Resource Summary Report

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Enrichr

RRID:SCR_001575
Type: Tool

Proper Citation

Enrichr (RRID:SCR_001575)

Resource Information

URL: http://amp.pharm.mssm.edu/Enrichr/

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Description: A web-based gene list enrichment analysis tool that provides various types of visualization summaries of collective functions of gene lists. It includes new gene-set libraries, an alternative approach to rank enriched terms, and various interactive visualization approaches to display enrichment results using the JavaScript library, Data Driven Documents (D3). The software can also be embedded into any tool that performs gene list analysis. System-wide profiling of genes and proteins in mammalian cells produce lists of differentially expressed genes / proteins that need to be further analyzed for their collective functions in order to extract new knowledge. Once unbiased lists of genes or proteins are generated from such experiments, these lists are used as input for computing enrichment with existing lists created from prior knowledge organized into gene-set libraries.

Abbreviations: Enrichr

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

Defining Citation: PMID:23586463

Keywords: bed, gene, software as a service, rna-seq, analyze, protein, function, gene list, visualization, bio.tools

Funding:

Availability: Open unspecified license

Resource Name: Enrichr

Resource ID: SCR_001575

Alternate IDs: biotools:enrichr, SciRes_000171

Alternate URLs: https://bio.tools/enrichr

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250517T055504+0000

Ratings and Alerts

No rating or validation information has been found for Enrichr.

No alerts have been found for Enrichr.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3538 mentions in open access literature.

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

Leopold M, et al. (2025) How the liver transcriptome and lipid composition influence the progression of nonalcoholic fatty liver disease to hepatocellular carcinoma in a murine model. Biochimica et biophysica acta. Molecular and cell biology of lipids, 1870(1), 159574.

Chen KA, et al. (2025) Post-operative Crohn's Disease Recurrence and Infectious Complications: A Transcriptomic Analysis. Digestive diseases and sciences, 70(1), 203.

Smith NJ, et al. (2025) Differentiation signals induce APOBEC3A expression via GRHL3 in squamous epithelia and squamous cell carcinoma. The EMBO journal, 44(1), 1.

Elewaut A, et al. (2025) Cancer cells impair monocyte-mediated T cell stimulation to evade immunity. Nature, 637(8046), 716.

Pollin G, et al. (2025) Emergent properties of the lysine methylome reveal regulatory roles via protein interactions and histone mimicry. Epigenomics, 17(1), 5.

Yamanashi Y, et al. (2025) Chemical catalyst manipulating cancer epigenome and transcription. Nature communications, 16(1), 887.

Jeong M, et al. (2025) An Investigation of the Anticancer Mechanism of Caesalpinia sappan L. Extract Against Colorectal Cancer by Integrating a Network Pharmacological Analysis and Experimental Validation. Plants (Basel, Switzerland), 14(2).

Oladapo A, et al. (2025) Single-Cell RNA-Seq Uncovers Robust Glial Cell Transcriptional Changes in Methamphetamine-Administered Mice. International journal of molecular sciences, 26(2).

Roodnat AW, et al. (2025) Investigating the miRNA-mRNA interactome of human trabecular meshwork cells treated with TGF-?1 provides insights into the pathogenesis of pseudoexfoliation glaucoma. PloS one, 20(1), e0318125.

He X, et al. (2025) Multi-Omics Assessment of Puff Volume-Mediated Salivary Biomarkers of Metal Exposure and Oxidative Injury Associated with Electronic Nicotine Delivery Systems. Environmental health perspectives, 133(1), 17005.

Lv J, et al. (2025) Downregulation of MLF1 safeguards cardiomyocytes against senescence-associated chromatin opening. Nucleic acids research, 53(2).

Gong JR, et al. (2025) Control of Cellular Differentiation Trajectories for Cancer Reversion. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(3), e2402132.

Cetin-Atalay R, et al. (2025) Sustained hypoxia but not intermittent hypoxia induces HIF-1? transcriptional response in human aortic endothelial cells. Molecular omics, 21(1), 19.

Debnath JP, et al. (2025) Identification of potential biomarkers for 2022 Mpox virus infection: a transcriptomic network analysis and machine learning approach. Scientific reports, 15(1), 2922.

Zheng Q, et al. (2025) Bidirectional histone monoaminylation dynamics regulate neural rhythmicity. Nature, 637(8047), 974.

Han H, et al. (2025) Identifying MTHFD1 and LGALS4 as Potential Therapeutic Targets in Prostate Cancer Through Multi-Omics Mendelian Randomization Analysis. Biomedicines, 13(1).

Scuderi G, et al. (2025) Comprehensive Analysis of TSPAN32 Regulatory Networks and Their Role in Immune Cell Biology. Biomolecules, 15(1).

Škandík M, et al. (2025) Age-associated microglial transcriptome leads to diminished immunogenicity and dysregulation of MCT4 and P2RY12/P2RY13 related functions. Cell death discovery, 11(1), 16.

Ahmadi M, et al. (2025) Bioinformatics analysis of mitochondrial metabolism-related genes demonstrates their importance in renal cell carcinoma. Discover oncology, 16(1), 28.

Liao C, et al. (2025) Single-nucleus transcriptomics reveals time-dependent and cell-type-specific effects of psilocybin on gene expression. bioRxiv : the preprint server for biology.