Resource Summary Report

Generated by RRID on Apr 18, 2025

GRASSIUS

RRID:SCR_012999
Type: Tool

Proper Citation

GRASSIUS (RRID:SCR_012999)

Resource Information

URL: http://grassius.org/

Proper Citation: GRASSIUS (RRID:SCR_012999)

Description: A public resource composed of a collection of databases, computational and experimental resources that relate to the control of gene expression in the grasses, and their relationship with agronomic traits. As knowledge on the interactions of transcription factors (TFs) and cis-regulatory elements in the promoters of the genes that they regulate continues to accumulate, the information is acquired by GRASSIUS, either through contributions by the community, or by literature analysis. The overarching objective of GRASSIUS is to provide a one-stop resource that will facilitate research and communication within the plant community with regards to genome-wide regulation of gene expression processes.

Abbreviations: GRASSIUS

Synonyms: Grass Regulatory Information Server

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

Defining Citation: PMID:18987217

Keywords: transcription factor, coregulator, promoter sequence, transcription factor orf clone, blast, genome browser

Funding: NSF

Availability: Free

Resource Name: GRASSIUS

Resource ID: SCR_012999

Alternate IDs: OMICS_00555

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250418T055333+0000

Ratings and Alerts

No rating or validation information has been found for GRASSIUS.

No alerts have been found for GRASSIUS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Xu H, et al. (2024) Identification of key genes for triacylglycerol biosynthesis and storage in herbaceous peony (Paeonia lactifolra Pall.) seeds based on full-length transcriptome. BMC genomics, 25(1), 601.

Chu YH, et al. (2024) Molecular mechanisms underlying gene regulatory variation of maize metabolic traits. The Plant cell, 36(9), 3709.

Borba AR, et al. (2023) Compartmentation of photosynthesis gene expression in C4 maize depends on time of day. Plant physiology, 193(4), 2306.

Xuhui L, et al. (2022) Full-length transcriptome analysis of maize root tips reveals the molecular mechanism of cold stress during the seedling stage. BMC plant biology, 22(1), 398.

de Souza Moraes T, et al. (2022) The TCP transcription factor HvTB2 heterodimerizes with VRS5 and controls spike architecture in barley. Plant reproduction, 35(3), 205.

Han Y, et al. (2021) Identification and evolution analysis of the JAZ gene family in maize. BMC genomics, 22(1), 256.

Nie Z, et al. (2021) Combined Transcriptome and Proteome Analysis of Maize (Zea mays L.) Reveals A Complementary Profile in Response to Phosphate Deficiency. Current issues in molecular biology, 43(2), 1142.

Ge M, et al. (2020) The NIN-like protein 5 (ZmNLP5) transcription factor is involved in modulating the nitrogen response in maize. The Plant journal : for cell and molecular biology, 102(2), 353.

Gomez-Cano F, et al. (2020) CamRegBase: a gene regulation database for the biofuel crop, Camelina sativa. Database : the journal of biological databases and curation, 2020.

Simões MS, et al. (2020) Differentiation of Tracheary Elements in Sugarcane Suspension Cells Involves Changes in Secondary Wall Deposition and Extensive Transcriptional Reprogramming. Frontiers in plant science, 11, 617020.

Martin RC, et al. (2020) Transcriptome analysis of responses in Brachypodium distachyon overexpressing the BdbZIP26 transcription factor. BMC plant biology, 20(1), 174.

Souza GM, et al. (2019) Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. GigaScience, 8(12).

Li W, et al. (2019) Effect of water-deficit on tassel development in maize. Gene, 681, 86.

Knauer S, et al. (2019) A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. Genome research, 29(12), 1962.

Huang J, et al. (2018) Distinct tissue-specific transcriptional regulation revealed by gene regulatory networks in maize. BMC plant biology, 18(1), 111.

Kandel R, et al. (2018) Potentials, Challenges, and Genetic and Genomic Resources for Sugarcane Biomass Improvement. Frontiers in plant science, 9, 151.

Forestan C, et al. (2018) Control of Maize Vegetative and Reproductive Development, Fertility, and rRNAs Silencing by HISTONE DEACETYLASE 108. Genetics, 208(4), 1443.

Miao Z, et al. (2017) A systems approach to a spatio-temporal understanding of the drought stress response in maize. Scientific reports, 7(1), 6590.

Yang F, et al. (2017) A Maize Gene Regulatory Network for Phenolic Metabolism. Molecular plant, 10(3), 498.

Li C, et al. (2017) Gene expression and plant hormone levels in two contrasting rice genotypes responding to brown planthopper infestation. BMC plant biology, 17(1), 57.