

Allen Cell Types Database

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This is the online help for the Allen Cell Types Database web application.

The Dataset

The Allen Cell Types Database contains a multimodal characterization of single brain cells by electrophysiology and morphology, as well as single-cell transcriptional data from nuclei or whole cells. These resources enable data-driven approaches to classification and are integrated with other Allen Brain Atlas applications. Data were collected from adult transgenic mice from fluorescent Cre-positive cells or Cre-negative cells, or from adult human neocortical cells.

The Allen Cell Types Database currently includes the following cell characterization datasets for mouse and human cells

- **Electrophysiology:** Whole-cell current clamp recordings made from identified, fluorescent Cre-positive neurons or nearby Cre-negative neurons in acute brain slices derived from adult mice. Whole-cell current clamp recordings made from adult human neocortical neurons in brain slices derived from surgical specimens.
- **Morphology:** reconstruction-quality, 2D image stacks containing the complete structure of mouse and human neurons filled and recorded from *in vitro* slice preparations and 3D reconstructions of the dendrites and the initial (spiny neurons) or complete axon (aspiny neurons) of each neuron.
- **Histology:** Images of immunohistochemical staining from human brain slices using antibodies chosen to evaluate tissue integrity, cell distribution and histopathology. The panel includes Nissl, NeuN, SMI-32, GFAP, PVALB, Iba1 and Ki67.
- **Transcriptomics:** single-cell RNA-sequencing with SMART-Seq v4 on fluorescent Cre-positive and Cre-negative cells enriched by FACS for mouse and fluorescent NeuN-positive (neuronal) or NeuN-negative (non-neuronal) nuclei enriched by FACS for human.
- **Generalized leaky integrate-and-fire (GLIF) models:** a series of point neuron models of increasing complexity to reproduce the spiking behaviors of the recorded neurons. Starting with a leaky integrate-and-fire model, more complex models attempt to model variable spike threshold, afterspike currents, and threshold adaptation.
- **Biophysical - perisomatic models:** compartmental model of neurons that account for the neural morphology and emulate electrophysiological responses by assuming biophysically detailed mechanisms for specific families of ionic conductances, with passive dendrites and active conductances at the soma.
- **Biophysical - all active models:** compartmental model of neurons that account for the neural morphology and emulate electrophysiological responses by assuming biophysically detailed mechanisms for specific families of ionic conductances, with active conductances throughout the cell.

Key features

- Registration to the mouse CCF, a 3-D anatomical framework with 3-D structural annotations.
- Data traces for the electrophysiology data from each neuron.
- Manually corrected and curated dendritic and axonal morphologies with annotation of neuronal compartments and extracted quantitative values for each reconstruction.
- RNA sequencing data derived from the LGd, VIS, and MOs for mouse and from the MTG for human.
- Search and visualization tools for exploring the single cell transcriptomics for LGd, and single cell electrophysiology, morphology, and modeling data.
- Data and models available for download via [Allen Brain Atlas API](#) and [Allen Software Development Kit \(SDK\)](#)

For complete details please see the white papers on our [Documentation](#) page.