

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 or information resource, data repository, database, service resource, storage service resource

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

Funding: BRAIN Initiative ;
NIMH MH114788

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 126 mentions in open access literature.

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

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.

Chang L, et al. (2026) The 30th Scientific Conference of the Society on NeuroImmune Pharmacology in Annapolis, Maryland, May 3rd - 6th, 2026. NeuroImmune pharmacology and therapeutics, 5(1), 1.

Wang Z, et al. (2026) Integrative Single-Cell Epigenomic Atlas Annotates the Regulatory Genome of the Adult Mouse Brain. bioRxiv : the preprint server for biology.

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.

, et al. (2026) A Community Standard Multispecies Cell Atlas of the Basal Ganglia. bioRxiv : the preprint server for biology.

Gao Y, et al. (2026) Conserved Cell Type Signatures Across the Brainstem and Spinal Cord in the Mouse Central Nervous System. bioRxiv : the preprint server for biology.

Mikolajewicz N, et al. (2026) Reactive oligodendrocytes promote glioblastoma progression through CCL5/CCR5-mediated glioma stem cell maintenance. Neuron, 114(2), 237.

Liu RF, et al. (2026) An atlas of primate insular cortex reveals a signal-processing strategy in von Economo neurons. Nature cell biology.

Spanò T, et al. (2026) Localized mRNAs and protein synthesis in cortical layer 1. Cell reports, 45(7), 117687.

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

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.

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

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).

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.

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.

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*.

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

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