

Resource Summary Report

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NeMOarchive

RRID:SCR_016152

Type: Tool

Proper Citation

NeMOarchive (RRID:SCR_016152)

Resource Information

URL: <https://nemoarchive.org/>

Proper Citation: NeMOarchive (RRID:SCR_016152)

Description: Data repository specifically focused on storage and dissemination of omic data generated from BRAIN Initiative and related brain research projects. Data repository and archive for BCDC and BICCN project, among others. NeMO data include genomic regions associated with brain abnormalities and disease, transcription factor binding sites and other regulatory elements, transcription activity, levels of cytosine modification, histone modification profiles and chromatin accessibility.

Abbreviations: NeMO

Synonyms: NeMO Archive, Neuroscience Multi-omic Data Archive, The Neuroscience Multi-Omic Archive, Neuroscience Multi-Omic Archive

Resource Type: data repository, service resource, database, storage service resource, data or information resource

Keywords: omic, neuroscience, neurobiology, bcdbc, biccn, nih, brain, genomic, region, abnormal, transcription, factor, binding, site, chromatin, regulatory, element, data

Funding: NIMH MH114788;
BRAIN Initiative

Availability: Free, Freely available

Resource Name: NeMOarchive

Resource ID: SCR_016152

Alternate URLs: <https://data.nemoarchive.org/>

Record Creation Time: 20220129T080329+0000

Ratings and Alerts

No rating or validation information has been found for NeMOarchive.

No alerts have been found for NeMOarchive.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 113 mentions in open access literature.

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

Grinberg AR, et al. (2026) Transcriptional Heterogeneity Reveals a Synaptic Gene Program in Developing and Adult Human Oligodendrocyte Precursor Cells. bioRxiv : the preprint server for biology.

Shwab EK, et al. (2025) Single cell transcriptomics reveals enrichment of aggregation-prone alpha-synuclein isoforms across synucleinopathies. bioRxiv : the preprint server for biology.

Zhou J, et al. (2025) scDCT: a conditional diffusion-based deep learning model for high-fidelity single-cell cross-modality translation. Briefings in bioinformatics, 26(4).

Ake F, et al. (2025) Quantification of transcript isoforms at the single-cell level using SCALPEL. Nature communications, 16(1), 6402.

Jin K, et al. (2025) Brain-wide cell-type-specific transcriptomic signatures of healthy ageing in mice. Nature, 638(8049), 182.

Gao Y, et al. (2025) Continuous cell-type diversification in mouse visual cortex development. Nature, 647(8088), 127.

Moon Y, et al. (2025) PolyASite v3.0: a multi-species atlas of polyadenylation sites inferred from single-cell RNA-sequencing data. Nucleic acids research, 53(D1), D197.

Park SJ, et al. (2025) The neurexin gene family regulates olfactory glomerular formation. Cell reports, 44(8), 116125.

Xu Y, et al. (2025) multiVIB: A unified probabilistic contrastive learning framework for atlas-scale integration of single-cell multi-omics data. bioRxiv : the preprint server for biology.

Gim DH, et al. (2025) Deciphering cell-type-and temporally specific matrisome expression signatures in human cortical development and neurodevelopmental disorders via scRNA-

seq meta-analysis. Nature communications, 16(1), 9907.

Shwab EK, et al. (2025) Comparative mapping of single-cell transcriptomic landscapes in neurodegenerative diseases. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(5), e70012.

Shi Q, et al. (2025) Spatial dissimilarity analysis in single-cell transcriptomics. Cell reports methods, 5(9), 101141.

Tasic B, et al. (2025) Exploring brain circuits, one cell type-or more- at a time. Neuron, 113(10), 1469.

Liu Y, et al. (2025) Human CLOCK enhances neocortical function. Nature neuroscience, 28(8), 1716.

Kim SJ, et al. (2025) A consensus definition for deep layer 6 excitatory neurons in mouse somatosensory, visual, and motor cortex. Cell reports, 44(9), 116167.

Mukamel EA, et al. (2025) Cell-type-specific enrichment of somatic aneuploidy in the mammalian brain. Neuron, 113(17), 2814.

van Velthoven CTJ, et al. (2025) Transcriptomic and spatial organization of telencephalic GABAergic neurons. Nature, 647(8088), 143.

Liao K, et al. (2025) Single-nucleus profiling decoding the subcortical visual pathway evolution of vertebrates. iScience, 28(4), 112128.

Miao Z, et al. (2024) Uniform quantification of single-nucleus ATAC-seq data with Paired-Insertion Counting (PIC) and a model-based insertion rate estimator. Nature methods, 21(1), 32.

Iyer S, et al. (2024) The BRAIN Initiative data-sharing ecosystem: Characteristics, challenges, benefits, and opportunities. eLife, 13.