

Resource Summary Report

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

G-SESAME - Gene Semantic Similarity Analysis and Measurement Tools

RRID:SCR_005816

Type: Tool

Proper Citation

G-SESAME - Gene Semantic Similarity Analysis and Measurement Tools
(RRID:SCR_005816)

Resource Information

URL: <http://bioinformatics.clemson.edu/G-SESAME/>

Proper Citation: G-SESAME - Gene Semantic Similarity Analysis and Measurement Tools (RRID:SCR_005816)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 2,2025. G-SESAME contains a set of tools. They include: tools for measuring the semantic similarity of GO terms; tools for measuring the functional similarity of genes; and tools for clustering genes based on their GO term annotation information. Platform: Online tool, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: G-SESAME

Synonyms: Gene Semantic Similarity Analysis Measurement Tools, Gene Semantic Similarity Analysis and Measurement Tools

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:19491312](#), [PMID:17344234](#)

Keywords: gene ontology, semantic similarity, functional similarity, cluster, gene, annotation, gene annotation

Funding: NSF DBI-0960586;
NSF DBI-0960443

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: G-SESAME - Gene Semantic Similarity Analysis and Measurement Tools

Resource ID: SCR_005816

Alternate IDs: nlx_149313

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260905T133132+0000

Ratings and Alerts

No rating or validation information has been found for G-SESAME - Gene Semantic Similarity Analysis and Measurement Tools.

No alerts have been found for G-SESAME - Gene Semantic Similarity Analysis and Measurement Tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Kim YH, et al. (2022) A time-dependently regulated gene network reveals that Aspergillus protease affects mitochondrial metabolism and airway epithelial cell barrier function via mitochondrial oxidants. Free radical biology & medicine, 185, 76.

Waleczek FJG, et al. (2022) Chemical and mechanical activation of resident cardiac macrophages in the living myocardial slice ex vivo model. Basic research in cardiology, 117(1), 63.

Yang Y, et al. (2016) Missing value imputation for microRNA expression data by using a GO-based similarity measure. BMC bioinformatics, 17 Suppl 1(Suppl 1), 10.

Dess?? N, et al. (2013) A comparative analysis of biomarker selection techniques. BioMed research international, 2013, 387673.

Pesquita C, et al. (2009) Semantic similarity in biomedical ontologies. PLoS computational biology, 5(7), e1000443.