Paul W. Hook, Ph.D.

phook2@jhmi.edu | pwh124@gmail.com | +1 (865) 719-5230 | pwh124.github.io
3400 N. Charles St., Clark Hall 107, Baltimore, MD 21218, USA

Curriculum Vitae

EDUCATION

Johns Hopkins University School of Medicine, Baltimore, MD 2014 – 2020
Ph.D., Human Genetics
Thesis title: "*Leveraging Mouse Genomic Data to Prioritize Genes and Variants Associated with Common, Complex Neurological Disease*"

The Pennsylvania State University, University Park, PA May 2012
B.S., Biochemistry and Molecular Biology

RESEARCH EXPERIENCE

Postdoctoral Fellow 2020 – Present
Whiting School of Engineering
Johns Hopkins University, Baltimore, MD
Advisor: Winston Timp

- Developed and optimized genomics approaches for measuring protein-DNA interactions using long-read sequencing. This included labeling protein-DNA binding sites with 6-methyladenine (6mA) and adapting CUT&RUN for nanopore sequencing
- Generated long-read open chromatin data with 5-methylcytosine (5mC) GpC labeling and analyzed DNA modifications from short-read and long-read sequencing as part of the Telomere-to-Telomere Consortium
- Planned experiments, generated data, and trained collaborators as part of a Small Business Innovation Research (SBIR) grant with Epicypher, Inc., to commercialize 6mA labeling for measuring protein-DNA binding
- Planned experiments, generated data, and managed collaborations for a variety of projects including developing methods to store data in DNA and developing software to analyze nanopore electrical signal data

Graduate Student 2014 – 2020
Johns Hopkins School of Medicine, Baltimore, MD
Advisor: Andrew McCallion

- Designed, performed, and analyzed bulk RNA-seq and single-cell RNA-seq experiments on mouse dopaminergic neurons and established a scoring paradigm for prioritizing genes from Parkinson disease GWAS loci
- Analyzed mouse chromatin data in order to identify cell populations relevant to neurological disease risk and to prioritize disease-relevant variation in disease-associated loci

Research Technologist 2012 – 2014
Johns Hopkins School of Medicine, Baltimore, MD
Advisor: Andrew McCallion

- Elucidated the functional consequences of disrupting genes on somitogenesis and heart development in zebrafish
- Implemented the use of Cas9 nuclease genome editing in zebrafish and human cell culture
- Performed lab administrative duties including inventory and ordering

Science Undergraduate Laboratory Internship Summer 2011
Department of Energy, Pacific Northwest National Laboratory, Sequim, WA
Advisor: Michael Huesemann

Chemical Research Intern 2010 – 2011
The Pennsylvania State University, University Park, PA
Advisor: Joseph Keiser

PLATFORM AND INVITED TALKS

Hook, P.W. "Using CUT&RUN/Tag with a portable nanopore sequencing device." American Society of Human Genetics Bioinformatics and Computational Methods SIG Seminar. Virtual. September 17, 2024. Link to recording: https://tinyurl.com/4wdsep7s

Hook, P.W. "Using CUT&RUN/Tag with a portable nanopore sequencing device." NHGRI Genome Technology Development Working Group bi-monthly meeting. Virtual. December 6, 2023.

Hook, P.W. "Targeted long-read sequencing for interrogation of cancer genetic loci." Association of Biomolecular Resources Facilities Annual Meeting, Palm Springs, CA, 2022.

Hook, P.W., McCallion, A.S. "Refining cell populations and fine-mapping variants for schizophrenia and bipolar disorder using mouse open chromatin profiles" The American Society of Human Genetics, Houston, TX, 2019.

Hook, P.W., McClymont S.A., Cannon, G.H., Law, W.D., Morton, A.J., Goff, L.A., McCallion, A.S. "Prioritizing genes for sporadic Parkinson disease using single-cell expression profiling of mouse dopaminergic neurons" 11th Leena Peltonen School of Human Genomics, Les Diablerets, Switzerland, 2018.

Hook, P.W., McClymont, S.A., Goff, L.A., McCallion, A.S. "RNA-seq analysis identifies phenotypic heterogeneity among *ex vivo* purified dopamine neurons and highlights their progressive temporal diversification" The American Society of Human Genetics, Vancouver, BC, Canada, 2016.

