Resource Summary Report

Generated by NIF on Apr 22, 2025

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

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: 20250422T055332+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 1726 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Pathak AK, et al. (2025) Thermal variation influences the transcriptome of the major malaria vector Anopheles stephensi. Communications biology, 8(1), 112.

Mangini G, et al. (2025) Genome-wide association study identifies QTL and candidate genes for grain size and weight in a Triticum turgidum collection. The plant genome, 18(1), e20562.

Phuagkhaopong S, et al. (2025) Anti-inflammatory effects of moxifloxacin and levofloxacin on cadmium-activated human astrocytes: Inhibition of proinflammatory cytokine release, TLR4/STAT3, and ERK/NF-?B signaling pathway. PloS one, 20(1), e0317281.

Periyakoil PK, et al. (2025) Deep topic modeling of spatial transcriptomics in the rheumatoid arthritis synovium identifies distinct classes of ectopic lymphoid structures. bioRxiv : the preprint server for biology.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: Phoxinus phoxinus) provide evidence of haplotype diversity. GigaScience, 14.

Dao B, et al. (2025) Crosstalk between genomic variants and DNA methylation in FLT3 mutant acute myeloid leukemia. Briefings in functional genomics, 24.

Siavoshi A, et al. (2025) Integration of Gastric Cancer RNA-Seq Datasets Along With PPI

Network Suggests That Nonhub Nodes Have the Potential to Become Biomarkers. Cancer reports (Hoboken, N.J.), 8(1), e70126.

Fan Z, et al. (2025) The landscape of plasma proteomic links to human organ imaging. medRxiv : the preprint server for health sciences.

Haque T, et al. (2025) Identification and Characterization of Key Genes Associated with Amelogenesis. European journal of dentistry, 19(1), 116.

Hidalgo P, et al. (2025) The protein composition of human adenovirus replication compartments. mBio, 16(1), e0214424.

Zhu X, et al. (2025) CircaKB: a comprehensive knowledgebase of circadian genes across multiple species. Nucleic acids research, 53(D1), D67.

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.

Kentistou KA, et al. (2025) Rare variant associations with birth weight identify genes involved in adipose tissue regulation, placental function and insulin-like growth factor signalling. Nature communications, 16(1), 648.

Ozisik O, et al. (2025) A collaborative network analysis for the interpretation of transcriptomics data in Huntington's disease. Scientific reports, 15(1), 1412.

Sen P, et al. (2025) A bipolar disorder-associated missense variant alters adenylyl cyclase 2 activity and promotes mania-like behavior. Molecular psychiatry, 30(1), 97.

Nishino K, et al. (2025) Functional dissection of metabolic trait-associated gene regulation in steady state and stimulated human skeletal muscle cells. bioRxiv : the preprint server for biology.

Fu X, et al. (2025) A foundation model of transcription across human cell types. Nature, 637(8047), 965.

Assis BA, et al. (2025) Genomic signatures of adaptation in native lizards exposed to human-introduced fire ants. Nature communications, 16(1), 89.

Wang S, et al. (2025) Unraveling the transcriptomic effects of leucine supplementation on muscle growth and performance in basketball athletes. PloS one, 20(1), e0316603.

Vigeland MD, et al. (2025) Gene Expression Correlates with Disability and Pain Intensity in Patients with Chronic Low Back Pain and Modic Changes in a Sex-Specific Manner. International journal of molecular sciences, 26(2).