Resource Summary Report

Generated by RRID on Apr 14, 2025

CummeRbund

RRID:SCR_014568
Type: Tool

Proper Citation

CummeRbund (RRID:SCR_014568)

Resource Information

URL: http://compbio.mit.edu/cummeRbund/index.html

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Description: Software R package used for simplifying and analyzing Cufflink RNA-Seq output. This program takes various output files from a cuffdiff run and creates a SQLite database of the results that will describe the appropriate relationships between the genes, transcripts, transcription start sites and CDS regions.

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

Keywords: r software, cufflink, rna-seq, sqlite, gene, transcript, transcription start site, cds region, r, rnaseq, rna seq, bio.tools, FASEB list

Funding:

Availability: Free, Freely available

Resource Name: CummeRbund

Resource ID: SCR_014568

Alternate IDs: biotools:cummerbund, OMICS_07349

Alternate URLs: https://bio.tools/cummerbund, https://sources.debian.org/src/r-bioc-cummerbund/

License: Artistic License 2.0

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250412T055813+0000

Ratings and Alerts

No rating or validation information has been found for CummeRbund.

No alerts have been found for CummeRbund.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 355 mentions in open access literature.

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

Xie F, et al. (2024) Repetitive transcranial magnetic stimulation alleviates motor impairment in Parkinson's disease: association with peripheral inflammatory regulatory T-cells and SYT6. Molecular neurodegeneration, 19(1), 80.

Tsai SH, et al. (2024) Peripheral peroxisomal ?-oxidation engages neuronal serotonin signaling to drive stress-induced aversive memory in C. elegans. Cell reports, 43(4), 113996.

Sharma A, et al. (2024) Deciphering the role of VapBC13 and VapBC26 toxin antitoxin systems in the pathophysiology of Mycobacterium tuberculosis. Communications biology, 7(1), 1417.

Chaubal R, et al. (2024) Surgical Tumor Resection Deregulates Hallmarks of Cancer in Resected Tissue and the Surrounding Microenvironment. Molecular cancer research : MCR, 22(6), 572.

Lan MY, et al. (2024) Unraveling the Pathogenetic Mechanisms Underlying the Association between Specific Mitochondrial DNA Haplogroups and Parkinson's Disease. Cells, 13(8).

Shang S, et al. (2024) 0.263 terahertz irradiation induced genes expression changes in Caenorhabditis elegans. iScience, 27(4), 109391.

Lages MA, et al. (2024) Remodulation of bacterial transcriptome after acquisition of foreign DNA: the case of irp-HPI high-pathogenicity island in Vibrio anguillarum. mSphere, 9(1), e0059623.

Lavado-Benito C, et al. (2024) GacA reduces virulence and increases competitiveness in

planta in the tumorigenic olive pathogen Pseudomonas savastanoi pv. savastanoi. Frontiers in plant science, 15, 1347982.

Daneshpour H, et al. (2023) Macroscopic quorum sensing sustains differentiating embryonic stem cells. Nature chemical biology, 19(5), 596.

Peng H, et al. (2023) SLC43A2 and NF?B signaling pathway regulate methionine/cystine restriction-induced ferroptosis in esophageal squamous cell carcinoma via a feedback loop. Cell death & disease, 14(6), 347.

Sands E, et al. (2023) Genetic and physiological responses to light quality in a deep ocean ecotype of Ostreococcus, an ecologically important photosynthetic picoeukaryote. Journal of experimental botany, 74(21), 6773.

Letelier J, et al. (2023) Mutation of vsx genes in zebrafish highlights the robustness of the retinal specification network. eLife, 12.

Jacksi M, et al. (2023) Absence of Scaffold Protein Tks4 Disrupts Several Signaling Pathways in Colon Cancer Cells. International journal of molecular sciences, 24(2).

Schorr AL, et al. (2023) An updated C. elegans nuclear body muscle transcriptome for studies in muscle formation and function. Skeletal muscle, 13(1), 4.

Murakami-Nishimagi Y, et al. (2023) Claudin-4-adhesion signaling drives breast cancer metabolism and progression via liver X receptor ?. Breast cancer research : BCR, 25(1), 41.

Poonperm R, et al. (2023) Replication dynamics identifies the folding principles of the inactive X chromosome. Nature structural & molecular biology, 30(8), 1224.

Dominici C, et al. (2022) Muscle stem cell polarity requires QKI-mediated alternative splicing of Integrin Alpha-7 (Itga7). Life science alliance, 5(5).

Sarkar SR, et al. (2022) DDX24 is required for muscle fiber organization and the suppression of wound-induced Wnt activity necessary for pole re-establishment during planarian regeneration. Developmental biology, 488, 11.

Paslaru L, et al. (2022) Comparative RNA-Sequencing Analysis Reveals High Complexity and Heterogeneity of Transcriptomic and Immune Profiles in Hepatocellular Carcinoma Tumors of Viral (HBV, HCV) and Non-Viral Etiology. Medicina (Kaunas, Lithuania), 58(12).

Zhang Q, et al. (2022) Identifying the Caenorhabditis elegans vulval transcriptome. G3 (Bethesda, Md.), 12(6).