Cufflinks
RRID:SCR_014597
Type: Tool

Proper Citation
Cufflinks (RRID:SCR_014597)

Resource Information

URL: http://cole-trapnell-lab.github.io/cufflinks/cuffmerge/

Description: A software which is used for transcriptome assembly and differential expression analysis for RNA-Seq. This software includes a script called cuffmerge that can be used to merge together several Cufflinks assemblies. It also handles running Cuffcompare as well as automatically filtering a number of transfrags that are likely to be artifacts. If the researcher has a reference GTF file, the researcher can provide it to the script to more effectively merge novel isoforms and maximize overall assembly quality.

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

Keywords: transcriptome, rna-seq, rna seq, cuffmerge, cufflink, cuffcompare, transfrags, artifacts, gtf file, transcriptome assembly, expression analysis

Resource ID: SCR_014597

References: DOI:10.1038/nbt.1621

Availability: Acknowledgement requested, Source code available on GitHub

Website Status: Last checked up

Alternate IDs: OMICS_01304, SCR_013307
Alternate URLs: https://github.com/cole-trapnell-lab/cufflinks

Mentions Count: 4678

Ratings and Alerts

No rating or validation information has been found for Cufflinks.

No alerts have been found for Cufflinks.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4678 mentions in open access literature.

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


Yim A, et al. (2020) mitoXplorer, a visual data mining platform to systematically analyze and visualize mitochondrial expression dynamics and mutations. Nucleic acids research, 48(2), 605-632.


