

**EPITRANSCRIPTOMICS: METHODS, TECHNOLOGIES & INNOVATION VIRTUAL SYMPOSIUM
JULY 24 - JULY 25, 2023**

10:15AM-10:30AM - WELCOME REMARKS

DR. SAMIE JAFFREY - WEILL CORNELL MEDICINE

DR. KATE MEYER - DUKE UNIVERSITY

DAY 1: SESSION 1

TOPIC OF SESSION: Emerging technologies for mapping m6A (Moderator: Dr. Samie Jaffrey - Weill Cornell Medicine)

SPEAKERS: (20min talks, 5mins Q&A)

10:30am -10:50am

Dr. Kate Meyer, Duke University - "**Transcriptome-wide profiling of m6A in single cells**"

10:55am - 11:15am

Dr. Schraga Schwartz, Weizmann Institute - "**Deciphering the code governing mRNA methylation**"

11:20am - 11:30am BREAK

11:30am - 11:50pm

Dr. Chengqi Yi, Peking University - "**Absolute quantification of RNA m6A methylome at the single-base resolution**"

11:55pm - 12:15pm

Dr. Weixin Tang: University of Chicago - "**Transcriptome-wide profiling & quantification of N6-methyladenosine by enzyme-assisted adenosine deamination**"

DAY 1: PANEL 1

PANEL TOPIC: How to choose the right approach for mapping m6A

PANELISTS (session is for all speakers and attendees)

12:20pm - 1:00pm

- **Moderator: Dr. Samie Jaffrey - Weill Cornell Medicine**
- Dr. Kate Meyer - Duke University
- Dr. Schraga Schwartz – Weizmann Institute
- Dr. Chengqi Yi - Peking University
- Dr. Weixin Tang - University of Chicago

1:00PM - 1:30PM - LUNCH

DAY 1: SESSION 2

TOPIC OF SESSION: New instrumentation for detecting and quantifying RNA modifications (Moderator: Dr. Kate Meyer, Duke University)

SPEAKERS: (20min talks, 5mins Q&A)

1:30pm - 1:50pm

Dr. Jonathan Göke - Genome Institute of Singapore: "**Identification of m6A RNA modifications at single molecule resolution using nanopore direct RNA-Seq data**"

1:55pm - 2:15pm

Dr. Shuo Huang - Nanjing University - "**Identification of epigenetically modified RNA nucleotides using a reactive nanopore sensor**"

2:20pm - 2:40pm

Dr. Eva Maria Novoa: Centre for Genomic Regulation: "**Decoding the epitranscriptome at single nucleotide & single molecule resolution using nanopore sequencing**"

2:45pm - 3:05pm

Dr. Logan Mulroney - Istituto Italiano Di Tecnologia - "**Investigating RNA modifications with Nanocompore**"

3:10pm - 3:20pm BREAK

DAY 1: PANEL 2

PANEL TOPIC: How to select and use ONT and other technologies for mapping modifications

PANELISTS (session is for all speakers and attendees)

3:20pm - 4:15pm

- **Moderator: Dr. Kate Meyer - Duke University**
- Dr. Jonas Korlach - PacBio (10 min presentation)
- Dr. Logan Mulroney - Istituto Italiano Di Tecnologia
- Dr. Eva Maria Novoa - Centre for Genomic Regulation
- Dr. Jonathan Göke - Genome Institute of Singapore
- Dr. Shuo Huang - Nanjing University

END OF DAY 1

DAY 2: SESSION 1

TOPIC OF SESSION: Methods for quantifying and mapping modified nucleotides in tRNA (Moderator: Dr. Scott Blanchard – St. Jude Research Hospital)

SPEAKERS: (20min talks, 5mins Q&A)

10:30am – 10:50am

Dr. Richard Gregory – Harvard University: “**Deciphering m7G and m3C methylomes and their role in tRNA biology**”

10:55am – 11:15am

Dr. Tao Pan – University of Chicago: “**Functional Genomics and Epitranscriptomics of tRNA from Cells to Microbiomes**”

11:20am – 11:40am

Dr. Shenglong Zhang – New York Institute of Technology – “**Empowering Mass Spectrometry: Large-Scale De Novo Direct & Unbiased Sequencing of RNA Modifications**”

11:45am – 12:05pm

Dr. Peter Dedon – M.I.T. – “**New analytical tools for functional epitranscriptomics**”

12:10pm - 12:20pm BREAK

DAY 2: PANEL 1

PANEL TOPIC: Methods for quantifying and mapping tRNA modifications

PANELISTS (session is for all speakers and attendees)

12:20pm - 1:00pm

- **Moderator: Dr. Scott Blanchard – St. Jude Research Hospital**
- Dr. Qi Chen - University of Utah (10 min Presentation)
- Dr. Richard Gregory - Harvard University
- Dr. Tao Pan - University of Chicago
- Dr. Shenglong Zhang - New York Institute of Technology
- Dr. Peter Dedon - M.I.T.

1:00PM - 1:30PM – LUNCH

DAY 2: SESSION 2

TOPIC OF SESSION: Methods for quantifying and mapping rRNA modifications Moderator: Dr. Davide Ruggero - University of California: San Francisco

SPEAKERS: (20min talks, 5mins Q&A)

1:30pm - 1:50pm

Dr. Yuri Motorin – University of Lorraine - "**Challenges and solutions in epitranscriptomic analysis by deep sequencing**"

1:55pm - 2:15pm

Dr. Davide Ruggero - University of California: San Francisco - "**rRNA modifications in health and disease**"

2:20pm - 2:40pm

Dr. Sarath Janga - Indiana Univ. School of Medicine - "**Single molecule mapping of RNA modifications and structures using direct RNA-sequencing**"

2:45pm - 3:05pm

Dr. Cynthia Burrows - University of Utah - "**Nanopore sequencing for 17 modifications in ribosomes under stress is aided by dwell-time analysis**"

3:10pm - 3:20pm BREAK

DAY 2: PANEL 2

PANEL TOPIC: What are the major challenges for rRNA modification detection?

PANELISTS (session is for all speakers and attendees)

3:20pm - 4:00pm

- **Moderator - Dr. Davide Ruggero - University of California: San Francisco**
- Dr. Yuri Motorin – University of Lorraine
- Dr. Sarath Janga - Indiana Univ. School of Medicine
- Dr. Cynthia Burrows - University of Utah

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DAY 2: SESSION 3

TOPIC OF SESSION: Emerging methods for installing and manipulating RNA modifications (Moderator: Dr. Shenglong Zhang - New York Institute of Technology)

SPEAKERS: (20min talks, 5mins Q&A)

4:00pm - 4:20pm

Dr. Prashant Mali, UC San Diego Health Sciences - "**Programmable Modulation of RNA editing: New Approaches, New Challenges**"

4:25pm - 4:45pm

Dr. Yi-Tao Yu, University of Rochester Medical Center - "**Pseudouridine-mediated nonsense suppression**"

4:50pm - 5:10pm

Dr. Josh Huang, Duke University - "**Programmable RNA sensing for cell monitoring and control**"

END OF SYMPOSIUM