

Resource Summary Report

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Monocle2

RRID:SCR_016339

Type: Tool

Proper Citation

Monocle2 (RRID:SCR_016339)

Resource Information

URL: <http://cole-trapnell-lab.github.io/monocle-release/docs/>

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Description: Software package for analyzing single cell gene expression, classifying and counting cells, performing differential expression analysis between subpopulations of cells, and reconstructing cellular trajectories. Works well with very large single-cell RNA-Seq experiments containing tens of thousands of cells or more. Used in computational analysis of gene expression data in single cell gene expression studies to profile transcriptional regulation in complex biological processes and highly heterogeneous cell populations.

Synonyms: Monocle 2

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

Defining Citation: [PMID:24658644](#)

Keywords: analysis, heterogenous, population, single, cell, gene, expression, data, large, single-cell RNA-Seq, transcriptional, regulation, heterogen

Funding: NIH DP2 HD088158;
Alfred P. Sloan Foundation Research Fellowship

Availability: Free, Available for download, Freely available

Resource Name: Monocle2

Resource ID: SCR_016339

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260805T044352+0000

Ratings and Alerts

No rating or validation information has been found for Monocle2.

No alerts have been found for Monocle2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 203 mentions in open access literature.

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

Chen J, et al. (2026) Integrated single-cell transcriptomics and proteomics elucidate the molecular mechanisms and detoxification strategy of rifampicin-induced hepatotoxicity. International journal of biological sciences, 22(1), 481.

Liang Y, et al. (2026) SLC39A10 drives M2 macrophage polarization and gastric cancer progression through the MAPK14(p38?) pathway. iScience, 29(1), 114400.

Lu L, et al. (2025) A Single-Cell Atlas of Crab Ovary Provides New Insights Into Oogenesis in Crustaceans. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2409688.

Zeng J, et al. (2025) CancerSCEM 2.0: an updated data resource of single-cell expression map across various human cancers. Nucleic acids research, 53(D1), D1278.

Wang K, et al. (2025) Exploring Key Genes of Glutathione Metabolism in Systemic Lupus Erythematosus Based on Mendelian Randomisation, Single-Cell RNA Sequencing and Multiple Machine Learning Approaches. IET systems biology, 19(1), e70021.

Zhao M, et al. (2025) Targeting MAPK14 by Lobeline Upregulates Slurp1-Mediated Inhibition of Alternative Activation of TAM and Retards Colorectal Cancer Growth. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(10), e2407900.

Huang ??? W, et al. (2025) A Single-cell Atlas of Developing Mouse Palates Reveals Cellular and Molecular Transitions in Periderm Cell Fate. Genomics, proteomics & bioinformatics, 23(1).

Jiang D, et al. (2025) Spatiotemporal single-cell analysis elucidates the cellular and molecular dynamics of human cornea aging. Genome medicine, 17(1), 56.

Ren C, et al. (2025) Single-Cell Insights Into Cellular Response in Abdominal Aortic Occlusion-Induced Hippocampal Injury. CNS neuroscience & therapeutics, 31(1), e70154.

Song K, et al. (2025) Construction of the Single-Cell Landscape of Hashimoto's Thyroiditis Tissue and Peripheral Blood by Single-Cell RNA Sequencing. Immunity, inflammation and disease, 13(2), e70153.

Wu Y, et al. (2025) Drosophila and mouse intestinal stem cells are spatiotemporally specified by Notch suppression and Wnt activation. *Science advances*, 11(49), eady7272.

Li S, et al. (2025) CXCR1 Depletion in Ly6C⁺ cDC2 Alleviates Acute Lung Injury via Modulation of Th17/Treg Balance. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(41), e06287.

Zhao ZH, et al. (2025) Spatiotemporal and single-cell atlases to dissect regional specific cell types of the developing ovary. *Communications biology*, 8(1), 849.

Cheng L, et al. (2025) PDGFR⁺+DPP4⁺ Fibroblasts-Macrophage Crosstalk Induces Orbital Fibrosis in Treatment-Resistant Thyroid Eye Disease via the GAS6-AXL Pathway. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(45), e11404.

Dong H, et al. (2025) Integrating single-cell RNA sequencing and spatial multi-omics reveals the molecular signature of regeneration after spinal cord injury. *Biomarker research*, 13(1), 130.

Xu G, et al. (2025) Unique Sertoli cell adaptations support enhanced spermatogenesis in chickens. *Journal of animal science and biotechnology*, 16(1), 170.

Chen J, et al. (2025) CD146⁺ CAFs mediate immunosuppression in gastric cancer via COL4A1: potential therapeutic targets. *Journal for immunotherapy of cancer*, 13(12).

Wang H, et al. (2025) Phenotypic plasticity and increased infiltration of peripheral blood-derived TREM1⁺ mono-macrophages following radiotherapy in rectal cancer. *Cell reports. Medicine*, 6(1), 101887.

Wang G, et al. (2025) Machine learning-based prediction reveals kinase MAP4K4 regulates neutrophil differentiation through phosphorylating apoptosis-related proteins. *PLoS computational biology*, 21(3), e1012877.

Lan H, et al. (2025) Multi-omics analysis of the dynamic role of STAR⁺ cells in regulating platinum-based chemotherapy responses and tumor microenvironment in serous ovarian carcinoma. *Frontiers in pharmacology*, 16, 1545762.