

Resource Summary Report

Generated by [ASWG](#) on Sep 18, 2026

REViGO

RRID:SCR_005825

Type: Tool

Proper Citation

REViGO (RRID:SCR_005825)

Resource Information

URL: <http://revigo.irb.hr/>

Proper Citation: REViGO (RRID:SCR_005825)

Description: Web server that summarizes lists of Gene Ontology terms by removing redundant terms and visualizing the remaining ones in scatterplots, interactive graphs, treemaps, or tag clouds. Platform: Online tool, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: REViGO

Synonyms: Reduce + Visualize Gene Ontology, REViGO - Reduce Visualize Gene Ontology, REViGO - Reduce & Visualize Gene Ontology, REViGO - Reduce and Visualize Gene Ontology, REViGO - Reduce + Visualize Gene Ontology

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

Defining Citation: [PMID:21789182](#), [PMID:20585573](#)

Keywords: gene ontology, visualization, statistical analysis, ontology or annotation visualization

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: REViGO

Resource ID: SCR_005825

Alternate IDs: OMICS_02283, nlx_149332

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260912T200139+0000

Ratings and Alerts

No rating or validation information has been found for REViGO.

No alerts have been found for REViGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2430 mentions in open access literature.

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

Shi X, et al. (2026) Rapid expansion of primary human vocal fold epithelial cells via targeted pathway inhibition and anchorage-independent sphere culture. *Cell reports methods*, 6(3), 101310.

Hadpech S, et al. (2026) Urinary proteins from stone formers promote calcium oxalate crystallization, growth and aggregation via oxidative modifications. *Journal of advanced research*, 81, 125.

Luo D, et al. (2026) Prenatal Alcohol Exposure and Mental Health Outcomes: A Two-Sample Mendelian Randomization Study of DNA Methylation Signatures. *medRxiv : the preprint server for health sciences*.

Becerril M, et al. (2026) Temperature changes reveal different transcriptional responses in the larvae of the bark beetle *Dendroctonus rhizophagus* during the cold season. *Scientific reports*, 16(1).

Pantazi V, et al. (2026) K63-linked ubiquitylation of S2P-RNAPII regulates transcription in a DNAPK inter-dependent manner in response to double-strand breaks. *Nucleic acids research*, 54(8).

Kramarenko DR, et al. (2026) Leveraging the shared and opposing genetic mechanisms in the heritable cardiomyopathies. *Research square*.

Deal SL, et al. (2026) RNAi-based screen for pigmentation in *Drosophila melanogaster* reveals regulators of brain dopamine and sleep. *iScience*, 29(1), 114388.

Gaudi AU, et al. (2026) Convergent evolution of scavenger cell development at brain borders. *Nature*, 651(8106), 743.

Witte Paz M, et al. (2026) TSSpredator-Web: A web-application for transcription start site prediction and exploration. *PloS one*, 21(3), e0326299.

López-García M, et al. (2026) In vitro Host-Parasite Models Combined With Proteomics Reveal Cell Type-Specific Responses of Early Migrating *Fasciola hepatica* Juveniles.

Molecular & cellular proteomics : MCP, 25(4), 101543.

Liang C, et al. (2026) Longitudinally altered default mode network and insula multimodal brain pattern in end-stage renal disease during sustained hemodialysis treatment. *iScience*, 29(6), 116008.

Ruan H, et al. (2026) Free apical surface hetero-cellular CDH1 homophilic binding is a major mediator of blastocyst-endometrium interaction in humans. *Human reproduction* (Oxford, England), 41(4), 563.

Röder N, et al. (2026) Pollution-Driven Selection in a Non-Biting Midge: Genome-Wide Responses to *Bacillus thuringiensis israelensis* and Copper. *Molecular ecology*, 35(3), e70263.

Lu L, et al. (2026) Genome-wide identification and dynamic transcriptome profiling of the DYW-type PPR family across greening of chlorotic leaves in pear (*Pyrus pyrifolia*). *Frontiers in plant science*, 17, 1767760.

Listrat A, et al. (2026) Transcriptional profiling of male mouse muscle across aging stages: a gene ontology analysis of the muscle matreotype. *BMC genomics*, 27(1).

Davis JM, et al. (2026) Benchmarking methods for genome annotation using nanopore direct RNA in a non-model crop plant. *Bioinformatics advances*, 6(1), vbag030.

Hirofuji A, et al. (2026) Mycn Reactivates the Cell Cycle in Adult Cardiomyocytes and Promotes Cardioprotection in Myocardial Infarction. *Journal of the American Heart Association*, 15(8), e046146.

Sun L, et al. (2026) Transcriptomic signatures of synaptic loss in Alzheimer's disease. *iScience*, 29(7), 116336.

Sandhu N, et al. (2026) GWAS reveals genetic interplay between root architecture and nitrogen uptake in *Aegilops tauschii*. *BMC plant biology*, 26(1).

Liu T, et al. (2026) Multi-omics elucidation of recombinant collagen-mediated modulation of mesenchymal stem cell functions. *Journal of advanced research*, 84, 305.