

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

NeMO Analytics

RRID:SCR_018164

Type: Tool

Proper Citation

NeMO Analytics (RRID:SCR_018164)

Resource Information

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

Proper Citation: NeMO Analytics (RRID:SCR_018164)

Description: Portal enabling web based visualization and analysis of multi omic data describing cell types in developing and adult brain, powered by gEAR and EpiViz. Release 1 on April 2019 includes single cell and bulk tissue RNAseq, ATACseq, and ChIPseq from fetal human prefrontal cortex, as well as from stem cell models of neural induction. Portal will expand to include multiple regions of developing and adult brain and additional analytical tools.

Synonyms: Neuroscience Multi-Omic Analytics

Resource Type: analysis service resource, data analysis service, data or information resource, portal, production service resource, service resource, topical portal

Keywords: Visualization, analysis, multi omic data, cell type, developing brain, adult brain, RNAseq, ATACseq, ChIPseq, fetal human prefrontal cortex, stem cell, neural induction, brain, data

Availability: Free, Freely available

Resource Name: NeMO Analytics

Resource ID: SCR_018164

Alternate IDs: SCR_018244

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260905T132832+0000

Ratings and Alerts

No rating or validation information has been found for NeMO Analytics.

No alerts have been found for NeMO Analytics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

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.

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

Sonthalia S, et al. (2024) A Curated Compendium of Transcriptomic Data for the Exploration of Neocortical Development. bioRxiv : the preprint server for biology.

Mato-Blanco X, et al. (2024) Early Developmental Origins of Cortical Disorders Modeled in Human Neural Stem Cells. bioRxiv : the preprint server for biology.

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

Hawrylycz M, et al. (2023) A guide to the BRAIN Initiative Cell Census Network data ecosystem. PLoS biology, 21(6), e3002133.

Naranjo O, et al. (2023) AKT signaling modulates latent viral reservoir viability in HIV-1-infected blood-brain barrier pericytes. The Journal of biological chemistry, 300(1), 105526.

Ament SA, et al. (2023) The Neuroscience Multi-Omic Archive: a BRAIN Initiative resource for single-cell transcriptomic and epigenomic data from the mammalian brain. Nucleic acids research, 51(D1), D1075.

Alhesain M, et al. (2023) Expression of the schizophrenia associated gene FEZ1 in the early developing fetal human forebrain. Frontiers in neuroscience, 17, 1249973.

Hertzano R, et al. (2022) Advancing discovery in hearing research via biologist-friendly access to multi-omic data. Human genetics, 141(3-4), 319.

Guo C, et al. (2021) Graded heterogeneity of metabotropic signaling underlies a continuum of cell-intrinsic temporal responses in unipolar brush cells. Nature communications, 12(1), 5491.

Yao Z, et al. (2021) A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. *Nature*, 598(7879), 103.

Zhu C, et al. (2021) Joint profiling of histone modifications and transcriptome in single cells from mouse brain. *Nature methods*, 18(3), 283.

Orvis J, et al. (2021) gEAR: Gene Expression Analysis Resource portal for community-driven, multi-omic data exploration. *Nature methods*, 18(8), 843.

Bakken TE, et al. (2021) Comparative cellular analysis of motor cortex in human, marmoset and mouse. *Nature*, 598(7879), 111.

Kancherla J, et al. (2020) Epiviz File Server: Query, transform and interactively explore data from indexed genomic files. *Bioinformatics (Oxford, England)*, 36(18), 4682.