



## Advances in Genomic Technology Development

The Jackson Laboratory, Farmington, Connecticut

June 11-13, 2024

All times listed are Eastern Daylight Time (GMT -4)

### Tuesday, June 11<sup>th</sup>

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8:15 am Registration Opens

8:30 am Shuttle from Farmington Inn – Farmington to JAX

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

### Session 1 – Genome Technologies: Protein Interactions and DNA and RNA

9:15 am **Photoactivable DNA binding molecules for Protein-DNA crosslinking.**  
*Lin Chen, Ph.D., University of Southern California (Abstract #6)*

9:30 am **ChIP-DIP: A multiplexed method for mapping proteins to DNA uncovers combinatorics controlling gene expression.**  
*Andrew Perez, California Institute of Technology (Abstract #13)*

9:45 am **Decoding global RNP topologies in splicing regulation.**  
*Zhipeng Lu, Ph.D., University of Southern California (Abstract #19)*

10:00 am **SpliceRUSH: an exon-centric screening platform for proximal and distal splicing-regulatory elements in a native sequence context.**  
*Chaolin Zhang, Ph.D., Columbia University (Abstract #35)*

10:15 am **INSCRIBE: High-sensitivity in situ capture of endogenous RNA-protein interactions in fixed cells and primary tissues.**  
*Gene Yeo, Ph.D., MBA, University of California, San Diego (Abstract #103)*

10:30 am **Break**

11:00 am **Keynote: New genomic methods to study nucleic acids and RNA-binding proteins.**  
*Chuan He, Ph.D., The University of Chicago*

12:00 pm **Lunch: Topic-based seating**

1:00 pm **Innovative Molecular Analysis Technologies (IMAT)**  
*Kelly Crotty Ph.D., Director of IMAT, National Cancer Institute*

## Session 2 – Spatial ‘Omics

1:15 pm **Slide-tags: Single-nucleus high-resolution multi-modal spatial genomics.**  
*Andrew J.C. Russell, Ph.D., Broad Institute of Harvard and MIT (Abstract #4)*

1:30 pm **DNA-optical barcoding technology for spatiotemporal single-cell analysis.**  
*Marissa Fahlberg, Ph.D., LASE Innovation (Abstract #17)*

1:45 pm **A multiplex in situ method to study the combinatorial code of epigenetic marks in single cells.**  
*Yanbo Chen, Yale University (Abstract #34)*

2:00 pm **Development of multi-color 3D super-localization liveFISH and liveFISH PAINT to investigate the chromatin dynamics at any genomic scale.**  
*Yanyu Zhu, Ph.D., Stanford University (Abstract #24)*

2:15 pm **A single plasmid system for multiplexed CRISPR gene tagging in induced pluripotent stem cells.**  
*Oscar Perez-Leal, M.D., Temple University (Abstract #22)*

2:30 pm **Break**

2:50 pm **Flash Talks – 2-minute poster previews invited from staff/trainee abstracts**

3:15 pm **Breakout Session – Refer to the pre-meeting survey to select your top 2**

Single-Molecule Protein Seq	RNA synthesis/seq/modifications	Epigenetics/Chromatin structure
Functional Genomics	DNA Synthesis	Multimic Profiling
Nanopore Sequencing	K99/R00 how-to	SBIR Grant Program

4:30 pm **Poster Session 1: Abstracts 1-49**

6:00 pm **Group Dinner – Butchers & Bakers**

8:00 pm **Shuttle from Butchers & Bakers – Farmington Inn**

8:30 am Shuttle from Farmington Inn – Farmington to JAX

### Session 3 – Single-Molecule Protein Sequencing

9:00 am Progress towards long-read single-molecule nanopore protein sequencing using unfoldase motors.  
*Jeff Nivala, Ph.D., University of Washington (Abstract #69)*

9:15 am Engineered nanopores for single-molecule protein sequencing.  
*Andrea Bonini, Ph.D., University of Groningen (Abstract #67)*

9:30 am Molecular determinants of current blockade produced by peptide transport through a nanopore.  
*Jingqian Liu, University of Illinois Urbana Champaign (Abstract #79)*

9:45 am Nanopore optimization for direct, single-molecule protein sequencing.  
*Eric Peterson, Ph.D., Electronic Biosciences, Inc. (Abstract #55)*

10:00 am Chemical tools to uncover hidden proteome.  
*Monika Raj, Ph.D., Emory University (Abstract #72)*

10:15 am Photo-fragmentation methods for single-molecule protein sequencing by nanopore mass spectrometry.  
*Derek Stein, Ph.D., Brown University (Abstract #77)*

10:30 am Break

### Commercialization Panel Discussion

11:00 am Moderators: *Ian Nova, Ph.D., NHGRI*  
*Mostafa Analoui, Ph.D., Quinnipiac University*

*Evan Macosko, M.D., Ph.D., representing Curio Biosciences*  
*Omar Abudayyeh, Ph.D., representing Tome Biosciences*  
*Sasha Levy, Ph.D., representing BacStitch DNA, Inc.*  
*Anna Marie Pyle, Ph.D., representing RNAConnect, Inc.*  
*Shenglong Zhang, Ph.D., representing DirectSeq Biosciences, Inc.*

