

PLEXdb - Plant Expression Database (RRID:SCR_006963)

Resource Information

URL: http://www.plexdb.org/index.php

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Description: PLEXdb (Plant Expression Database) is a unified gene expression resource for plants and plant pathogens. PLEXdb is a genotype to phenotype, hypothesis building information warehouse, leveraging highly parallel expression data with seamless portals to related genetic, physical, and pathway data. The integrated tools of PLEXdb allow investigators to use commonalities in plant biology for a comparative approach to functional genomics through use of large-scale expression profiling data sets.

Abbreviations: PLEXdb

Synonyms: PLEXdb - Gene expression resources for plants and plant pathogens, Plant Expression Database

Resource Type: service resource, production service resource, data analysis service, database, topical portal, analysis service resource, data or information resource, portal, storage service resource, data repository

Defining Citation: PMID:22084198

Keywords: gene expression, plant, plant pathogen, genotype, phenotype, genetic, physical, pathway, plant biology, compare, functional genomics, expression profiling, expression atlas, pathogen, genome, anova, cluster, bio.tools

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Resource Name: PLEXdb - Plant Expression Database

Resource ID: SCR_006963

Alternate IDs: biotools:plexdb, nlx_149236

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

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250519T204321+0000

Ratings and Alerts

No rating or validation information has been found for PLEXdb - Plant Expression Database.

No alerts have been found for PLEXdb - Plant Expression Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Su Y, et al. (2020) GhCIPK6a increases salt tolerance in transgenic upland cotton by involving in ROS scavenging and MAPK signaling pathways. BMC plant biology, 20(1), 421.

Li F, et al. (2020) Genome-wide analysis of the AREB/ABF gene lineage in land plants and functional analysis of TaABF3 in Arabidopsis. BMC plant biology, 20(1), 558.

Hong WJ, et al. (2019) Infrastructures of systems biology that facilitate functional genomic study in rice. Rice (New York, N.Y.), 12(1), 15.

Zhao M, et al. (2018) Molecular Evolution and Expression Divergence of HMT Gene Family in Plants. International journal of molecular sciences, 19(4).

Zhao M, et al. (2018) Molecular evolution and expression divergence of three key Met biosynthetic genes in plants: CGS, HMT and MMT. PeerJ, 6, e6023.

Zhang H, et al. (2018) Molecular characterization of the TaWTG1 in bread wheat (Triticum aestivum L.). Gene, 678, 23.

Guo XJ, et al. (2017) Global identification, structural analysis and expression characterization of bHLH transcription factors in wheat. BMC plant biology, 17(1), 90.

Feng G, et al. (2017) Evolution of the 3R-MYB Gene Family in Plants. Genome biology and evolution, 9(4), 1013.

Yamasaki Y, et al. (2017) Seed maturation associated transcriptional programs and regulatory networks underlying genotypic difference in seed dormancy and size/weight in wheat (Triticum aestivum L.). BMC plant biology, 17(1), 154.

Li M, et al. (2016) Evolution and Functional Insights of Different Ancestral Orthologous Clades of Chitin Synthase Genes in the Fungal Tree of Life. Frontiers in plant science, 7, 37.

Ren C, et al. (2016) Genome-wide identification and characterization of the NF-Y gene family in grape (vitis vinifera L.). BMC genomics, 17(1), 605.

Du H, et al. (2016) Genome-Wide Analysis, Classification, Evolution, and Expression Analysis of the Cytochrome P450 93 Family in Land Plants. PloS one, 11(10), e0165020.

Li Y, et al. (2016) Application of Glycerol for Induced Powdery Mildew Resistance in Triticum aestivum L. Frontiers in physiology, 7, 413.

Daigle C, et al. (2015) Genome-wide analysis of MAPKKKs shows expansion and evolution of a new MEKK class involved in solanaceous species sexual reproduction. BMC genomics, 16, 1037.

D'Orso F, et al. (2015) Conservation of AtTZF1, AtTZF2, and AtTZF3 homolog gene regulation by salt stress in evolutionarily distant plant species. Frontiers in plant science, 6, 394.

Sun T, et al. (2015) Identification and comprehensive analyses of the CBL and CIPK gene families in wheat (Triticum aestivum L.). BMC plant biology, 15, 269.

Xu Y, et al. (2014) SoyFN: a knowledge database of soybean functional networks. Database : the journal of biological databases and curation, 2014, bau019.

Zhao Z, et al. (2014) Correction: Comparative analysis of fungal genomes reveals different plant cell wall degrading capacity in fungi. BMC genomics, 15, 6.

Chen Y, et al. (2014) Comparative genomic analysis of the Sm gene family in rice and maize. Gene, 539(2), 238.

Liu X, et al. (2010) A network approach to predict pathogenic genes for Fusarium graminearum. PloS one, 5(10).