



RiboClub 2018
September 23-27

RNomics: Big data, analysis and mechanism of action.
Hotel et Villégiature Chéribourg
2603 Chemin du Parc
Orford (Magog) Quebec, Canada

Sunday, September 23th

15:00 – 18:00	Registration for early arrivals
18:00 – 19:30	Welcome reception
19:30 – 21:30	Opening dinner



Monday, September 24th

- 08:00 – 08:45 Registration
- 08:45 – 08:55 Opening Notes (Sherif Abou Elela)
- 08:55 – 09:00 Presentation of Keynote speaker (**Benoit Chabot**)
- 09:00 – 10:00 **Keynote presentation**
Hidden treasures of the RNA world: RBPs from moonlighting to riboregulation
Matthias W. Hentze, EMBL Heidelberg, Heidelberg
- 10:00 – 10:30 Coffee break

Session 1: **Transcription and RNA synthesis**

Chair: **Shona Murphy**

- 10:30 – 10:35 Introduction by **Shona Murphy**
- 10:35 – 10:55 Photo-dependent control of transcription elongation
Jean-François Nadon, Université de Sherbrooke, Sherbrooke
- 10:55 – 11:15 Nus factors prevent Rho-dependent transcription termination of CRISPR arrays in diverse bacterial species
Joseph Wade, University at Albany-SUNY, Albany
- 11:15 – 11:35 Influenza A virus cap-snatching profiling reveals inhibition of the cellular response at the earliest steps of infection
Martin Pelchat, University of Ottawa, Ottawa
- 11:35 – 11:55 Common mechanism of transcription termination at coding and noncoding RNA genes in fission yeast
François Bachand, Université de Sherbrooke, Sherbrooke
- 11:55 – 12:15 The mysterious world of pol II CTD kinases
Shona Murphy, University of Oxford, UK
- 12:15 – 14:00 Networking Lunch



Session 2: RNP Maturation and Function

Chair: **Benoit Chabot**

- 14:00 – 14:05 Introduction by **Benoit Chabot**
- 14:05 – 14:25 Early Recognition in the spliceosome
Andrew MacMillan, University of Alberta, Edmonton
- 14:25 – 14:45 Investigating the biological function of an extremely reduced splicing system
Stephen Rader, University of Northern British Columbia, Prince George
- 14:45 – 15:05 Alternative splicing in apoptotic resistance associated with senescence
Mathieu Deschênes, Université de Sherbrooke, Sherbrooke
- 15:05 – 15:25 The exon junction complex undergoes a compositional switch that alters overall mRNP structure and nonsense-mediated mRNA decay activity
Guramrit Singh, The Ohio State University, Ohio
- 15:25 – 15:45 Genome-wide CRISPR-Cas9 interrogation of splicing networks reveals a mechanism for recognition of autism-misregulated neuronal microexons
Thomas Gonatopoulos-Pournatzis, University of Toronto, Toronto
- 15:45 – 16:10 Coffee break

Session 3: Transcriptomics and Bioinformatics of Splicing

Chair: **Jernej Ule**

- 16:10 – 16:15 Introduction by **Jernej Ule**
- 16:15 – 16:35 Big RNA splicing data - challenges and advancements
Mathieu Quesnel-Vallières, University of Pennsylvania, Philadelphia
- 16:35 – 16:55 Multiple spliced alignment and visualization of gene structure alignment
Aïda Ouangraoua, Université de Sherbrooke, Sherbrooke
- 16:55 – 17:15 The exon junction complex shapes the transcriptome by repressing recursive splicing
Jernej Ule, Institute of Neurology, London



- 17:15 – 17:35 Proteome remodeling by neuronal microexons across bilaterian animals
Manuel Irimia, Centre for Genomic Regulation (CRG), Barcelona
- 17:35 – 17:55 What transcriptomes tell us about disease
Nuno L. Barbosa Morais, IMM Lisboa, Lisbon
- 18:00 – 19:30 Dinner
- 19:30 – 20:30 Gairdner event - After Dinner Speaker
Introduction by Brendan Bell, Université de Sherbrooke
Davor Solter, 2018 Gairdner Award winner
- 20:30 – 21:30 Poster competition IA: (Odd numbers)
- 21:30 – 22:30 Poster competition IB: (Even numbers)
- 22:30 – 24:00 Get Together (Bistro)



Tuesday, September 25th

07:00 – 08:30 Breakfast

**Session 4:
Ribosome Profiling and transcriptomics**

Chair: **Alan G. Hinnebusch**

08:30 – 08:35 Introduction by Alan G. Hinnebusch

08:35 – 08:55 Identifying translated isoforms from ribosome profiling data
Uwe Ohler, Max Delbrück Center for Molecular Medicine, Berlin

