Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 23, 2025

NeMOarchive

RRID:SCR_016152
Type: Tool

Proper Citation

NeMOarchive (RRID:SCR_016152)

Resource Information

URL: https://nemoarchive.org/

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

Keywords: omic, neuroscience, neurobiology, bcbc, 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

Record Last Update: 20250423T060916+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 96 mentions in open access literature.

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

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.

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.

Kim SJ, et al. (2024) A consensus definition for deep layer 6 excitatory neurons in mouse neocortex. bioRxiv : the preprint server for biology.

Ling E, et al. (2024) Concerted neuron-astrocyte gene expression declines in aging and schizophrenia. bioRxiv : the preprint server for biology.

van Velthoven CTJ, et al. (2024) The transcriptomic and spatial organization of telencephalic GABAergic neuronal types. bioRxiv : the preprint server for biology.

Gao Y, et al. (2024) Continuous cell type diversification throughout the embryonic and postnatal mouse visual cortex development. bioRxiv : the preprint server for biology.

Shwab EK, et al. (2024) Comparative mapping of single-cell transcriptomic landscapes in neurodegenerative diseases. bioRxiv : the preprint server for biology.

Cao Y, et al. (2024) scButterfly: a versatile single-cell cross-modality translation method via dual-aligned variational autoencoders. Nature communications, 15(1), 2973.

Dembrow NC, et al. (2024) Areal specializations in the morpho-electric and transcriptomic properties of primate layer 5 extratelencephalic projection neurons. Cell reports, 43(9), 114718.

Rigden DJ, et al. (2023) The 2023 Nucleic Acids Research Database Issue and the online molecular biology database collection. Nucleic acids research, 51(D1), D1.

Jin K, et al. (2023) Cell-type specific molecular signatures of aging revealed in a brain-wide transcriptomic cell-type atlas. bioRxiv : the preprint server for biology.

Yao Z, et al. (2023) A high-resolution transcriptomic and spatial atlas of cell types in the whole mouse brain. bioRxiv : the preprint server for biology.

Chen A, et al. (2023) Single-cell spatial transcriptome reveals cell-type organization in the macaque cortex. Cell, 186(17), 3726.

Yampolskaya M, et al. (2023) scTOP: physics-inspired order parameters for cellular identification and visualization. Development (Cambridge, England), 150(21).

Pool AH, et al. (2023) Recovery of missing single-cell RNA-sequencing data with optimized transcriptomic references. Nature methods, 20(10), 1506.

Krienen FM, et al. (2023) A marmoset brain cell census reveals regional specialization of cellular identities. Science advances, 9(41), eadk3986.

Micali N, et al. (2023) Molecular programs of regional specification and neural stem cell fate progression in macaque telencephalon. Science (New York, N.Y.), 382(6667), eadf3786.

Price KM, et al. (2023) Identification of brain cell types underlying genetic association with word reading and correlated traits. Molecular psychiatry, 28(4), 1719.

Suresh H, et al. (2023) Comparative single-cell transcriptomic analysis of primate brains highlights human-specific regulatory evolution. Nature ecology & evolution, 7(11), 1930.