

Resource Summary Report

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Allen Institute Mouse Whole Cortex and Hippocampus SMART-seq

RRID:SCR_019013

Type: Tool

Proper Citation

Allen Institute Mouse Whole Cortex and Hippocampus SMART-seq (RRID:SCR_019013)

Resource Information

URL: <https://portal.brain-map.org/atlasses-and-data/rnaseq/mouse-whole-cortex-and-hippocampus-smart-seq>

Proper Citation: Allen Institute Mouse Whole Cortex and Hippocampus SMART-seq (RRID:SCR_019013)

Description: Collection of data set including single cell transcriptomes from multiple cortical areas and hippocampal formation. Samples were collected from dissections of brain regions from 8 week old male and female mice, primarily from pan GABAergic, pan glutamatergic, and pan neuronal transgenic lines, with addition of more specific transgenic lines and some retrogradely labeled cells in VISp and ALM.

Synonyms: Mouse Whole Cortex and Hippocampus SMART-seq

Resource Type: data or information resource, spatially referenced dataset, atlas

Keywords: Data collection, single cell transcriptomes, multiple cortical area, hippocampal formation, eight week old mice brain sample, pan GABAergic line, pan glutamatergic line, pan neuronal transgenic line

Availability: Free, Freely available

Resource Name: Allen Institute Mouse Whole Cortex and Hippocampus SMART-seq

Resource ID: SCR_019013

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260815T182933+0000

Ratings and Alerts

No rating or validation information has been found for Allen Institute Mouse Whole Cortex and Hippocampus SMART-seq.

No alerts have been found for Allen Institute Mouse Whole Cortex and Hippocampus SMART-seq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

King A, et al. (2026) Endothelial Adgrl2 Expression and Alternative Splicing Controls the Cerebrovasculature. The Journal of neuroscience : the official journal of the Society for Neuroscience, 46(16).

Villanueva EB, et al. (2026) Distinct and combined interferon- γ -receptor-1 loss in neurons and astrocytes disrupt brain energy metabolism and drive Parkinsonian dementia. Journal of biomedical science, 33(1).

Liao C, et al. (2025) Single-nucleus transcriptomics reveals time-dependent and cell-type-specific effects of psilocybin on gene expression. bioRxiv : the preprint server for biology.

Alexander RPD, et al. (2025) Delta opioid receptors engage multiple signaling cascades to differentially modulate prefrontal GABA release with input and target specificity. Cell reports, 44(2), 115293.

Fu X, et al. (2024) BIDCell: Biologically-informed self-supervised learning for segmentation of subcellular spatial transcriptomics data. Nature communications, 15(1), 509.

Safari MS, et al. (2024) Glucose-1,6-bisphosphate: A new gatekeeper of cerebral mitochondrial pyruvate uptake. Molecular metabolism, 88, 102018.

Wei Y, et al. (2024) Expression characteristics and potential function of non-coding RNA in mouse cortical cells. Frontiers in molecular neuroscience, 17, 1365978.

Triller G, et al. (2023) A trypanosome-derived immunotherapeutics platform elicits potent high-affinity antibodies, negating the effects of the synthetic opioid fentanyl. Cell reports, 42(2), 112049.

Sun ED, et al. (2023) TISSUE: uncertainty-calibrated prediction of single-cell spatial transcriptomics improves downstream analyses. bioRxiv : the preprint server for biology.

Bhattacharjee A, et al. (2023) Spatial transcriptomics reveals the distinct organization of mouse prefrontal cortex and neuronal subtypes regulating chronic pain. Nature neuroscience, 26(11), 1880.

Coleman K, et al. (2023) SpaDecon: cell-type deconvolution in spatial transcriptomics with semi-supervised learning. *Communications biology*, 6(1), 378.

Lund JB, et al. (2022) AntiSplodge: a neural-network-based RNA-profile deconvolution pipeline designed for spatial transcriptomics. *NAR genomics and bioinformatics*, 4(4), lqac073.

Oudenaarden C, et al. (2022) Upregulated functional gene expression programmes in tumour pericytes mark progression in patients with low-grade glioma. *Molecular oncology*, 16(2), 405.

Theofilatos D, et al. (2022) Protocol to isolate mature thymic T cell subsets using fluorescence-activated cell sorting for assessing gene expression by RNA-seq and transcription factor binding across the genome by CUT&RUN. *STAR protocols*, 3(4), 101839.

Zlatic SA, et al. (2022) Convergent cerebrospinal fluid proteomes and metabolic ontologies in humans and animal models of Rett syndrome. *iScience*, 25(9), 104966.

Yao Z, et al. (2021) A taxonomy of transcriptomic cell types across the isocortex and hippocampal formation. *Cell*, 184(12), 3222.

Tomikawa J, et al. (2021) Cell division- and DNA replication-free reprogramming of somatic nuclei for embryonic transcription. *iScience*, 24(11), 103290.

Cleary B, et al. (2021) Compressed sensing for highly efficient imaging transcriptomics. *Nature biotechnology*, 39(8), 936.

Uchigashima M, et al. (2020) Specific Neuroligin3-?Neurexin1 signaling regulates GABAergic synaptic function in mouse hippocampus. *eLife*, 9.