

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: 20260801T190258+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 790 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kr??ger 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.

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.

Roh J, et al. (2025) Gene Profiling Analyses of Synovium Tissues in Korean Osteoarthritis Patients. In vivo (Athens, Greece), 39(6), 3128.

Pankow S, et al. (2025) In vivo conformational space and defects of misfolded CFTR variants by covalent protein painting. Nature communications, 16(1), 10131.

Meucci S, et al. (2025) Biological Processes Underlying Genetic Adaptation of Larches to Cold and Dry Winter Conditions in Eastern Siberia. Ecology and evolution, 15(2), e70940.

Madden CF, et al. (2025) Defying Death: A Multi-Omics Approach to Understanding Desiccation Tolerance and Senescence in Eragrostis nindensis. Plants (Basel, Switzerland), 14(21).

- Sun M, et al. (2025) Molecular and immune landscape of melanoma: a risk stratification model for precision oncology. *Discover oncology*, 16(1), 667.
- Horn A, et al. (2025) Transcriptional and functional characterization in the terpenoid precursor pathway of the early land plant *Physcomitrium patens*. *Plant biology (Stuttgart, Germany)*, 27(1), 29.
- Wang C, et al. (2025) Bioinformatics Analysis Screening and Identification of Key Biomarkers and Drug Targets in Human Glioblastoma. *Current medicinal chemistry*, 32(25), 5260.
- Ran Q, et al. (2025) Eniluracil blocks AREG signalling-induced pro-inflammatory fibroblasts of melanoma in heart failure. *ESC heart failure*, 12(1), 525.
- Carlton M, et al. (2025) Salivary Proteome Is Altered in Children With Small Area Thermal Burns. *Proteomics. Clinical applications*, 19(2), e202300107.
- Cui G, et al. (2025) Deciphering the regulatory mechanisms of potato cold-induced sweetening via integrated time-course transcriptome and metabolome analysis. *Frontiers in plant science*, 16, 1551265.
- Sudhindar PD, et al. (2025) Urinary renal epithelial cells can be used for NPHP1 phenotyping and a personalized therapeutic strategy. *Journal of cell science*, 138(20).
- Dagva SU, et al. (2025) Effect of fieldwork-friendly coffee blender-based extraction methods and leaf tissue storage on the transcriptome of non-model plants. *Journal of plant research*, 138(3), 511.
- Martinez-Hernandez JE, et al. (2025) Comparative and systems analyses of *Leishmania* spp. non-coding RNAs through developmental stages. *PLoS neglected tropical diseases*, 19(5), e0013108.
- Cuaspu O, et al. (2025) Transcriptome analysis of *Thevetia peruviana* cell suspensions treated with methyl jasmonate reveals genes involved in phenolics, flavonoids and cardiac glycosides biosynthesis. *Frontiers in plant science*, 16, 1593315.
- Herrmann A, et al. (2025) Chemical genetics reveals cross-regulation of plant developmental signaling by the immune peptide-receptor pathway. *Science advances*, 11(6), eads3718.
- Semmy D, et al. (2025) ER Stress Ire1-Xbp1s Pathway Maintains Youthful Epidermal Basal Layer Through the Regulation of Cell Proliferation. *Aging cell*, 24(12), e70258.