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

Defining Citation: PMID:23586463

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

Availability: Free, Freely available

Resource Name: Enrichr

Resource ID: SCR_001575

Alternate IDs: biotools:enrichr, SciRes_000171

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

License: Open unspecified license

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260801T190155+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 4351 mentions in open access literature.

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

Dipali SS, et al. (2026) Self-Organizing Ovarian Somatic Organoids Preserve Cellular Heterogeneity and Reveal Cellular Contributions to Ovarian Aging. Aging cell, 25(1), e70333.

Wilhelm SJ, et al. (2026) Diverse Misfolding Mutant Digestive Enzymes Cause Chronic Pancreatitis Through Common Pathways. Cellular and molecular gastroenterology and hepatology, 20(2), 101638.

Bauer A, et al. (2026) Transcriptomics- and 3D imaging-based characterization of the lymphatic vasculature in human skin. The Journal of experimental medicine, 223(1).

Mbano IM, et al. (2026) Single-cell and spatial profiling highlights TB-induced myofibroblasts as drivers of lung pathology. The Journal of experimental medicine, 223(3).

Luan R, et al. (2026) Pan-cancer multi-omics reveals DCAF7 as an immune-modulating prognostic driver and Wnt/?-catenin activator in hepatocellular carcinoma. Clinical and translational medicine, 16(1), e70572.

Ferreira JV, et al. (2026) LAMP2A regulates endosomal protein composition and membrane identity in exosome biogenesis. iScience, 29(1), 114305.

Nguyen JH, et al. (2025) Developmental pyrethroid exposure disrupts molecular pathways for MAP kinase and circadian rhythms in mouse brain. Physiological genomics, 57(4), 240.

Lall D, et al. (2025) An organ-chip model of sporadic ALS using iPSC-derived spinal cord motor neurons and an integrated blood-brain-like barrier. Cell stem cell, 32(7), 1139.

Rademacher K, et al. (2025) Chronic hyperactivation of midbrain dopamine neurons causes preferential dopamine neuron degeneration. eLife, 13.

Burns MS, et al. (2025) Distinct molecular patterns in R6/2 HD mouse brain: Insights from spatiotemporal transcriptomics. Neuron, 113(15), 2416.

Humblin E, et al. (2025) The costimulatory molecule ICOS limits memory-like properties and function of exhausted PD-1+CD8+ T cells. Immunity, 58(8), 1966.

Russ-Silsby J, et al. (2025) Complete loss of PAX4 causes transient neonatal diabetes in humans. Molecular metabolism, 99, 102201.

Ayabe H, et al. (2025) Cellular crosstalk mediated by TGF-? drives epithelial-mesenchymal transition in patient-derived multi-compartment biliary organoids. Nature communications, 16(1), 6575.

Hollis HC, et al. (2025) Reconstructed cell-type-specific rhythms in human brain link Alzheimer's pathology, circadian stress, and ribosomal disruption. Neuron, 113(17), 2822.

Larsen RK, et al. (2025) Non-cell-autonomous tumor promotion in DICER1 cancer predisposition. Developmental cell.

Berg K, et al. (2025) Endocardial primary cilia and blood flow regulate EndoMT during endocardial cushion development. Nature cardiovascular research, 4(9), 1114.

Sharma G, et al. (2025) IGF2BP3 redirects glycolytic flux to promote one-carbon metabolism and RNA methylation. Cell reports, 116330.

Hoffmann J, et al. (2025) Steatohepatitis-induced vascular niche alterations promote melanoma metastasis. Cancer & metabolism, 13(1), 5.

Nibeyro G, et al. (2025) Evaluating Gene Fusions as Prognostic Biomarkers and Therapeutic Targets in Immune Checkpoint Blockade-Treated Advanced Melanoma: A Retrospective Analysis. Cancer research communications, 5(8), 1332.

Alfaro-García JP, et al. (2025) Characterization of the Temporal Dynamics of the Endothelial-Mesenchymal-like Transition Induced by Soluble Factors from Dengue Virus Infection in Microvascular Endothelial Cells. International journal of molecular sciences, 26(5).