

# 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>

**Proper Citation:** BiNGO: A Biological Networks Gene Ontology tool (RRID:SCR\_005736)

**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

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## 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.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 806 mentions in open access literature.

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

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).

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.

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

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.

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.

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

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

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.

- 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.
- Wu QQ, et al. (2026) Integrated Analysis of Bulk and Single-Cell Transcriptomics Identifies Prognostic Biomarkers in Breast Cancer Metastasis. *Biochemical genetics*, 64(3), 3940.
- 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.
- 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).
- 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.
- 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.
- Roh J, et al. (2025) Gene Profiling Analyses of Synovium Tissues in Korean Osteoarthritis Patients. *In vivo (Athens, Greece)*, 39(6), 3128.
- 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.