Resource Summary Report

Generated by RRID on Aug 15, 2026

Arriba

RRID:SCR_025854
Type: Tool

Proper Citation

Arriba (RRID:SCR_025854)

Resource Information

URL: https://github.com/suhrig/arriba/

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Description: Software tool for gene fusion detection from RNA-Seq data. Fusion detection algorithm specifically designed to meet demanding requirements of HTS-assisted precision oncology. Capable of detecting aberrant transcripts that are not called by most fusion detection methods but may be clinically relevant. This includes tumor suppressor genes that are occasionally inactivated by rearrangements within the gene or by translocations to introns or intergenic regions.

Resource Type: data processing software, software application, data analysis software, source code, software resource

Defining Citation: PMID:33441414

Keywords: gene fusion detection, RNA-Seq data, detecting aberrant transcripts,

Funding: Heidelberg Center for Personalized Oncology ;
Dietmar Hopp Foundation ;
Ontario Institute for Cancer Research ;
Government of Ontario

Availability: Free, Available for download, Freely available

Resource Name: Arriba

Resource ID: SCR_025854

License: MIT/Expat License

Record Creation Time: 20241005T053245+0000

Record Last Update: 20260815T042908+0000

Ratings and Alerts

No rating or validation information has been found for Arriba.

No alerts have been found for Arriba.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Hofvander J, et al. (2026) Transcriptomic Subgroups in Soft Tissue Tumors Correlate with Morphologic Subtype, Genomic Features, and Outcome. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1825.

Hübschmann D, et al. (2026) The Knowledge Connector decision support system for multiomics-based precision oncology. Nature communications, 17(1), 742.

Chen JP, et al. (2026) A novel PML::RARA fusion in acute promyelocytic leukemia: a case report and literature review. Frontiers in oncology, 16, 1784103.

Hlevnjak M, et al. (2026) Delivering precision oncology in metastatic breast cancer: Clinical impact of comprehensive genomic profiling-The CATCH experience. International journal of cancer, 158(6), 1675.

Raby M, et al. (2026) Ovarian central nervous system-type tumors: integrated neuropathological and methylation-based classification reveals site-related features. Acta neuropathologica communications, 14(1).

Nichetti F, et al. (2026) Deep molecular profiling of biliary tract cancer uncovers novel biological mechanisms and therapeutic opportunities. ESMO open, 11(5), 106082.

Federico A, et al. (2026) Molecular and clinical stratification of astroblastomas: Three distinct fusion-defined groups informing risk-adapted treatment strategies. Neuro-oncology, 28(4), 1005.

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

Gao T, et al. (2025) Self-assembled patient-derived tumor-like cell clusters for personalized drug testing in diverse sarcomas. Cell reports. Medicine, 6(3), 101990.

Xu Y, et al. (2025) Exploring treatment-driven subclonal evolution of prognostic triple biomarkers: Dual gene fusions and chimeric RNA variants in novel subtypes of acute myeloid leukemia patients with KMT2A rearrangement. Drug resistance updates : reviews

and commentaries in antimicrobial and anticancer chemotherapy, 79, 101199.

Soupir A, et al. (2025) Genomic, transcriptomic, and immunogenomic landscape of over 1300 sarcomas of diverse histology subtypes. Nature communications, 16(1), 4206.

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.

Vissers JHA, et al. (2025) Pathologist-initiated whole genome and transcriptome sequencing demonstrates diagnostic utility in resolving difficult-to-diagnose tumors. Genome medicine, 17(1), 107.

Terashima Y, et al. (2025) Discovery of Novel RASGRF2 Fusions as a Therapeutic Target in Lung Adenocarcinoma of Never or Light Smokers. Cancer science.

Nibeyro G, et al. (2025) Evaluating Gene Fusions as Prognostic Biomarkers and Therapeutic Targets in Immune Checkpoint Blockade-Treated Advanced Melanoma: A Retrospective Analysis. Cancer research communications, 5(8), 1332.

Song Y, et al. (2025) Integrated Transcriptomic Landscape and Deep Learning Based Survival Prediction in Uterine Sarcomas. Cancer research and treatment, 57(1), 250.

Balko J, et al. (2025) Novel and unusual USP6 fusion partners in aneurysmal bone cyst and their role in pathogenesis and histopathological evaluation of this disease. Journal of clinical pathology, 78(6), 399.

Varghese AM, et al. (2025) Clinicogenomic landscape of pancreatic adenocarcinoma identifies KRAS mutant dosage as prognostic of overall survival. Nature medicine, 31(2), 466.

Brož P, et al. (2025) Molecular Landscape of Pediatric Low-Grade Gliomas: Insights From RNA-NGS and Bioinformatic Analysis. Genes, chromosomes & cancer, 64(10), e70085.

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