Resource Summary Report

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GoMapMan

RRID:SCR_005060
Type: Tool

Proper Citation

GoMapMan (RRID:SCR_005060)

Resource Information

URL: http://www.gomapman.org/

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Description: An open web-accessible resource for gene functional annotations in the plant sciences to facilitate improvement, consolidation and visualization of gene annotations across several plant species. It is based on the MapMan ontology, organized in the form of a hierarchical tree of biological concepts, which describe gene functions. Currently, genes of the model species Arabidopsis, potato, tomato, rice, and tobacco are included. The main features are (i) dynamic and interactive gene product annotation through various curation options; (ii) consolidation of gene annotations for different plant species through the integration of orthologue group information; (iii) traceability of gene ontology changes and annotations; (iv) integration of external knowledge about genes from different public resources; and (v) providing gathered information to high-throughput analysis tools via dynamically generated export files. All of the GoMapMan functionalities are openly available, with the restriction on the curation functions, which require prior registration to ensure traceability of the implemented changes.

Abbreviations: GoMapMan

Resource Type: database, service resource, data or information resource

Defining Citation: PMID:24194592

Keywords: functional annotation, function, annotation, gene, visualization, ortholog, ontology, microarray, gene annotation, bio.tools

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Resource Name: GoMapMan

Resource ID: SCR_005060

Alternate IDs: biotools:gomapman, OMICS_02280

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

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T015514+0000

Ratings and Alerts

No rating or validation information has been found for GoMapMan.

No alerts have been found for GoMapMan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 28 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Scotti R, et al. (2024) Transcriptional reprogramming of tomato (Solanum lycopersicum L.) roots treated with humic acids and filter sterilized compost tea. BMC plant biology, 24(1), 894.

Bleker C, et al. (2024) Stress Knowledge Map: A knowledge graph resource for systems biology analysis of plant stress responses. Plant communications, 5(6), 100920.

Tomaž Š, et al. (2023) A mini-TGA protein modulates gene expression through heterogeneous association with transcription factors. Plant physiology, 191(3), 1934.

Yang X, et al. (2023) RNA-seq profiling in leaf tissues of two soybean (Glycine max [L.] Merr.) cultivars that show contrasting responses to drought stress during early developmental stages. Molecular breeding : new strategies in plant improvement, 43(5), 42.

Osmani Z, et al. (2021) Identification of a defense response gene involved in signaling pathways against PVA and PVY in potato. GM crops & food, 12(1), 86.

Abreha KB, et al. (2021) Leaf Apoplast of Field-Grown Potato Analyzed by Quantitative Proteomics and Activity-Based Protein Profiling. International journal of molecular sciences, 22(21).

Misra G, et al. (2021) Genome-wide association coupled gene to gene interaction studies unveil novel epistatic targets among major effect loci impacting rice grain chalkiness. Plant biotechnology journal, 19(5), 910.

Plackett ARG, et al. (2021) Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. Current biology : CB, 31(20), 4560.

Prinsi B, et al. (2020) Root Proteomic Analysis of Two Grapevine Rootstock Genotypes Showing Different Susceptibility to Salt Stress. International journal of molecular sciences, 21(3).

Karlusich JJP, et al. (2020) Transcriptional and Metabolic Profiling of Potato Plants Expressing a Plastid-Targeted Electron Shuttle Reveal Modulation of Genes Associated to Drought Tolerance by Chloroplast Redox Poise. International journal of molecular sciences, 21(19).

Costello R, et al. (2020) Gene Duplication Accelerates the Pace of Protein Gain and Loss from Plant Organelles. Molecular biology and evolution, 37(4), 969.

Meng W, et al. (2020) RICE ACYL-COA-BINDING PROTEIN6 Affects Acyl-CoA Homeostasis and Growth in Rice. Rice (New York, N.Y.), 13(1), 75.

Lukan T, et al. (2020) Precision transcriptomics of viral foci reveals the spatial regulation of immune-signaling genes and identifies RBOHD as an important player in the incompatible interaction between potato virus Y and potato. The Plant journal : for cell and molecular biology, 104(3), 645.

De Palma M, et al. (2019) Transcriptome reprogramming, epigenetic modifications and alternative splicing orchestrate the tomato root response to the beneficial fungus Trichoderma harzianum. Horticulture research, 6, 5.

Shan J, et al. (2019) The underlying pathway involved in inter-subspecific hybrid male sterility in rice. Genomics, 111(6), 1447.

Prinsi B, et al. (2018) Root proteomic and metabolic analyses reveal specific responses to drought stress in differently tolerant grapevine rootstocks. BMC plant biology, 18(1), 126.

Cunha CP, et al. (2017) Ethylene-induced transcriptional and hormonal responses at the onset of sugarcane ripening. Scientific reports, 7, 43364.

Pierella Karlusich JJ, et al. (2017) Chloroplast Redox Status Modulates Genome-Wide Plant Responses during the Non-host Interaction of Tobacco with the Hemibiotrophic Bacterium Xanthomonas campestris pv. vesicatoria. Frontiers in plant science, 8, 1158.

Marmiroli M, et al. (2017) Target proteins reprogrammed by As and As?+?Si treatments in Solanum lycopersicum L. fruit. BMC plant biology, 17(1), 210.

Wang L, et al. (2017) System-Level and Granger Network Analysis of Integrated Proteomic and Metabolomic Dynamics Identifies Key Points of Grape Berry Development at the Interface of Primary and Secondary Metabolism. Frontiers in plant science, 8, 1066.