

Resource Summary Report

Generated by [NIF](#) on Aug 22, 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 resource, software toolkit

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: 20260821T194143+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 60 mentions in open access literature.

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

de Menezes MN, et al. (2026) High efficiency CRISPR knock-in demonstrates that TCF1 is insufficient to reverse T cell exhaustion. Nature communications, 17(1).

Masuda K, et al. (2026) Distinct CD8+ T cell types associated with COVID-19 severity in unvaccinated HLA-A2+ patients. iScience, 29(6), 115880.

Liu S, et al. (2026) PRECISE-seq reveals disease-relevant TCR repertoires with phenotypic plasticity. The Journal of experimental medicine, 223(6).

Younis S, et al. (2026) EBV reprograms autoreactive anti-CNS B cells as antigen presenting cells in multiple sclerosis. bioRxiv : the preprint server for biology.

Han J, et al. (2026) RNA-binding proteins Zfp36l1 and Zfp36l2 protect against premature thymic involution. Cellular & molecular immunology, 23(5), 505.

Panas D, et al. (2026) Interactive analysis of single-cell trajectories in 3D space with Cell Journey. GigaScience, 15.

Rigby RE, et al. (2026) Single-cell analysis of signalling and transcriptional responses to type I interferons. EMBO reports, 27(9), 2491.

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.

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.

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).

Noyer L, et al. (2025) ORAI1 mutation with mixed loss and gain of function properties causes immunodeficiency and HLH. *Journal of human immunity*, 1(4).

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

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*.

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

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.

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*.

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

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.