

Resource Summary Report

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EnrichmentMap

RRID:SCR_016052

Type: Tool

Proper Citation

EnrichmentMap (RRID:SCR_016052)

Resource Information

URL: <http://baderlab.org/Software/EnrichmentMap>

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Description: Source code of a Cytoscape plugin for functional enrichment visualization. It organizes gene-sets, such as pathways and Gene Ontology terms, into a network to reveal which mutually overlapping gene-sets cluster together.

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

Defining Citation: [PMID:21085593](#)

Keywords: cytoscape, functional, visualization, enrichment, gene, mapping, genome, pathway, network, cluster, bio.tools

Funding: Canada Foundation for Innovation ;
Heart and Stroke Foundation of Canada ;
NHGRI P41 HG041118;
Ontario Genomics Institute ;
Ontario Research Fund (ORF)

Resource Name: EnrichmentMap

Resource ID: SCR_016052

Alternate IDs: biotools:enrichmentmap

Alternate URLs: <https://github.com/BaderLab/EnrichmentMapApp>,
<https://bio.tools/enrichmentmap>

License: GNU LGPL

Record Creation Time: 20220129T080328+0000

Ratings and Alerts

No rating or validation information has been found for EnrichmentMap.

No alerts have been found for EnrichmentMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 590 mentions in open access literature.

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

Yogo A, et al. (2026) Spatial Transcriptomics Reveals Location-Specific Tumor Cell Subtypes and Signaling within Multifocal Small Intestinal Neuroendocrine Tumors. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(10), 2098.

Nguyen A, et al. (2026) Pre-Encoded IFN-I Sensitivity Exacerbates Memory T Cell Senescence in Solid Tumors. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(35), e04474.

Kristensen SG, et al. (2026) Molecular signatures of oocyte viability identified by follicular fluid proteomics. Scientific reports, 16(1).

Singhal C, et al. (2026) CUL3LRB E3 ubiquitin ligases control thermosensory growth in Arabidopsis by differentially regulating HY5 and PIF4 protein stability. Science advances, 12(10), eaec7817.

Li Z, et al. (2026) Integration of radiomics, deep learning, transcriptomics, and metabolomics reveals prognostic risk stratification and underlying biological mechanisms in colorectal cancer. NPJ precision oncology, 10(1).

Quaynor SK, et al. (2026) Consensus-based Detection of Aetiologic Copy Number Variants For Syndromic Orofacial Clefts Utilising Whole Exome Sequencing of Case Parent Trios. Research square.

Fan Y, et al. (2026) Uncovering shared and tissue-specific molecular adaptations to intermittent fasting in liver, brain, and muscle. eLife, 14.

Yefet LS, et al. (2026) Assessment of molecular tools in pediatric, adolescent, and young adult meningioma highlights the need for lifespan precision in neuro-oncology. Neuro-oncology, 28(3), 765.

Kang H, et al. (2026) RNA-seq evaluation of equine alveolar macrophages and monocyte-derived macrophages exposed to an inflammatory stimulus (short communication). BMC veterinary research, 22(1).

Zhang X, et al. (2026) Anti-Inflammatory Effects of Marine-Derived Resorcylic Acid Lactone Derivatives in Ulcerative Colitis via the MAPK/ERK Pathway. Marine drugs, 24(2).

Brinkmann M, et al. (2026) SummArIzeR: simplifying cross-database enrichment result clustering and annotation via large language models. Bioinformatics (Oxford, England), 42(3).

Jonas W, et al. (2026) Cholesterol-rich diet exacerbates steatohepatitis in the STAM mouse model. Scientific reports, 16(1).

Cheong I, et al. (2026) Integration of human and mouse single-cell transcriptomes of the developing cerebellum nominates cells-of-origin for group 3 and 4 medulloblastoma. BMC cancer, 26(1).

Yan X, et al. (2026) UBE2S promotes small cell lung cancer transformation and progression via monitoring metabolic remodeling and cell cycle. Journal of translational medicine, 24(1).

Zhang K, et al. (2026) Multi-tissue transcriptomic profiling of foxtail millet in response to drought and rewatering. BMC plant biology, 26(1).

Bosch JA, et al. (2026) Multi-omic mapping of Drosophila protein secretomes reveals tissue-specific origins and inter-organ trafficking. Nature communications, 17(1).

Edge JC, et al. (2026) Bovine endometrial organoids: a new tool to study conceptus-maternal interactions in mammals†. Biology of reproduction, 114(4), 1241.

Zhang Y, et al. (2026) Explainable AI multiomics analysis reveals shared and divergent host responses in COVID-19 and influenza. NPJ digital medicine, 9(1), 111.

Petrenya N, et al. (2026) Genome-wide profiling of salivary promoter-region DNA methylation in periodontitis: the Tromsø Study. BMC medical genomics, 19(1).

Zhang X, et al. (2026) Volumetric mechanoplasticity couples melanoma drug tolerance to susceptibility to CD8+ T cell killing. bioRxiv : the preprint server for biology.