Tyler **Bradshaw, PhD**

MOLECULAR, CELLULAR, AND COMPUTATIONAL BIOLOGIST

Durham NC, USA

☎ (+1) 952-212-4563 | ✉ twesleyb10@gmail.com | ⬤ twesleyb | in twbradshaw

Summary

I am a diligent and driven computational and molecular biologist. In my PhD work, I combined cutting-edge spatial and proximity proteomics tools to solve problems in molecular neuroscience. My interdisciplinary expertise spans molecular biology approaches and computational analysisI am a self-taught programmer and data scientist, and have pioneered novel computational pipelines and molecular techniques in numerous projects aimed at understanding the organization of the neuronal proteome and its dysregulation in disease. I am interested in a career where I can continue to draw together ideas and approaches spread across the fields of cell biology and computer science.

Work Experience

Graduate Research Assistant   *Fall 2016 - May 2021*

SODERLING LABORATORY, DUKE UNIVERSITY   *Department of Neurobiology*

- Developed a novel spatial proteomics analysis pipeline for clustering and statistical inference in spatial proteomics, published in *eLife*.
- Applied and developed CRISPR-based methods for genetic depletion and tagging of endogenous proteins–work which lead to founding of CasTag BioSciences.
- Performed synaptosome subcellular fractionation to assess synaptic protein changes in multiple mouse models of human brain disorders.
- Designed peptide libraries for multiple-reaction monitoring targeted proteomics.
- Experience working with numerous model organisms including immortalized cell lines, bacteria, yeast, and mice.
- Applied and analyzed BioID-based proximity proteomics for identification of subcellular specific compartments.
- Normalization and analysis of RNA transcriptomics and protein proteomics datasets.
- Design and troubleshooting of molecular biology and computational approaches.
- Awarded the Ruth L. Kirschstein National Research Service Award Fellowship to study a protein of unknown function and the mechanisms by which its loss causes a rare epilepsy disorder.

Research Technician   *May 2014 - May 2016*

SODERLING LABORATORY, DUKE UNIVERSITY   *Department of Cell Biology*

- Performed protein co-immunoprecipitation and proximity proteomics for identification of protein-protein interactions and revealing protein interactomes *in vivo*–my work was a part of the first application of BioID *in vivo*, published in the journal *Science*.
- Performed immunoblotting, immunostaining, and cell and tissue culture for assessing protein expression and localization *in vitro* and *in vivo*.
- Molecular cloning and generation of adeno-associated virus for transgene expression *in vivo*.
- Maintained mouse colony with >30 strains of mice; performed mouse surgery, husbandry, genotyping, and analysis of mouse behavior.

Skills

Computational Biology
- Linear models and linear mixed-models in R
- Analysis of NGS data with edgeR
- Clustering and visualization of protein networks in R and Python using the Leiden algorithm
- Data visualization in R using ggplot2
- Working with bioinformatics databases like NCBI, UCSC, ENSEMBL, and UniProt
- Analysis of biological network organization and function
- DevOps toolchain: Windows, Linux, Tmux, Vim, R, Python, Julia, Cytoscape, Adobe Illustrator, and PowerPoint
- Bioinformatics software development and version control with Git and GitHub
- Markup languages like Markdown, RMarkdown, and LaTeX

Molecular Biology
- Molecular cloning and plasmid design
- Molecular biology using immortalized human cell lines, E. coli, and yeast
- Protein purification, co-immunoprecipitation and immunoblotting
- Production of adeno associated virus and stereotaxic injection into mouse brain tissue
- Subcellular fractionation and tandem mass tag multiplex proteomics
- Histology, immunohistochemistry, and quantitative fluorescent microscopy
- Adherent cell culture and transfection

Education

Duke University, Department of Neurobiology   *Durham, NC*

DOCTOR OF PHILOSOPHY - NEUROBIOLOGY   *Fall 2016 - May 2021*

- Dissertation: *Statistical Inference and Community Detection in Proximity and Spatial Proteomics*; my thesis work establishes a framework for the analysis of proximity and spatial proteomics, extending protein-level inference in spatial proteomics to the level of protein-groups or modules and generates hypotheses that identify foci of biological function and dysfunction which may underlie the neuropathology of disease.

University of Washington   *Seattle, Washington*

Bachelor of Science - Molecular, Cellular and Developmental Biology   *Fall 2010 - Spring 2014*

- My undergraduate research focused on the pathobiological mechanisms of type I and type II diabetes. In the the Surgical Outcomes Research Center, I worked with Ossabaw pigs to study mechanisms of weight-loss following bariatric surgery. In the Bornfeldt lab, I performed some of my first molecular biology experiments aimed at studying mechanisms of type I diabetes accelerated atherosclerosis.

Honors & Awards

2018-2021 **Ruth L. Kirschstein National Research Service Award**, NIH NRSA 5F31NS113738-03   *Duke University*

Epilepsy, the condition of spontaneous recurrent seizures, is a devastating neurological disorder. Rare genetic mutations provide unique opportunities to understand the molecular mechanisms that drive susceptibility to seizures and epilepsy. This work studied a human epilepsy candidate gene towards generating a deeper understanding of the molecular mechanisms underlying epilepsy.

