

Resource Summary Report

Generated by [dkNET](#) on Apr 22, 2025

GoBean - a Java application for Gene Ontology enrichment analysis

RRID:SCR_005808

Type: Tool

Proper Citation

GoBean - a Java application for Gene Ontology enrichment analysis (RRID:SCR_005808)

Resource Information

URL:

http://ftp://ftp.geneontology.org/pub/go/www/GO.tools_by_type.term_enrichment.shtml#gobean

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Description: GoBean is a Java application for gene ontology enrichment analysis. It utilizes the NetBeans platform framework. Features * Graphical comparison of multiple enrichment analysis results * Versatile filter facility for focused analysis of enrichment results * Effective exploitation of the graphical/hierarchical structure of GO * Evidence code based association filtering * Supports local data files such as the ontology obo file and gene association files * Supports late enrichment methods and multiple testing corrections * Built-in ID conversion for common species using Ensembl biomart service Platform: Windows compatible, Mac OS X compatible, Linux compatible

Abbreviations: GoBean

Resource Type: software resource, data processing software, software application

Defining Citation: [PMID:22360891](#)

Keywords: java, gene ontology, ontology, gene association, analysis, enrichment, term enrichment

Funding:

Availability: Free for academic use

Resource Name: GoBean - a Java application for Gene Ontology enrichment analysis

Resource ID: SCR_005808

Alternate IDs: nlx_149296

Old URLs: <http://neon.gachon.ac.kr/GoBean/>

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250422T055255+0000

Ratings and Alerts

No rating or validation information has been found for GoBean - a Java application for Gene Ontology enrichment analysis.

No alerts have been found for GoBean - a Java application for Gene Ontology enrichment analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Sun M, et al. (2024) Extracellular vesicles derived from dental follicle stem cells regulate tooth eruption by inhibiting osteoclast differentiation. *Frontiers in cell and developmental biology*, 12, 1503481.

Deutsch EW, et al. (2023) The ProteomeXchange consortium at 10 years: 2023 update. *Nucleic acids research*, 51(D1), D1539.

Meng Y, et al. (2022) Novel factors contributing to fungal pathogenicity at early stages of *Setosphaeria turcica* infection. *Molecular plant pathology*, 23(1), 32.

Jadhao S, et al. (2022) RBCeq: A robust and scalable algorithm for accurate genetic blood typing. *EBioMedicine*, 76, 103759.

Chen H, et al. (2022) Two novel AMHR2 gene variants in monozygotic twins with persistent Müllerian duct syndrome: A case report and functional study. *Molecular genetics & genomic medicine*, 10(8), e1999.

Ji X, et al. (2022) Pituitary-Gland-Based Genes Participates in Intrauterine Growth Restriction in Piglets. *Genes*, 13(11).

Salifou K, et al. (2021) Chromatin-associated MRN complex protects highly transcribing genes from genomic instability. *Science advances*, 7(21).

Liu X, et al. (2020) Predicting Cancer Tissue-of-Origin by a Machine Learning Method Using DNA Somatic Mutation Data. *Frontiers in genetics*, 11, 674.

Wise MJ, et al. (2016) dCITE: Measuring Necessary Cladistic Information Can Help You Reduce Polytoomy Artefacts in Trees. *PloS one*, 11(11), e0166991.

Fusar-Poli P, et al. (2016) Towards a Standard Psychometric Diagnostic Interview for Subjects at Ultra High Risk of Psychosis: CAARMS versus SIPS. *Psychiatry journal*, 2016, 7146341.

Hanrahan SJ, et al. (2016) Long-Term Task- and Dopamine-Dependent Dynamics of Subthalamic Local Field Potentials in Parkinson's Disease. *Brain sciences*, 6(4).

Reiss DJ, et al. (2015) cMonkey2: Automated, systematic, integrated detection of co-regulated gene modules for any organism. *Nucleic acids research*, 43(13), e87.

Pereira-Leal JB, et al. (2014) A comprehensive assessment of the transcriptome of cork oak (*Quercus suber*) through EST sequencing. *BMC genomics*, 15(1), 371.

Wise MJ, et al. (2013) Mean protein evolutionary distance: a method for comparative protein evolution and its application. *PloS one*, 8(4), e61276.

Vlachos I, et al. (2013) Neural system prediction and identification challenge. *Frontiers in neuroinformatics*, 7, 43.

Villanueva-Cañas JL, et al. (2013) Improving genome-wide scans of positive selection by using protein isoforms of similar length. *Genome biology and evolution*, 5(2), 457.

Teo BG, et al. (2013) A deformable generic 3D model of haptoral anchor of Monogenean. *PloS one*, 8(10), e77650.

Zycinski G, et al. (2013) Knowledge Driven Variable Selection (KDVS) - a new approach to enrichment analysis of gene signatures obtained from high-throughput data. *Source code for biology and medicine*, 8(1), 2.

Rubinstein WS, et al. (2013) The NIH genetic testing registry: a new, centralized database of genetic tests to enable access to comprehensive information and improve transparency. *Nucleic acids research*, 41(Database issue), D925.

Richmond P, et al. (2011) Democratic population decisions result in robust policy-gradient learning: a parametric study with GPU simulations. *PloS one*, 6(5), e18539.