

Resource Summary Report

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STARsolo

RRID:SCR_021542

Type: Tool

Proper Citation

STARsolo (RRID:SCR_021542)

Resource Information

URL: <https://github.com/alexdobin/STAR/blob/master/docs/STARsolo.md>

Proper Citation: STARsolo (RRID:SCR_021542)

Description: Software tool for accurate, fast and versatile mapping/quantification of single cell and single nucleus RNA-seq data. Used for mapping, demultiplexing and quantification for single cell RNA-seq. Comprehensive turnkey solution for quantifying gene expression in single-cell/nucleus RNA-seq data, built into RNA-seq aligner STAR.

Resource Type: data analysis software, data analytics software, data processing software, software application, software resource

Defining Citation: [DOI:10.1101/2021.05.05.442755](https://doi.org/10.1101/2021.05.05.442755)

Keywords: mapping, quantification, single cell, single nucleus, RNA-seq data, quantifying gene expression

Availability: Free, Available for download, Freely available

Resource Name: STARsolo

Resource ID: SCR_021542

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260905T132941+0000

Ratings and Alerts

No rating or validation information has been found for STARsolo.

No alerts have been found for STARsolo.

Data and Source Information

Usage and Citation Metrics

We found 127 mentions in open access literature.

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

Ilie MD, et al. (2026) Mast cells act as pro-angiogenic and pro-tumorigenic players in pituitary gonadotroph tumors. *Neuro-oncology*, 28(1), 175.

Hannig L, et al. (2026) GPR124 regulates hyaloid blood vessel regression and is associated with endothelial-mesenchymal transition. *Scientific reports*, 16(1).

Takahama M, et al. (2026) Secreted phospholipase PLA2G5 acts as a hemolytic factor in sepsis. *The Journal of clinical investigation*, 136(9).

Soelter TM, et al. (2026) Cell-type-specific alternative splicing in the brain and kidney of a *Setbp1*S858R Schinzel-Giedion syndrome mouse. *Disease models & mechanisms*, 19(2).

Rasetto NB, et al. (2026) Cell-state mapping reveals a reversible neuroblast accumulation in the aging mouse hippocampus. *bioRxiv : the preprint server for biology*.

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Yao J, et al. (2026) Evaluating genetic ancestry inference from single-cell transcriptomic datasets. *HGG advances*, 7(2), 100564.

Bandesh K, et al. (2026) Deep single-cell decoding of human pancreatic islets reveals T2D β -cell gene expression defects. *The EMBO journal*, 45(11), 3978.

Carrizo GE, et al. (2026) The transition from monocyte to tissue-resident macrophage requires DHPS. *Nature*, 651(8106), 763.

Sarropoulos I, et al. (2026) The evolution of gene regulation in mammalian cerebellum development. *Science (New York, N.Y.)*, 391(6784), eadw9154.

Pham CN, et al. (2026) Spermidine Reproduces the Anti-Inflammatory Effects of Intermittent Fasting and Prevents Urate and Calcium Pyrophosphate Crystal-Induced Inflammation. *Arthritis & rheumatology (Hoboken, N.J.)*, 78(2), 449.

Kar A, et al. (2026) Lessons from single cell omics: admixed American ancestry and sex confer cardiometabolic disease risk in Mexicans. *Genome medicine*, 18(1).

Buissant des Amorie JR, et al. (2026) Emergence of oncofetal plasticity is ubiquitous in early colorectal cancers. *Nature*, 654(8117), 229.

Plessier F, et al. (2026) Cellular and transcriptional trajectories of neural fate specification in sea anemone uncover two modes of adult neurogenesis. *Nature communications*, 17(1).

Johnson HJ, et al. (2026) Optogenetic WNT signaling drives germ layer self-organization in a human gastruloid model. *bioRxiv : the preprint server for biology*.

Lattke M, et al. (2026) Single-cell atlas of the developing Down syndrome brain cortex. *Nature medicine*, 32(3), 1061.

Kim H, et al. (2026) Myelin antigen capture in the CNS by B cells expressing EBV latent membrane protein 1 leads to demyelinating lesion formation. *Cell*.

Lee CN, et al. (2025) Spatial joint profiling of DNA methylome and transcriptome in mammalian tissues. *bioRxiv : the preprint server for biology*.

Teske M, et al. (2025) Targeted CRISPR-Cas9 screening identifies core transcription factors controlling murine haemato-endothelial fate commitment. *Nature communications*, 16(1), 11412.

Mukherjee S, et al. (2025) Tumor-associated neutrophil precursors impair homologous DNA repair and promote sensitivity to PARP inhibition. *Nature communications*, 16(1), 6999.