08:55 – 09:15 Dissecting the roles of eIF2 and eIF3 during translation using TCP-seq
Thomas Preiss, The John Curtin School of Medical Research, Canberra

09:15 – 09:35 Reconstituting distinct functions of DEAD-box RNA helicases Ded1, Dbp1, and eIF4A in stimulating translation initiation of structured native yeast mRNAs
Alan G. Hinnebusch, NIH, Bethesda

09:35 – 9:55 Translating the cancer genome one codon at a time and its therapeutic implications
Davide Ruggero, UCSF, San Francisco

09:55 – 10:15 Endogenous rRNA sequence variation can regulate gene expression and phenotype
Scott Blanchard, Weill Cornell Medical College, New York

10:15 – 10:45 Coffee break

**Session 5:
Translation Mechanisms and Function**

Chair: **Neva Caliskan**

10:45 – 10:50 Introduction by **Neva Caliskan**

10:50 – 11:10 eIF2 α Methylation by PRMT7 is Required for S51 Phosphorylation and Subsequent Stress Granule Formation
Jocelyn Côté, University of Ottawa, Ottawa



- 11:10 – 11:30 Eukaryotic initiation factor 5B (eIF5B) is a regulatory hub for non-canonical translation initiation in glioblastoma progression
Joseph A. Ross, University of Lethbridge, Lethbridge
- 11:30 – 11:50 The conserved translational ATPase YchF interacts with tRNA and the ribosomal A-site for ribosome quality control
Harland E. Brandon, University of Lethbridge, Lethbridge
- 11:50 – 12:10 Small synthetic molecule-stabilized RNA pseudoknot as an activator for –1 ribosomal frameshifting
Neva Caliskan, Helmholtz Institute for RNA-based Infectious Research (HIRI/HZI), Würzburg
- 12:10 – 12:20 Group Photo
- 12:20 – 13:50 Lunch
- 13:00 – 13:50 Virtual computational RNA community meeting

Session 6: Translation Regulation

Chair: **Christine Clayton**

- 13:50 – 13:55 Introduction by **Christine Clayton**
- 13:55 – 14:15 Human La binds the poly(A) tail to promote cap-independent translation
Mark Bayfield, York University, Toronto
- 14:15 – 14:35 The suppressive cap-binding-complex factor 4EIP is required for normal differentiation
Christine Clayton, University (ZMBH), Heidelberg
- 14:35 – 14:55 Investigating nPABP, a mammalian neural poly(A) binding protein that represses mRNA translation
Sahil Sharma, Lady Davis Institute for Medical Research, Montréal
- 14:55 – 15:15 Translation activation by mRNA secondary structures revealed by small RNA regulation
Maude Guillier, CNRS, Paris
- 15:15 – 15:35 Elucidating the interplay between RNA structure and translation during vertebrate embryogenesis
Jean-Denis Beaudoin, Yale University School of Medicine, New Haven



15:35 – 16:00 Coffee Break

**Session 7:
RNA Degradation**

Chair: **Joel G. Belasco**

16:00 – 16:05 Introduction by **Joel G. Belasco**

16:05 – 16:25 Mechanisms of bacterial mRNA degradation
Joel G. Belasco, New York University School of Medicine, New York

16:25 – 16:45 Posttranscriptional feedback regulation of S-adenosylmethionine production
Nicholas K. Conrad, University of Texas Southwestern Medical Center, Dallas

16:45 – 17:05 Deconvolving the RNA life cycle from high-resolution time-resolved protein-RNA interaction data
Sander Granneman, University of Edinburgh, Edinburgh

17:05 – 17:25 Human antigen R (HuR) mediates cancer-induced muscle wasting by regulating PGC1 α -dependent muscle fiber type specification
Imed Gallouzi, McGill University, Montreal

17:25 – 17:30 Students' Award Introduction (students' representatives)

17:30 – 17:45 Best Talk Award of the RiboWest (introduced by Students' Representative)

17:45 – 18:00 Best Seminar Award (introduced by Students' Representative)

18:00 – 19:00 Poster competition IIA (Even numbers), Cocktail and light snacks

19:00 – 20:00 Poster competition IIB: (Odd numbers), Cocktail and light snacks

20:00 – 21:30 Dinner

21:30 – 24:00 Get Together (Bistro)



Wednesday, September 26th

07:00 – 08:30 Breakfast

**Session 8:
Eukaryotic Non-Coding RNA**

Chair: **René F. Ketting**

08:30 – 08:35 Introduction by **René F. Ketting**

08:35 – 08:55 Tissue-based map of the snoRNome
Michelle Scott, Université de Sherbrooke, Sherbrooke

