

Resource Summary Report

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BiNGO: A Biological Networks Gene Ontology tool

RRID:SCR_005736

Type: Tool

Proper Citation

BiNGO: A Biological Networks Gene Ontology tool (RRID:SCR_005736)

Resource Information

URL: <http://www.psb.ugent.be/cbd/papers/BiNGO/Home.html>

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Description: The Biological Networks Gene Ontology tool (BiNGO) is an open-source Java tool to determine which Gene Ontology (GO) terms are significantly overrepresented in a set of genes. BiNGO can be used either on a list of genes, pasted as text, or interactively on subgraphs of biological networks visualized in Cytoscape. BiNGO maps the predominant functional themes of the tested gene set on the GO hierarchy, and takes advantage of Cytoscape's versatile visualization environment to produce an intuitive and customizable visual representation of the results. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: BiNGO

Synonyms: Biological Networks Gene Ontology

Resource Type: software resource

Defining Citation: [PMID:15972284](#)

Keywords: gene ontology, gene, ontology, statistical analysis, term enrichment, biological network, plugin, bio.tools

Availability: Open unspecified license - Free for academic use

Resource Name: BiNGO: A Biological Networks Gene Ontology tool

Resource ID: SCR_005736

Alternate IDs: nlx_149196, biotools:bingo

Alternate URLs: <https://bio.tools/bingo>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260821T193747+0000

Ratings and Alerts

No rating or validation information has been found for BiNGO: A Biological Networks Gene Ontology tool.

No alerts have been found for BiNGO: A Biological Networks Gene Ontology tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 806 mentions in open access literature.

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

Golpasand S, et al. (2026) Genomic dissection of methane emission traits in cattle: A meta-GWAS and heritability analysis across populations. PloS one, 21(4), e0344752.

Fattel L, et al. (2026) Go Big or go home: a new gene ontology subset that improves plant gene function prediction. Plant methods, 22(1).

Singhal C, et al. (2026) CUL3LRB E3 ubiquitin ligases control thermosensory growth in Arabidopsis by differentially regulating HY5 and PIF4 protein stability. Science advances, 12(10), eaec7817.

Droc G, et al. (2026) A Super-Pangenome for Cultivated Citrus Reveals Evolutionary Features During the Allopatric Phase of Their Reticulate Evolution. Plant biotechnology journal, 24(5), 3345.

Hou C, et al. (2026) Site-Specific and Quantitative O-GlcNAc Proteomics for Hepatocellular Carcinoma. Journal of proteome research, 25(4), 1892.

Liu Z, et al. (2026) Machine Learning-Informed Nano Co-Assembly Inhibits Fibroblast Activation Protein and Improves Drug Delivery in Fibrotic Tissue. Advanced materials (Deerfield Beach, Fla.), 38(17), e19805.

Gao MJ, et al. (2026) SCL15 Promotes Seed Longevity Acquisition in Arabidopsis thaliana by Enhancing Antioxidant and Repair Mechanisms During Maturation. Physiologia plantarum, 178(3), e70907.

Rameshi N, et al. (2026) Transcriptomic and physiological analysis of Dunaliella salina under sistian deep water in Iran. Scientific reports, 16(1).

- Fernández-Bernaldez A, et al. (2026) Integrative skin-blood transcriptomic analysis identifies circulating biomarkers reflecting disease activity in atopic dermatitis. *Frontiers in allergy*, 7, 1837776.
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- Chitarra W, et al. (2026) Mitigating grapevine esca disease: an innovative integrated management strategy to reduce incidence and severity by enhancing plant physiology and defence mechanisms. *BMC plant biology*, 26(1).
- Stilwell PA, et al. (2026) The genome of *Istocheta aldrichi* (Diptera: Tachinidae), a parasitoid of the Japanese beetle, *Popillia japonica* (Coleoptera: Scarabaeidae). *G3 (Bethesda, Md.)*, 16(4).
- Sánchez E, et al. (2026) Integrated Gene Regulatory Network Analysis Reveals Coordinated Transcriptional Reprogramming in the *Arabidopsis thaliana*-*Trichoderma atroviride* Interaction. *Plants (Basel, Switzerland)*, 15(4).
- Pittalà MGG, et al. (2026) SPROUTS_DB: An Implemented Database of Contaminants for Extracellular Vesicle Proteomics Studies. *Proteomics*, 26(7), 69.
- Wang L, et al. (2026) Comprehensive analysis of mRNA-microRNA-lncRNA expression profiles in post-traumatic elbow heterotopic ossification using RNA sequencing and experimental validation. *Annals of medicine*, 58(1), 2611612.
- Zhang K, et al. (2026) Multi-tissue transcriptomic profiling of foxtail millet in response to drought and rewatering. *BMC plant biology*, 26(1).
- Gao MJ, et al. (2025) SCL15 Regulates the Release of Seed Dormancy in *Arabidopsis thaliana* by Integrating the Circadian Clock, Hormonal Signals and Cell Wall Remodelling. *Physiologia plantarum*, 177(5), e70467.
- Krüger T, et al. (2025) DOG1 controls dormancy independently of ABA core signaling kinases regulation by preventing AFP dephosphorylation through AHG1. *Science advances*, 11(9), eadr8502.
- do Carmo Santos ML, et al. (2025) The family of glutathione peroxidase proteins and their role against biotic stress in plants: a systematic review. *Frontiers in plant science*, 16, 1425880.
- Shafieizadegan S, et al. (2025) The molecular impact of miR-326 in acute lymphoblastic leukemia and its cross talk with P53. *Annals of hematology*, 104(4), 2417.