

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

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

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: 20260729T044504+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 50 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Palii CG, et al. (2025) Trimodal Single-Cell Gene Regulatory Networks Reveal Principles of Stemness Loss and Cell Fate Acquisition in Human Hematopoiesis. bioRxiv : the preprint server for biology.

Bennabi I, et al. (2025) Size-dependent temporal decoupling of morphogenesis and transcriptional programs in pseudoembryos. Science advances, 11(34), eadv7790.

Truchi M, et al. (2025) Aging affects reprogramming of pulmonary capillary endothelial cells after lung injury in male mice. Nature communications, 16(1), 7234.

Salehi S, et al. (2025) Disrupted priming within draining lymph nodes drives immune quiescence in gastric cancer. bioRxiv : the preprint server for biology.

Rodrigues KA, et al. (2025) Vaccines combining slow release and follicle targeting of antigens increase germinal center B cell diversity and clonal expansion. Science translational medicine, 17(803), eadw7499.

Nguyen AA, et al. (2025) Sequential Lymphotoxin Beta Receptor and Retinoic Acid Receptor signals regulate cDC2 fates. Research square.

Muñoz Sandoval D, et al. (2025) Plasmodium falciparum infection induces T cell tolerance that is associated with decreased disease severity upon re-infection. The Journal of experimental medicine, 222(7).

Pisu D, et al. (2025) Spatially-distinct programming of macrophage diversity within the granulomas of Mycobacterium tuberculosis infected nonhuman primates. bioRxiv : the preprint server for biology.

Kim J, et al. (2025) Functional maturation of preterm intestinal epithelium through CFTR activation. Communications biology, 8(1), 540.

Hu W, et al. (2025) Temporal and Context-Dependent Requirements for the Transcription Factor Foxp3 Expression in Regulatory T Cells. Research square.

Zheng MZM, et al. (2025) Deconvoluting TCR-dependent and -independent activation is vital for reliable Ag-specific CD4+ T cell characterization by AIM assay. Science advances,

11(17), eadv3491.

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.

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

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.