

Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

Scrattch.Hicat

RRID:SCR_018099

Type: Tool

Proper Citation

Scrattch.Hicat (RRID:SCR_018099)

Resource Information

URL: <https://github.com/AllenInstitute/scrattch.hicat>

Proper Citation: Scrattch.Hicat (RRID:SCR_018099)

Description: Software R package as hierarchical, iterative clustering for analysis of transcriptomics data.Used for single cell RNA-seq analysis for transcriptomic type characterization from Allen Institute.

Synonyms: Scrattch Hierarchical, Iterative Clustering for Analysis of Transcriptomics

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

Keywords: Hierarchical, iterative clustering, analysis, transcriptomics, data, single cell RNAseq, Allen Institute

Availability: Free, Available for download, Freely available

Resource Name: Scrattch.Hicat

Resource ID: SCR_018099

License: 2-clause BSD license

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260912T200255+0000

Ratings and Alerts

No rating or validation information has been found for Scrattch.Hicat.

No alerts have been found for Scrattch.Hicat.

Data and Source Information

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Hunker AC, et al. (2026) Technical and biological sources of noise confound multiplexed enhancer AAV screening. Nature communications, 17(1).

Megat S, et al. (2025) CREB3 gain of function variants protect against ALS. Nature communications, 16(1), 2942.

Jin K, et al. (2025) Brain-wide cell-type-specific transcriptomic signatures of healthy ageing in mice. Nature, 638(8049), 182.

Hunker AC, et al. (2025) Enhancer AAV toolbox for accessing and perturbing striatal cell types and circuits. Neuron, 113(10), 1507.

Gao Y, et al. (2025) Continuous cell-type diversification in mouse visual cortex development. Nature, 647(8088), 127.

Matthews EA, et al. (2025) RNA-programmable cell-type monitoring and manipulation in the human cortex with CellREADR. Cell reports, 44(8), 116037.

Reig-Viader R, et al. (2025) Synaptic proteome diversity is shaped by the levels of glutamate receptors and their regulatory proteins. Nature communications, 16(1), 10487.

Ben-Simon Y, et al. (2024) A suite of enhancer AAVs and transgenic mouse lines for genetic access to cortical cell types. bioRxiv : the preprint server for biology.

Gao Y, et al. (2024) Continuous cell type diversification throughout the embryonic and postnatal mouse visual cortex development. bioRxiv : the preprint server for biology.

Matthews EA, et al. (2024) RNA-programmable cell type monitoring and manipulation in the human cortex with CellREADR. bioRxiv : the preprint server for biology.

Hunker AC, et al. (2024) Enhancer AAV toolbox for accessing and perturbing striatal cell types and circuits. bioRxiv : the preprint server for biology.

Yao Z, et al. (2023) A high-resolution transcriptomic and spatial atlas of cell types in the whole mouse brain. Nature, 624(7991), 317.

Zhang Y, et al. (2023) Reference-based cell type matching of in situ image-based spatial transcriptomics data on primary visual cortex of mouse brain. Scientific reports, 13(1), 9567.

Sorensen SA, et al. (2023) Connecting single-cell transcriptomes to projectomes in mouse visual cortex. bioRxiv : the preprint server for biology.

Johansen N, et al. (2023) Interindividual variation in human cortical cell type abundance and expression. *Science* (New York, N.Y.), 382(6667), eadf2359.

Luo C, et al. (2022) Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. *Cell genomics*, 2(3).

Ishii K, et al. (2022) A neurogenetic mechanism of experience-dependent suppression of aggression. *Science advances*, 8(36), eabg3203.

Ortiz-??lvarez G, et al. (2022) p53/p21 pathway activation contributes to the ependymal fate decision downstream of GemC1. *Cell reports*, 41(11), 111810.

Yao Z, et al. (2021) A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. *Nature*, 598(7879), 103.

Mich JK, et al. (2021) Functional enhancer elements drive subclass-selective expression from mouse to primate neocortex. *Cell reports*, 34(13), 108754.