12:30 pm Buffet Lunch

### Session 4 – Synthetic Nucleic Acid Synthesis

1:30 pm Towards High-throughput BIG DNA Writing.  
*Antonio Vela Gartner, NYU Langone Health (Abstract #2)*

- 1:45 pm Scalable DNA engineering by mating bacteria in arrays and pools.  
*Sasha Levy, Ph.D., BacStitch DNA, Inc. (Abstract #18)*
- 2:00 pm Generating sequence variants by templated gene synthesis.  
*Harris Wang, Ph.D., Columbia University (Abstract #33)*
- 2:15 pm Progress towards a low-cost benchtop inkjet enzymatic DNA synthesizer.  
*Damiano Verardo, Ph.D., DNA Script (Abstract #62)*
- 2:30 pm Development of Genome-Build as a universal method to synthesize genomes  
*Christopher Warren, Ph.D., Proteovista (Abstract #80)*
- 2:45 pm Flash Talks – 2-minute poster previews invited from staff/trainee abstracts
- 3:10 pm Break
- 3:30 pm **Keynote: A Tale of 2 Strands: From Genomes to Origami, Vaccines, Data Storage, and Back.**  
*Mark Bathe, Ph.D., Massachusetts Institute of Technology*
- 4:30 pm Poster Session 2: Abstracts 50 – 98
- 6:00 pm Group Dinner – Shuttle to Five Churches Brewing 193 Arch St, New Britain, CT  
8:15 pm Shuttle from Five Churches Brewing – Farmington Inn

## Thursday, June 13<sup>th</sup>

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- 8:30 am Shuttle from Farmington Inn – Farmington to JAX

### Session 5 – Sequencing Technology Development

- 9:00 am High accuracy nanopore sequencing.  
*Andrew Laszlo, Ph.D., University of Washington (Abstract #60)*
- 9:15 am Navigating the pitfalls of long-read based DNA modification detection.  
*Gang Fang, Ph.D., Icahn School of Medicine at Mount Sinai (Abstract #10)*
- 9:30 am Complete genomes of a multi-generational pedigree to expand studies of genetic and epigenetic inheritance.  
*Karen Miga, Ph.D., University of California, Santa Cruz (Abstract #68)*
- 9:45 am Measuring the epigenome with nanopore sequencing.  
*Winston Timp, Ph.D., Johns Hopkins University (Abstract #78)*
- 10:00 am Psi modification profiling and dynamics in the human transcriptome  
*Sara Rouhanifard Ph.D., Northeastern University (Abstract #73)*
- 10:15 am Break

## Session 6 – 2024 Opportunity Fund Previews

- 10:30 pm      **Transfer RNA epitranscriptome by multi-target sequencing and top-down mass spectrometry.**  
*Shenglong Zhang, Ph.D., New York Institute of Technology*  
*Tao Pan, Ph.D., University of Chicago*
- High-throughput interrogation of transcription factor binding within the mammalian brain.**  
*Bing Ren, Ph.D., University of California, San Diego*  
*Alejandro Chavez, Ph.D., University of California, San Diego*
- Transliteration of a 8 base alphabet into 4 bases in eukaryotic cells.**  
*Steven Benner, Ph.D., Foundation for Applied Molecular Evolution*  
*Jef Boeke, Ph.D., NYU Langone Health*
- Imaging-free spatial transcriptomics.**  
*Fei Chen, Ph.D., Broad Institute of Harvard and MIT*  
*Evan Macosko, M.D., Ph.D., Broad Institute of Harvard and MIT*
- 11:00 am      **Keynote: New machine learning models for single-cell and regulatory genomics.**  
*Christina Leslie, Ph.D., Memorial Sloan Kettering Cancer Center*
- 12:00 pm      **Buffet Lunch**

## Session 7 – Single-Cell Genomics and Chromatin Structure

- 1:00 pm      **A novel flexible approach for high-throughput single-cell phenotyping and genotyping.**  
*Magali Soumillon Ph.D., Flexomics (Abstract #29)*
- 1:15 pm      **Single-cell massively parallel reporter gene assays (scMPRA).**  
*Barak Cohen, Ph.D., Washington University in St. Louis (Abstract #7)*
- 1:30 pm      **Massively parallel in vivo Perturb-seq reveals cell type-specific transcriptional networks in cortical development.**  
*Xin Jin, Ph.D., Scripps Research (Abstract #64)*
- 1:45 pm      **High-throughput measurements of gene expression and chromatin state changes upon targeted gene activation.**  
*Lacra Bintu, Ph.D., Stanford University (Abstract #1)*
- 2:00 pm      **TEM-seq: An ultrasensitive, multi-omic method that directly links chromatin features to DNA methylation.**  
*Bryan Venters, Ph.D., EpiCypher, Inc. (Abstract #14)*
- 2:15 pm      **Genomic sequence context and histone marks regulate pioneer binding to nucleosomes.**  
*Martha Bulyk, Ph.D., Brigham and Women's Hospital and Harvard Medical School (Abstract #3)*

2:30 pm Break

## Session 8 – Wrap-up and Future Directions

2:50 pm **Breakout session wrap-up and TDCC Future Directions**  
*Mark Adams, Ph.D., The Jackson Laboratory*  
*Stephanie Morris, Ph.D., NHGRI*

3:50 pm Adjourn

4:00 pm Shuttle from JAX - Farmington Inn

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