# STAR

**RRID:** SCR_004463  
**Type:** Tool

## Proper Citation

STAR (RRID:SCR_004463)

## Resource Information

**URL:** [http://code.google.com/p/rna-star/](http://code.google.com/p/rna-star/)

**Proper Citation:** STAR (RRID:SCR_004463)

**Description:** Software performing alignment of high-throughput RNA-seq data. Aligns RNA-seq reads to reference genome using uncompressed suffix arrays.

**Synonyms:** Spliced Transcripts Alignment to Reference, Spliced Transcripts Alignment to a Reference (STAR), rna-star, ultrafast universal RNA-seq aligner

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

**Defining Citation:** [PMID:23104886](https://www.ncbi.nlm.nih.gov/pubmed/23104886), [DOI:10.1093/bioinformatics/bts635](https://doi.org/10.1093/bioinformatics/bts635)

**Keywords:** RNA-seq data, alignment, RNA-seq reads alignment, reference genome, using uncompressed suffix arrays, bio.tools

**Funding Agency:** NHGRI

**Availability:** Free, Available for download, Freely available

**Resource Name:** STAR

**Resource ID:** SCR_004463

**Alternate IDs:** biotools:star, OMICS_01254, SCR_015899

Record Creation Time: 20220129T080224+0000

Record Last Update: 20240616T053306+0000

Ratings and Alerts

No rating or validation information has been found for STAR.

No alerts have been found for STAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12431 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Kellett DO, et al. (2024) Transcriptional response of the heart to vagus nerve stimulation. Physiological genomics, 56(2), 167.


Stankovi? D, et al. (2024) Xrp1 governs the stress response program to spliceosome dysfunction. Nucleic acids research, 52(5), 2093.

Mohr ME, et al. (2024) Cardiomyocyte-fibroblast interaction regulates ferroptosis and fibrosis after myocardial injury. iScience, 27(3), 109219.

Murray GC, et al. (2024) Testing SIPA1L2 as a modifier of CMT1A using mouse models. Journal of neuropathology and experimental neurology.


Lin P, et al. (2024) RBBP6 maintains glioblastoma stem cells through CPSF3-dependent alternative polyadenylation. Cell discovery, 10(1), 32.

Wienke J, et al. (2024) Integrative analysis of neuroblastoma by single-cell RNA sequencing identifies the NECTIN2-TIGIT axis as a target for immunotherapy. Cancer cell, 42(2), 283.


