RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS
SATURDAY, JULY 7 • ROOM: GRAND BALLROOM B

10:15 AM-10:20 AM Introduction

10:20 AM-11:00 AM Invited Talk 1

Michael Seiler, H3 Biomedicine, United States

11:00 AM-11:20 AM Ammar Naqvi, Children’s Hospital of Philadelphia, United States
Aberrant splicing in B-cell acute lymphoblastic leukemia

11:20 AM-11:40 AM Marina Reixachs, Universitat Pompeu Fabra, Spain
Measuring ribosome profiling at isoform level: towards unveiling the functional impact of alternative splicing

11:40 AM-12:00 PM Auinash Kalsotra, University of Illinois at Urbana-Champaign, United States
Overexpression of a non-muscle Rbfox2 splice isoform drives cardiac dysfunctions in Myotonic Dystrophy type 1

12:00 PM-12:10 PM Pooja Sethiya, University Of Macau, Macao
Integrating different transcription profiling data to determine mRNA stability upon host-pathogen interaction

12:10 PM-12:20 PM Weizhong Li, Sun Yat-sen University, China
ncRPheDB: identify and prioritize associations between noncoding RNAs and disease phenotypes based on novel evidential metrics

12:20 PM-12:30 PM Vanessa Aguiar-Pulido, Cornell University, United States
High-throughput single-cell transcriptomics profiling interneuron specification during brain development

12:30 PM-12:40 PM Zhen Tan, University of Rochester, United States
TurboFold II: RNA Structural Alignment and Secondary Structure Prediction Informed by Multiple Homologs

12:40 PM-2:00 PM LUNCH (ON OWN)

Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:20 PM Jean-Pierre Glouzon, University of Sherbrooke, Canada
Proceedings Presentation: aliFreeFold: an alignment-free approach to predict secondary structure from homologous RNA sequences

2:20 PM-2:40 PM Dezhong Deng, School of EECS, Oregon State University, United States
LinearFold: Linear-Time Prediction of RNA Secondary Structures

2:40 PM-3:00 PM Anton Petrov, EMBL-EBI, United Kingdom
Rfam: The transition to a genome-centric sequence database

3:00 PM-3:20 PM Jan Gorodkin, University of Copenhagen, Denmark
Enhanced prediction of CRISPR-Cas9 off-targets through modeling of nucleic acid duplex interactions

3:20 PM-3:40 PM Lucia Lorenzi, Ghent University, Belgium
RNA atlas: a nucleotide resolution map of the human transcriptome

3:40 PM-4:00 PM Vincent Boivin, Université de Sherbrooke, Canada
Uncovering new non-coding RNA genes in human with TGIRT-Seq.

4:00 PM-4:40 PM COFFEE BREAK WITH EXHIBITORS

RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:00 PM Yasubumi Sakakibara, Keio University, Japan
Proceedings Presentation: Convolutional neural networks for classification of alignments of non-coding RNA sequences

5:00 PM-5:20 PM Jean-Michel Garant, Université de Sherbrooke, Canada
RNA G-quadruplex prediction to investigate a novel RNA regulation model.

5:20 PM-6:00 PM Stirling Churchman, Harvard University, United States
Exploring the nascent transcriptome with direct RNA nanopore sequencing
RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS
SUNDAY, JULY 8 • ROOM: GRAND BALLROOM B

10:15 AM-10:20 AM Introduction

10:20 AM-11:00 AM Gene Yeo, UCSD University, United States
Large-scale studies of RNA binding proteins by eCLIP and proximity labeling

11:00 AM-11:20 AM Mark Gerstein, Yale University, United States
RADAR: Annotation and prioritization of variants in the post-transcriptional regulome for RNA-binding proteins

11:20 AM-11:40 AM Reazur Rahman, Brandeis University, United States
Identification of RNA-Binding Protein Targets with HyperTRIBE

11:40 AM-12:00 PM Carla Mann, Iowa State University, United States
RPIDisorder: A machine learning method for improved prediction of RNA-Protein interaction partners

12:00 PM-12:10 PM Bojan Losic, Icahn School of Medicine at Mount Sinai Hospital, United States
Using co-expression networks and predictive models to infer circular RNA regulatory function in colitis models

12:10 PM-12:20 PM Hendrik Weisser, STORM Therapeutics Limited, United Kingdom
New tools for RNA epigenetics: an open-source approach to RNA modification analysis

12:20 PM-12:30 PM Renana Sabi, Tel Aviv University, Israel
Novel Insights into Gene Expression Regulation during Meiosis Revealed by Translation Elongation Dynamics

12:30 PM-12:40 PM Dimitra Karagkouni, University of Thessaly, Hellenic Pasteur Institute, Greece
Usher in a new era of CLIP-guided detection of miRNA targets

2:00 PM-2:10 PM Dana Wyman, University of California, Irvine, Center for Complex
Generating full-length, high quality human transcriptomes from PacBio Iso-seq data

2:10 PM-2:20 PM TBD
Long noncoding RNA (IncRNA)-Protein coding gene (PCG) regulatory networks responsive to diverse xenobiotics in rat liver

3:00 PM-3:20 PM Christopher Jürges, Institut für Virologie und Immunbiologie, Julius-Maximilians-Universität Würzburg, Germany
Proceedings Presentation: Dissecting newly transcribed and old RNA using GRAND-SLAM

3:20 PM-3:40 PM Andrew Thurman, University of Iowa, United States
Gene isoform abundance quantification with third generation transcriptome sequencing

3:40 PM-4:00 PM Steven E. Brenner, University of California, Berkeley, United States
Revealing the hidden transcriptome: Analysis of nonsense-mediated mRNA decay target reveals mechanistic insights

4:00 PM-4:40 PM COFFEE BREAK WITH EXHIBITORS
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:00 PM Donny Licatalosi, Case Western Reserve University, United States
Stage-specific mRNA regulatory programs drive mammalian gametogenesis

5:00 PM-5:20 PM Namshik Han, University of Cambridge, United Kingdom
Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci

5:20 PM-6:00 PM Chaolin Zhang, Columbia University, United States
Modeling RNA-binding protein specificity using single-nucleotide-resolution binding maps: a case study of LIN28 and two subclasses of let-7 microRNAs