

# Resource Summary Report

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## GoMapMan

RRID:SCR\_005060

Type: Tool

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### Proper Citation

GoMapMan (RRID:SCR\_005060)

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### 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:** data or information resource, database, service resource

**Defining Citation:** [PMID:24194592](#)

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

**Funding:** Slovenian Research Agency J4-2228;  
Slovenian Research Agency P2-0103

**Availability:** Creative Commons Attribution-NonCommercial-ShareAlike License

**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:** 20260829T182931+0000

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## Ratings and Alerts

No rating or validation information has been found for GoMapMan.

No alerts have been found for GoMapMan.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 29 mentions in open access literature.

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

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.

Gallo V, et al. (2022) Protein Analysis of *A. halleri* and *N. caerulescens* Hyperaccumulators When Exposed to Nano and Ionic Forms of Cd and Zn. *Nanomaterials* (Basel, Switzerland), 12(23).

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.

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.

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).

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.

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.

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).

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.

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.

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.

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.