

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

TopHat

RRID:SCR_013035

Type: Tool

Proper Citation

TopHat (RRID:SCR_013035)

Resource Information

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

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

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: 20260731T042852+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 9575 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Shen M, et al. (2026) H3K9 acetylation-dependent CHAC1 transcription in dihydroartemisinin-induced hepatic stellate cell ferroptosis. Chinese medical journal, 139(1), 93.

Tan J, et al. (2026) Photosystem Perturbation by Staygreen Mutations Confers Allele-Dependent Defences Against Infections of Pathogens With Different Lifestyles and Abiotic Stress Tolerance. Plant, cell & environment, 49(1), 585.

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

Welti J, et al. (2025) NXP800 Activates the Unfolded Protein Response, Altering AR and E2F Function to Impact Castration-Resistant Prostate Cancer Growth. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(6), 1109.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. GigaScience, 14.

Yue F, et al. (2025) Mitochondrial fatty acid oxidation regulates adult muscle stem cell function through modulating metabolic flux and protein acetylation. *The EMBO journal*, 44(9), 2566.

Hayashi Y, et al. (2025) Glial cells missing 1 triggers gliosis and angiogenesis after neonatal brain injury. *iScience*, 28(11), 113860.

Milo Rasouly H, et al. (2025) Exome analysis links kidney malformations to developmental disorders and reveals causal genes. *Nature communications*, 16(1), 7290.

Freytag D, et al. (2025) Lymphopenia drives T cell exhaustion in immunodeficient STING gain-of-function mice. *EMBO molecular medicine*, 17(9), 2438.

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.

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

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.

Lin W, et al. (2025) The transcriptional analysis of pepper shed light on a proviral role of light-harvesting chlorophyll a/b binding protein 13 during infection of pepper mild mottle virus. *Frontiers in plant science*, 16, 1533151.

Lou Z, et al. (2025) Assessment of immune modulation strategies to enhance survival and integration of human neural progenitor cells in rodent models of spinal cord injury. *Stem cells translational medicine*, 14(2).

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.

Senuma W, et al. (2025) The sensor histidine kinase PhcS participates in the regulation of quorum sensing-dependent virulence genes in *Ralstonia pseudosolanacearum* strain OE1-1. *Microbiology spectrum*, 13(4), e0005925.

Tian X, et al. (2025) Expression pattern, subcellular localization of *Aspergillus oryzae* ergosterol synthases, and their effects on ergosterol and fatty acid metabolism. *Applied and environmental microbiology*, 91(4), e0227324.

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.

Fu J, et al. (2025) Development of delayed pulmonary toxicities and transcriptional changes in pre-existing interstitial lung disease mice after partial thoracic irradiation. *Radiation oncology (London, England)*, 20(1), 20.

Li L, et al. (2025) Cell-Type Specific Circuits in the Mammillary Body for Place and Object Recognition Memory. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(13), e2409397.