

Resource Summary Report

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CellBender

RRID:SCR_025990

Type: Tool

Proper Citation

CellBender (RRID:SCR_025990)

Resource Information

URL: <https://github.com/broadinstitute/CellBender>

Proper Citation: CellBender (RRID:SCR_025990)

Description: Software package for eliminating technical artifacts from high-throughput single-cell RNA sequencing data. Deep generative model for noise removal in droplet-based single-cell RNA sequencing.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:37550580](#)

Keywords: Deep generative model, noise removal, eliminating technical artifacts, high-throughput single-cell RNA sequencing data,

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Alternate URLs: <https://cellbender.readthedocs.io/en/latest/>

License: BSD-3-Clause license

Record Creation Time: 20241026T053255+0000

Record Last Update: 20260801T042935+0000

Ratings and Alerts

No rating or validation information has been found for CellBender.

No alerts have been found for CellBender.

Data and Source Information

Usage and Citation Metrics

We found 175 mentions in open access literature.

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

Lasse Opsahl EL, et al. (2026) Fibroblast STAT3 Activation Drives Organ-Specific Premetastatic Niche Formation. *Cancer research*, 86(1), 22.

Mbano IM, et al. (2026) Single-cell and spatial profiling highlights TB-induced myofibroblasts as drivers of lung pathology. *The Journal of experimental medicine*, 223(3).

Pita-Juarez Y, et al. (2025) A single-nucleus and spatial transcriptomic atlas of the COVID-19 liver reveals topological, functional, and regenerative organ disruption in patients. *Genome biology*, 26(1), 56.

Vogt KE, et al. (2025) Sleep need driven oscillation of glutamate synaptic phenotype. *eLife*, 13.

Goldman OV, et al. (2025) Mosquito Cell Atlas: A single-nucleus transcriptomic atlas of the adult *Aedes aegypti* mosquito. *bioRxiv : the preprint server for biology*.

So J, et al. (2025) Robust single-nucleus RNA sequencing reveals depot-specific cell population dynamics in adipose tissue remodeling during obesity. *eLife*, 13.

Hanics J, et al. (2025) Neuronal activity modulates the expression of secretagoin, a Ca²⁺ sensor protein, during mammalian forebrain development. *Acta physiologica (Oxford, England)*, 241(5), e70031.

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. *Genomics & informatics*, 23(1), 13.

Nusser A, et al. (2025) Developmental trajectory and evolutionary origin of thymic mimetic cells. *Nature*, 643(8073), 1066.

Alegbe T, et al. (2025) Cell-type-resolved genetic regulatory variation shapes inflammatory bowel disease risk. *medRxiv : the preprint server for health sciences*.

Beernaert B, et al. (2025) Chromosomal instability shapes the tumor microenvironment of esophageal adenocarcinoma via a cGAS-chemokine-myeloid axis. *bioRxiv : the preprint server for biology*.

Umei TC, et al. (2025) Serine synthesis pathway regulates cardiac differentiation from human pluripotent stem cells. *iScience*, 28(7), 112843.

Patil KV, et al. (2025) The citrullinating enzyme PADI4 governs progenitor cell proliferation and translation in developing hair follicles. *Science advances*, 11(37), eadx4511.

Zhang H, et al. (2025) Fosl2 facilitates chromatin accessibility to determine developmental events during follicular maturation. *Nature communications*, 16(1), 8955.

Inamo J, et al. (2025) Comparative single-cell and spatial profiling of anti-SSA-positive and anti-centromere-positive Sjögren's disease reveals common and distinct immune activation and fibroblast-mediated inflammation. *Nature communications*, 16(1), 8299.

Wang Y, et al. (2025) Vascular endothelial-specific loss of TGF-beta signaling as a model for choroidal neovascularization and central nervous system vascular inflammation. *eLife*, 14.

Zheng C, et al. (2025) Distinct transcriptomic and epigenomic responses of mature oligodendrocytes during disease progression in a mouse model of multiple sclerosis. *Nature neuroscience*, 28(12), 2612.

Viswanadham VV, et al. (2025) Combined somatic mutation and transcriptome analysis reveals region-specific differences in clonal architecture in human cortex. *Cell reports*, 44(11), 116458.

Schmitz MT, et al. (2025) ANTIPODE Provides a Global View of Cell Type Homology and Transcriptomic Divergence in the Developing Mammalian Brain. *bioRxiv : the preprint server for biology*.

Youness M, et al. (2025) Location and aetiology are determinants of fibroblast activation and heterogeneity in the failing human heart. *Genome medicine*, 17(1), 155.