

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

**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:** 20260905T132748+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 9083 mentions in open access literature.

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

Xue Y, et al. (2026) Mucosal-associated invariant T cells recognize a tumor-derived metabolite in the DNA synthesis pathway. *Frontiers in immunology*, 17, 1797918.

Kuo HH, et al. (2026) Patient-derived organoids across cancers reveal conserved tumor heterogeneity and actionable therapeutic vulnerabilities. *Science advances*, 12(26), eadz3351.

Boudjadi S, et al. (2026) Involvement of the FGF8/FGF Receptor Signaling Pathway in the Maintenance and Progression of Fusion-Positive Rhabdomyosarcoma. *Molecular cancer therapeutics*, 25(3), 493.

Komura S, et al. (2026) Expression of Glycoprotein B (gB) Correlates With Poor Prognosis in Nasopharyngeal Carcinoma. *Cancer science*, 117(5), 1481.

Kim DH, et al. (2026) Tumor Exosomal L1 Cell Adhesion Molecule Promotes Brain Metastasis of Lung Cancer. *Research (Washington, D.C.)*, 9, 1126.

Nakajo S, et al. (2026) Hypoxic CAF studies unveil PTHrP?vitamin D?RAS axis as pivotal in the CAF. *Oncology reports*, 55(6).

Gautier M, et al. (2026) A regulatory circuitry driving a noradrenergic to mesenchymal transition highlights YAP/TAZ as critical players in neuroblastoma plasticity. *Cell reports*, 45(5), 117351.

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.

Das D, et al. (2026) Immune landscape of gingivo-buccal oral cancer indicates high enrichment of immune-related gene sets in tumors of a large proportion of patients. *Molecular medicine (Cambridge, Mass.)*, 32(1).

Cuba Z, et al. (2026) Fixed-Bed Bioreactor Culture Enhances Yield and Reparative Properties of hTERT Mesenchymal Stem Cell Extracellular Vesicles. *Cells*, 15(7).

Lee CH, et al. (2026) [3-11C]Pyruvate PET detects alterations in cardiac pyruvate metabolism induced by doxorubicin chemotherapy. *Npj imaging*, 4(1).

Yue Z, et al. (2026) Subcellular Redistribution of Endomembrane GPR15 Promotes NAD<sup>+</sup>-Mediated Metabolic Reprogramming and Boosts 5-FU Chemosensitivity in Colorectal Cancer. *Cancer research*, 86(9), 2253.

Tang C, et al. (2026) HnRPD/AUF1 facilitates human ovarian cancer progression through activating FLI1 and maintaining cisplatin resistance. *Molecular cancer*, 25(1).

Lee JM, et al. (2026) Radiologic phenotype-specific transcriptomic signatures in lung tissues from patients with Mycobacterium avium complex pulmonary disease. *European journal of medical research*, 31(1), 299.

Kubota S, et al. (2026)  $\gamma$ -Glutamylcyclotransferase Depletion Induces p15<sup>INK4b</sup> and p21<sup>Cip1</sup>-mediated Senescence via TGF- $\beta$ 2/SMAD3 Pathway Activation in Breast Cancer Cells. *Cancer genomics & proteomics*, 23(2), 195.

He Z, et al. (2026) Transcriptome sequencing and weighted correlation network analysis reveal the molecular mechanism of growth variation in highly resistant transgenic double Bt poplar. *BMC plant biology*, 26(1).

Gao L, et al. (2026) Transcriptome Sequencing Unveils a Novel Mechanism Underlying Breed Distinctions Between Thin- and Fat-Tailed Sheep. *Genes*, 17(2).

Zhang Z, et al. (2026) Fuzheng Huayu formula ameliorates chronic cholestatic liver injury by upregulating PPAR $\alpha$  in mice. *Chinese medicine*, 21(1).

Machida T, et al. (2026) LSD1 inhibitor, TAS1440, disrupts INSM1-LSD1 complex activating tumor-suppressive pathways via transcriptional reprogramming in neuroendocrine SCLC. *Nature communications*, 17(1).

Grau J, et al. (2026) Improved reconstruction of transcripts and coding sequences from RNA-seq data. *Nucleic acids research*, 54(4).