

# Resource Summary Report

Generated by [NIF](#) on Aug 25, 2026

## MapMyCells

RRID:SCR\_024672

Type: Tool

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### Proper Citation

MapMyCells (RRID:SCR\_024672)

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### Resource Information

**URL:** <https://portal.brain-map.org/atlasses-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/atlasses-and-data/bkp/mapmycells/mapmycells-use-case->

single-cell-genomics

**Record Creation Time:** 20231103T050226+0000

**Record Last Update:** 20260821T194258+0000

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## Ratings and Alerts

No rating or validation information has been found for MapMyCells.

No alerts have been found for MapMyCells.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 60 mentions in open access literature.

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

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.

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.

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.

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

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

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

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

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

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.

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.

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.

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