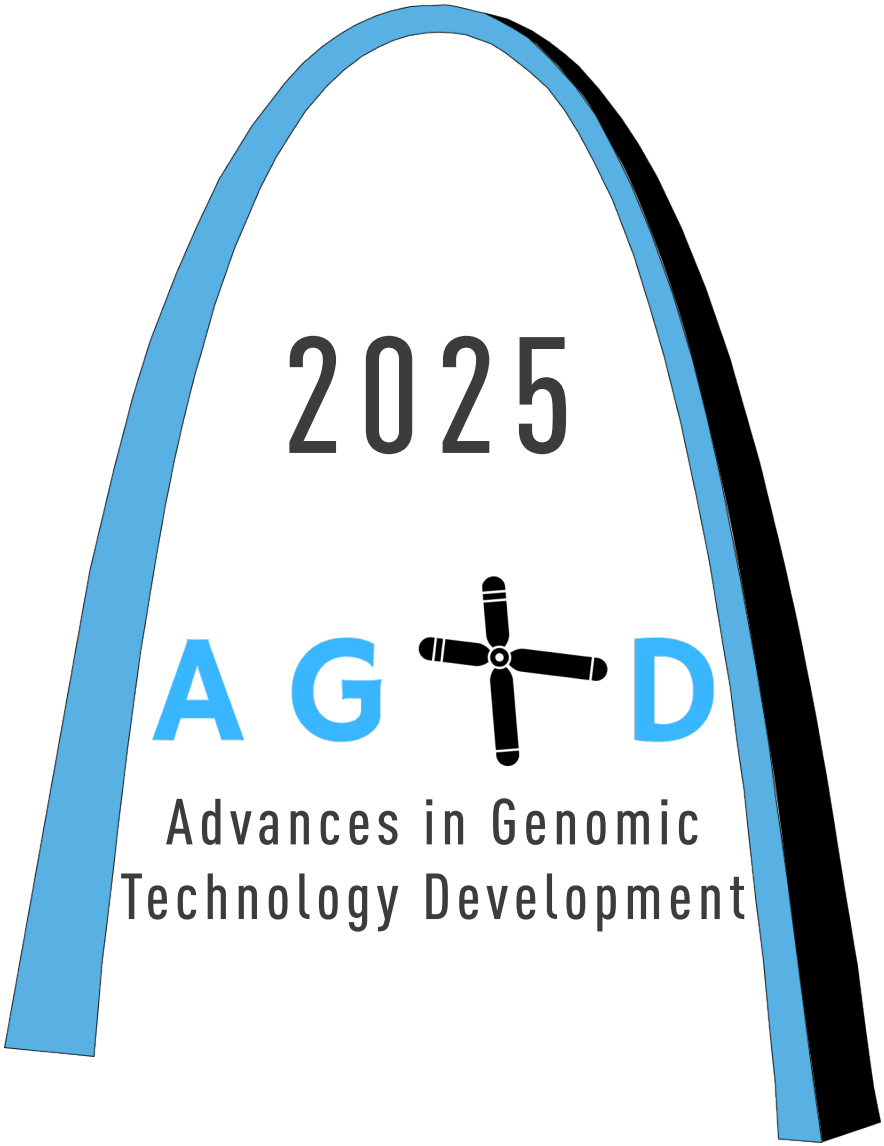

2025

AGTD

Advances in Genomic Technology Development

ANNUAL MEETING

Washington University in St. Louis

June 10 - 12, 2025 • St. Louis, Missouri

GENOME TDCC

NIH National Human Genome Research Institute

The Jackson Laboratory

Supported by NHGRI Project 2U24HG011735 and The Jackson Laboratory

Dear Friends and Colleagues,

On behalf of the National Human Genome Research Institute (NHGRI), Technology Development Coordinating Center (TDCC), and Washington University in St. Louis, we are excited to welcome you to the 2025 Advances in Genomic Technology Development (AGTD) meeting. We thank Washington University in St. Louis for being this year's host. We hope you will take the opportunities over these three days to renew and establish friendships and collaborations and to learn about one another's research programs. The TDCC community has continued to expand this past year, with 21 new grant awards, including 20 new PIs. Presentations by groups that are new since the previous AGTD meeting are annotated with (*) in the program.

