

Resource Summary Report

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ToppCluster

RRID:SCR_001503

Type: Tool

Proper Citation

ToppCluster (RRID:SCR_001503)

Resource Information

URL: <http://toppcluster.cchmc.org/>

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Description: A tool for performing multi-cluster gene functional enrichment analyses on large scale data (microarray experiments with many time-points, cell-types, tissue-types, etc.). It facilitates co-analysis of multiple gene lists and yields as output a rich functional map showing the shared and list-specific functional features. The output can be visualized in tabular, heatmap or network formats using built-in options as well as third-party software. It uses the hypergeometric test to obtain functional enrichment achieved via the gene list enrichment analysis option available in ToppGene.

Abbreviations: ToppCluster

Synonyms: ToppCluster: A multiple gene list feature analyzer for the dissection of biological systems

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

Defining Citation: [PMID:20484371](#)

Keywords: term enrichment, gene, analysis, gene enrichment analysis, connectivity, heatmap, ortholog, microarray, function, bio.tools

Funding: NIDDK 1U01DK70219;
NIDDK P30DK078392;
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NIDCR U01DE020049

Availability: Free

Resource Name: ToppCluster

Resource ID: SCR_001503

Alternate IDs: OMICS_02225, nlx_152801, biotools:toppcluster

Alternate URLs: <https://bio.tools/toppcluster>

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260903T235750+0000

Ratings and Alerts

No rating or validation information has been found for ToppCluster .

No alerts have been found for ToppCluster .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 152 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Brandon AE, et al. (2026) Protein kinase C epsilon deletion in AgRP neurons modulates hypothalamic glucose sensing and improves glucose tolerance in mice. *Molecular metabolism*, 104, 102320.

Huber J, et al. (2026) The Sh3Pxd2bnee^{-/-} mouse: an attractive model unveiling novel developmental features in Frank-ter-Haar Syndrome. *Development (Cambridge, England)*.

Madhuravasal Krishnan J, et al. (2025) The synthetic opioid fentanyl increases HIV replication in macrophages. *PloS one*, 20(2), e0298341.

Bell MB, et al. (2025) Brain Transcriptome Changes Associated With an Acute Increase of Protein O-GlcNAcylation and Implications for Neurodegenerative Disease. *Journal of neurochemistry*, 169(1), e16302.

Liu J, et al. (2025) The Epstein-Barr virus deubiquitinase BPLF1 regulates stress-induced ribosome UFMylation and reticulophagy. *Autophagy*, 21(5), 996.

Ayala-Torres C, et al. (2025) Regulation of N-degron recognin-mediated autophagy by the SARS-CoV-2 PLpro ubiquitin deconjugase. *Autophagy*, 21(5), 1019.

Deng EB, et al. (2025) A Tonic Signaling Code Predicts CAR-T Cell Efficacy in Diffuse Midline Glioma. *bioRxiv : the preprint server for biology*.

Wu LMN, et al. (2025) Single-cell and Spatial Omics Reveals Region-Specific Plasticity and Therapeutic Vulnerabilities in Metastatic High-Risk Neuroblastoma. *bioRxiv : the*

preprint server for biology.

Malaymar Pinar D, et al. (2025) Nuclear Factor I Family Members are Key Transcription Factors Regulating Gene Expression. *Molecular & cellular proteomics : MCP*, 24(1), 100890.

Solta A, et al. (2025) Unveiling the powerhouse: ASCL1-driven small cell lung cancer is characterized by higher numbers of mitochondria and enhanced oxidative phosphorylation. *Cancer & metabolism*, 13(1), 16.

Kim Y, et al. (2025) Mitochondrial proteome landscape unveils key insights into melanoma severity and treatment strategies. *Cancer*, 131(13), e35897.

Mao G, et al. (2025) Identification and experimental validation of biomarkers related to mitochondrial and programmed cell death in obsessive-compulsive disorder. *Scientific reports*, 15(1), 31971.

Braun T, et al. (2024) Diet-omics in the Study of Urban and Rural Crohn disease Evolution (SOURCE) cohort. *Nature communications*, 15(1), 3764.

Gammie SC, et al. (2024) Large-scale gene expression changes in APP/PSEN1 and GFAP mutation models exhibit high congruence with Alzheimer's disease. *PloS one*, 19(1), e0291995.

Ayuso-García P, et al. (2024) Neddylation orchestrates the complex transcriptional and posttranscriptional program that drives Schwann cell myelination. *Science advances*, 10(15), eadm7600.

Krishnan JM, et al. (2024) Effect of fentanyl on HIV expression in peripheral blood mononuclear cells. *Frontiers in microbiology*, 15, 1463441.

Kahraman S, et al. (2024) m6A mRNA methylation by METTL14 regulates early pancreatic cell differentiation. *The EMBO journal*.

Roider E, et al. (2024) MITF regulates IDH1, NNT, and a transcriptional program protecting melanoma from reactive oxygen species. *Scientific reports*, 14(1), 21527.

Yoshida M, et al. (2024) Transcriptome analysis of long non-coding RNAs in *Mycobacterium avium* complex-infected macrophages. *Frontiers in immunology*, 15, 1374437.

Huang K, et al. (2024) Effect of acidosis on adipose-derived stem cell impairment and gene expression. *Regenerative therapy*, 25, 331.