

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

MapMyCells

RRID:SCR_024672

Type: Tool

Proper Citation

MapMyCells (RRID:SCR_024672)

Resource Information

URL: <https://portal.brain-map.org/atlas-and-data/bkp/mapmycells>

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Description: MapMyCells maps single cell and spatial transcriptomics data sets to massive, high-quality, and high-resolution cell type taxonomies. It enables speeding up the creation of brain reference atlases by facilitating the integration of datasets from the scientific community with a shared reference. MapMyCells is part of the growing Brain Knowledge Platform. Its key advantage is scale: researchers can provide up to 327 million cell-gene pairs from their own data, a huge leap forward for working with whole-brain datasets. Allen Institute and its collaborators continue to add new reference taxonomies and algorithms to MapMyCells.

Synonyms: Map My Cells, Allen MapMyCells

Resource Type: algorithm resource, software application, software resource, web application

Keywords: mapping of single cell and spatial transcriptomics data, mapping to whole mouse brain taxonomy, mapping to human brain taxonomy, correlation mapping, hierarchical mapping, label transfer

Funding: NIMH U24MH130918;
Paul G. Allen Foundation

Availability: Free, Freely available

Resource Name: MapMyCells

Resource ID: SCR_024672

Alternate URLs: <https://knowledge.brain-map.org/mapmycells/process/>,
<https://portal.brain-map.org/atlas-and-data/bkp/mapmycells/mapmycells-use-case->

single-cell-genomics

Record Creation Time: 20231103T050226+0000

Record Last Update: 20260905T133033+0000

Ratings and Alerts

No rating or validation information has been found for MapMyCells.

No alerts have been found for MapMyCells.

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 [PRECISE-TBI](#) .

Daniele E, et al. (2026) ACSA2 is not astrocyte-specific: implications for cell sorting strategies in the rodent brain. *Frontiers in cellular neuroscience*, 20, 1756677.

Yong HC, et al. (2026) A transcriptomic axis aligns with in vivo functional dynamics in hippocampal inhibitory circuits. *bioRxiv : the preprint server for biology*.

Zheng X, et al. (2026) In vivo multiomic Perturb-seq with enhanced nuclear gRNA capture. *bioRxiv : the preprint server for biology*.

Barkasi M, et al. (2026) Logistic regression for estimating functional effects with spatial transcriptomics. *Nucleic acids research*, 54(9).

Ray PL, et al. (2026) A layered standards framework for integrating single-cell and spatial omics data into brain cell atlases. *bioRxiv : the preprint server for biology*.

Kunst M, et al. (2026) SCALPEL: A pipeline for processing large-scale spatial transcriptomics data. *bioRxiv : the preprint server for biology*.

Burger S, et al. (2026) Inter-individual variation of cellular and gene-expression properties of the human striatum. *bioRxiv : the preprint server for biology*.

Fu B, et al. (2026) The molecular asynchrony of single cells. *bioRxiv : the preprint server for biology*.

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

Furdan S, et al. (2026) Conserved Kir channel mechanisms governing intrinsic excitability in human and rodent parvalbumin neurons. *Communications biology*, 9(1).

Schmitz MT, et al. (2026) A consensus spinal cord cell type atlas across mouse, macaque, and human. *bioRxiv : the preprint server for biology*.

Liang Z, et al. (2026) CellNiche represents cellular microenvironments in atlas-scale spatial omics data with contrastive learning. *Nature communications*, 17(1).

Radaelli C, et al. (2026) HCN channels reveal conserved and divergent physiology in supragranular pyramidal neurons in primate species. *Communications biology*, 9(1), 279.

Sloan NX, et al. (2026) Uncovering the signatures of aging and senescence in the human dorsolateral prefrontal cortex. *Cell genomics*, 6(2), 101127.

Sonthalia S, et al. (2026) NeMO Analytics: a compendium of transcriptomic data for the exploration of neocortical development. *Nature neuroscience*, 29(4), 978.

Lee E, et al. (2026) Angiopoietin-2 aggravates Alzheimer's disease by promoting blood-brain barrier dysfunction and neuroinflammation. *Cell reports*, 116621.

Robbins AB, et al. (2026) Temporal single-cell atlas of full-length Huntington's disease mouse model defines stage-specific signatures of corticostriatal dysfunction. *bioRxiv : the preprint server for biology*.

Baumgartner NE, et al. (2026) The lateral septum orchestrates state-dependent modulation of associative threat memory dynamics across the ovarian hormone cycle. *bioRxiv : the preprint server for biology*.

Green AA, et al. (2026) Cell-type specific impact of opioid use disorder and HIV on the human forebrain and cerebellum. *bioRxiv : the preprint server for biology*.

Minerva AR, et al. (2026) Stress resilience is associated with transcriptional remodeling in the VTA. *Cell reports*, 45(2), 116867.