

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;
NCRR U54 RR025216;
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: 20260821T193624+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 [dkNET](#) .

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).

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.

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

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.

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.

Deng EB, et al. (2025) A Tonic Signaling Code Predicts CAR-T Cell Efficacy in Diffuse Midline Glioma. *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.

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

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