

# Paul W. Hook, Ph.D.

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## Curriculum Vitae

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### 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*

**MENTORING 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*

Worked with two Ph.D. candidates at Johns Hopkins University to perfect their presentations for the Empower Your Pitch, three-minute thesis competition. One mentee advanced to the final round of competition.

**Career panel**

July 14, 2022

*NIH Advanced Genomic Technology Development (AGTD) Annual Meeting*

Represented postdoctoral fellows on a career panel meant to discuss career options and provide advice on how to prepare and pursue different career paths.

**LEADERSHIP****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 to increase the value of a 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)*

Reviewed abstracts for the ASHG annual meeting in the categories of "Bioinformatics and Computational Approaches" (2019) and "Epigenetic mechanisms of disease and genome function" (2024).

## **TEACHING AND OUTREACH EXPERIENCE**

### **Instructor**

Spring 2024

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

- Planned content and adapted wet-lab and dry-lab protocols for three modules including dirt microbiome sequencing, targeted human genome sequencing, and genome assembly of a scorpion genome
- Managed the class through the Canvas Learning Management System and graded lab reports for all three modules
- Recruited, organized, and trained both undergraduate- and masters-level teaching assistants
- Received an instructor teaching effectiveness mean score higher than both the school- and department-level mean scores

### **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*

## **PREPRINTS AND PEER-REVIEWED PUBLICATIONS ([Google Scholar Page](#))**

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>

Volkel, K.D., **Hook, P.W.**, Keung, A., Timp, W., and Tuck, J.M. (2024). Nanopore Decoding with Speed and Versatility for Data Storage. *bioRxiv*, 2024.06.18.599582.  
DOI: <https://doi.org/10.1101/2024.06.18.599582>

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). FramedD: 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>

## **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

## **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” 11<sup>th</sup> 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.**, 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.

## **PROFESSIONAL ASSOCIATIONS**

The American Society of Human Genetics

2015 - Present