OmicsHQ: Accelerating Single-Cell Discovery Through Analysis-Ready Data

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Background

Single-cell genomics has fundamentally transformed biology in recent decades, yet data remain fragmented across disparate sources, with inconsistent metadata and processing standards that make cross-study comparison difficult and time-consuming.

OmicsHQ addresses these challenges by providing a unified, expertly curated catalog of over 9,000 single-cell and single-nuclei RNA-sequencing studies, including nearly 1,200 processed, analysis- and AI-ready datasets aggregated from multiple public repositories into a single searchable platform. OmicsHQ includes 14 atlases that integrate standardized, analysis-ready datasets across specific tissues to provide insights into cellular heterogeneity across various conditions such as cancer, autoimmune and infectious diseases, thus supporting identification of new therapeutic targets.

OmicsHQ

Catalog App

OmicsHQ ? Login

Single-Cell Catalog

Results contain a total of 9183 studies and 1179 processed datasets

Filter for datasets or cell type atlases

Search... *Entry point for dataset discovery* Filters Can't find it? Suggest a Study Datasets Atlases

Filter Options

Filters

Processed Unprocessed All

Publication Date

From mm/dd/yyyy To mm/dd/yyyy

Organization Data

Status (2)

scAlliance1 (1)

Common Filters

Organism (4) Clear Selected

Human (14)

Mouse (2)

Cynomolgus Monkey (0)

Rhesus Monkey (0)

Tissue (640)

Disease (433) Clear Selected

multiple sclerosis

multiple sclerosis (14)

relapsing-remitting multiple sclerosis (2)

secondary progressive multiple sclerosis (1)

Technique (43)

Repository (26)

Advanced Filters

Cell Types (1236)

Processing Workflow (4)

Tissue Collections (10)

Disease Collections (7)

Atlas (14)

Browse single-cell RNA-seq datasets or filter by publication date, status, organism, tissue, disease, technique, repository, cell type, processing workflow, tissue collections, disease collections or atlases to refine results

Study | Disease | Technique | Repository ID

Study Level View

Cell type mapping reveals tissue niches and interactions in subcortical multiple sclerosis lesions. | Human | brain white matter | multiple sclerosis | 10x 3' v3 | GSE279180

Processed Shortname: **Lerma-Martin_2024_Nat_Neurosci**

PMID: **39501036**

Multiple sclerosis (MS) is a chronic inflammatory disease of the central nervous system. Inflammation is gradually compartmentalized and restricted to specific tissue niches such a...

Publication: 11/5/2024 Authors: Lerma-Martin,Celia;Badia-I-Mompel,Pau;Rami...

Journal: Nature Neuroscience

Toggle for dataset details

Datasets v

Dataset Details

Study Description: The authors performed paired single-nuclei RNA-sequencing and spatial transcriptomics analysis on the subcortical white matter tissue from 6 controls and 6 multiple sclerosis human donors.

