**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.

**Resource Name:** CummeRbund

**Proper Citation:** CummeRbund (RRID:SCR_014568)

**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
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 upon loss 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),


