

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

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: 20260808T190030+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 227 mentions in open access literature.

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

Wei Y, et al. (2026) Integrating single-cell RNA-seq and bulk RNA-seq to identify hub pathways and diagnostic biomarkers in active pulmonary tuberculosis. BMC infectious diseases, 26(1).

Zhang Y, et al. (2026) Excitatory neurons and astrocytes-specific dysregulation and aberrant interactions are vulnerable to FCDI as suggested by single-cell spatial transcriptomics. Clinical and translational medicine, 16(5), e70673.

Kim BG, et al. (2026) T-Cell Immune Dysfunction and Progression to Severe COVID-19 in Asthma Revealed by Single-Cell RNA Sequencing. Tuberculosis and respiratory diseases, 89(1), 38.

Jeong J, et al. (2026) Developmental dynamics of skeletal muscle can be recapitulated in vitro from pig embryonic stem cells. Stem cell reports, 21(6), 102921.

Li S, et al. (2026) Generation of CCR4/CD7 Bispecific CAR-T Cells Resistant to Fratricide and Exhaustion. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(35), e21443.

Baurès M, et al. (2026) Targeting pre-existing club-like cells in prostate cancer potentiates androgen deprivation therapy. EMBO molecular medicine, 18(3), 943.

Yang J, et al. (2026) A Malignant Subpopulation of H2AFZ+ Cells Interacts with Myeloid Cells to Promote an Anti-inflammatory Microenvironment and Drive Hepatic Metastasis, Revealing an Immunotherapeutic Strategy for Pancreatic Ductal Adenocarcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2479.

Tang S, et al. (2026) Single-cell RNA sequencing analysis reveals the evolution and regulatory features of specialized endothelial cell subsets in non-traumatic osteonecrosis of the femoral head. Biology direct, 21(1).

Zhan L, et al. (2026) Single-bacterium metabolome revealing heterogeneous cellular states in bacterial populations. Nature communications, 17(1).

Wang BL, et al. (2026) Multi-Omics reveals SPP1 + malignant and CXCR4+ TAM crosstalk predicts immunotherapy response in lung adenocarcinoma. *Discover oncology*, 17(1).

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.

Pan Y, et al. (2026) Colorectal Cancer Organoid Model Reveals the Mechanisms of Irinotecan Resistance at Single-Cell Resolution. *Cancer medicine*, 15(2), e71550.

Zhang H, et al. (2026) Single-cell profiling of bone metastasis ecosystems reveals pivotal role of INSR+AEC in clear cell renal cell carcinoma. *Translational oncology*, 64, 102650.

Sun W, et al. (2026) Reconstruction of T cell infiltration in an osteosarcoma PDX-organoid interactive biobank for personalized immunotherapy. *Cell reports. Medicine*, 7(3), 102644.

Zhang L, et al. (2026) Bcl11a orchestrates multilineage integrity in aging hematopoiesis by regulating multipotent progenitor fate decisions. *Cell reports*, 45(7), 117716.

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

Wang BS, et al. (2026) Single-cell multiomic approaches define a gradual, spatially regulated epigenetic and transcriptional transition from embryonic to adult neural stem cells. *Stem cell reports*, 21(7), 102967.

Zhang XK, et al. (2025) Multi-omics reveals key cell types and gene families regulating eggshell strength in chicken uteri. *Zoological research*, 46(6), 1396.

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.

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.