CummeRbund

RRID:SCR_014568
Type: Tool

Proper Citation

CummeRbund (RRID:SCR_014568)

Resource Information

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

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.

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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

Resource ID: SCR_014568

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

Availability: Open Source

Website Status: Last checked up

Mentions Count: 262

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 262 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](#).


Hong AL, et al. (2019) Renal medullary carcinomas depend uponloss and are sensitive to proteasome inhibition. eLife, 8.


Arora R, et al. (2019) Transcriptome profiling of longissimus thoracis muscles identifies highly connected differentially expressed genes in meat type sheep of India. PloS one, 14(6),


