

Resource Summary Report

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TopHat-Fusion

RRID:SCR_011899

Type: Tool

Proper Citation

TopHat-Fusion (RRID:SCR_011899)

Resource Information

URL: 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: 20260829T182411+0000

Ratings and Alerts

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

No alerts have been found for TopHat-Fusion.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 162 mentions in open access literature.

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

Che J, et al. (2026) Analytical and clinical validation of CancerMaster, an automated targeted NGS panel, for tumor-only precision oncology. Scientific reports, 16(1).

Teng M, et al. (2025) Circular RMST cooperates with lineage-driving transcription factors to govern neuroendocrine transdifferentiation. Cancer cell, 43(5), 891.

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.

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.

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

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).

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

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.

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

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

Abebe BK, et al. (2025) Exploring the regulatory mechanisms of differentially expressed circRNAs during bovine intramuscular adipogenic differentiation. BMC genomics, 27(1), 58.

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.

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*.

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.

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.

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

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.