Resource Summary Report

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Cell Ranger ATAC

RRID:SCR_021160
Type: Tool

Proper Citation

Cell Ranger ATAC (RRID:SCR_021160)

Resource Information

URL: https://support.10xgenomics.com/single-cell-atac/software/pipelines/latest/what-is-cell-ranger-atac

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Description: Software tool as set of analysis pipelines that process Chromium Single Cell ATAC data. Cell Ranger ATAC includes four pipelines relevant to single cell chromatin accessibility experiments.Used to investigate number of chromatin-accessibility signatures.

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

Keywords: Process Chromium Single Cell ATAC data, single cell chromatin, chromatin accessibility signatures

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Cell Ranger ATAC

Resource ID: SCR_021160

Record Creation Time: 20220129T080354+0000

Record Last Update: 20250426T060757+0000

Ratings and Alerts

No rating or validation information has been found for Cell Ranger ATAC.

No alerts have been found for Cell Ranger ATAC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Cao C, et al. (2024) CXCR4 orchestrates the TOX-programmed exhausted phenotype of CD8+ T cells via JAK2/STAT3 pathway. Cell genomics, 4(10), 100659.

Garnica J, et al. (2024) T-follicular helper cells are epigenetically poised to transdifferentiate into T-regulatory type 1 cells. eLife, 13.

Kim JH, et al. (2023) Integrative analysis of single-cell RNA-seq and ATAC-seq reveals heterogeneity of induced pluripotent stem cell-derived hepatic organoids. iScience, 26(9), 107675.

Yu Z, et al. (2023) Integrative Single-Cell Analysis Reveals Transcriptional and Epigenetic Regulatory Features of Clear Cell Renal Cell Carcinoma. Cancer research, 83(5), 700.

Hickey JW, et al. (2023) Organization of the human intestine at single-cell resolution. Nature, 619(7970), 572.

Becker WR, et al. (2022) Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. Nature genetics, 54(7), 985.

Finkbeiner C, et al. (2022) Single-cell ATAC-seq of fetal human retina and stem-cell-derived retinal organoids shows changing chromatin landscapes during cell fate acquisition. Cell reports, 38(4), 110294.

Yang L, et al. (2022) Human and mouse trigeminal ganglia cell atlas implicates multiple cell types in migraine. Neuron, 110(11), 1806.

Khateb M, et al. (2022) Transcriptomics, regulatory syntax, and enhancer identification in mesoderm-induced ESCs at single-cell resolution. Cell reports, 40(7), 111219.

Miyao T, et al. (2022) Integrative analysis of scRNA-seq and scATAC-seq revealed transit-amplifying thymic epithelial cells expressing autoimmune regulator. eLife, 11.

Sinha S, et al. (2021) Profiling Chromatin Accessibility at Single-cell Resolution. Genomics, proteomics & bioinformatics, 19(2), 172.

Wimmers F, et al. (2021) The single-cell epigenomic and transcriptional landscape of immunity to influenza vaccination. Cell, 184(15), 3915.

Marand AP, et al. (2021) A cis-regulatory atlas in maize at single-cell resolution. Cell, 184(11), 3041.

Penkala IJ, et al. (2021) Age-dependent alveolar epithelial plasticity orchestrates lung homeostasis and regeneration. Cell stem cell, 28(10), 1775.

Marand AP, et al. (2021) Profiling single-cell chromatin accessibility in plants. STAR protocols, 2(3), 100737.

Schwartz GW, et al. (2021) TooManyPeaks identifies drug-resistant-specific regulatory elements from single-cell leukemic epigenomes. Cell reports, 36(8), 109575.

Penter L, et al. (2021) Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. Cancer discovery, 11(12), 3048.

Cui M, et al. (2020) Dynamic Transcriptional Responses to Injury of Regenerative and Non-regenerative Cardiomyocytes Revealed by Single-Nucleus RNA Sequencing. Developmental cell, 53(1), 102.

Pervolarakis N, et al. (2020) Integrated Single-Cell Transcriptomics and Chromatin Accessibility Analysis Reveals Regulators of Mammary Epithelial Cell Identity. Cell reports, 33(3), 108273.