POSTER PRESENTATIONS

Hook, P.W., Venters, B.J., Hickman, A.R, Timp, W. "Streamlined, multimodal, epigenetic measurements using CUT&RUN combined with nanopore sequencing." The American Society of Human Genetics Annual Meeting, Denver, CO, 2024

Hook, P.W., Timp, W. "Using CUT&RUN/Tag with a portable nanopore sequencing device." The American Society of Human Genetics Annual Meeting, Washington, DC, 2023

Hook, P.W., Hosea, J.A., Morina, L.B., Ebenstein, Y., Simpson, J., Timp, W. "Measuring the epigenome with nanopore sequencing." The Advances in Genomic Technology Development Annual Meeting, La Jolla, California, 2023.

Hook, P.W., Timp, W. "Protein-DNA interactions at the bench: CUT&RUN/Tag with nanopore sequencing." The Advances in Genome Biology and Technology Annual Meeting, Hollywood, FL, 2023.

Hook, P.W., Krueger, F., Timp, W. "Adapting Enzymatic Methyl-seq (EM-seq) for long-read nanopore sequencing." Nanopore Community Meeting, New York City, NY, 2022.

Hook, P.W., Krueger, F., Timp, W. "Adapting Enzymatic Methyl-seq (EM-seq) for long read sequencing." The Advances in Genome Biology and Technology Annual Meeting, Orlando, FL, 2022.

LEADERSHIP EXPERIENCE

Student Faculty Representative 2016 – 2020
Human Genetics Pre-Doctoral Training Program
Johns Hopkins University School of Medicine, Baltimore, MD

Served as a representative to program leadership for the students in the Human Genetics graduate program. This involved regular meetings with the program's board as well as advocating for students to program leadership when necessary.

Membership Engagement Committee 2020 – 2023
The American Society of Human Genetics (ASHG)

Served on a committee of ASHG members (20+) working with ASHG staff to analyze what society members wanted from a membership and working to increase the value of a society membership. This included:

- Developing special interest groups (SIGs) and leading the Bioinformatics and Computational Methods SIG for two years
- Proposing a virtual, society-exclusive social media platform that led to the creation of ASHG Connect
- Attending frequent, virtual planning meetings and in-person planning meetings at ASHG annual conferences

Shared Interest Group (SIG) Chair 2022 – 2024
Bioinformatics and Computational Methods SIG
The American Society of Human Genetics (ASHG)

- Worked with ASHG staff to create and run the Bioinformatics and Computational Methods SIG
- Developed and executed inclusive strategies to maximize participation
- Lead a webinar introducing the SIGs and conversations on the ASHG social media platform, ASHG Connect
- Organized and led an in-person meet-up at the ASHG annual conference in 2023.

ASHG 2022 Annual Meeting Planning Advisory Group 2021-2022
The American Society of Human Genetics (ASHG)

Provided advice and perspective to ASHG staff as they planned the first, in-person, post-pandemic, ASHG annual conference.

Planning Committee 2021-2022, 2023-2024
NIH Advanced Genomic Technology Development (AGTD) Annual Meeting

Worked with the organizers of the AGTD annual meeting to review abstracts, organize sessions, and plan activities during the meeting.

ASHG Annual Meeting Abstract Review 2019, 2024
The American Society of Human Genetics (ASHG)

TEACHING AND OUTREACH EXPERIENCE

Instructor Spring 2024
EN.580.454: Methods in Nucleic Acid Sequencing Lab
Johns Hopkins University, Baltimore, MD

Lab tour and strawberry DNA extraction demonstration March 23, 2023
Galaxy Team Meeting 2023
Johns Hopkins University, Baltimore, MD

Teaching Assistant Fall 2016
Evolution of Ideas in Human Genetics
Johns Hopkins University School of Medicine, Baltimore, MD

Presenter November 14, 2015
The Genome Geeks Are In
Smithsonian National Museum of Natural History, Washington, DC

Peer Learning Assistant Fall 2011
BMB 430: Developmental Biology
The Pennsylvania State University, University Park, PA

MENTORING AND TRAINING EXPERIENCE

Research Mentoring (Postdoctoral Fellow) 2020 – Present
Timp Lab, John Hopkins University

Trained and supervised my peers in a variety of scientific aspects including wet-bench and computational techniques, the planning and performing of experiments, and the writing and editing of manuscripts, abstracts, and grants. These individuals included:

- Undergraduate students (2), one of which went to graduate school in Human Genetics
- Technicians (2)
- Graduate students (8), two of which have graduated and have jobs at biotechnology companies
- Postdoctoral Fellows (3)

Research Mentoring (Graduate school) 2014 – 2020
McCallion Lab, Johns Hopkins University School of Medicine

Trained and supervised my peers on various molecular biology techniques including single-cell RNA-seq and techniques related to working with mice and zebrafish. These individuals included:

- A graduate student and rotation students (3)
- Technicians (5), two of which went on to graduate school and one of which went on to medical school

Peer Mentoring Leader 2017 – 2020
Institute of Genetic Medicine Peer Mentoring Families
Johns Hopkins University School of Medicine, Baltimore, MD

Served as the head of Human Genetics peer mentoring “family.” This involved mentoring a small group of students (between 5-10 at any given time) at all stages of graduate school from newly accepted students to those close to graduating. As head of the “family,” I would periodically organize small events for the entire group and have one-on-one conversations.

