

# Resource Summary Report

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## GoBean - a Java application for Gene Ontology enrichment analysis

RRID:SCR\_005808

Type: Tool

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### Proper Citation

GoBean - a Java application for Gene Ontology enrichment analysis (RRID:SCR\_005808)

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### Resource Information

**URL:**

[http://ftp://ftp.geneontology.org/pub/go/www/GO.tools\\_by\\_type.term\\_enrichment.shtml#gobean](http://ftp://ftp.geneontology.org/pub/go/www/GO.tools_by_type.term_enrichment.shtml#gobean)

**Proper Citation:** GoBean - a Java application for Gene Ontology enrichment analysis (RRID:SCR\_005808)

**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, software application, data processing software

**Defining Citation:** [PMID:22360891](#)

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

**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:** 20260804T043248+0000

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## 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.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 22 mentions in open access literature.

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

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.

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.

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

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 Polytomy 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.
- Teo BG, et al. (2013) A deformable generic 3D model of haptoral anchor of Monogenean. *PloS one*, 8(10), e77650.
- 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.
- Wise MJ, et al. (2013) Mean protein evolutionary distance: a method for comparative protein evolution and its application. *PloS one*, 8(4), e61276.
- 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.
- 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.
- 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.