Cufflinks

RRID:SCR_014597
Type: Tool

Proper Citation

Cufflinks (RRID:SCR_014597)

Resource Information

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

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Description: Software tool for transcriptome assembly and differential expression analysis for RNA-Seq. Includes 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.

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

Defining Citation: DOI:10.1038/nbt.1621

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

Availability: Acknowledgement requested, Source code available on GitHub

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Alternate IDs: biotools:cufflinks, OMICS_01304, SCR_013307

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 7976 mentions in open access literature.

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

Huang LC, et al. (2024) BRCA1 and ELK-1 regulate neural progenitor cell fate in the optic tectum in response to visual experience in Xenopus laevis tadpoles. Proceedings of the National Academy of Sciences of the United States of America, 121(3), e2316542121.


Zhou R, et al. (2024) Decreased YB-1 expression denervates brown adipose tissue and contributes to age-related metabolic dysfunction. Cell proliferation, 57(1), e13520.


An X, et al. (2024) WTAP-mediated m6A modification of FRZB triggers the inflammatory response via the Wnt signaling pathway in osteoarthritis. Experimental & molecular medicine, 56(1), 156.


Huang X, et al. (2024) Transcriptomic and targeted metabolome analyses revealed the regulatory mechanisms of the synthesis of bioactive compounds in Citrus grandis 'tomentosa'. PeerJ, 12, e16881.