Dataset ID: **Lerma-Martin_2024_Nat_Neurosci-GSE279180** Batch: **batch13**

Download Explore Figures

No. Of Cells: **102,956**

Workflow: **scds_cellranger_7**

SC Technology: **10x 3' v3**

Donor Organism: **Human**

Donor Disease: **multiple sclerosis, Healthy Subject**

No. Of Donors: **12**

Sample Tissue: **brain white matter**

Sample Pathology: **Abnormal, Healthy**

No. Of Samples: **16**

CellxGene

Dataset Explorer – CellxGene Visualizations

cellxgene 2157_Lerma...ata-annotated

Celltypist_Cell_Annotation

Celltypist_Cell_Type_Ontology_ID

Celltypist_Cell_Type_Ontology_Name

author_cell_id

author_cell_type

author_cell_type_cell_ontology_id

author_cell_type_cell_ontology_name

author_major_cell_type

authors: C. Lerma-... z, L. Schirmer

basic_qc: PASS

cell_batch

cell_technology_type: RNA assay

doi: 10.1038/s...}-024-01796-z

donor_age

donor_age_unit: Year

donor_alcohol_use_history: Not reported

donor_cancer_type: NA

donor_disease

Control 24585

MS 78371

donor_disease_doid_id

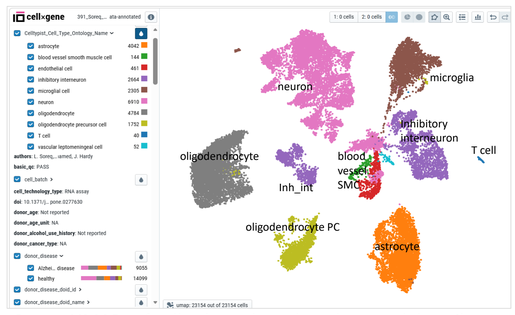
1: 0 cells 2: 0 cells

T cell, stromal cell, microglial cell, pericyte, capillary endothelial cell, endothelial cell, venule, astrocyte, B cell, oligodendrocy...recursor cell, nan, oligodendrocyte, lamp5 GABAerg...l interneuron, neuron, L2/3-6 intrat...tergic neuron

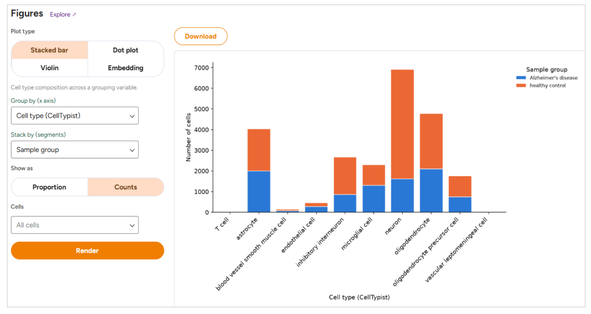
umap: 0 out of 102956 cells

Explore and Compare Datasets

Use CELLxGENE suite of tools to explore, analyze and annotate single-cell datasets



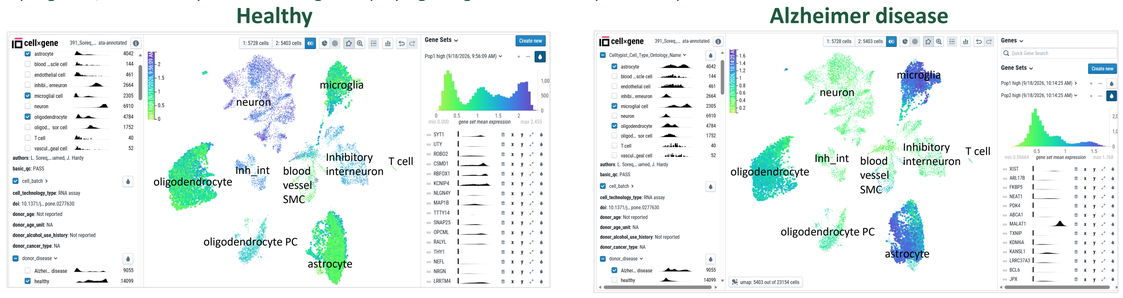
Create UMAPs of cell subsets based on data model attributes



Explore cell types in healthy vs diseased samples

Soreq et al., 2023, analyzed differences in gene expression in over 25,000 single-nuclei from control vs Alzheimer disease brain samples. They found an increase in the frequency of microglia, astrocytes and oligodendrocytes, as well as shared and distinct gene programs, with astrocytes and microglia displaying the greatest transcriptomic impacts.

