SEA-AD: What's New, November 2026

New Data

- **Multi-region ATAC-seq data**: Cell by peak matrices showing the chromatin accessibility for each supertype in each brain region is available on AWS.
- **Quantitative neuropathology:** Image-based pathology quantifications that connect molecular changes with neuropathological burden are now available in primary visual cortex + extrastriate occipital cortex (V1C-ESOC) and will shortly be available in caudate nucleus + putamen + globus pallidus (Ca-Pu-GP) on AWS.
- **** Multi-region data set:** Single-nucleus RNA-seq, ATAC-seq, and Multiome from ~7 million nuclei across ten neo- and allocortical regions spanning the full arc of AD staging in the same 84-donor cohort and aligned to a unified taxonomy.

New Science

- **Caudate paper:** "The Caudate Nucleus Exhibits Distinct Pathology and Cell Type-Specific Responses Across Alzheimer's Disease" has been accepted at Cell Genomics and expands SEA-AD beyond cortex to provide the first detailed characterization of Alzheimer's disease-associated changes in a major subcortical structure.
- **** Multi-region paper:** The study identifies a stereotyped sequence of cellular and molecular changes across neo- and allocortex, unexpected vulnerability of primary visual cortex neurons, and neuronal hyperexcitability as a potential convergent mechanism of vulnerability.
- **** Computational studies**: Studies introducing computational and statistical approaches for modeling disease progression and extracting insight from SEA-AD data.

New on SEA-AD.org

- **Prototype data exploration tools:** New public prototype applications are being made available as part of a 'SEA-AD Sandbox' to gather community feedback, including:
  - A multiregion gene-expression viewer spanning all ten brain regions.
  - A quantitative neuropathology viewer supporting donor- and region-level exploration of pathology measurements.
- **ABC Atlas integration expanded:** SEA-AD multiregion, caudate, and original MTG datasets are now accessible through the Allen Brain Cell Atlas with interactive visualization, gene-expression exploration, and notebook-based programmatic access.
- **Beginner-friendly data access:** A new Jupyter notebook provides guided access to and exploration of SEA-AD snRNA-seq data from MTG for users with limited coding experience.
- **** New Data, Tools, and Resources:** New data releases are accompanied by expanded tools, code, documentation, and access options that support exploration and downstream analysis.

*** Available from July 2026. For a complete list, see the **SEA-AD: What's New, July 2026** document.*

Coming soon

- **Caudate spatial data**: A spatial-transcriptomics resource for the caudate nucleus will soon be available for interactive and programmatic access as part of the ABC Atlas.
- **Caudate latent space**: A new UMAP for caudate snRNA-seq data which deemphasizes donor differences in favor of cell type and disease changes is coming soon.

In development

- **Community microglial taxonomy**: A community reference spanning ~1.5 million microglia is in development, with planned support for mapping and exploration through SEA-AD ecosystem resources.