

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

## GOHyperGAll

RRID:SCR\_005766

Type: Tool

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### Proper Citation

GOHyperGAll (RRID:SCR\_005766)

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### Resource Information

**URL:** [http://manuals.bioinformatics.ucr.edu/home/R\\_BioCondManual#GOHyperGAll](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 processing software, software application, data analysis software, 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:** 20260731T042715+0000

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### Ratings and Alerts

No rating or validation information has been found for GOHyperGAll.

No alerts have been found for GOHyperGAll.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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.