AGTD is an invitation-only meeting. By participating in the meeting, we all agree to abide by a Code of Conduct (found at the back of the program) that establishes a respectful environment and interactions. We encourage presentation of unpublished results, but also recognize that disclosure may affect intellectual property protection and encourage you to consult with an IP expert if you have concerns before your presentation. There should be NO sharing of any information from presentations, posters, or informal discussions through social media or with anyone other than AGTD attendees.

Several groups will be participating in AGTD via Zoom this year due to institutional constraints on funding for travel. We encourage Zoom participants to be actively engaged, including through posting questions in the Zoom chat.

The TDCC's goal is to enhance the impact of the advances made by grantees in NHGRI's Genome Technology Development Program by supporting collaboration among grantees and outreach to the broader scientific community that highlights new technologies developed through the program. We look forward to your input on how the TDCC can best support you in the year ahead.

Mark Adams, Ph.D.
Professor & Interim Scientific Director
The Jackson Laboratory for Genomic Medicine

Stephanie Morris, Ph.D.
Program Lead, Genome Technology Program
Division of Genome Sciences
National Human Genome Research Institute

Barak Cohen, Ph.D.
Alvin Goldfarb Distinguished Professor of Computational Biology
Department of Genetics
Washington University in St. Louis

Tuesday, June 10, 2025

8:15 am Registration

9:00 am Welcome & Introduction
Mark Adams, Ph.D., The Jackson Laboratory
Stephanie Morris, Ph.D., NHGRI

Genome Regulation

Session Moderator: Yuning Zhang, Ph.D., Washington University in St. Louis

9:15 am Long-range Massively Parallel Reporter Assay Reveals Rules of Distant Enhancer-Promoter Interactions. | *Yawei Wu, Washington University in St. Louis (abstract 82)*

9:30 am Direct multi-omics: Linking DNA methylation to chromatin targets via CUT&RUN-EM | *Connor Frasier, MS, EpiCypher, Inc. (abstract 20)*

9:45 am ChIP-DIP: A Novel Tool for Comprehensive Profiling of DNA-Protein Interactions in Complex Biological Systems.
Benjamin Yeh, California Institute of Technology (abstract 83)

10:00 am Integrated Analysis of Multimodal Single Molecule Epigenetic Measurements with Long Read Sequencing.
Oberon Dixon-Luinenburg, University of California, Berkeley (abstract 71)

10:15 am Precise Measurement of Molecular Phenotypes with Barcoded Reporters. | *Nicholas Ingolia, Ph.D., University of California, Berkeley (abstract 27)*

10:30 am Coffee Break

10:50 am Keynote: Microfluidics for high-throughput and quantitative *in vitro* characterization of human allelic variants.
Polly Fordyce, Ph.D., Stanford University

11:40 am Lunch: Meet & Greet - Assigned Seating

RNA Sequencing Technologies

Session Moderator: Keqing Nian, Northeastern University

12:50 pm Deciphering the Non-Canonical snoRNA Targetome.
Bei Liu, Ph.D., University of Chicago (abstract 35)

1:05 pm Re-reading RNA to Obtain High Accuracy.
Anna Schibel, Ph.D., Electronic BioSciences, Inc. (abstract 62)

1:20 pm A 2-Read Nanopore Direct Seq Approach to Map tRNA Modifications. | *Ya-Ming Hou Ph.D., Thomas Jefferson University (abstract 26)*

1:35 pm Synthetic mRNA Control Set for Nanopore-Based Pseudouridine Modification Profiling in Human Transcriptomes. | *Sara Rouhanifard, Ph.D., Northeastern University (abstract 65)*

