IRB-SIG 2016 Program - Friday, July 8

7:30 a.m. - 8:30 a.m. Registration

Session 1	RNA processing
08:30 - 08:40	
08:40 - 09:15	Opening notes Invited speaker: Christine Mayr. 3'UTR-mediated protein complex formation determines protein
	functions
09:15 - 09:30	Michael Hamilton. Alternative and differential polyadenylation detection from single molecule long sequencing
09:30 - 09:45	Alina Selega. Statistical modelling of protein–RNA binding time series reveals widespread control of mRNA degradation in stress response
09:45 - 10:00	Meredith Corley. An RNA structure mediated post– transcriptional model of α –1–antitrypsin deficiency
10:00 - 10:15	Steven Brenner. Polysome fractionation analysis reveals nonsense-mediated mRNA decay targets are monosomal and supports model That 3' UTR length is a weak predictor of NMD
10:15 - 10:45	Coffee Break
Session 2	RNA IN DIFFERENTIATION, CELL FUNCTION, AND DISEASE
10:45 - 11:00	Yi Xing. SURVIV: Survival Analysis of mRNA Isoform Variation
11:20 - 11:35	Jorge Vaquero. A new view of transcriptome complexity and regulation through the lens of local splicing variations
11:35 - 11:50	Elena Sotillo. Alternative Splicing of CD19 in relapsed B-cell acute lymphoblastic leukemia
11:30 - 11:45	Benjamin Cieply. Multiphasic and dynamic changes in alternative splicing during induction of pluripotency are coordinated by numerous RNA binding proteins
11:45 - 12:20	Invited speaker: Simon (Hualin) Xi. From Genome Biology to Drug Discovery: Integrative Mining of Human Transcriptomics Data for Novel Therapeutic Targets
12:30 - 13:45	Lunch
12:30 – 13:45 Session 3	Lunch CHARACTERIZATION OF RNA SEQUENCE AND STRUCTURE
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