

Resource Summary Report

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Comprehensive Systems-Biology Database

RRID:SCR_008185

Type: Tool

Proper Citation

Comprehensive Systems-Biology Database (RRID:SCR_008185)

Resource Information

URL: <http://csbdb.mpimp-golm.mpg.de/>

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Description: CSB.DB presents the results of bio-statistical analysis on gene expression data in association with additional biochemical and physiological knowledge. The main aim of this database platform is to provide tools that support insight into life's complexity pyramid with a special focus on the integration of data from transcript and metabolite profiling experiments. The main focus of the CSB project is the generation of new easily accessible knowledge about the relationship and the hierarchy of cellular components. Thus new progress towards understanding life's complexity pyramid is made. For this aim statistical and computational algorithms are applied to organism specific data derived from publicly available multi-parallel technologies, currently such as expression profiles. The underlying data are derived from various research activities. Thus CSB project provides an integrated and centralized public resource allowing universal access on the generated knowledge CSB.DB: A Comprehensive Systems-Biology Database. The derived knowledge should support the formulation of new hypotheses about the respective functional involvement of genes beyond their (inter-) relationships. Another major goal of the CSB project is to supply the researchers with necessary information to formulate these new hypotheses without demanding any a-priori statistical knowledge of the user. The CSB project mainly focuses on application of required statistical tests as well as to assist the user during exploration of results with information / help files to support hypothesis generation

Synonyms: CSB.DB

Resource Type: database, data or information resource

Keywords: expression, gene, generation, algorithm, arabidopsis thaliana databases, biochemical, biology, bio-statistical, cellular, compound, computational, hierarchy, metabolite, organism, physiological, plant, system, transcript

Resource Name: Comprehensive Systems-Biology Database

Resource ID: SCR_008185

Alternate IDs: nif-0000-21102

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260808T190420+0000

Ratings and Alerts

No rating or validation information has been found for Comprehensive Systems-Biology Database.

No alerts have been found for Comprehensive Systems-Biology Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Shahzad R, et al. (2021) β -Sitosterol differentially regulates key metabolites for growth improvement and stress tolerance in rice plants during prolonged UV-B stress. Journal, genetic engineering & biotechnology, 19(1), 79.

Bustamante MA, et al. (2019) The effect of anaerobic digestate derived composts on the metabolite composition and thermal behaviour of rosemary. Scientific reports, 9(1), 6489.

de Marcos Lousa C, et al. (2016) Subcellular localization and trafficking of phytolongins (non-SNARE longins) in the plant secretory pathway. Journal of experimental botany, 67(9), 2627.

Zhao X, et al. (2014) Comparative metabolite profiling of two rice genotypes with contrasting salt stress tolerance at the seedling stage. PloS one, 9(9), e108020.

Provart N, et al. (2012) Correlation networks visualization. Frontiers in plant science, 3, 240.

Junker A, et al. (2012) Visual analysis of transcriptome data in the context of anatomical structures and biological networks. Frontiers in plant science, 3, 252.

Mönke G, et al. (2012) Toward the identification and regulation of the Arabidopsis thaliana ABI3 regulon. Nucleic acids research, 40(17), 8240.

van Verk MC, et al. (2011) Prospecting for genes involved in transcriptional regulation of plant defenses, a bioinformatics approach. BMC plant biology, 11, 88.

Carroll AJ, et al. (2010) The MetabolomeExpress Project: enabling web-based processing, analysis and transparent dissemination of GC/MS metabolomics datasets. *BMC bioinformatics*, 11, 376.

Hehl R, et al. (2008) Internet Resources for Gene Expression Analysis in *Arabidopsis thaliana*. *Current genomics*, 9(6), 375.

Mustroph A, et al. (2007) Characterisation of the ATP-dependent phosphofructokinase gene family from *Arabidopsis thaliana*. *FEBS letters*, 581(13), 2401.