

Resource Summary Report

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Gene Map Annotator and Pathway Profiler

RRID:SCR_005094

Type: Tool

Proper Citation

Gene Map Annotator and Pathway Profiler (RRID:SCR_005094)

Resource Information

URL: <http://www.genmapp.org/>

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Description: GenMAPP is a free computer application designed to visualize gene expression and other genomic data on maps representing biological pathways and groupings of genes. Integrated with GenMAPP are programs to perform a global analysis of gene expression or genomic data in the context of hundreds of pathway MAPPs and thousands of Gene Ontology Terms (MAPPFinder), import lists of genes/proteins to build new MAPPs (MAPPBuilder), and export archives of MAPPs and expression/genomic data to the web. The main features underlying GenMAPP are: *Draw pathways with easy to use graphics tools *Color genes on MAPP files based on user-imported genomic data *Query data against MAPPs and the GeneOntology Enhanced features include the simultaneous view of multiple color sets, expanded species-specific gene databases and custom database options.

Synonyms: GenMAPP

Resource Type: data visualization software, software resource, software application, data processing software

Defining Citation: [PMID:17588266](#)

Keywords: expression, gene, analysis, biological, mapping, microarray, network, pathway, protein, visualization, ontology, proteomics, FASEB list

Funding: Agilent Foundation ;
BayGenomics ;
NIGMS

Resource Name: Gene Map Annotator and Pathway Profiler

Resource ID: SCR_005094

Alternate IDs: nif-0000-00244

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260804T043247+0000

Ratings and Alerts

No rating or validation information has been found for Gene Map Annotator and Pathway Profiler.

No alerts have been found for Gene Map Annotator and Pathway Profiler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 211 mentions in open access literature.

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

Lv FL, et al. (2025) Cabozantinib selectively induces proteasomal degradation of p53 somatic mutant Y220C and impedes tumor growth. The Journal of biological chemistry, 301(2), 108167.

Tsuchiya J, et al. (2024) Hepatitis B Virus-KMT2B Integration Drives Hepatic Oncogenic Processes in a Human Gene-edited Induced Pluripotent Stem Cells-derived Model. Cellular and molecular gastroenterology and hepatology, 19(2), 101422.

Ramonell RP, et al. (2023) Single-cell analysis of human nasal mucosal IgE antibody secreting cells reveals a newly minted phenotype. Mucosal immunology, 16(3), 287.

Ma W, et al. (2023) Dermokine mutations contribute to epithelial-mesenchymal transition and advanced melanoma through ERK/MAPK pathways. PloS one, 18(7), e0285806.

Agretti P, et al. (2022) Gene expression profile in functioning and non-functioning nodules of autonomous multinodular goiter from an area of iodine deficiency: unexpected common characteristics between the two entities. Journal of endocrinological investigation, 45(2), 399.

Lu L, et al. (2022) The circRNA expression profile of colorectal inflammatory cancer transformation revealed potential predictive biomarkers. Aging, 14(22), 9280.

Ghatnatti V, et al. (2021) Identification of potential and novel target genes in pituitary prolactinoma by bioinformatics analysis. AIMS neuroscience, 8(2), 254.

Matsumoto K, et al. (2021) Identification of neutrophil $\alpha 2$ -integrin LFA-1 as a potential mechanistic biomarker in ANCA-associated vasculitis via microarray and validation

analyses. *Arthritis research & therapy*, 23(1), 136.

Weber SR, et al. (2021) Proteomic Analyses of Vitreous in Proliferative Diabetic Retinopathy: Prior Studies and Future Outlook. *Journal of clinical medicine*, 10(11).

Joshi H, et al. (2021) Identification of Key Pathways and Genes in Obesity Using Bioinformatics Analysis and Molecular Docking Studies. *Frontiers in endocrinology*, 12, 628907.

Yano K, et al. (2021) PRPF19 regulates p53-dependent cellular senescence by modulating alternative splicing of MDM4 mRNA. *The Journal of biological chemistry*, 297(1), 100882.

Han KI, et al. (2021) Gene expression analysis of inflammation-related genes in macrophages treated with β -(1 $\rightarrow$ 3, 1 $\rightarrow$ 6)-D-glucan extracted from *Streptococcus mutans*. *International journal of biological macromolecules*, 166, 45.

Yin GN, et al. (2021) Transcriptional profiling of mouse cavernous pericytes under high-glucose conditions: Implications for diabetic angiopathy. *Investigative and clinical urology*, 62(1), 100.

Prashanth G, et al. (2021) Potential Molecular Mechanisms and Remdesivir Treatment for Acute Respiratory Syndrome Corona Virus 2 Infection/COVID 19 Through RNA Sequencing and Bioinformatics Analysis. *Bioinformatics and biology insights*, 15, 11779322211067365.

Vastrad B, et al. (2020) Bioinformatics analyses of significant genes, related pathways, and candidate diagnostic biomarkers and molecular targets in SARS-CoV-2/COVID-19. *Gene reports*, 21, 100956.

Golinski ML, et al. (2020) CD11c⁺ B Cells Are Mainly Memory Cells, Precursors of Antibody Secreting Cells in Healthy Donors. *Frontiers in immunology*, 11, 32.

Barakat AK, et al. (2020) Citalopram-induced pathways regulation and tentative treatment-outcome-predicting biomarkers in lymphoblastoid cell lines from depression patients. *Translational psychiatry*, 10(1), 210.

Bushau-Sprinkle A, et al. (2020) NHERF1 Loss Upregulates Enzymes of the Pentose Phosphate Pathway in Kidney Cortex. *Antioxidants (Basel, Switzerland)*, 9(9).

Ezekian JE, et al. (2020) Variant R94C in TNNT2-Encoded Troponin T Predisposes to Pediatric Restrictive Cardiomyopathy and Sudden Death Through Impaired Thin Filament Relaxation Resulting in Myocardial Diastolic Dysfunction. *Journal of the American Heart Association*, 9(5), e015111.

Huang X, et al. (2020) Depletion of exosomal circLDLR in follicle fluid derepresses miR-1294 function and inhibits estradiol production via CYP19A1 in polycystic ovary syndrome. *Aging*, 12(15), 15414.