Three Minute Thesis Competition Mentor Spring 2024
Johns Hopkins University PHutures Office

Career panel July 14, 2022
NIH Advanced Genomic Technology Development (AGTD) Annual Meeting

HONORS AND AWARDS

ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Semifinalist 2019
The American Society of Human Genetics – Houston, TX
"Refining cell populations and fine-mapping variants for schizophrenia and bipolar disorder using mouse open chromatin profiles"

C.W. Cotterman Award 2018
The American Society of Human Genetics – San Diego, CA
"*Single-Cell RNA-Seq of Mouse Dopaminergic Neurons Informs Candidate Gene Selection for Sporadic Parkinson Disease*"

Leena Peltonen School of Human Genomics Trainee Summer 2018
Les Diablerets, Switzerland

Graduated with Distinction May 2012
Eberly College of Science
The Pennsylvania State University, University Park, PA

Dean's List 2008-2012
Eberly College of Science
The Pennsylvania State University, University Park, PA

Gail A. and Thomas G. Ernst Scholarship 2009 – 2011

Kimberly Clark Bright Futures Scholarship 2008 – 2012

PROFESSIONAL ASSOCIATIONS

The American Society of Human Genetics 2015 - Present

PREPRINTS AND PEER-REVIEWED PUBLICATIONS (Google Scholar Page)

Volkel, K.D., **Hook, P.W.**, Keung, A., Timp, W., and Tuck, J.M. (2025). Nanopore decoding with speed and versatility for data storage. *Bioinformatics*, Volume 41, Issue 1, btaf006. https://doi.org/10.1093/bioinformatics/btaf006

Mahlke, M.A., Lumerman, L., Nath, P., Chittenden, C., Hoyt, S., Koeppel, J., Xu, Y., Raphael, R., Zaffina, K., **Hook, P.W.**, et al. (2025). Epigenetically dynamic human centromeres are maintained within a stable DNA methylation signature. *bioRxiv,* 2025.02.03.636285. https://doi.org/10.1101/2025.02.03.636285.

Lin, K.N., Volkel, K., Cao, C., **Hook, P.W.**, Polak, R.E., Clark, A.S., San Miguel, A., Timp, W., Tuck, J.M., Velev, O.D., et al. (2024). A primordial DNA store and compute engine. *Nat. Nanotechnol.*, 1–11. DOI: https://doi.org/10.1038/s41565-024-01771-6

Guerrero Zuniga, A., Aikin, T.J., McKenney, C., Lendner, Y., Phung, A., **Hook, P.W.**, Meltzer, A., Timp, W., and Regot, S. (2024). Sustained ERK signaling promotes G2 cell cycle exit and primes cells for whole-genome duplication. *Developmental Cell 59*, 1–13.
DOI: https://doi.org/10.1016/j.devcel.2024.03.032

Kovaka, S., **Hook, P.W.**, Jenike, K.M., Shivakumar, V., Morina, L.B. Razaghi, R., Timp, W., Schatz, M .C (2024). Uncalled4 improves nanopore DNA and RNA modification detection via fast and accurate signal alignment. *bioRxiv*, 2024.03.05.58351.
DOI: https://doi.org/10.1101/2024.03.05.583511

Volkel, K.D, Lin, K.N., **Hook, P.W.**, Timp, W., Keung, A.J., and Tuck, J.M (2023). FrameD: framework for DNA-based data storage design, verification, and validation. *Bioinformatics*, Volume 39, Issue 10, October 2023, btad572.
DOI: https://doi.org/10.1093/bioinformatics/btad572

Rhie, A., Nurk, S., Cechova, M., Hoyt, S.J., Taylor, D.J., Altemose, N., **Hook, P.W.**, Koren, S., Rautiainen, M., Alexandrov, I.A., …, Eichler, E.E, O'Neill, R., Schatz, M.C., Miga, K.H., Makova, K.D., and Phillippy, A.M. (2023). The complete sequence of a human Y chromosome. *Nature*, 1–11. DOI: https://doi.org/10.1038/s41586-023-06457-y

