Determining gene expression during neural differentiation through coupled protein localization and RNA-seq in single cells

Project Deliverables
- We will initially optimize the pairing in high cell populations, titrating from 500,000 to 10 cells within ~4-6 months
- Next, we will optimize for single cells over the next ~4-6 months
- Application to ~5,000 single cells throughout neural differentiation will begin over the last ~4 months and continue into the following year

Potential Impact
- This will be the first pairing of factor profiling and scRNA-seq within one individual cell
- This will revolutionize our ability to interpret mechanistically how factors impact the transcriptome.

References and/or Acknowledgements
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Context
- Heterogeneity across cell populations and tissues, as well as limitations in profiling technologies in rare populations limits our capacity to understand cellular biology

Project Description
- We propose to integrate these techniques to address an important biological question during development

Motivation
- We developed the first single cell technique to profile protein location on DNA.
- There has been huge advancement in assessing the transcriptome (via single cell RNA-seq)

Pairing single cell -omic technologies

Sarah J. Hainer
Department of Biological Sciences
University of Pittsburgh

We will apply this technology during neural differentiation to assess the role of a conserved and essential protein complex called BAF.