1:50 pm * Integrating LC-MS/MS and Nanopore Sequencing to Enable the Direct and Quantitative Detection of RNA Modifications.
Kristin Koutmou, Ph.D., University of Michigan (abstract 30)

2:05 pm Direct RNA sequencing using electro-optical zero mode waveguides and custom click fluorescent nucleotides.
Meni Wanunu, Ph.D., Northeastern University (abstract 80)

2:20 pm Towards Adding Pseudouridine Identification at Single Base Resolution to EpiPlex, a Proximity Barcoding Platform for the Multiplexed Detection of RNA Modifications.
Gudrun Stengel, Ph.D., Alida Biosciences, Inc. (abstract 69)

2:35 pm Coffee Break

2:55 pm Keynote: Understanding Variant Effects At Scale.
Lea Starita, Ph.D., University of Washington

Flash Talks & Poster Previews

3:45 pm

Micheal White, Ph.D., Washington University in St. Louis
Chunzhe Lu, Ph.D., University of Groningen
Yimin Chen, University at Albany
Amr Makhamreh, Northeastern University
Ali Fallahi, Northeastern University
Kyril Kavetsky, University of Pennsylvania
Shubham Khetan, Ph.D., Harvard Medical School
Kevin Bardon, Ph.D., Northeastern University
Shangsi Lin, University at Albany
Keqing Nian, Northeastern University
Julia Reinsch, University of Oregon
Yuning Zhang, Ph.D., Washington University in St. Louis

4:20 pm — Poster Session I

6:00 pm — Group Dinner - SqWire (1415 South 18th Street)

8:00 pm — Shuttle returns to DoubleTree by Hilton

Wednesday, June 11, 2025

8:30 am — Keynote: Molecular Technologies to Monitor and Manipulate Cells.
Seth Shipman, Ph.D., University of California, San Francisco

Sequencing Technologies

Session Moderator: Andrew Stein, Northeastern University

9:15 am — High Accuracy Nanopore Sequencing. | *Jonathan Craig, Ph.D., University of Washington (abstract 22)*

9:30 am — Improving Biological Nanopores for Precision Nucleic Acid Sequencing Using a Computational Microscope.
Min Chen, Ph.D., University of Massachusetts at Amherst (abstract 10)

9:45 am * Super-Resolution Single-Molecule Sequencing Based on Hybridization Kinetics of a Repertoire of Oligonucleotides.
Kalim Mir, Ph.D., XGenomes, Corp. (abstract 55)

10:00 am Photo-Fragmentation Methods for Single-Molecule Protein Sequencing by Nanopore Mass Spectrometry.
Derek Stein, Ph.D., Brown University (abstract 13)

10:15 am Coffee Break

Single-Cell Technologies

Session Moderator: Milan Sanghvi, University of California, San Diego

10:35 am * Cytope: High-Dimensional Single-Cell Spatial Multiomics Through Spatial Hashing of Live Tissue Sections.
George Hartoularos, Ph.D., Survey Genomics, Inc. (abstract 24)

10:50 am A Perturbation Cell Atlas of KOLF2.1J hiPSCs
Yesh Doctor, University of California, San Diego (abstract 84)

11:05 am Multiplex Gene Tagging of Stem Cells for the Development of Kidney Organoids for Drug Discovery.
Oscar Perez-Leal, M.D., Temple University (abstract 57)

Commercialization Panel Discussion

Session Moderator: Mark Adams, Ph.D., The Jackson Laboratory

11:20 am *James McCarter, M.D., Ph.D., BioGenerator Ventures*
Kalim Mir, Ph.D., XGenomes, Corp.
Gudrun Stengel, Ph.D., Alida Biosciences, Inc.

