

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 30, 2026

g:Profiler

RRID:SCR_006809

Type: Tool

Proper Citation

g:Profiler (RRID:SCR_006809)

Resource Information

URL: <http://biit.cs.ut.ee/gprofiler/>

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Description: Web server for functional enrichment analysis and conversions of gene lists. Web based tool for functional profiling of gene lists from large scale experiments. Has web interface with powerful visualization. Used for analyzing data from any organism.

Synonyms: G:Profiler, g:profiler, gProfiler

Resource Type: service resource, data analysis service, data access protocol, software resource, production service resource, web service, analysis service resource

Defining Citation: [PMID:21646343](#), [PMID:17478515](#), [PMID:31066453](#)

Keywords: gene, high-throughput, genomics, visualization, statistical analysis, slimmer-type tool, term enrichment, protein interaction, functional similarity, analysis, coexpression, gene id, network enrichment analysis, orthology mapping, genomic locus, ontology or annotation visualization, other analysis, ortholog, functional profile, gene list, ontology, pathway, transcription factor, microRNA, regulatory motif, protein-protein interaction, biomolecule, gene expression, gene, homology, single nucleotide polymorphism, DNA polymorphism, chromosome, network analysis, disease gene, r

Funding: Estonian Research Council grants ;
European Regional Development Fund for CoE of Estonian ICT research EXCITE projects

Availability: Free, Freely available

Resource Name: g:Profiler

Resource ID: SCR_006809

Alternate IDs: OMICS_02223, nif-0000-31975

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260729T044140+0000

Ratings and Alerts

No rating or validation information has been found for g:Profiler.

No alerts have been found for g:Profiler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2078 mentions in open access literature.

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

Gou X, et al. (2026) Identification of a Two-Gene Biomarker Correlated with Sensitivity to Combined PARP7 Inhibition and AHR Activation in Cancer Cells. Cancer research communications, 6(1), 5.

Daniel MM, et al. (2026) Integrative Bioinformatics Reveals Novel Molecular Mechanisms and Therapeutic Targets in Acute Myeloid Leukaemia. Journal of cellular and molecular medicine, 30(1), e71007.

Jiang H, et al. (2026) SenSeqNet: A Deep Learning Framework for Cellular Senescence Detection From Protein Sequences. Aging cell, 25(1), e70344.

Woods RM, et al. (2026) Developmental modulation of schizophrenia risk gene methylation in offspring exhibiting cognitive deficits following maternal immune activation. Molecular psychiatry, 31(1), 418.

Yu Z, et al. (2026) Multi-trait genome-wide analysis identified risk loci and candidate drugs for heart failure. HGG advances, 7(1), 100540.

Burgos-Ruiz AM, et al. (2026) A single-cell multiomics roadmap of zebrafish spermatogenesis reveals regulatory principles of male germline formation. Molecular systems biology, 22(1), 42.

Jensen D, et al. (2026) Adolescent White Matter Maturation Mediates Epigenetic Associations With Cognitive Development. Developmental neurobiology, 86(1), e70000.

Yamada S, et al. (2026) Long-Term Biobanked Dental Pulp Stem Cells Retain Angiogenic Potential for Vascularised Tissue Engineering-Laboratory Investigation. International endodontic journal, 59(1), 105.

Breen K, et al. (2026) Duration of contact sports play associated with aberrant DNA methylation in human frontal cortex. Research square.

Park YJ, et al. (2026) Spatiotemporal translation of sperm acrosome associated proteins during early capacitation modulates sperm fertilizing ability. Journal of advanced research, 79, 313.

Birappa G, et al. (2026) Single-cell RNA sequence analysis reveals USP32 as a therapeutic target to mitigate PD-L1-driven colorectal tumorigenesis in vitro and in vivo. Theranostics, 16(2), 986.

Granda Farias A, et al. (2025) Phenotypic screens for SIRPA expression reveal RAB21 as a general regulator of macrophage surface identity. Cell reports, 44(7), 115921.

Snitow ME, et al. (2025) Stc1-expressing myofibroblasts are a developmentally distinct lineage cleared through apoptosis in the neonatal lung. Cell reports, 45(1), 116750.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. Molecular cell, 85(1), 24.

Culbert BM, et al. (2025) Effects of environmental salinity on global and endocrine-specific transcriptomic profiles in the caudal neurosecretory system of salmonid fishes. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(6), e70477.

Tatarakis A, et al. (2025) Requirements for establishment and epigenetic stability of mammalian heterochromatin. Molecular cell, 85(18), 3388.

Ramirez Reyes B, et al. (2025) Homeostatic antiviral protection of the neonatal gut epithelium by interferon lambda. Cell reports, 44(2), 115243.

Kim LA, et al. (2025) Circulating RNA Markers Associated with Adenoma-Carcinoma Sequence in Colorectal Cancer. International journal of molecular sciences, 26(4).

Richman CM, et al. (2025) Carbonic Anhydrase Inhibition Sensitizes Group 3 Medulloblastoma to Radiotherapy. Cancer research, 85(19), 3737.

Podsiywa??ow-Bartnicka P, et al. (2025) Transcriptional readthrough precedes alternative splicing programs triggered in CML cells by imatinib. bioRxiv : the preprint server for biology.