Presentations

Statistical inference and community detection in proximity and spatial proteomics: resolving organization of the neuronal proteome   *Department of Neurobiology*

Dissertation Presentation   *March 22nd, 2021*

- Dissertation seminar given to Duke faculty and students

Evaluting changes in the synaptic protein architecture in mouse autism disorders   *Neurobiology Retreat*

Poster Presentation   *November 2018*

- Research poster presentation

Seizures and Ube3a synergistically impair a sociability circuit in a mouse model of autism   *Department of Neurobiology, Duke University*

Student Seminar Presentation   *2018*

- Presentation to Duke Neurobiology faculty and students

A Targeted-Proteomics Approach to Interrogate the Synaptopathology Underlying Monogenic Autism Spectrum Disorders   *Neurobiology Retreat, Wrightsville Beach, NC*

Poster Presentation   *2017*

- Presentation to Duke Neurobiology faculty and students

Development of a Targeted-Proteomics Approach to Identify Underlying Mechanisms of Synaptic Pathologies   *The Society for Neuroscience, San Diego, CA*

Poster Presentation   *2017*

- Presentation to Duke Neurobiology faculty and students

Unraveling the Molecular Mechanisms of Inhibitory Synaptic Function in vivo   *Cell Biology Retreat, Beaufort, NC*

Poster Presentation   *2015*

- Presentation to Duke Neurobiology faculty and students

Exploring diabetes-derived intestinal changes that promote atherosclerosis   *Bornfeldt Laboratory, University of Washington, Seattle WA*

Honors Research Manuscript   *2014*

- Presentation to SOURCE faculty and students

Obesity, Insulin Resistance, and Type 2 Dibetes in Ossabaw Swine   *Surgical Outcome Research Center, Seattle WA*

Presentation   *2013*

- Presentation to SOURCE faculty and students

Publications

Courtland and Bradshaw *et al.,* (2021)   *eLife*

Contributions: Conceptualization, Software development, Analysis, Visualization, Writing   *2021*

- *Genetic Disruption of WASHC4 Drives Endo-lysosomal Dysfunction and Cognitive-Movement Impairments in Mice and Human.* Jamie Courtland, **Tyler Bradshaw**, Greg Waitt, Erik Soderblom, Tricia Ho, Anna Rajab, Ricardo Vancini, Il Hwan Kim, Scott Soderling. eLife 2021 March 22; 10:e61590 **doi:** 10.7554/eLife.61590.

Uezu *et al.,* (2019)
eLife

Contributions: Conceptualization, Writing - review and editing
2019

- *Essential role for InSyn1 in dystroglycan complex integrity and cognitive behaviors in mice.* Akiyoshi Uezu, Erin Hisey, Yoshihiko Kobayashi, Yudong Gao, **Tyler Bradshaw**, Patrick Devlin, Ramona Rodriguiz, Purushothama Rao Tata, and Scott Soderling. eLife 2019 Dec 12;8:e50712. **doi:** 10.7554/eLife.50712.

Gao *et al.,* (2018)
Neuron

Contributions: Investigation, Method development, Writing - review and editing
2018

- *Plug-and-Play Protein Modification Using Homology-Independent Universal Genome Engineering.* Yudong Gao, Erin Hisey, **Tyler Bradshaw**, Eda Erata, Walter E. Brown, Jamie L. Courtland, Akiyoshi Uezu, Yu Xiang, Yarui Diao, and Scott H. Soderling. Neuron 2018 July 1; S0896-6273(19)30523-9. **doi:** 10.1016/j.neuron.2019.05.047

Uezu *et al.,* (2016)
Science

Contributions: Investigation, Formal analysis, Visualization, Writing - review and editing
2016

- *Identification of an Elaborate Complex Mediating Postsynaptic Inhibition.* Akiyoshi Uezu, Daniel J. Kanak, **Tyler Bradshaw**, Erik J. Soderblom, Christina M. Catavero, Alain C. Burette, Richard J. Weinberg, and Scott H. Soderling. Science 2016 Sep 9; 353(6304): 1123–1129. **doi:** 10.1126/science.aag0821

Coursework

Machine Learning Summer School
Duke University

Primary Instructors: Lawrence Carin and David Carlson
June 17-21, 2019

- Course focused on recent advances in machine learning including deep learning and methods that allow ML algorithms to train effectively on massive datasets with an emphasis on image and video analysis, natural language processing, reinforcement learning, and data synthesis/modeling.

Targeted Proteomics Course
University of Washington

Primary Instructors: Michael MacCoss and Brendan MacLean
July 24-28, 2017

- Course aimed at a range of targeted proteomics techniques using SRM, PRM, DIA/SWATH, and MS1 filtering including topics like system suitability, plasma proteomics, statistical methods for designing and analyzing these experiments and using Skyline and MSstats software.