# Resource Summary Report

Generated by RRID on May 13, 2025

# Monocle3

RRID:SCR_018685
Type: Tool

## Proper Citation

Monocle3 (RRID:SCR_018685)

## Resource Information

**URL:** https://cole-trapnell-lab.github.io/monocle3/

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**Description:** Software analysis toolkit for single cell RNA-seq. Used for single cell RNA-Seq experiments. Unsupervised algorithm that increases temporal resolution of transcriptome dynamics using single-cell RNA-Seq data collected at multiple time points.

**Synonyms:** Monocle, Monocle 3

**Resource Type:** data processing software, software application, software toolkit, software resource, data analysis software

**Defining Citation:** PMID:24658644

**Keywords:** Data analysis, singel cell RNAseq data, single cell RNAseq experiment, transcriptome dynamics

**Funding:** NIH Office of the Director DP2 OD00667;
NIGMS P01 GM099117;
NIH Office of the Director DP2 0D008514;
NHGRI P50 HG006193;
Single Cell Genomics initiative

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

**Resource Name:** Monocle3

**Resource ID:** SCR_018685

**Alternate URLs:** https://github.com/cole-trapnell-lab/monocle3

**License:** MIT License

**Record Creation Time:** 20220129T080341+0000

**Record Last Update:** 20250513T062009+0000

## Ratings and Alerts

No rating or validation information has been found for Monocle3.

No alerts have been found for Monocle3.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 205 mentions in open access literature.

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

Lv Y, et al. (2025) CD14loCD301b+ macrophages gathering as a proangiogenic marker in adipose tissues. Journal of lipid research, 66(1), 100720.

Jin W, et al. (2025) Bayesian-optimized deep learning for identifying essential genes of mitophagy and fostering therapies to combat drug resistance in human cancers. Journal of cellular and molecular medicine, 29(2), e18254.

Montagne JM, et al. (2025) CD137 agonism enhances anti-PD1 induced activation of expanded CD8+ T cell clones in a neoadjuvant pancreatic cancer clinical trial. iScience, 28(1), 111569.

Masuda K, et al. (2025) Distinct CD8+ T-cell types Associated with COVID-19 Severity in Unvaccinated HLA-A2+ Patients. bioRxiv : the preprint server for biology.

Liu Y, et al. (2025) Differential transcriptomic profiling of lipid metabolism and collagen remodeling in fast- and slow-twitch skeletal muscles in aging. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(2), e70335.

Lee LR, et al. (2025) Glutathione accelerates the cell cycle and cellular reprogramming in plant regeneration. Developmental cell.

Wang L, et al. (2024) Sorafenib inhibits ossification of the posterior longitudinal ligament by

blocking LOXL2-mediated vascularization. Bone research, 12(1), 24.

Scarfò R, et al. (2024) CD32 captures committed haemogenic endothelial cells during human embryonic development. Nature cell biology, 26(5), 719.

Croizer H, et al. (2024) Deciphering the spatial landscape and plasticity of immunosuppressive fibroblasts in breast cancer. Nature communications, 15(1), 2806.

Lian W, et al. (2024) Single-cell sequencing reveals increased LAMB3-positive basal keratinocytes and ZNF90-positive fibroblasts in autologous cultured epithelium. Communications biology, 7(1), 79.

Sun Y, et al. (2024) Single-cell transcriptomic analyses of tumor microenvironment and molecular reprograming landscape of metastatic laryngeal squamous cell carcinoma. Communications biology, 7(1), 63.

Su Y, et al. (2024) Distribution-Agnostic Deep Learning Enables Accurate Single-Cell Data Recovery and Transcriptional Regulation Interpretation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(16), e2307280.

Zhi M, et al. (2024) Elucidation of the pluripotent potential of bovine embryonic lineages facilitates the establishment of formative stem cell lines. Cellular and molecular life sciences : CMLS, 81(1), 427.

Mozin E, et al. (2024) Dystrophin deficiency impairs cell junction formation during embryonic myogenesis from pluripotent stem cells. iScience, 27(7), 110242.

Duan J, et al. (2024) LoRA-TV: read depth profile-based clustering of tumor cells in single-cell sequencing. Briefings in bioinformatics, 25(4).

Yi N, et al. (2024) Functional variation among mesenchymal stem cells derived from different tissue sources. PeerJ, 12, e17616.

Cao L, et al. (2024) From single-cell to spatial transcriptomics: decoding the glioma stem cell niche and its clinical implications. Frontiers in immunology, 15, 1475235.

Yao J, et al. (2024) Integration of multi-omics data revealed the orphan CpG islands and enhancer-dominated c is-regulatory network in glioma. iScience, 27(10), 110946.

Zhao F, et al. (2024) Integrated single-cell transcriptomic analyses identify a novel lineage plasticity-related cancer cell type involved in prostate cancer progression. EBioMedicine, 109, 105398.

Magnani E, et al. (2024) Epigenetic Disordering Drives Stemness, Senescence Escape and Tumor Heterogeneity. bioRxiv : the preprint server for biology.