

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

STAR-Fusion

RRID:SCR_025853

Type: Tool

Proper Citation

STAR-Fusion (RRID:SCR_025853)

Resource Information

URL: <https://github.com/STAR-Fusion/STAR-Fusion>

Proper Citation: STAR-Fusion (RRID:SCR_025853)

Description: Software tool to leverage chimeric and discordant read alignments identified by STAR aligner to predict fusions. Component of Trinity Cancer Transcriptome Analysis Toolkit. Used to identify candidate fusion transcripts supported by Illumina reads. Maps junction reads and spanning reads to reference annotation set.

Resource Type: software resource, source code

Defining Citation: [PMID:31639029](#)

Keywords: identify candidate fusion transcripts, predict fusions, leverages chimeric and discordant read alignments, chimeric, discordant, read alignment,

Funding: Howard Hughes Medical Institute ;
Klarman Cell Observatory ;
NCI U24CA180922;
NCI R50CA211461;
NCI R21CA209940;
NCI U01CA214846

Availability: Free, Available for download, Freely available

Resource Name: STAR-Fusion

Resource ID: SCR_025853

License: BSD-3-Clause license

Record Creation Time: 20241005T053245+0000

Record Last Update: 20260804T043851+0000

Ratings and Alerts

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

No alerts have been found for STAR-Fusion.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Wong K, et al. (2025) Wnt/??-catenin activation by mutually exclusive FBXW11 and CTNNB1 hotspot mutations drives salivary basal cell adenoma. Nature communications, 16(1), 4657.

Park YH, et al. (2025) Genomic alterations linked to recurrence risk in high-grade serous ovarian cancer revealed by deep targeted sequencing. Scientific reports, 15(1), 44155.

Qin Q, et al. (2025) Accurate fusion transcript identification from long- and short-read isoform sequencing at bulk or single-cell resolution. Genome research, 35(4), 967.

Nauseef JT, et al. (2025) A complex phylogeny of lineage plasticity in metastatic castration resistant prostate cancer. NPJ precision oncology, 9(1), 91.

Knox JJ, et al. (2025) Whole genome and transcriptome profiling in advanced pancreatic cancer patients on the COMPASS trial. Nature communications, 16(1), 5919.

Shinozaki T, et al. (2025) Basal-shift transformation leads to EGFR therapy-resistance in human lung adenocarcinoma. Nature communications, 16(1), 4369.

Vandiver AR, et al. (2025) Chimeric mitochondrial RNA transcripts predict mitochondrial genome deletion mutations in mitochondrial genetic diseases and aging. Genome research, 35(1), 55.

Zhao W, et al. (2025) A prognostic signature for lung adenocarcinoma in people who have never smoked. bioRxiv : the preprint server for biology.

Ferreira I, et al. (2025) The molecular cartography of malignant and benign sebaceous tumours. Nature communications, 17(1), 14.

Sol Ruiz M, et al. (2025) Genetic characterization of pediatric B-cell acute lymphoblastic leukemia in Argentina uncovers molecular heterogeneity and novel variants. Frontiers in pharmacology, 16, 1701680.

Haas R, et al. (2024) The Proteogenomics of Prostate Cancer Radioresistance. Cancer research communications, 4(9), 2463.

Qin Q, et al. (2024) CTAT-LR-fusion: accurate fusion transcript identification from long and short read isoform sequencing at bulk or single cell resolution. *bioRxiv : the preprint server for biology*.

Zheng D, et al. (2024) Brd4::Nutm1 fusion gene initiates NUT carcinoma in vivo. *Life science alliance*, 7(7).

Nunes L, et al. (2024) Prognostic genome and transcriptome signatures in colorectal cancers. *Nature*, 633(8028), 137.

Kim JC, et al. (2023) Transcriptomic classes of BCR-ABL1 lymphoblastic leukemia. *Nature genetics*, 55(7), 1186.

Bertrums EJM, et al. (2023) Comprehensive molecular and clinical characterization of NUP98 fusions in pediatric acute myeloid leukemia. *Haematologica*, 108(8), 2044.

Park YH, et al. (2023) Longitudinal multi-omics study of palbociclib resistance in HR-positive/HER2-negative metastatic breast cancer. *Genome medicine*, 15(1), 55.

Mulkiđjan RS, et al. (2023) ALK, ROS1, RET and NTRK1-3 Gene Fusions in Colorectal and Non-Colorectal Microsatellite-Unstable Cancers. *International journal of molecular sciences*, 24(17).

Patel RA, et al. (2022) Comprehensive assessment of anaplastic lymphoma kinase in localized and metastatic prostate cancer reveals targetable alterations. *Cancer research communications*, 2(5), 277.

Song H, et al. (2022) Single-cell analysis of human primary prostate cancer reveals the heterogeneity of tumor-associated epithelial cell states. *Nature communications*, 13(1), 141.