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/atlases-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 processing software, data analysis software, service resource, data visualization software, software resource, software application

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

Funding:

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,

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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 73 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Gimenez GA, et al. (2025) A Study on Potential Sources of Perineuronal Net-Associated Sema3A in Cerebellar Nuclei Reveals Toxicity of Non-Invasive AAV-Mediated Cre Expression in the Central Nervous System. International journal of molecular sciences, 26(2).

García-Ruiz S, et al. (2025) Splicing accuracy varies across human introns, tissues, age and disease. Nature communications, 16(1), 1068.

Zhao H, et al. (2024) Identifying novel proteins for suicide attempt by integrating proteomes from brain and blood with genome-wide association data. Neuropsychopharmacology : official publication of the American College of Neuropsychopharmacology, 49(8), 1255.

Bai Z, et al. (2024) Spatially Exploring RNA Biology in Archival Formalin-Fixed Paraffin-Embedded Tissues. bioRxiv : the preprint server for biology.

Machold R, et al. (2024) Genetic approaches to elucidating cortical and hippocampal GABAergic interneuron diversity. Frontiers in cellular neuroscience, 18, 1414955.

Yokoyama K, et al. (2024) Visualization of myelin-forming oligodendrocytes in the adult mouse brain. Journal of neurochemistry.

Montani C, et al. (2024) Sex-biasing influence of autism-associated Ube3a gene overdosage at connectomic, behavioral, and transcriptomic levels. Science advances, 10(28), eadg1421.

Pichet Binette A, et al. (2024) Proteomic changes in Alzheimer's disease associated with progressive A? plaque and tau tangle pathologies. Nature neuroscience, 27(10), 1880.

Tian J, et al. (2024) Hippocampal transcriptome-wide association study and pathway analysis of mitochondrial solute carriers in Alzheimer's disease. Translational psychiatry, 14(1), 250.

Bahl E, et al. (2024) Using deep learning to quantify neuronal activation from single-cell and spatial transcriptomic data. Nature communications, 15(1), 779.

K C R, et al. (2024) Zmiz1 is a novel regulator of brain development associated with autism and intellectual disability. Frontiers in psychiatry, 15, 1375492.

Dear R, et al. (2024) Cortical gene expression architecture links healthy neurodevelopment to the imaging, transcriptomics and genetics of autism and schizophrenia. Nature neuroscience, 27(6), 1075.

García-Ruiz S, et al. (2023) Splicing accuracy varies across human introns, tissues and age. bioRxiv : the preprint server for biology.

Fuentes-Fayos AC, et al. (2023) Metformin and simvastatin exert additive antitumour effects in glioblastoma via senescence-state: clinical and translational evidence. EBioMedicine, 90, 104484.

Sadria M, et al. (2023) Adversarial training improves model interpretability in single-cell RNA-seq analysis. Bioinformatics advances, 3(1), vbad166.

Johansen N, et al. (2023) Projecting RNA measurements onto single cell atlases to extract cell type-specific expression profiles using scProjection. Nature communications, 14(1), 5192.

Lukacs IP, et al. (2023) Differential effects of group III metabotropic glutamate receptors on spontaneous inhibitory synaptic currents in spine-innervating double bouquet and parvalbumin-expressing dendrite-targeting GABAergic interneurons in human neocortex. Cerebral cortex (New York, N.Y. : 1991), 33(5), 2101.

Machold R, et al. (2023) Id2 GABAergic interneurons comprise a neglected fourth major group of cortical inhibitory cells. eLife, 12.

Zeighami Y, et al. (2023) A comparison of anatomic and cellular transcriptome structures across 40 human brain diseases. PLoS biology, 21(4), e3002058.

Schreglmann SR, et al. (2023) Age-related telomere attrition in the human putamen. Aging cell, 22(7), e13861.