Resource Summary Report

Generated by dkNET on Apr 22, 2025

Rank Rank Hypergeometric Overlap

RRID:SCR_014024
Type: Tool

Proper Citation

Rank Rank Hypergeometric Overlap (RRID:SCR_014024)

Resource Information

URL: http://systems.crump.ucla.edu/rankrank/rankranksimple.php

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Description: Software tool that compares two gene expression signatures. Each signature is processed as a ranked list based on expression differences between two classes of samples. The signatures can be input either as raw expression data and sample and class labels, or as a preranked gene list.

Abbreviations: RRHO

Resource Type: software resource, sequence analysis software, data analysis software, data processing software, software application

Defining Citation: PMID:20660011

Keywords: algorithm, gene expression, gene expression signature, raw expression data, preranked

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: Rank Rank Hypergeometric Overlap

Resource ID: SCR_014024

Alternate URLs: http://www.bioconductor.org/packages/release/bioc/html/RRHO.html,

License URLs: http://oip.ucla.edu/graeber-lab-bioinformatic-software

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250422T055751+0000

Ratings and Alerts

No rating or validation information has been found for Rank Rank Hypergeometric Overlap.

No alerts have been found for Rank Rank Hypergeometric Overlap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Vandenbempt V, et al. (2024) HAMSAB diet ameliorates dysfunctional signaling in pancreatic islets in autoimmune diabetes. iScience, 27(1), 108694.

Hong J, et al. (2024) Multiomics profiling of buffy coat and plasma unveils etiology-specific signatures in hepatocellular carcinoma. Clinical and molecular hepatology, 30(3), 360.

Booher WC, et al. (2023) Hippocampal RNA sequencing in mice selectively bred for high and low activity. Genes, brain, and behavior, 22(2), e12832.

Peng S, et al. (2023) Identification of novel targets and pathways to distinguish suicide dependent or independent on depression diagnosis. Scientific reports, 13(1), 2488.

Seeling C, et al. (2021) Molecular features and vulnerabilities of recurrent chordomas. Journal of experimental & clinical cancer research : CR, 40(1), 244.

Javeed N, et al. (2021) Pro-inflammatory ? cell small extracellular vesicles induce ? cell failure through activation of the CXCL10/CXCR3 axis in diabetes. Cell reports, 36(8), 109613.

Bentsen MA, et al. (2020) Transcriptomic analysis links diverse hypothalamic cell types to fibroblast growth factor 1-induced sustained diabetes remission. Nature communications, 11(1), 4458.

Vijayaraj P, et al. (2019) Modeling Progressive Fibrosis with Pluripotent Stem Cells Identifies

an Anti-fibrotic Small Molecule. Cell reports, 29(11), 3488.

Lim SB, et al. (2019) Compendiums of cancer transcriptomes for machine learning applications. Scientific data, 6(1), 194.

Tol MJ, et al. (2018) HEPES activates a MiT/TFE-dependent lysosomal-autophagic gene network in cultured cells: A call for caution. Autophagy, 14(3), 437.

Shimada E, et al. (2018) PNPase knockout results in mtDNA loss and an altered metabolic gene expression program. PloS one, 13(7), e0200925.

Smith BA, et al. (2018) A Human Adult Stem Cell Signature Marks Aggressive Variants across Epithelial Cancers. Cell reports, 24(12), 3353.

Kraaijeveld K, et al. (2018) Regulatory and sequence evolution in response to selection for improved associative learning ability in Nasonia vitripennis. BMC genomics, 19(1), 892.

Lardone RD, et al. (2016) Cross-platform comparison of independent datasets identifies an immune signature associated with improved survival in metastatic melanoma. Oncotarget, 7(12), 14415.

Hong CS, et al. (2016) MCT1 Modulates Cancer Cell Pyruvate Export and Growth of Tumors that Co-express MCT1 and MCT4. Cell reports, 14(7), 1590.

Franke B, et al. (2016) Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature neuroscience, 19(3), 420.

Haan S, et al. (2015) The oncogenic FIP1L1-PDGFR? fusion protein displays skewed signaling properties compared to its wild-type PDGFR? counterpart. JAK-STAT, 4(1), e1062596.

Snoek LB, et al. (2012) Genetical Genomics Reveals Large Scale Genotype-By-Environment Interactions in Arabidopsis thaliana. Frontiers in genetics, 3, 317.