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: service resource, production service resource, data analysis service, analysis service resource, 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: 20250517T055503+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 137 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

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.

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

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

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.

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.

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

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

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

Sosnovski KE, et al. (2023) Reduced LHFPL3-AS2 IncRNA expression is linked to altered epithelial polarity and proliferation, and to ileal ulceration in Crohn disease. Scientific reports, 13(1), 20513.

Whyte SS, et al. (2023) Integrated analysis using ToppMiR uncovers altered miRNA-?mRNA regulatory networks in pediatric hepatocellular carcinoma-A pilot study. Cancer reports (Hoboken, N.J.), 6(1), e1685.

Tejwani L, et al. (2023) Reduction of nemo-like kinase increases lysosome biogenesis and ameliorates TDP-43-related neurodegeneration. The Journal of clinical investigation, 133(16).

Madhuravasal Krishnan J, et al. (2023) The Synthetic Opioid Fentanyl Increases HIV Replication and Chemokine Co-Receptor Expression in Lymphocyte Cell Lines. Viruses, 15(4).

Fonseca PAS, et al. (2023) Multi-breed host rumen epithelium transcriptome and microbiome associations and their relationship with beef cattle feed efficiency. Scientific reports, 13(1), 16209.

Sosnovski KE, et al. (2023) GATA6-AS1 Regulates Intestinal Epithelial Mitochondrial Functions, and its Reduced Expression is Linked to Intestinal Inflammation and Less Favourable Disease Course in Ulcerative Colitis. Journal of Crohn's & colitis, 17(6), 960.

Dubois-Chevalier J, et al. (2023) An extended transcription factor regulatory network controls hepatocyte identity. EMBO reports, 24(9), e57020.

Kolli U, et al. (2023) Multi-omics analysis revealing the interplay between gut microbiome and the host following opioid use. Gut microbes, 15(2), 2246184.

Bolte AC, et al. (2023) The meningeal transcriptional response to traumatic brain injury and aging. eLife, 12.

Younas N, et al. (2023) Differential interactome mapping of aggregation prone/prion-like proteins under stress: novel links to stress granule biology. Cell & bioscience, 13(1), 221.