# Public single-cell RNA-sequencing data

Public single-cell RNA-sequencing (scRNA-seq) data refers to scRNA-seq datasets that are publicly available for researchers to access and analyze. These datasets contain gene expression information from individual cells, allowing researchers to study the molecular diversity of cell populations and identify novel cell types and gene expression patterns.

There are several publicly available scRNA-seq databases and repositories, including the Gene Expression Omnibus (GEO), the European Bioinformatics Institute (EBI) Expression Atlas, the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA), and the Single Cell Portal. These databases contain scRNA-seq datasets from a wide range of organisms, tissues, and cell types.

Public scRNA-seq datasets have been used in numerous studies to investigate various biological processes and diseases. For example, scRNA-seq datasets have been used to study the immune response to viral infections, the development of neuronal circuits, and the heterogeneity of cancer cells. Public scRNA-seq datasets have also been used to develop computational tools and methods for scRNA-seq data analysis.

The availability of public scRNA-seq datasets has facilitated the advancement of single-cell genomics research and has enabled researchers to ask new questions and make new discoveries.

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The purpose of a study by Piperi et al. was to investigate the clinical significance of SSADH expression in human gliomas. Using public single-cell RNA-sequencing data from glioma surgical resections, Piperi et al. initially grouped cancer cells according to ALDH5A1 (Aldehyde dehydrogenase 5 family member A1) expression, which encodes SSADH. Gene ontology enrichment analysis of genes differentially expressed between cancer cells expressing high or low levels of ALDH5A1, highlighted enrichment in genes implicated in the cell morphogenesis and motility. In glioblastoma cell lines, ALDH5A1 knockdown inhibited cell proliferation, induced apoptosis, and reduced their migratory potential. This was accompanied by a reduction in the mRNA levels of the adherens junction molecule ADAM-15 and deregulation in the expression of EMT biomarkers, with increased CDH1 and decreased vimentin mRNA levels. Evaluation of SSADH expression in a cohort of 95 gliomas using immunohistochemistry showed that SSADH expression was significantly elevated in cancer tissues compared to normal brain tissues, without any significant correlation with clinicopathological characteristics. In summary, data show that SSADH is upregulated in glioma irrespective of the histological grade, and its expression sustains glioma cell motility [1)]

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Piperi C, Saurty-Seerunghen MS, Levidou G, Sepsa A, Trigka EA, Klonou A, Markouli M, Strepkos D, Spyropoulou A, Kanakoglou DS, Lakiotaki E, Karatrasoglou EA, Boviatsis E, El-Habr EA, Korkolopoulou P. Glioma Cells Expressing High Levels of ALDH5A1 Exhibit Enhanced Migration Transcriptional Signature in Patient Tumors. Neurotherapeutics. 2023 Mar 28. doi: 10.1007/s13311-023-01354-8. Epub ahead of print. PMID: 36976494.