Resource Summary Report

Generated by NIF on Apr 8, 2025

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

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

Funding:

Availability: Acknowledgement requested, Source code available on GitHub

Resource Name: Cufflinks

Resource ID: SCR_014597

Alternate IDs: biotools:cufflinks, OMICS_01304, SCR_013307

Alternate URLs: https://github.com/cole-trapnell-lab/cufflinks, https://bio.tools/cufflinks, https://sources.debian.org/src/cufflinks/

Record Creation Time: 20220129T080321+0000

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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 8415 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Yan Y, et al. (2025) Degenerated vision, altered lipid metabolism, and expanded chemoreceptor repertoires enable Lindaspio polybranchiata to thrive in deep-sea cold seeps. BMC biology, 23(1), 13.

Shah K, et al. (2025) Gibberellin-3 induced dormancy and suppression of flower bud formation in pitaya (Hylocereus polyrhizus). BMC plant biology, 25(1), 47.

Li J, et al. (2025) Jasmonic acid plays an important role in mediating retrograde signaling under mitochondrial translational stress to balance plant growth and defense. Plant communications, 6(1), 101133.

Kim SJ, et al. (2025) Disruption of bioenergetics enhances the radio-sensitivity of patient-derived glioblastoma tumorspheres. Translational oncology, 51, 102197.

Sun Q, et al. (2025) Pervasive RNA-binding protein enrichment on TAD boundaries regulates TAD organization. Nucleic acids research, 53(1).

Shi J, et al. (2025) Saponins enhance the stability and cost-efficiency of human embryonic stem cell culture. Cell regeneration (London, England), 14(1), 3.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (Eleusine indica). Scientific data, 12(1), 156.

Shaikh K, et al. (2025) ZFAND6 promotes TRAF2-dependent mitophagy to restrain cGAS-STING signaling. iScience, 28(1), 111544.

Yan X, et al. (2025) CMSP exerts anti-tumor effects on small cell lung cancer cells by inducing mitochondrial dysfunction and ferroptosis. Open medicine (Warsaw, Poland), 20(1), 20241100.

McColl KS, et al. (2025) Identification of HEPACAM2 as a novel and specific marker of small cell carcinoma. Cancer, 131(1), e35557.

Zhang W, et al. (2025) Chromosome-level genome assembly of tetraploid Chinese cherry (Prunus pseudocerasus). Scientific data, 12(1), 136.

Wang C, et al. (2025) Identifying Candidate Genes Related to Soybean (Glycine max) Seed Coat Color via RNA-Seq and Coexpression Network Analysis. Genes, 16(1).

Li L, et al. (2025) A Chromosomal-level genome assembly and annotation of fat greenling (Hexagrammos otakii). Scientific data, 12(1), 78.

Chen L, et al. (2025) MOF-derived intelligent arenobufagin nanocomposites with glucose metabolism inhibition for enhanced bioenergetic therapy and integrated photothermal-chemodynamic-chemotherapy. Journal of nanobiotechnology, 23(1), 19.

Ma L, et al. (2025) lncRNA, miRNA, and mRNA of plasma and tumor-derived exosomes of cardiac myxoma-related ischaemic stroke. Scientific data, 12(1), 91.

Yang Y, et al. (2025) A Chromosome-Scale Genome of Trametes versicolor and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene Biosynthesis. Journal of fungi (Basel, Switzerland), 11(1).

Song XQ, et al. (2025) Copy number amplification of FLAD1 promotes the progression of triple-negative breast cancer through lipid metabolism. Nature communications, 16(1), 1241.

Zhang J, et al. (2025) Nutrient status alters developmental fates via a switch in mitochondrial homeodynamics. Nature communications, 16(1), 1258.

Sio YY, et al. (2025) Functional Polymorphisms Regulate FOXO1 Transcript Expression and Contribute to the Risk and Symptom Severity of HDM-Induced Allergic Rhinitis. International archives of allergy and immunology, 186(1), 1.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries. Molecular horticulture, 5(1), 6.