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, resource, service resource, data analysis service, production service resource

Defining Citation: PMID:20484371

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

Funding Agency: NIDDK, NIDDK, NCRR, NIDCR

Availability: Free

Resource Name: ToppCluster

Resource ID: SCR_001503

Alternate IDs: OMICS_02225, nlx_152801, biotools:toppcluster

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

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: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 128 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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

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.

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.

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).

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).

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

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.

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.

Challa NVD, et al. (2023) GSDMD gene knockout alleviates hyperoxia-induced hippocampal brain injury in neonatal mice. Journal of neuroinflammation, 20(1), 205.

Nguyen V, et al. (2023) Supporting materials: Endothelial cells differentiated from patient dermal fibroblast-derived induced pluripotent stem cells resemble vascular malformations of Port Wine Birthmark. bioRxiv : the preprint server for biology.

Yang X, et al. (2022) Protein palmitoylation regulates extracellular vesicle production and function in sepsis. Journal of extracellular biology, 1(7).

Ennerfelt H, et al. (2022) SYK coordinates neuroprotective microglial responses in neurodegenerative disease. Cell, 185(22), 4135.

You Y, et al. (2022) Human neural cell type-specific extracellular vesicle proteome defines disease-related molecules associated with activated astrocytes in Alzheimer's disease brain. Journal of extracellular vesicles, 11(1), e12183.

Sharma M, et al. (2022) Mesenchymal Stem Cell-derived Extracellular Vesicles Prevent Experimental Bronchopulmonary Dysplasia Complicated By Pulmonary Hypertension. Stem cells translational medicine, 11(8), 828.

Raja GL, et al. (2022) In utero exposure to endocrine disruptors and developmental neurotoxicity: Implications for behavioural and neurological disorders in adult life. Environmental research, 203, 111829.

Wang Z, et al. (2022) Transcription Analysis of Liver and Muscle Tissues from Landrace Finishing Pigs with Different Feed Conversion Ratios. Genes, 13(11).