

Resource Summary Report

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ChromDB- the chromatin database

RRID:SCR_007597

Type: Tool

Proper Citation

ChromDB- the chromatin database (RRID:SCR_007597)

Resource Information

URL: <http://www.chromdb.org>

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Description: ChromDB is a chromatin database. Three types of sequences are included in the database: genomic-based (predominantly plant sequences); transcript-based (EST contigs or cDNAs for plants lacking a sequenced genome); and NCBI RefSeq sequences for a variety of model animal organisms. The Gene Record Page for any sequence indicates the type of sequence. The broad mission of ChromDB is display, annotate, and curate sequences of two broad functional classes of biologically important proteins: chromatin-associated proteins (CAPs) and RNA interference-associated proteins. Plant proteins are the major focus of the work supported by The Plant Genome Research Program (PGRP) of the National Science Foundation. Our intent is to produce intensively curated sequence information and make it available to the research and teaching community in support of comparative analyses toward understanding the chromatin proteome in plants, especially in important crop species. In order to do a comparative analysis, it is necessary to include non-plant proteins in the database. Non-plant genes are not curated to the degree carried out for plants and to automate the process of data import, our non-plant genes are from the RefSeq database of NCBI. We reason that the inclusion of non-plant, model organisms will broaden the relevance and usefulness of ChromDB to the entire chromatin community and will provide a more complete data set for phylogenetic analyses in support of the evolution of the plant chromatin proteome. ChromDB is funded by a grant from the National Science Foundation Plant Genome Research Project(#DBI-0421679).

Synonyms: ChromDB

Resource Type: data or information resource, database

Keywords: chromatin, chromatin-associated protein, crop species chromatin, plant chromatin proteome, plant protein, rna interference-associated proteins, FASEB list

Resource Name: ChromDB- the chromatin database

Resource ID: SCR_007597

Alternate IDs: nif-0000-02661

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260912T200148+0000

Ratings and Alerts

No rating or validation information has been found for ChromDB- the chromatin database.

No alerts have been found for ChromDB- the chromatin database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Zhang L, et al. (2023) MoJMJD6, a Nuclear Protein, Regulates Conidial Germination and Appressorium Formation at the Early Stage of Pathogenesis in *Magnaporthe oryzae*. The plant pathology journal, 39(4), 361.

Da L, et al. (2023) RoseAP: an analytical platform for gene function of *Rosa rugosa*. Frontiers in plant science, 14, 1197119.

Chao J, et al. (2023) Genomic insight into domestication of rubber tree. Nature communications, 14(1), 4651.

Hussain A, et al. (2022) N-Methyltransferase CaASHH3 Acts as a Positive Regulator of Immunity against Bacterial Pathogens in Pepper. International journal of molecular sciences, 23(12).

Shang FH, et al. (2021) Identification of grape H3K4 genes and their expression profiles during grape fruit ripening and postharvest ROS treatment. Genomics, 113(6), 3793.

Fang H, et al. (2021) Reprogramming of Histone H3 Lysine Methylation During Plant Sexual Reproduction. Frontiers in plant science, 12, 782450.

Jiang S, et al. (2020) Methylation of MdMYB1 locus mediated by RdDM pathway regulates anthocyanin biosynthesis in apple. Plant biotechnology journal, 18(8), 1736.

Shahmir F, et al. (2020) Identification, Gene Structure, and Expression of BnMicEmUP: A Gene Upregulated in Embryogenic *Brassica napus* Microspores. Frontiers in plant science, 11, 576008.

Zhang D, et al. (2019) Identification and Expression Analysis of Snf2 Family Proteins in Tomato (*Solanum lycopersicum*). *International journal of genomics*, 2019, 5080935.

Guo T, et al. (2019) Mutations in the Rice OsCHR4 Gene, Encoding a CHD3 Family Chromatin Remodeler, Induce Narrow and Rolled Leaves with Increased Cuticular Wax. *International journal of molecular sciences*, 20(10).

Jiang S, et al. (2019) MdGSTF6, activated by MdMYB1, plays an essential role in anthocyanin accumulation in apple. *Horticulture research*, 6, 40.

Xiang J, et al. (2017) Transcriptomic Analysis of Gibberellin- and Paclobutrazol-Treated Rice Seedlings under Submergence. *International journal of molecular sciences*, 18(10).

Huh A, et al. (2017) MoJMJ1, Encoding a Histone Demethylase Containing JmjC Domain, Is Required for Pathogenic Development of the Rice Blast Fungus, *Magnaporthe oryzae*. *The plant pathology journal*, 33(2), 193.

Yu X, et al. (2016) The Core Subunit of A Chromatin-Remodeling Complex, ZmCHB101, Plays Essential Roles in Maize Growth and Development. *Scientific reports*, 6, 38504.

Huber M, et al. (2016) A Latex Metabolite Benefits Plant Fitness under Root Herbivore Attack. *PLoS biology*, 14(1), e1002332.

Michniewicz M, et al. (2015) Gateway-compatible tissue-specific vectors for plant transformation. *BMC research notes*, 8, 63.

J??gu T, et al. (2015) A SWI/SNF Chromatin Remodelling Protein Controls Cytokinin Production through the Regulation of Chromatin Architecture. *PloS one*, 10(10), e0138276.

Xu J, et al. (2015) Genome-wide identification of sweet orange (*Citrus sinensis*) histone modification gene families and their expression analysis during the fruit development and fruit-blue mold infection process. *Frontiers in plant science*, 6, 607.

Dubin MJ, et al. (2015) DNA methylation in *Arabidopsis* has a genetic basis and shows evidence of local adaptation. *eLife*, 4, e05255.

Shi J, et al. (2014) Epigenetic regulation of rice flowering and reproduction. *Frontiers in plant science*, 5, 803.