

This Zenodo deposit contains a publicly available description of the Dataset:

## "PD5D\_MTG\_snRNAseq\_hybsel".

### Dataset Description:

This dataset contains the raw data in FASTQ format for single-nucleus RNA sequencing (snRNAseq) enriched with Agilent SureSelect for reads from a list of targeted transcripts for human middle temporal gyrus (MTG) samples from Parkinson's patients and healthy controls. This data comes from the same 10X libraries as PD5D\_MTG\_snRNAseq, except with the additional enrichment step before sequencing. It's part of the PD5D cohort, where the same subjects were also profiled with other omics assays incl. genotyping, single-cell ATACseq, and spatial transcriptomics.

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**Dataset Name:** scherzer-pmdbs-sn-rnaseq-mtg-hybsel, v1.0

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**ASAP Project:** Parkinson5D: deconstructing proximal disease mechanisms across cells, space, and progression

**Project Description:** Here we will develop a molecular atlas of Parkinson's disease (PD) useful for mapping GWAS/familial genetics to proximal mechanisms in five dimensions: brain cells (1D), brain space (3D), and disease stage (1D). We will reveal how genetic variants modulate transcription in specific cells in specific topographic locations of midbrain and cortex during the progression of neuropathology from healthy brains to prodromal to symptomatic disease. This research will for the first time integrate whole genome sequencing, single-nucleus transcriptomics, and high-resolution spatial transcriptomics of 100 human brains with cell-specific mechanistic analyses in model systems.

**Submission Date:** 2024-06-25

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This dataset is made available to researchers via the ASAP CRN Cloud: [cloud.parkinsonsroadmap.org](https://cloud.parkinsonsroadmap.org). Instructions for how to request access can be found in the [User Manual](#).

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This Zenodo deposit was created by the ASAP CRN Cloud staff on behalf of the dataset authors. It provides a citable reference for a CRN Cloud Dataset