

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## TopHat-Fusion

RRID:SCR\_011899

Type: Tool

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### Proper Citation

TopHat-Fusion (RRID:SCR\_011899)

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### Resource Information

**URL:** [http://tophat.cbcb.umd.edu/fusion\\_index.html](http://tophat.cbcb.umd.edu/fusion_index.html)

**Proper Citation:** TopHat-Fusion (RRID:SCR\_011899)

**Description:** An algorithm for Discovery of Novel Fusion Transcripts with the ability to align reads across fusion points, which results from the breakage and re-joining of two different chromosomes, or from rearrangements within a chromosome.

**Abbreviations:** TopHat-Fusion

**Synonyms:** TopHat-Fusion: An algorithm for Discovery of Novel Fusion Transcripts

**Resource Type:** software resource

**Defining Citation:** [PMID:21835007](#)

**Keywords:** bio.tools

**Resource Name:** TopHat-Fusion

**Resource ID:** SCR\_011899

**Alternate IDs:** OMICS\_01359, biotools:tophat-fusion

**Alternate URLs:** <https://bio.tools/tophat-fusion>

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20260725T190726+0000

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### Ratings and Alerts

No rating or validation information has been found for TopHat-Fusion.

No alerts have been found for TopHat-Fusion.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 159 mentions in open access literature.

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

Wu J, et al. (2025) Whole-transcriptome analysis reveals the profiles and roles of coding and non-coding RNAs during hair follicle cycling in Rex rabbits. *BMC genomics*, 26(1), 74.

Wang TZ, et al. (2025) Mining, validating, and quantifying circular RNA transcriptome from total RNA as a biomarker or target. *Scientific reports*, 15(1), 20418.

Tu J, et al. (2025) Identification of Riboflavin Metabolism Pathway in HepG2 Cells Expressing Genotype IV Swine Hepatitis E Virus ORF3 Protein. *Veterinary sciences*, 12(9).

Shah M, et al. (2025) Peptide-based therapeutics targeting the SLC39A14-PIWIL2 fusion in hepatocellular carcinoma. *Genomics & informatics*, 23(1), 28.

Lin H, et al. (2025) Whole Transcriptome-Based ceRNA Regulatory Network Analysis of Radiation-Induced Esophageal Epithelial Cell Injury. *Biologics : targets & therapy*, 19, 231.

Zhao L, et al. (2025) The biomarker potential of circPOLD1 and its binding protein YBX1 in cervical carcinogenesis. *Journal of translational medicine*, 23(1), 506.

Zhang S, et al. (2025) CircCdh7 induces astrogliosis and neuroinflammation to trigger hypertensive effects in the rostral ventrolateral medulla. *Cell & bioscience*, 15(1), 141.

Yang C, et al. (2025) CeRNA profiling and the role in regulating gonadal development in gold pompano. *BMC genomics*, 26(1), 43.

Datar GK, et al. (2025) Nuclear Phase Separation Drives NPM1-mutant Acute Myeloid Leukemia. *bioRxiv : the preprint server for biology*.

Anselmino N, et al. (2024) Integrative Molecular Analyses of the MD Anderson Prostate Cancer Patient-derived Xenograft (MDA PCa PDX) Series. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(10), 2272.

Zheng W, et al. (2024) CircYthdc2 generates polypeptides through two translation strategies to facilitate virus escape. *Cellular and molecular life sciences : CMLS*, 81(1), 91.

Zhang M, et al. (2024) Circular RNA HMGCS1 sponges MIR4521 to aggravate type 2 diabetes-induced vascular endothelial dysfunction. *eLife*, 13.

Xiao L, et al. (2024) Whole-transcriptome sequencing revealed the ceRNA regulatory network during the proliferation and differentiation of goose myoblast. *Poultry science*, 103(11), 104173.

DiPeri TP, et al. (2024) Utilizing Patient-derived Xenografts to Model Precision Oncology for Biliary Tract Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*.

Das A, et al. (2023) Identification of potential proteins translated from circular RNA splice variants. *European journal of cell biology*, 102(1), 151286.

Gentien D, et al. (2023) Multi-omics comparison of malignant and normal uveal melanocytes reveals molecular features of uveal melanoma. *Cell reports*, 42(9), 113132.

Dai W, et al. (2023) Hedgehog-Gli1-derived exosomal circ-0011536 mediates peripheral neural remodeling in pancreatic cancer by modulating the miR-451a/VGF axis. *Journal of experimental & clinical cancer research : CR*, 42(1), 329.

Deng J, et al. (2023) Specific intracellular retention of circSKA3 promotes colorectal cancer metastasis by attenuating ubiquitination and degradation of SLUG. *Cell death & disease*, 14(11), 750.

Liu J, et al. (2023) Transcriptome RNA Sequencing Reveals That Circular RNAs Are Abundantly Expressed in Embryonic Breast Muscle of Duck. *Veterinary sciences*, 10(2).

Mokhtari M, et al. (2023) WASF3 overexpression affects the expression of circular RNA hsa-circ-0100153, which promotes breast cancer progression by sponging hsa-miR-31, hsa-miR-767-3p, and hsa-miR-935. *Heliyon*, 9(12), e22874.