

Resource Summary Report

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Transcriptomics Explorer

RRID:SCR_017567

Type: Tool

Proper Citation

Transcriptomics Explorer (RRID:SCR_017567)

Resource Information

URL: <https://portal.brain-map.org/atlasses-and-data/rnaseq>

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Description: Software tool to visualize and analyze transcriptomics data and transcriptomic cell types for mouse and human, all directly in web browser. To explore gene expression heatmap across cell types in datasets, search for genes of interest, explore tSNE visualization, colored by cell types or expression of genes of interest, visualize dataset's sampling strategy to see how cells and nuclei were sampled across brain areas, cortical layer, and other dimensions, find cell type of interest in one visualization and see its characteristics in different visualization. Used for Allen Brain Map Cell Types Database to Browse Data: Human - Multiple Cortical Areas, and Mouse - Cortex and Hippocampus.

Resource Type: data analysis software, data processing software, data visualization software, service resource, software application, software resource

Keywords: Visualize, analyze, transcriptomic, data, cell, type, mouse, human, Allen, database, multiple, cortical, area, cortex, hippocampus

Availability: Free, Freely available

Resource Name: Transcriptomics Explorer

Resource ID: SCR_017567

Alternate URLs: <https://celltypes.brain-map.org/rnaseq/human/cortex>,
<https://celltypes.brain-map.org/rnaseq/mouse/cortex-and-hippocampus>,

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260905T132826+0000

Ratings and Alerts

No rating or validation information has been found for Transcriptomics Explorer.

No alerts have been found for Transcriptomics Explorer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 108 mentions in open access literature.

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

Cheng M, et al. (2026) Neuronal and glial networks interact with traumatic brain injury to modulate cognition in ABCD study. NPJ systems biology and applications, 12(1).

Coulon A, et al. (2026) Non-microglial downregulation of PLCG2 impairs synaptic function and elicits Alzheimer disease-related hallmarks. bioRxiv : the preprint server for biology.

Yonemaru H, et al. (2026) Hippocampal transcriptome profiling in a 22q11.2 deletion syndrome mouse model: comparison with human schizophrenia. Molecular brain, 19(1).

Hristovska I, et al. (2026) Identification of distinct and shared biomarker panels in different manifestations of cerebral small-vessel disease through proteomic profiling. Nature aging, 6(3), 703.

Hanno Y, et al. (2026) Targeting notch signaling to restore neural development and behavior in mouse models of ASD. Nature communications, 17(1).

Arsentiev KA, et al. (2026) EMILIN-1 in the tumor microenvironment: insights from CNS tumors and beyond. Frontiers in oncology, 16, 1771697.

Zerbes T, et al. (2026) A self-complementary recombinant adeno-associated virus vector coding for an anchorless prion protein carrying the G127V mutation extends survival in a rodent prion disease model. bioRxiv : the preprint server for biology.

Zhang Y, et al. (2026) Robust integration and annotation of single-cell and spatial omics data using interpretable gene programs. Cell genomics, 6(4), 101105.

Sarropoulos I, et al. (2026) The evolution of gene regulation in mammalian cerebellum development. Science (New York, N.Y.), 391(6784), eadw9154.

Zhao T, et al. (2026) Discovering paracrine regulators of cell type composition from spatial transcriptomics using SPER. Bioinformatics advances, 6(1), vbag011.

Lu L, et al. (2026) Proteomic signatures of the APOE ϵ 4 and APOE ϵ 2 genetic variants and Alzheimer's disease. Nature aging, 6(5), 1138.

Liu X, et al. (2025) Brain Network Controllability and Its Regional Gene Expression Profile Associated With Suicidal Tendencies in Major Depressive Disorder Patients. *Depression and anxiety*, 2025, 6529148.

Mills WA, et al. (2025) Microglial cyclooxygenase-1 modulates cerebral capillary basal tone in vivo in mice. *Nature communications*, 16(1), 5704.

Kim HG, et al. (2025) The WAVE complex in developmental and adulthood brain disorders. *Experimental & molecular medicine*, 57(1), 13.

McKeever PM, et al. (2025) Single-nucleus transcriptome atlas of orbitofrontal cortex in ALS with a deep learning-based decoding of alternative polyadenylation mechanisms. *Cell genomics*, 101007.

Hong A, et al. (2025) Multi-omic relay velocity modeling uncovers dynamic chromatin-transcription regulation across cell states. *Nature communications*, 17(1), 566.

Li Y, et al. (2025) SOAR elucidates biological insights and empowers drug discovery through spatial transcriptomics. *Science advances*, 11(24), eadt7450.

Sung E, et al. (2025) Augmenting the human interactome for disease prediction through gene networks inferred from human cell atlas. *Animal cells and systems*, 29(1), 11.

Wang X, et al. (2025) Chromatin remodeling factor BAF155 coordinates oligodendroglial-neuronal communications linked to regional myelination and autism-like behavioral deficits in mice. *Nature communications*, 17(1), 1165.

Chinopoulos C, et al. (2025) Underestimation of mitochondrial respiratory capacity in gray matter voxels of the human brain map due to limited OXPHOS and TCA cycle in astrocytes. *Frontiers in cellular neuroscience*, 19, 1661231.