Resource Summary Report

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scanpy

RRID:SCR_018139
Type: Tool

Proper Citation

scanpy (RRID:SCR_018139)

Resource Information

URL: https://github.com/theislab/scanpy

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Description: Software Python tool for large scale single cell gene expression data analysis. Integrates analysis possibilities of established R-based frameworks, provides pre processing, visualization, graph-drawing and diffusion maps, clustering, identification of marker genes for clusters via differential expression tests and pseudo temporal ordering via diffusion pseudo time.

Synonyms: Single Cell Analysis in Python

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

Defining Citation: PMID:29409532

Keywords: Large scale, single cell, gene expression, data analysis, R, pre processing, visualization, graph drawing, diffusion map, clustering, marker gene, differential expression test, bio.tools

Funding: Helmholtz Postdoc Programme ;
German Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: scanpy

Resource ID: SCR_018139

Alternate IDs: biotools:scanpy, BioTools:scanpy

Alternate URLs: https://icb-scanpy.readthedocs-hosted.com/en/stable/, https://bio.tools/scanpy, https://bio.tools/scanpy, https://bio.tools/scanpy

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Ratings and Alerts

No rating or validation information has been found for scanpy.

No alerts have been found for scanpy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 172 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Goclowski CL, et al. (2025) Galaxy as a gateway to bioinformatics: Multi-Interface Galaxy Hands-on Training Suite (MIGHTS) for scRNA-seq. GigaScience, 14.

Holden JM, et al. (2025) Chronic hyperglycemia alters retinal astrocyte microstructure and uptake of cholera toxin B in a murine model of diabetes. Journal of neurochemistry, 169(1), e16237.

Fowler JL, et al. (2024) Lineage-tracing hematopoietic stem cell origins in vivo to efficiently make human HLF+ HOXA+ hematopoietic progenitors from pluripotent stem cells. Developmental cell, 59(9), 1110.

Wang W, et al. (2024) Single-cell analysis of tumor microenvironment and cell adhesion reveals that interleukin-1 beta promotes cancer cell proliferation in breast cancer. Animal models and experimental medicine, 7(5), 617.

Ricker CA, et al. (2024) Historical perspective and future directions: computational science in immuno-oncology. Journal for immunotherapy of cancer, 12(1).

Ratnasiri K, et al. (2024) Systems immunology of transcriptional responses to viral infection

identifies conserved antiviral pathways across macaques and humans. Cell reports, 43(2), 113706.

Li PL, et al. (2024) Microgel-based carriers enhance skeletal stem cell reprogramming towards immunomodulatory phenotype in osteoarthritic therapy. Bioactive materials, 34, 204.

Nie W, et al. (2024) Spatially Informed Graph Structure Learning Extracts Insights from Spatial Transcriptomics. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(45), e2403572.

Samson SC, et al. (2024) Tenascin-C in the early lung cancer tumor microenvironment promotes progression through integrin ?v?1 and FAK. bioRxiv : the preprint server for biology.

Ko KP, et al. (2024) Tumor niche network-defined subtypes predict immunotherapy response of esophageal squamous cell cancer. iScience, 27(5), 109795.

Düdükcü Ö, et al. (2024) Molecular diversity and migration of GABAergic neurons in the developing ventral midbrain. iScience, 27(11), 111239.

Murphy B, et al. (2024) Intraperitoneal activation of myeloid cells clears ascites and reveals IL27-dependent regression of metastatic ovarian cancer. bioRxiv : the preprint server for biology.

Lv T, et al. (2024) EAGS: efficient and adaptive Gaussian smoothing applied to high-resolved spatial transcriptomics. GigaScience, 13(1).

Gonzalez-Ferrer J, et al. (2024) SIMS: A deep-learning label transfer tool for single-cell RNA sequencing analysis. Cell genomics, 4(6), 100581.

Poovathingal S, et al. (2024) Nova-ST: Nano-patterned ultra-dense platform for spatial transcriptomics. Cell reports methods, 4(8), 100831.

Wang Y, et al. (2024) Identification of JUN gene and cellular microenvironment in response to PD-1 blockade treatment in lung cancer patients via single-cell RNA sequencing. Aging, 16(12), 10348.

Wu Y, et al. (2024) A spatiotemporal transcriptomic atlas of mouse placentation. Cell discovery, 10(1), 110.

Likasitwatanakul P, et al. (2024) Chemical perturbations impacting histone acetylation govern colorectal cancer differentiation. bioRxiv : the preprint server for biology.

Dorgau B, et al. (2024) Deciphering the spatiotemporal transcriptional and chromatin accessibility of human retinal organoid development at the single-cell level. iScience, 27(4), 109397.

Linneberg-Agerholm M, et al. (2024) The primitive endoderm supports lineage plasticity to enable regulative development. Cell, 187(15), 4010.