

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

GOHyperGAll

RRID:SCR_005766

Type: Tool

Proper Citation

GOHyperGAll (RRID:SCR_005766)

Resource Information

URL: http://manuals.bioinformatics.ucr.edu/home/R_BioCondManual#GOHyperGAll

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Description: To test a sample population of genes for overrepresentation of GO terms, the R/BioC function GOHyperGAll computes for all GO nodes a hypergeometric distribution test and returns the corresponding p-values. A subsequent filter function performs a GO Slim analysis using default or custom GO Slim categories. Basic knowledge about R and BioConductor is required for using this tool. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GOHyperGAll

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

Defining Citation: [PMID:18354039](#)

Keywords: gene, gene ontology, annotation, statistical analysis, slimmer-type tool

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GOHyperGAll

Resource ID: SCR_005766

Alternate IDs: nlx_149267

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260905T132541+0000

Ratings and Alerts

No rating or validation information has been found for GOHyperGAll.

No alerts have been found for GOHyperGAll.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Butsayawarapat P, et al. (2019) Comparative Transcriptome Analysis of Waterlogging-Sensitive and Tolerant Zombi Pea (*Vigna Vexillata*) Reveals Energy Conservation and Root Plasticity Controlling Waterlogging Tolerance. *Plants* (Basel, Switzerland), 8(8).

Ah-Fong AMV, et al. (2017) Lifestyle, gene gain and loss, and transcriptional remodeling cause divergence in the transcriptomes of *Phytophthora infestans* and *Pythium ultimum* during potato tuber colonization. *BMC genomics*, 18(1), 764.

Ah-Fong AM, et al. (2017) RNA-seq of life stages of the oomycete *Phytophthora infestans* reveals dynamic changes in metabolic, signal transduction, and pathogenesis genes and a major role for calcium signaling in development. *BMC genomics*, 18(1), 198.

Juntawong P, et al. (2014) Elucidation of the molecular responses to waterlogging in *Jatropha* roots by transcriptome profiling. *Frontiers in plant science*, 5, 658.