12:20 pm Buffet Lunch

Breakout Room Discussion

1:20 pm
- Navigating the application process for faculty positions
- AI use in science communication
- AI machine learning and data analysis
- Publication landscape
- NHGRI/TDCC new initiatives

2:30 pm Coffee Break

RNA Synthesis, Isolation, and Splicing

Session Moderator: Bei Liu, Ph.D., University of Chicago

2:50 pm * Automated Microfluidic Platform for Transcriptional Site-Specific Labelling of RNA. | *Diwakaran Rathinam Palaniswamy, University of Massachusetts at Amherst (abstract 14)*

3:05 pm A Rapid Method for Global and Targeted miRNA Next Generation Sequencing. | *Varsha Rao, Ph.D., Claret Bioscience (abstract 63)*

3:20 pm A Quick and Robust Platform for Circular RNA Isolation, Discovery, and Profiling. | *Prashant Khade, Ph.D., Ribo-Therapeutics LLC (abstract 60)*

3:35 pm Harnessing Marathon Reverse Transcriptase for RNA Analysis: From Alternative Splicing Diversification to Revealing the circRNA Transcriptome.
Anna Marie Pyle Ph.D., Yale University (abstract 21)

3:50 pm Decoding Global RNP Topologies in Splicing Regulation.
Zhipeng Lu, Ph.D., University of Southern California (abstract 51)

4:05 pm Poster Session

5:30 pm Dinner - Shuttle to Majorette (7150 Manchester Ave)
8:00 pm Shuttle - Majorette to DoubleTree by Hilton

Thursday, June 12, 2025

8:30 am Keynote: Mapping the cellular determinants of genome editing in human cells.
Britt Adamson, Ph.D., Princeton University

Single-Molecule Protein Sequencing

Session Moderator: Monika Kumari, Ph.D., University of Illinois Urbana-Champaign

9:15 am Stepping Towards Nanopore Single Molecule Protein Sequencing Using Unfoldase Motors. | *Daphne Kontogiorgos-Heintz, University of Washington (abstract 29)*

9:30 am Identification of Native Full-Length Proteins with Single Amino Acid Resolution Using Nanopores. | *Chunzhe Lu, Ph.D., University of Groningen (abstract 36)*

9:45 am Toward Direct, Single-Molecule Protein Sequencing Using Engineered Nanopores. | *Eric Ervin, Ph.D., Electronic BioSciences, Inc. (abstract 17)*

10:00 am Chemical Tools for labeling Posttranslational Modifications. *Monika Raj, Ph.D., Emory University (abstract 61)*

10:15 am Coffee Break

Spatial 'Omics

Session Moderator: Ayushi Hedge, Yale University

10:35 am * Expansion in situ Genome Sequencing Links Nuclear Abnormalities to Hotspots of Aberrant Euchromatin Repression. | *Jason Buenrostro Ph.D., Broad Institute of MIT and Harvard University (abstract 4)*

10:50 am * AI-Guided Laser Capture Microscopy for Genome-Wide Single-Cell Spatial Transcriptomics. | *Hu Cang, Ph.D., University of California, Irvine (abstract 6)*

11:05 am Sequencing-free Whole Genome Spatial Transcriptomics at Molecular Resolution in Intact Tissue. | *Siyuan Wang, Ph.D., Yale University (abstract 78)*

11:20 am Deconvolving the Temporal Dynamics of Organogenesis via Deep-Tissue Spatial Transcriptomics. | *Reza Kalhor, Ph.D., Johns Hopkins University (abstract 28)*

11:35 am * Visualizing Enhancer-Promoter Contact Using Chromatin Expansion Microscopy. | *Liyun Miao, Ph.D., Yale University (abstract 25)*

Wrap-up

11:50 am Closing Remarks | *Mark Adams, Ph.D., The Jackson Laboratory Stephanie Morris, Ph.D., NHGRI*

12:00 pm Boxed lunch available.

