## **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:** <a href="https://portal.brain-map.org/atlases-and-data/rnaseq/mouse-whole-cortex-and-hippocampus-smart-seq">https://portal.brain-map.org/atlases-and-data/rnaseq/mouse-whole-cortex-and-hippocampus-smart-seq</a>

**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, atlas, spatially referenced dataset

**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

#### **Funding:**

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:** 20250501T081517+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 15 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

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.

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

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

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

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.

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

Bhattacherjee 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.

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.