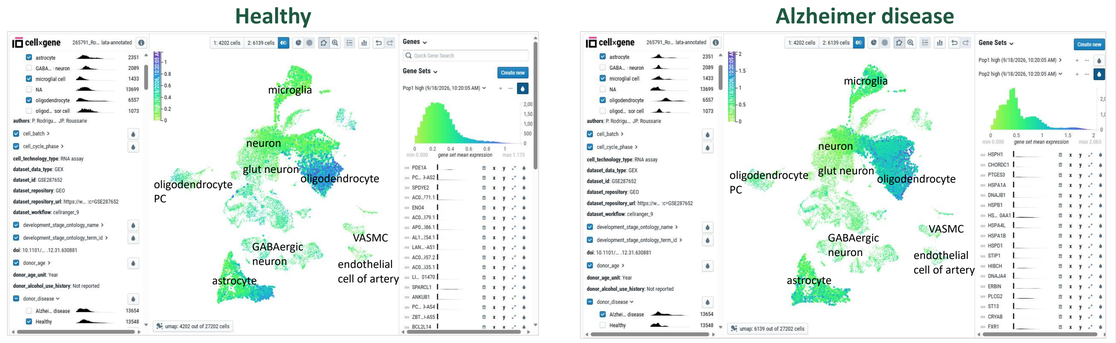
Healthy **Alzheimer disease**



Astrocytes, microglia and oligodendrocytes from healthy vs AD samples were used to compute differentially expressed genes (DEGs).

Rodriguez-Rodriguez et al., 2025 identified early responses to amyloid pathology by microglia, astrocytes and oligodendrocytes in entorhinal cortex samples of Alzheimer disease vs control donors, including pathways related to cell stress.

Healthy **Alzheimer disease**



Healthy vs AD samples of astrocytes, microglia and oligodendrocytes were selected in a second study to compute DEGs between gene sets. The top 50 DEGs in each gene set can be downloaded for further analysis.

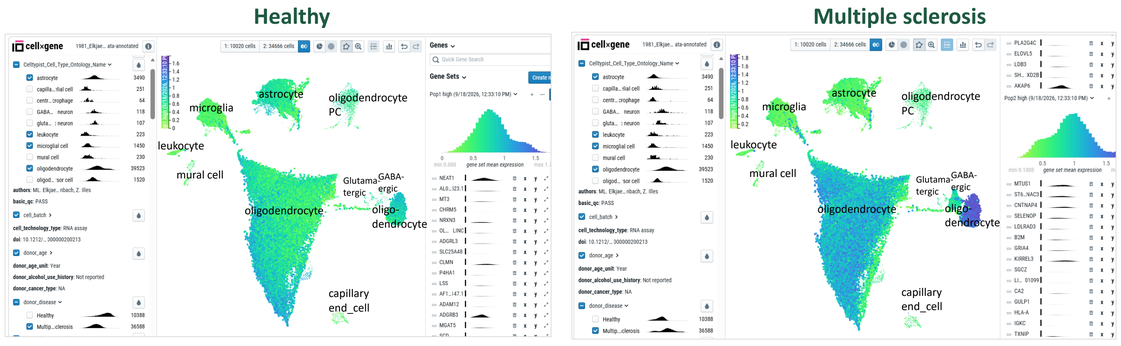
Independent studies (Soreq et al., 2023 and Rodriguez-Rodriguez et al., 2025) visualized using CellxGene in OmicsHQ show activated astrocytes, microglia and oligodendrocytes in Alzheimer disease vs. control samples, consistent with established disease biology.

1. Soreq et al. PLoS One. 2023. doi: 10.1371/journal.pone.0277630.
2. Rodriguez-Rodriguez et al. bioRxiv [Preprint] 2025.doi:10.1101/2024.12.31.630881.

Compare top differentially expressed genes across independent Multiple sclerosis studies

Elkjaer et al., 2024 uncovered an MS-specific oligodendrocyte genetic signature with an inflammatory profile, functional B-cell subsets with differential location and specific tendencies toward certain lesion types and a distinct metabolic astrocyte phenotype.

