Resource Summary Report

Generated by NIF on May 19, 2025

TopHat

RRID:SCR_013035
Type: Tool

Proper Citation

TopHat (RRID:SCR_013035)

Resource Information

URL: http://ccb.jhu.edu/software/tophat/index.shtml

Proper Citation: TopHat (RRID:SCR_013035)

Description: Software tool for fast and high throughput alignment of shotgun cDNA sequencing reads generated by transcriptomics technologies. Fast splice junction mapper for RNA-Seq reads. Aligns RNA-Seq reads to mammalian-sized genomes using ultra high-throughput short read aligner Bowtie, and then analyzes mapping results to identify splice junctions between exons.TopHat2 is accurate alignment of transcriptomes in presence of insertions, deletions and gene fusions.

Synonyms: tophat, TopHat1, Tophat2

Resource Type: software application, alignment software, data analysis software, data processing software, sequence analysis software, image analysis software, software resource

Defining Citation: PMID:23618408, PMID:19289445, DOI:10.1093/bioinformatics/btp120

Keywords: align, RNA-Seq, read, cDNA, sequencing, transcriptomics, fast, splice, junction, mapper, exon, analysis, bio.tools

Funding: NHGRI R01 HG006102;
NHGRI R01 HG006677

Availability: Free, Available for download, Freely available

Resource Name: TopHat

Resource ID: SCR_013035

Alternate IDs: biotools:tophat, OMICS_01257

Alternate URLs: https://github.com/infphilo/tophat, https://bio.tools/tophat, https://sources.debian.org/src/tophat/

Old URLs: http://tophat.cbcb.umd.edu/

License: Boost Software License 1.0

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250517T060055+0000

Ratings and Alerts

- Used for RNA-Seq by the Human Islet Research Network community. Contact(s): Diane Saunders, Marcela Brissova, John Walker, Dale Greiner, Al Powers - Human Islets Research Network https://hirnetwork.org/

No alerts have been found for TopHat.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9281 mentions in open access literature.

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

Wang Z, et al. (2025) A high-quality assembly revealing the PMEL gene for the unique plumage phenotype in Liancheng ducks. GigaScience, 14.

Zhu W, et al. (2025) Self-Healing Hyaluronic Acid-based Hydrogel with miRNA140-5p Loaded MON-PEI Nanoparticles for Chondrocyte Regeneration: Schiff Base Self-Assembly Approach. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(1), e2406479.

Kim SJ, et al. (2025) Disruption of bioenergetics enhances the radio-sensitivity of patient-derived glioblastoma tumorspheres. Translational oncology, 51, 102197.

Raiter A, et al. (2025) Galectin-3 secreted by triple-negative breast cancer cells regulates T cell function. Neoplasia (New York, N.Y.), 60, 101117.

Zhang L, et al. (2025) The transcription factor CREB regulates epithelial-mesenchymal transition of lens epithelial cells by phosphorylation-dependent and phosphorylation-independent mechanisms. The Journal of biological chemistry, 301(1), 108064.

Marchand V, et al. (2025) Monocytes generated by interleukin-6-treated human hematopoietic stem and progenitor cells secrete calprotectin that inhibits erythropoiesis. iScience, 28(1), 111522.

Zhang RX, et al. (2025) FNDC1 is a myokine that promotes myogenesis and muscle regeneration. The EMBO journal, 44(1), 30.

Zhong Y, et al. (2025) ZmCCD8 regulates sugar and amino acid accumulation in maize kernels via strigolactone signalling. Plant biotechnology journal, 23(2), 492.

McColl KS, et al. (2025) Identification of HEPACAM2 as a novel and specific marker of small cell carcinoma. Cancer, 131(1), e35557.

Zhang W, et al. (2025) Chromosome-level genome assembly of tetraploid Chinese cherry (Prunus pseudocerasus). Scientific data, 12(1), 136.

Vogels DHJ, et al. (2025) Proteomics Reveals Mechanisms of Delayed Keratoconus Progression: A Study of Corneas Following Two Light-Activated Crosslinking Treatments. Investigative ophthalmology & visual science, 66(1), 64.

Sio YY, et al. (2025) Functional Polymorphisms Regulate FOXO1 Transcript Expression and Contribute to the Risk and Symptom Severity of HDM-Induced Allergic Rhinitis. International archives of allergy and immunology, 186(1), 1.

Priego N, et al. (2025) TIMP1 Mediates Astrocyte-Dependent Local Immunosuppression in Brain Metastasis Acting on Infiltrating CD8+ T Cells. Cancer discovery, 15(1), 179.

Meng X, et al. (2025) Metabolic rewiring controlled by HIF-1? tunes IgA-producing B-cell differentiation and intestinal inflammation. Cellular & molecular immunology, 22(1), 54.

Policarpo R, et al. (2025) The MIR-NAT MAPT-AS1 does not regulate Tau expression in human neurons. PloS one, 20(1), e0314973.

Kido T, et al. (2025) The X-Linked Tumor Suppressor TSPX Regulates Genes Involved in the EGFR Signaling Pathway and Cell Viability to Suppress Lung Adenocarcinoma. Genes, 16(1).

Jani C, et al. (2025) VPS18 contributes to phagosome membrane integrity in Mycobacterium tuberculosis-infected macrophages. Science advances, 11(5), eadr6166.

Xu Z, et al. (2025) Creeping Stem 1 regulates directional auxin transport for lodging resistance in soybean. Plant biotechnology journal, 23(2), 377.

Kang KA, et al. (2025) Epigenetic Regulation of Nuclear Factor Erythroid-2-Related Factor 2 in Colorectal Cancer Cells Resistant to Ionizing Radiation. Biomolecules & therapeutics, 33(1), 182.

Rosato BE, et al. (2025) RAS signaling pathway is essential in regulating PIEZO1-mediated hepatic iron overload in dehydrated hereditary stomatocytosis. American journal of hematology, 100(1), 52.