Resource Summary Report

Generated by RRID on Apr 8, 2025

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

Funding:

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: 20250214T183213+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 152 mentions in open access literature.

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

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.

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

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

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.

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.

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.

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).

Chakravarthi VP, et al. (2023) LH/hCG Regulation of Circular RNA in Mural Granulosa Cells during the Periovulatory Period in Mice. International journal of molecular sciences, 24(17).

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.

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.

Tripathi S, et al. (2023) Defining the condensate landscape of fusion oncoproteins. Nature communications, 14(1), 6008.

Zhang S, et al. (2023) CircRNA Galntl6 sponges miR-335 to ameliorate stress-induced hypertension through upregulating Lig3 in rostral ventrolateral medulla. Redox biology, 64, 102782.

Wang Y, et al. (2023) Multi-omics of Circular RNAs and Their Responses to Hormones in Moso Bamboo (Phyllostachys edulis). Genomics, proteomics & bioinformatics, 21(4), 866.

Cortes-Ciriano I, et al. (2023) Genomic Patterns of Malignant Peripheral Nerve Sheath Tumor (MPNST) Evolution Correlate with Clinical Outcome and Are Detectable in Cell-Free DNA. Cancer discovery, 13(3), 654.

Buratin A, et al. (2023) Systematic benchmarking of statistical methods to assess differential expression of circular RNAs. Briefings in bioinformatics, 24(1).

Cao H, et al. (2022) Circular RNA screening identifies circMYLK4 as a regulator of fast/slow myofibers in porcine skeletal muscles. Molecular genetics and genomics : MGG, 297(1), 87.