- End -

Keynote Speakers

Britt Adamson is an Assistant Professor in the Department of Molecular Biology and the Lewis-Sigler Institute for Integrative Genomics at Princeton University. She is also a member of the Genomic Instability and Cancer Genetics Program at the Rutgers Cancer Institute of New Jersey. Dr. Adamson started her training in 2004 at the Massachusetts Institute of Technology in the laboratory of Angelika Amon. In 2007, she joined the lab of Stephen Elledge at Harvard Medical School, where she used functional genomics approaches to study DNA repair in human cells. She earned her PhD from Harvard Medical School in 2012. Dr. Adamson then worked with Jonathan Weissman at the University of California, San Francisco, where she received a postdoctoral fellowship from the Damon Runyon Cancer Research Foundation. Her postdoctoral work pioneered new approaches for functional genomics in human cells, technologies that now enable dissection of cellular pathways with unprecedented resolution. With her lab at Princeton, Dr. Adamson continues to use and develop cutting-edge experimental tools, including genetic screening methods and single-cell RNA- sequencing, to study genome editing and DNA repair, as well as other areas of interest to the group. Dr. Adamson is the recipient of a 2020 Searle Scholars Award and Rutgers Cancer Institute of New Jersey New Investigator Award.

Polly Fordyce is an Associate Professor of Bioengineering and Genetics and Institute Scholar of ChEM-H at Stanford, where her lab develops and applies new microfluidic platforms for quantitative and high-throughput biophysics, biochemistry, and single-cell biology. She graduated from the University of Colorado at Boulder with undergraduate degrees in physics and biology before moving to Stanford University, where she earned a Ph.D. in physics for work with Professor Steve Block developing instrumentation and assays for single-molecule studies of kinesin motor proteins. For her postdoctoral research, she worked with Professor Joe DeRisi to develop a new microfluidic platform for understanding how transcription factors recognize and bind their DNA targets as well as a new technology for bead-based multiplexing. She is the recipient of an NSF CAREER Award, NIH New Innovator and Pioneer Awards, the Stanford President's Award for Excellence in Diversity, and she is a Chan Zuckerberg Biohub Investigator and Fellow of the AIMBE and AAAS.

Seth Shipman is an Associate Investigator in the Gladstone Institute for Data Science and Biotechnology and an Associate Professor of Bioengineering at UCSF. Seth holds a BA and PhD in Neuroscience from Wesleyan University and UCSF, respectively, and completed his postdoctoral training at Harvard Medical School. The Shipman Lab is focused on developing molecular technology that will make a difference in the understanding and treatment of human disease. In recent years, the lab has built molecular machines to edit genomes, record molecular events, and manipulate transcriptional circuits using repurposed components of bacterial immune systems, like the CRISPR system and the retron system. Seth has received a number of honors for his work, including an NIH New Innovator Award, the Pew Biomedical Scholar Award, and a Chan Zuckerberg Investigator of the SF Biohub.

Lea Starita is an Associate Professor of Genome Sciences at the University of Washington and the Brotman Baty Institute for Precision Medicine. The main goal of the Starita lab is to put an end to Variants of Uncertain Significance (VUS) to make genetic medicine more informative, equitable and impactful. Our lab has shown that multiplexed assays of variant effect (MAVE) can powerfully inform variant classification to move VUS to more definitive classifications. To continue toward this goal, my current research program has four main directions: 1) scaling existing MAVEs for broad application, 2) developing new MAVE technology to unlock access to new and more informative phenotypes, and 3) working with local and international partners to develop guidelines for clinical translation and 4) working with clinical partners to build resources to increase MAVE uptake in the clinic.

The Jackson Laboratory is an independent, nonprofit biomedical research institution with a National Cancer Institute-designated Cancer Center, and nearly 3,000 employees in locations across the United States (Maine, Connecticut, California), China and Japan. Its mission is to discover precise genomic solutions for disease and empower the global biomedical community in the shared quest to improve human health.

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