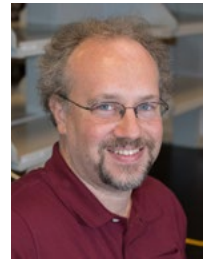




## Webinar: Mapping the epigenome of neural progenitors in the embryonic mouse forebrain using cell sorting and single cell transcriptomics to characterize inter neuron diversity

Monday, July 31, 2023

8:00 PDT | 11:00 EDT | 16:00 BST | 17:00 CEST



The epigenetic landscape changes continually during cell proliferation and differentiation throughout development. A comprehensive characterization of epigenomic organization in the embryonic mouse forebrain will enhance understanding of normal development and provide insight into mechanisms of neurological disease.

In this webinar, Timothy Petros, PhD, discusses his research on how intrinsic genetic programs and environmental signals interact to generate interneuron diversity. His group uses the SH800 cell sorter to enrich cells and nuclei suspensions from brain dissections. They identified thousands of differentially accessible peaks, many restricted to distinct progenitor cell types and/or brain regions. This dataset defines an epigenomic landscape and reveals a diverse chromatin landscape. The data can be used to explore how perturbation of gene regulation in GABAergic inhibitory interneuron progenitors affects gene expression, chromatin organization, and ultimately cell fate.



### Who Should Attend

This webinar will provide insights for researchers who want to learn about the strategies for characterization of the epigenetic landscape during embryonic neurogenesis and the methodologies used for successfully generating an Epigenome Atlas.

### Certificate of attendance

All webinar participants can request a certificate of attendance and a learning outcomes summary document for continuing education purposes.

Join this webinar to:

- Understand how to characterize changes of chromatin accessibility at enhancers and promoters that are tightly coupled to transcript abundance during neurodevelopment.
- Learn how a single-cell assay for transposase-accessible chromatin with sequencing (scATAC-Seq), in combination with Cut&Tag and Hi-C/ Capture-C, can be used to generate an "Epigenome Atlas" of the embryonic mouse brain.
- Identify strategies for rapid isolation of single cells or nuclei from embryonic mouse brain with microfluidics-based cell sorting for use in transcriptional profiling of the brain progenitor cells.

### Speaker

**Dr. Timothy J. Petros**, Unit on Cellular and Molecular Neurodevelopment  
Eunice Kennedy Shriver National Institute of Child Health and Human Development

Dr. Timothy Petros obtained his PhD from Columbia University. He has used in vitro stem cell techniques and genetic manipulations in vivo to explore the intrinsic genetic programs and extrinsic environmental factors that regulate interneuron differentiation. He joined NICHD in 2017, where he continues to explore the genetic and epigenetic mechanisms that regulate initial interneuron fate decisions during neurogenesis.