

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

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: 20260729T044512+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 106 mentions in open access literature.

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

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*.

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

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

Loo TM, et al. (2025) Senescence-associated lysosomal dysfunction impairs cystine deprivation-induced lipid peroxidation and ferroptosis. *Nature communications*, 16(1), 6617.

Tombor LS, et al. (2025) Immunoregulatory Endothelial Cells Interact With T Cells After Myocardial Infarction. *Circulation research*, 137(6), 866.

Ma L, et al. (2025) Exploring the Molecular Mechanisms of Fisetin in Treating Periodontitis Through Multiomics and Network Pharmacology. *International dental journal*, 75(3), 2204.

Neugebauer E, et al. (2025) Herpesviruses mimic zygotic genome activation to promote viral replication. *Nature communications*, 16(1), 710.

Lim K, et al. (2025) A novel human fetal lung-derived alveolar organoid model reveals mechanisms of surfactant protein C maturation relevant to interstitial lung disease. *The EMBO journal*, 44(3), 639.

Tamminga SM, et al. (2025) Single-cell sequencing of human Langerhans cells identifies altered gene expression profiles in patients with atopic dermatitis. *ImmunoHorizons*, 9(2).

Rodrigues Sousa E, et al. (2025) CRIPTO's multifaceted role in driving aggressive prostate cancer unveiled by in vivo, organoid, and patient data. *Oncogene*, 44(7), 462.

van der Maarel LE, et al. (2025) PITX2 dosage-dependent changes in pacemaker cell state underlie sinus node dysfunction and atrial arrhythmias. *Nature communications*, 16(1), 11197.

Belfort BDW, et al. (2025) Comparative analysis of AAV serotypes for transduction of olfactory sensory neurons. *Frontiers in neuroscience*, 19, 1531122.

Vinsland E, et al. (2025) Cell atlas of the developing human meninges reveals a dura origin of meningioma. *bioRxiv : the preprint server for biology*.

Chan PY, et al. (2025) The synthetic lethal interaction between CDS1 and CDS2 is a vulnerability in uveal melanoma and across multiple tumor types. *Nature genetics*, 57(7), 1672.

Guan J, et al. (2025) Distinct Transcriptomic Profiles of Cultured Anterior and Posterior Populations of Human Infant Scleral Fibroblasts: Including Dopamine Receptors. *Investigative ophthalmology & visual science*, 66(5), 29.

Yao J, et al. (2025) Evaluating genetic-ancestry inference from single-cell RNA-seq data. *bioRxiv : the preprint server for biology*.

Bennabi I, et al. (2025) Size-dependent temporal decoupling of morphogenesis and transcriptional programs in pseudoembryos. *Science advances*, 11(34), eadv7790.

Ruiz-Amezcu P, et al. (2025) A Single-Nucleus Transcriptomic Atlas of the Mouse Lumbar Spinal Cord: Functional Implications of Non-Coding RNAs. *Biotech (Basel (Switzerland))*, 14(3).

Shah V, et al. (2025) Fundamental errors in RNA velocity arising from the omission of cell growth. *bioRxiv : the preprint server for biology*.