08:55 – 09:15 A nested 2-level cross-validation ensemble learning pipeline suggests a negative pressure against crosstalk snoRNA-mRNA interactions in *Saccharomyces Cerevisae*
Antoine Paul Soulé, McGill University, Montreal

09:15 – 09:35 Molecular mechanisms driving small RNA pathways in germ cells
René F. Ketting, Institute of Molecular Biology gGmbH, Mainz

09:35 – 09:55 Evf2 ultraconserved enhancer (UCE) lncRNA regulates UCE target gene selection and activity through cohesin recruitment and cis and trans mechanisms
Jhumku D. Kohtz, Northwestern University & Stanley Manne Children's Research Institute, Chicago

09:55 – 10:15 Mechanisms regulating dyskerin SUMOylation and effects of X-linked dyskeratosis congenita mutations on dyskerin function
Chantal Autexier, McGill University, Montreal

10:15 – 10:35 ADAR1 RNA editing mediated dsRNA sensing in innate immunity
Jin Billy Li, Stanford University, Stanford

10:35 – 11:05 Coffee Break



**Session 9:
Bacterial Non-Coding RNA**

Chair: **Cari Vanderpool**

- 11:05 – 11:10 Introduction by **Cari Vanderpool**
- 11:10 – 11:30 Determinants of target prioritization and regulatory hierarchy for the bacterial small RNA SgrS
Cari Vanderpool, University of Illinois at Urbana-Champaign, Champaign
- 11:30 – 11:50 A systems approach to bacterial cell stress and small non-coding RNAs
Eric D. Brown, McMaster University, Hamilton, Canada
- 11:50 – 12:10 Real-time Imaging of Cotranscriptional Folding During Transcription Elongation
Jonathan Grondin, Université de Sherbrooke, Sherbrooke
- 12:10 – 14:00 Lunch
- 13:15 – 14:00 Business meeting

**Session 10:
RNA-Seq, System Biology and Networks**

Chair: **Jack D. Keene**

- 14:00 – 14:05 Introduction by **Jack D. Keene**
- 14:05 – 14:25 Efficient regulatory circuits by a protein and a small RNA encoded in a single gene
Hanah Margalit, The Hebrew University of Jerusalem, Jerusalem
- 14:25 – 14:45 Post-transcriptional Regulation in RAS-induced malignant cells
Jack D. Keene, Duke University Medical Center, Durham
- 14:45 – 15:05 Dissecting the role of SINE non-coding RNAs in aging and amyloid pathology: An integrative RNA genomics approach
Athanasios Zovoilis, University of Lethbridge, Lethbridge
- 15:05 – 15:25 Widespread & functional RNA circularization in localized prostate cancer
Sujun Chen, Princess Margaret Cancer Center, Toronto
- 15:25 – 15:55 Coffee Break



**Session 11:
New Methods for Bioinformatics and Transcriptomics**

Chair: **Lydia L. Sohn**

- 15:55 – 16:00 Introduction by **Lydia L. Sohn**
- 16:00 – 16:20 Inferring the targets of RNA-binding proteins
Quaid Morris, University of Toronto, Toronto
- 16:20 – 16:40 Mechano-NPS: An electronic method to mechanically phenotype cells
Lydia L. Sohn, University of California, Berkeley
- 16:40 – 17:00 Cataloguing recurrent long-range interactions in RNA structures exhibits embedded hierarchies in network families
Vladimir Reinharz, Institute of Basic Science, Ulju-gun
- 17:00 – 17:20 Fission yeast transcriptional heterogeneity surveyed by single cell RNA sequencing
Samuel Marguerat, MRC London Institute of Medical Sciences, London
- 17:20 – 18:20 **Students' Choice Seminar**
Ribosome heterogeneity in translating the genetic code
Introduction by student representatives
Maria Barna, Stanford University, Stanford
- 18:20 – 20:30 Banquet
- 20:30 – 20:35 Presentations of the travel awards
Éric Massé, Université de Sherbrooke
- 20:35 – 20:40 Poster prizes
Michelle Scott, Université de Sherbrooke
- 20:40 – 20:45 Blue Jacket Award
Benoit Chabot, Université de Sherbrooke
- 20:45 – 20:55 RNA Group Notes and Progress
François Bachand, Université de Sherbrooke
- 21:00 – .. Special Presentation of Quebec Folk Music and Dance



Thursday, September 27th

07:00 – 09:30 Breakfast and Departure.