Resource Summary Report

Generated by <u>dkNET</u> on May 8, 2025

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

Funding:

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: 20250420T014301+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 765 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Ran Q, et al. (2025) Eniluracil blocks AREG signalling-induced pro-inflammatory fibroblasts of melanoma in heart failure. ESC heart failure, 12(1), 525.

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.

Wos G, et al. (2024) Comparative Transcriptomic Reveals Greater Similarities in Response to Temperature Than to Invasive Alien Predator in the Damselfly Ischnura elegans Across Different Geographic Scales. Evolutionary applications, 17(9), e70002.

De Oliveira IB, et al. (2024) Apoplastomes of contrasting cacao genotypes to witches' broom disease reveals differential accumulation of PR proteins. Frontiers in plant science, 15, 1387153.

Poquita-Du RC, et al. (2024) Genome-wide analysis to uncover how Pocillopora acuta survives the challenging intertidal environment. Scientific reports, 14(1), 8538.

Cione E, et al. (2024) Profiling of differentially expressed MicroRNAs in familial

hypercholesterolemia via direct hybridization. Non-coding RNA research, 9(3), 796.

Vakirlis N, et al. (2024) Large-scale investigation of species-specific orphan genes in the human gut microbiome elucidates their evolutionary origins. Genome research, 34(6), 888.

Garmany A, et al. (2024) Decoded cardiopoietic cell secretome linkage to heart repair biosignature. Stem cells translational medicine, 13(11), 1144.

Delclos PJ, et al. (2024) Trans regulation of an odorant binding protein by a proto-Y chromosome affects male courtship in house fly. eLife, 13.

Poquita-Du RC, et al. (2024) Genome-Wide Comparisons Reveal Extensive Divergence Within the Lichen Photobiont Genus, Trebouxia. Genome biology and evolution, 16(10).

Lereim RR, et al. (2024) Natalizumab promotes anti-inflammatory and repair effects in multiple sclerosis. PloS one, 19(3), e0300914.

Yue H, et al. (2024) Host genotype-specific rhizosphere fungus enhances drought resistance in wheat. Microbiome, 12(1), 44.

Feng X, et al. (2024) Genomic evidence for rediploidization and adaptive evolution following the whole-genome triplication. Nature communications, 15(1), 1635.

Yun HY, et al. (2024) Leucine rich repeat LGI family member 3: Integrative analyses support its prognostic association with pancreatic adenocarcinoma. Medicine, 103(8), e37183.

Liu Q, et al. (2024) The combination of RNA-seq transcriptomics and data-independent acquisition proteomics reveal the mechanisms and function of different gooses testicular development at different stages of laying cycle. Poultry science, 103(10), 104007.

Avalos PN, et al. (2024) Extracellular vesicles promote proliferation in an animal model of regeneration. bioRxiv : the preprint server for biology.

Chodkowski JL, et al. (2024) Bioactive exometabolites drive maintenance competition in simple bacterial communities. mSystems, 9(4), e0006424.

Madej E, et al. (2024) The involvement of RIPK4 in TNF-?-stimulated IL-6 and IL-8 production by melanoma cells. Journal of cancer research and clinical oncology, 150(4), 209.

Tun W, et al. (2024) OsWRKY26 negatively regulates bacterial blight resistance by suppressing OsXa39 expression. Frontiers in plant science, 15, 1519039.

Yang W, et al. (2024) Mice with type I interferon signaling deficiency are prone to epilepsy upon HSV-1 infection. Virologica Sinica, 39(2), 251.