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: A package of the R software which is 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: Resource, software resource, data processing software, data analysis software, sequence analysis software, software application

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

Parent Organization: Harvard University; Cambridge; United States, Massachusetts Institute of Technology; Massachusetts; USA

Availability: Open Source

Website Status: Last checked up

Resource Name: CummeRbund

Resource ID: SCR_014568

Alternate IDs: biotools:cummerbund

Alternate URLs: https://bio.tools/cummerbund
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 297 mentions in open access literature.

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


Martín-Vicente M, et al. (2020) Downregulation of A20 Expression Increases the Immune Response and Apoptosis and Reduces Virus Production in Cells Infected by the Human Respiratory Syncytial Virus. Vaccines, 8(1).


Lu S, et al. (2020) Smooth muscle-derived progenitor cell myofibroblast differentiation through KLF4 downregulation promotes arterial remodeling and fibrosis. JCI insight, 5(23).


