Resource Summary Report

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CITE-seq-Count

RRID:SCR_019239
Type: Tool

Proper Citation

CITE-seq-Count (RRID:SCR_019239)

Resource Information

URL: https://hoohm.github.io/CITE-seq-Count/

Proper Citation: CITE-seq-Count (RRID:SCR_019239)

Description: Software python package that allows to count antibody TAGS from CITE-seq and/or cell hashing experiment. Software tool that allows to get UMI counts from single cell protein assay. Used to count (UMI counts) antibody-derived-tags (ADTs) or Cell Hashing tags (HTOs) in raw sequencing reads and build count matrix.

Synonyms: CITE-seq-Count v1.4.0, Cellular Indexing of Transcriptomes and Epitopes by Sequencing Count

Resource Type: software toolkit, software resource

Keywords: antibody TAGS count, CITE-seq, cell hashing experiment, antibody derived tags, cell hashing tags, raw sequencing reads, build count matrix, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CITE-seq-Count

Resource ID: SCR_019239

Alternate IDs: biotools:https:cite-seq-count

Alternate URLs: https://cite-seq.com/computational-tools/, https://bio.tools/cite-seq-count

Record Creation Time: 20220129T080344+0000

Record Last Update: 20250331T061713+0000

Ratings and Alerts

No rating or validation information has been found for CITE-seq-Count.

No alerts have been found for CITE-seq-Count.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Nyirenda J, et al. (2024) Spatially resolved single-cell atlas unveils a distinct cellular signature of fatal lung COVID-19 in a Malawian population. Nature medicine, 30(12), 3765.

Truchi M, et al. (2024) Detecting subtle transcriptomic perturbations induced by lncRNAs knock-down in single-cell CRISPRi screening using a new sparse supervised autoencoder neural network. Frontiers in bioinformatics, 4, 1340339.

Morgan DM, et al. (2024) Full-length single-cell BCR sequencing paired with RNA sequencing reveals convergent responses to pneumococcal vaccination. Communications biology, 7(1), 1208.

Russell D, et al. (2024) CD38+ Alveolar macrophages mediate early control of M. tuberculosis proliferation in the lung. Research square.

Lucibello F, et al. (2024) Divergent local and systemic antitumor response in primary uveal melanomas. The Journal of experimental medicine, 221(6).

Karnaukhov VK, et al. (2024) Innate-like T cell subset commitment in the murine thymus is independent of TCR characteristics and occurs during proliferation. Proceedings of the National Academy of Sciences of the United States of America, 121(14), e2311348121.

Pisu D, et al. (2024) The frequency of CD38+ alveolar macrophages correlates with early control of M. tuberculosis in the murine lung. Nature communications, 15(1), 8522.

Bagheri M, et al. (2024) Pharmacological induction of chromatin remodeling drives chemosensitization in triple-negative breast cancer. Cell reports. Medicine, 5(4), 101504.

Rodrigues KA, et al. (2024) Vaccines combining slow delivery and follicle targeting of antigens increase germinal center B cell clonal diversity and clonal expansion. bioRxiv : the preprint server for biology.

Zenk F, et al. (2024) Single-cell epigenomic reconstruction of developmental trajectories from pluripotency in human neural organoid systems. Nature neuroscience, 27(7), 1376.

Patir A, et al. (2024) Phenotypic and spatial heterogeneity of brain myeloid cells after stroke is associated with cell ontogeny, tissue damage, and brain connectivity. Cell reports, 43(5), 114250.

Quek C, et al. (2024) Single-cell spatial multiomics reveals tumor microenvironment vulnerabilities in cancer resistance to immunotherapy. Cell reports, 43(7), 114392.

Bagheri M, et al. (2023) Pharmacological Induction of mesenchymal-epithelial transition chemosensitizes breast cancer cells and prevents metastatic progression. bioRxiv : the preprint server for biology.

Ben-Chetrit N, et al. (2023) Breast Cancer Macrophage Heterogeneity and Self-renewal are Determined by Spatial Localization. bioRxiv : the preprint server for biology.

Kotov DI, et al. (2023) Early cellular mechanisms of type I interferon-driven susceptibility to tuberculosis. Cell, 186(25), 5536.

Madaci L, et al. (2023) Single-Cell Transcriptome Analysis of Acute Myeloid Leukemia Cells Using Methanol Fixation and Cryopreservation. Diseases (Basel, Switzerland), 12(1).

Ma L, et al. (2023) Vaccine-boosted CAR T crosstalk with host immunity to reject tumors with antigen heterogeneity. Cell, 186(15), 3148.

Mulè MP, et al. (2023) Multiscale integration of human and single-cell variations reveals unadjuvanted vaccine high responders are naturally adjuvanted. medRxiv : the preprint server for health sciences.

Madaci L, et al. (2023) The Contribution of Multiplexing Single Cell RNA Sequencing in Acute Myeloid Leukemia. Diseases (Basel, Switzerland), 11(3).

Mead BE, et al. (2022) Screening for modulators of the cellular composition of gut epithelia via organoid models of intestinal stem cell differentiation. Nature biomedical engineering, 6(4), 476.