

Program, July 18th

- 07.30 - 08.45 Registration
- 09.00 - 09.00 Opening: Ben Blencowe
- 09.15 - 10.15 Keynote lecture: *Global patterns in condition- and tissue-specific RNA processing*, **Chris Burge**. Department of Biology, MIT, Cambridge, USA.
- 10.15 - 10.45** *Coffee break*

GLOBAL ANALYSES AND NEW TECHNOLOGIES

Chair: Brendan Frey

- 10.45 - 11.25 *Digital analysis of gene expression and alternative splicing by high throughput sequencing*, **Xiang-Dong Fu**. University of California - San Diego, USA.
- 11.25 - 11.45 *Detecting Alternative Splicing in Deep Sequencing Data*, **Fan Meng**. University of Michigan, USA.
- 11.45 - 12.05 *Deep surveying of alternative splicing complexity in the human transcriptome by next generation sequencing*, **Qun Pan**. University of Toronto, Canada.
- 12.05 - 12.25 *MADS: a new and improved method for analysis of differential alternative splicing by exon-tiling microarrays*, **Yi Xing**. University of Iowa, USA
- 12.25 - 12.45 *Practical optimization of large scale primer probe selection using the flexible febit Geniom platform*. **Anthony P. Caruso**. Febit Inc.
- 12.45 - 13.50** *Lunch break*
- 13.50 - 14.10 *Genome-wide Analysis of Alternative Splicing using High-Density Oligonucleotide Microarrays*. **Alan Williams**. Affymetrix, Inc. USA

SPLICING REGULATION IN EUKARYOTES

Chair: Uwe Ohler

- 14.10 - 14.50 *A functional exploration of the eukaryotic mRNA processing machinery*, **Brenton Graveley**. University of Connecticut Health Center, USA.
- 14.50 - 15.10 *Evolution of ultraconserved, unproductive splicing in SR genes*, **Steven Brenner**. University of California Berkeley, USA
- 15.10 - 15.30 *Exon creation and establishment in human genes*, **Andre Corvelo**. Pompeu Fabra University, Spain
- 15.30 - 16.00** *Coffee break*
- 16.00 - 16.20 *Intron loss, gain, and alternative splicing in Drosophila*, **Jasmin Coulombe-Huntington**. McGill University, Canada.

SPECIFIC MECHANISMS OF SPLICING REGULATION I

Chair: Eduardo Eyras

- 16.20 - 17.00 *Pre-mRNA splicing factors: old players in new games*, **Javier Cáceres**. MRC Human Genetics Unit, Edinburgh, UK
- 17.00 - 18.30** Poster session
- followed by** *Conference dinner*

Program, July 19th

07.30 - 08.45 Registration

SPECIFIC MECHANISMS OF SPLICING REGULATION II

Chair: Eduardo Eyras

- 09.00 - 09.40 Mechanisms of alternative mRNA processing in the brain revealed by HITS-CLIP(I), **Donny D. Licatalosi**. The Rockefeller University, USA.
- 09.40 - 10.20 *RRM-RNA complexes - toward an RRM-RNA recognition code?* **Frederic Allain**. Institute of Molecular Biology and Biophysics, Zurich, Switzerland
- 10.20 - 10.45** *Coffee break*
- 10.45 - 11.05 *Engineer artificial splicing factors with designed specificity*, **Yang Wang**. Department of Pharmacology, School of Medicine, UNC at Chapel Hill, US.
- 11.05 - 11.25 *Identification of the sequence preferences of RNA binding proteins using a microarray approach*, **Debashish Ray**. University of Toronto, Canada.
- 11.25 - 11.45 *Identification and characterization of nSR100, a novel neuronal splicing regulator*, **John A. Calarco**. University of Toronto, Toronto, Canada.

SPLICING, VARIATION AND DISEASE

Chair: Graziano Pesole

- 11.45 - 12:25 *Identifying alternative hyper-splicing signatures in MG-thymoma by exon arrays*, **Hermona Soreq**. The Hebrew University, Jerusalem, Israel.
- 12.30 - 13.50** *Lunch break*
- 14.00 - 14.40 *Alternative splicing markers in cancer and their regulation by RNA binding proteins*, **Benoit Chabot**. Université de Sherbrooke, Canada.
- 14.40 - 15.00 *Visualizing the weakest links: nucleotides vulnerable to mutations that affect splicing*, **Stephen Mount**. University of Maryland, USA
- 15.00 - 15.20 *Common splicing mutations detected by individual information analysis of single nucleotide polymorphisms*. **Peter Rogan**. University of Western Ontario, London Ontario, Canada
- 15.30 - 16.00** *Coffee break*

DEFINITION OF REGULATORY MOTIFS AND PATTERNS

Chair: Benoit Chabot

- 16.00 - 16.40 *A predictive model of tissue-dependent alternative splicing*, **Brendan Frey**. University of Toronto, Canada.
- 16.40 - 17.00 *Predicting splicing factor binding sites from their genomic context*, **Martin Akerman**. Technion – Israel Institute of Technology, Haifa, Israel
- 17.00 - 17.20 *Application of Bayesian methods to motif detection in RNA*, **Ofer Shai**, University of Toronto. Canada
- 17.20 - 17.40 *Multiple classes of human introns revealed by n-mer co-occurrence probabilities and graph clustering*, **Rodger Voelker**, University of Oregon, Eugene, OR, USA
- 17.40 Conclusion