Hook, P.W., and Timp, W. (2023). Beyond assembly: the increasing flexibility of single-molecule sequencing technology. *Nat. Rev. Genet. 24*, 627–641.
DOI: https://doi.org/10.1038/s41576-023-00600-1

Boyd, R.J., McClymont, S.A., Barrientos, N.B., **Hook, P.W.**, Law, W.D., Rose, R.J., Waite, E.L., Rathinavelu, J., Avramopoulos, D., and McCallion, A.S. (2023). Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons. *BMC Genomics 24*, 306. DOI: https://doi.org/10.1186/s12864-023-09398-y

Razaghi, R., **Hook, P.W.**, Ou, S., Schatz, M. C., Hansen, K. D., Jain, M., & Timp, W. (2022). Modbamtools: Analysis of single-molecule epigenetic data for long-range profiling, heterogeneity, and clustering. *bioRxiv*, 2022.07.07.499188.
DOI: https://doi.org/10.1101/2022.07.07.499188

Gershman, A., Sauria, M.E.G., Guitart, X., Vollger, M.R., **Hook, P.W.**, Hoyt, S.J., Jain, M., Shumate, A., Razaghi, R., Koren, S., Altemose, N., Caldas, G.V., Logsdon, G.A., Rhie, A., Eichler, E.E., Schatz, M.C., O'Neill, R.J., Phillippy, A.M., Miga, K.H., & Timp, W. (2022). Epigenetic patterns in a complete human genome. *Science*, *376* (6588), eabj5089.
DOI: https://doi.org/10.1126/science.abj5089

Soto-Beasley, A.I., Walton, R.L., Valentino, R.R., **Hook, P.W.**, Labbé, C., Heckman, M.G., Johnson, P.W., Goff, L.A., Uitti, R.J., McLean, P.J., Springer, W., McCallion, A.S., Wszolek, Z.K., & Ross, O.A. (2020). Screening non-*MAPT* genes of the Chr17q21 H1 haplotype in Parkinson's disease. *Parkinsonism & Related Disorders*, *78*, 138–144.
DOI: https://doi.org/10.1016/j.parkreldis.2020.07.022

Hook, P.W., & McCallion, A.S. (2020). Leveraging mouse chromatin data for heritability enrichment informs common disease architecture and reveals cortical layer contributions to schizophrenia. *Genome Research*, *30* (4): 528–39. DOI: https://doi.org/10.1101/gr.256578.119

McClymont, S.A, **Hook, P.W.**, Soto, A.I., Reed, X., Law, W.D., Kerans, S.J., Waite, E.L., Briceno, N.J., Thole, J.F., Heckman, M.G., Diehl, N.N., Wszolek, Z.K., Moore, C.D., Zhu, H., Akiyama, J.A., Dickel, D.E., Visel, A., Pennacchio, L.A., Ross, O.A., Beer, M.A., McCallion, A.S. (2018). Parkinson Associated *SNCA* Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. *The American Journal of Human Genetics*, *103* (6), 874–892.
DOI: https://doi.org/10.1016/j.ajhg.2018.10.018

Hook, P.W., McClymont, S.A., Cannon, G.H., Law, W.D., Morton, A.J., Goff, L.A., & McCallion, A.S. (2018). Single-Cell RNA-Seq of Mouse Dopaminergic Neurons Informs Candidate Gene Selection for Sporadic Parkinson Disease. *The American Journal of Human Genetics*, *102* (3), 427–446. DOI: https://doi.org/10.1016/j.ajhg.2018.02.001

Turner, T.N., Hormozdiari, F., Duyzend, M.H., McClymont, S.A., **Hook, P.W.**, Iossifov, I., … Eichler, E.E. (2016). Genome Sequencing of Autism-Affected Families Reveals Disruption of Putative Noncoding Regulatory DNA. *The American Journal of Human Genetics*, *98* (1), 58–74. DOI: https://doi.org/10.1016/j.ajhg.2015.11.023

Maragh, S., Miller, R.A., Bessling, S.L., Wang, G., **Hook, P.W.**, & McCallion, A.S. (2014). Rbm24a and Rbm24b are required for normal somitogenesis. *PLoS ONE*, *9* (8).
DOI: https://doi.org/10.1371/journal.pone.0105460

Van Wagenen, J., Miller, T.W., Hobbs, S., **Hook, P.**, Crowe, B., and Huesemann, M. (2012). Effects of light and temperature on fatty acid production in *Nannochloropsis salina*. *Energies 5*, 731–740. DOI: https://doi.org/10.3390/en5030731