

# Resource Summary Report

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## Cufflinks

RRID:SCR\_014597

Type: Tool

### Proper Citation

Cufflinks (RRID:SCR\_014597)

### Resource Information

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

**Proper Citation:** Cufflinks (RRID:SCR\_014597)

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

**Defining Citation:** [DOI:10.1038/nbt.1621](https://doi.org/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

**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

**Record Last Update:** 20260731T042923+0000

### Ratings and Alerts

No rating or validation information has been found for Cufflinks.

No alerts have been found for Cufflinks.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 8838 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Yu YH, et al. (2026) Transcriptome and microbiota analysis reveal differences in the cecum of weaning pigs in response to different dietary crude protein levels. *Animal bioscience*, 39(1), 250135.

Li JJ, et al. (2026) NSD2 targeting reverses plasticity and drug resistance in prostate cancer. *Nature*, 649(8095), 216.

Jing J, et al. (2026) Recombinant tissue plasminogen activator protects neurons after intracerebral hemorrhage through activating the PI3K/AKT/mTOR pathway. *Neural regeneration research*, 21(4), 1574.

Chen Q, et al. (2026) SAMD4A inhibits abdominal aortic aneurysm development and VSMC phenotypic transformation through targeting KDM2B. *Journal of advanced research*, 79, 223.

Sun B, et al. (2026) CDK1?induced regulation of p53 phosphorylation at Ser315 mediates cell cycle arrest and apoptosis of macrophages infected with clinical isolates of *Mycobacterium tuberculosis*. *Molecular medicine reports*, 33(1).

Rosen JC, et al. (2026) Modeling response to the KRAS-G12C inhibitor AZD4625 in KRASG12C NSCLC patient-derived xenografts reveals insights into primary resistance mechanisms. *British journal of cancer*, 134(1), 165.

Zhu X, et al. (2026) PARP1 stabilizes FOXN3 to suppress pulmonary fibrosis through p38-related feedback regulation. *Science advances*, 12(1), eady1681.

Scott MC, et al. (2025) Deep profiling deconstructs features associated with memory CD8+ T cell tissue residence. *Immunity*, 58(1), 162.

Gilbert MB, et al. (2025) Neuropeptides specify and reprogram division of labor in the leafcutter ant *Atta cephalotes*. *Cell*, 188(15), 3974.

Hayashi Y, et al. (2025) Glial cells missing 1 triggers gliosis and angiogenesis after neonatal brain injury. *iScience*, 28(11), 113860.

de Sousa GR, et al. (2025) Loss of LDOC1 by chromatin compaction in mesenchymal tumor cells is required for PFA1 ependymoma growth. *Neuro-oncology*, 27(6), 1597.

Löönd F, et al. (2025) DLBCL Cells Emerge after CD19 CAR T Cells with Cross-Antigen Resistance and a Gene Signature Predictive of Clinical CAR T-cell Response. *Blood cancer discovery*, 6(6), 580.

Singh P, et al. (2025) Alternative mRNA splicing in anthracycline-induced cardiomyopathy - a COG-ALTE03N1 report. *Cardio-oncology (London, England)*, 11(1), 47.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Welti J, et al. (2025) NXP800 Activates the Unfolded Protein Response, Altering AR and E2F Function to Impact Castration-Resistant Prostate Cancer Growth. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(6), 1109.

Goel S, et al. (2025) A Phase II Study of Abemaciclib for Patients with Retinoblastoma-Positive, Metastatic Triple-Negative Breast Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(8), 1427.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

Huang X, et al. (2025) CDK4/6 Inhibition Reverses MEIS2 Suppression of CRL4 CRBN to Enhance Immunomodulatory Drug Therapy in Multiple Myeloma. *bioRxiv : the preprint server for biology*.

DeSisto J, et al. (2025) PRMT5 Maintains Tumor Stem Cells to Promote Pediatric High-Grade Glioma Tumorigenesis. *Molecular cancer research : MCR*, 23(2), 107.