

Resource Summary Report

Generated by [dkNET](#) on Sep 16, 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 R21CA209940;
NCI R50CA211461;
NCI U01CA214846;
NCI U24CA180922

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: 20260912T200453+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 47 mentions in open access literature.

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

Panagopoulos I, et al. (2026) Fusion gene heterogeneity and kinase enrichment in high-grade serous carcinomas. *Neoplasia* (New York, N.Y.), 79, 101332.

Hang JF, et al. (2026) Out-of-frame CBX3::ALK fusion drives ALK activation and therapy response. *Cell reports. Medicine*, 7(4), 102697.

Wang K, et al. (2026) Ontogeny Dictates Oncogenic Potential, Lineage Hierarchy, and Therapy Response in Pediatric Leukemia. *Cancer discovery*, 16(3), 541.

Ohlstrom DJ, et al. (2026) Longitudinal Profiling of Tumor and Immune Compartments Uncovers Patterns of Dysregulation and Associations with Response in Multiple Myeloma. *Blood cancer discovery*, 7(2), 266.

Kuo HH, et al. (2026) Patient-derived organoids across cancers reveal conserved tumor heterogeneity and actionable therapeutic vulnerabilities. *Science advances*, 12(26), ead3351.

Williams JS, et al. (2026) Patient-derived pediatric brain tumor orthotopic xenografts and tumor organoids faithfully recapitulate primary tumors. *Science advances*, 12(16), eaea4966.

Abd El-Salam M, et al. (2026) Synergistic effects through targeting the PI3K and IGFR pathways in treating lung cancer carrying activation alterations along the PI3K pathway. *Translational oncology*, 67, 102753.

Yun KH, et al. (2026) Phase IB/II Trial with Correlative Analyses of Doxorubicin plus Durvalumab Combination in Patients with Advanced Soft Tissue Sarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1686.

Sun L, et al. (2026) Genomic Profile and Clinicopathologic Analyses of Wild-Type Gastrointestinal Stromal Tumors. *Molecular cancer research : MCR*, 24(4), 232.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Yemelyanenko J, et al. (2026) C-Terminal Truncation and Fusion Partner Determine Oncogenicity of FGFR3. *Cancer research*, 86(6), 1372.

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.

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.

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.

Gaziev I, et al. (2025) Accurate RET Fusion Detection in Solid Tumors Using RNA Sequencing Coverage Imbalance Analysis. *International journal of molecular sciences*, 26(23).

Rice SV, et al. (2025) Fast and sensitive detection of targeted gene fusions using frequency minimizers and fuzzy pattern matching with Fuzzion2. *Cell reports methods*, 5(12), 101238.

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.

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

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

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