

# Program - Friday, July 11

7:30 a.m. – 8:30 a.m. Registration

## SESSION 1

- 08:30 - 08:40 Opening notes
- 08:40 - 09:15 **Invited speaker: John Calarco.** *Shining a light on the diversity of messages in the nervous system*
- 09:15 - 09:30 **Maria Carmo-Fonseca.** *5 seconds to splice*
- 09:30 - 09:45 **Courtney French.** *Transcriptome analysis reveals thousands of targets of nonsense-mediated mRNA decay that offer clues to the mechanism in different species*
- 09:45 - 10:00 **Hyeshik Chang.** *TAIL-seq: Genome-wide determination of poly(A) tail length and 3' end modifications*
- 10:00 - 10:15 **Lawrence Chasin.** *Saturation mutagenesis of a human exon*
- 10:15 - 10:45 Coffee Break

## SESSION 2

- 10:45 - 11:20 **Invited speaker: Kristen Lynch.** *Interplay of signaling and splicing during T cell activation*
- 11:20 - 11:35 **Auinash Kalsotra.** *Identification of a conserved and cell-type specific program of regulated mRNA splicing in postnatal liver development.*
- 11:35 - 11:50 **Fátima Sánchez-Cabo.** *Understanding the regulation of alternative splicing changes in heart disease*
- 11:50 - 12:20 **Invited speaker: Aviv Regev/Rahul Satija** *From culture to clinic : single cell profiling of the mammalian immune system.*
- 12:20 - 13:30 Lunch

## SESSION 3

- 13:30 - 14:05 **Invited speaker: Christina Leslie.** *Context-specific 3'UTR isoform expression and miRNA regulation*
- 14:05 - 14:20 **Angela Brooks.** *The landscape of RNA splicing alterations in human cancers*
- 14:20 - 14:35 **Sara Gosline.** *Beyond Argonaute: understanding microRNA dysregulation in cancer and its effect on protein interaction and transcriptional regulatory networks*
- 14:35 - 14:50 **Will Fairbrother.** *Massively parallel reporter assays reveal splicing defects in 20% missense disease alleles*
- 14:50 - 15:25 **Invited speaker: Chris Burge.** *Origins and impacts of new exons*
- 15:25 - 16:00 Coffee Break (and start of poster session)

## SESSION 4

- 16:00 - 17:30 **Poster session**
- 17:30 - 17:45 **Arvind Subramaniam.** *Mechanistic constraints for modelling translation from genome-wide measurements of ribosome occupancy*
- 17:45 - 18:00 **Alexander Junge.** *RNAalignClust: Discovering ncRNA families by sequence-structure-based clustering of multiple sequence alignments*
- 18:00 - 18:15 **Stephen Mount.** *Specialized reference transcriptomes for Sailfish*
- 18:15 - 18:50 **Invited speaker: Quaid Morris.** *The eukaryotic RNA-protein interaction code*
- 18:50 – 19:00 Concluding notes, poster prize announcement
- 19:30 IRB-SIG dinner**