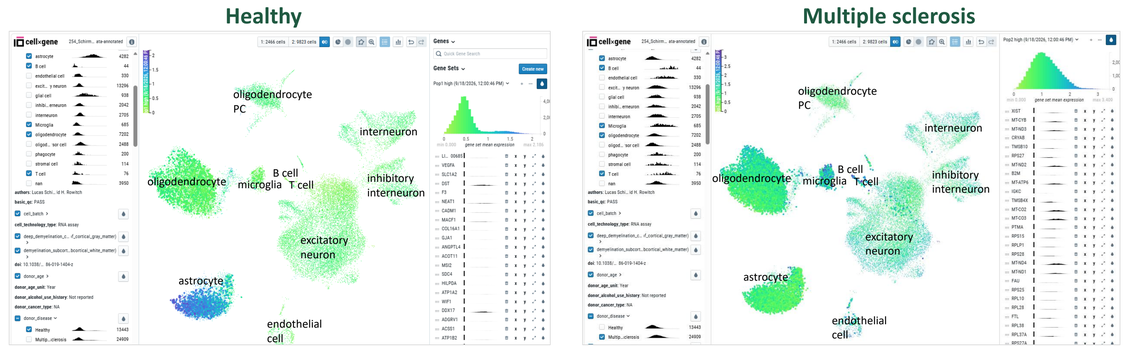
Healthy **Multiple sclerosis**



Cell subsets of astrocytes, microglia, oligodendrocytes and immune cells were selected in healthy vs MS samples to compute DEGs between gene sets. The top 50 DEGs in each gene set can be downloaded for further analysis.

Schirmer et al., 2019 assessed changes in expression in multiple cell lineages in MS lesions and found signatures of stressed oligodendrocytes, reactive astrocytes and activated microglia mapped most strongly to the rim of MS plaques.

Healthy **Multiple sclerosis**



Cell subsets of astrocytes, microglia, oligodendrocytes, B cells and T cells were selected in healthy vs MS samples to compute DEGs between gene sets. The top 50 DEGs in each gene set can be downloaded for further analysis.

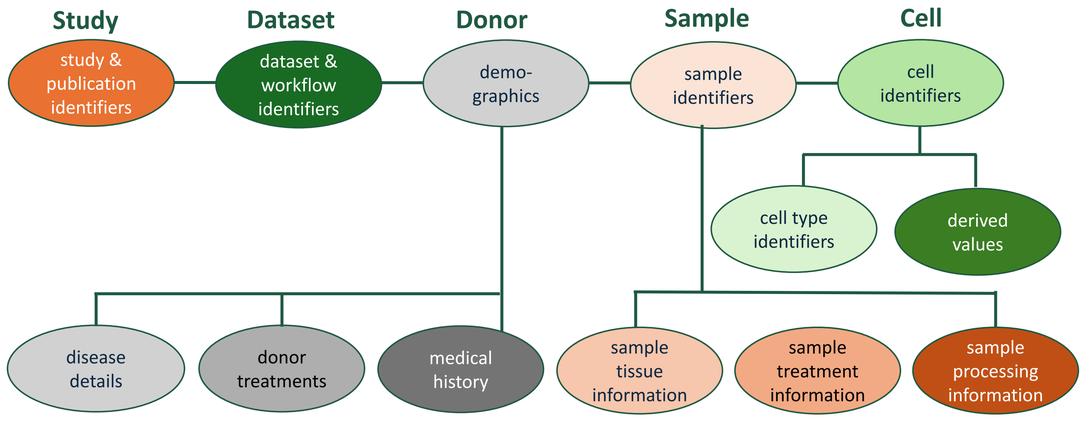
Comparison of top differentially expressed genes in independent studies (Elkjaer et al., 2024 and Schirmer et al., 2019) visualized using CellxGene in OmicsHQ show MS-specific gene signatures of reactive astrocytes, activated microglia, oligodendrocytes and immune cells that can lead to deeper insights into MS lesion pathogenesis.

3. Elkjaer et al. Neurol Neuroimmunol Neuroinflamm. 2024 doi:10.1212/NXI.0000000000200213.
4. Schirmer et al. Nature. 2019 Sep;573(7772):75-82. doi: 10.1038/s41586-019-1404-z.

Single Cell data alliance

Data Model

Nearly 1200 datasets in OmicsHQ are processed according to the Single Cell data alliance data model



Custom 5 entity, 92 attribute data model is flexible enough to be used for a wide range of experimental purposes

All processed datasets undergo a rigorous multi-step workflow:

- prescreening for completeness and pipeline compatibility
- harmonization using consistent ontology-aligned metadata
- processing through a reproducible bioinformatics pipeline
- independent quality control
- flexible data delivery (h5ad, seurat, TileDB)
- direct download or command-line access

Every dataset is validated and immediately usable for downstream analysis

- Consistent standards across datasets
- Processed, harmonized, AI/ML machine readable
- Ready for immediate analysis

OmicsHQ

Confidentiality Level: GENERAL/INTERNAL