

Toronto NGS Symposium 2015:

Improving Genomics through Collaboration and Innovation

AGENDA

Thursday, October 22nd, 2015

Mt. Sinai Ben Sadowski Auditorium (18th floor) – 600 University Ave, Toronto

8:00 am – 9:25 am	Registration and morning wake-up Foyer outside Ben Sadowski Auditorium MSH 18th floor
9:25 am – 9:30 am	Introductory Remarks Jeffrey Seitz, VP of Sales, D-MARK Biosciences Inc.
9:30 am – 10:10 am	Mohammad Akbari, Women’s College Hospital “The Power of Founder Population in Gene Discovery”
10:10 am – 10:50 am	Mathieu Lupien, Princess Margaret Cancer Centre “Alterations in the Regulators of the 3-Dimensional Genome in Breast Cancer”
10:50 am – 11:10 am	Coffee Break Foyer, Ben Sadowski Auditorium
11:10 am – 11:50 am	Shadi Shokralla, Biodiversity Institute of Ontario “Next-generation sequencing for environmental DNA research: significance and applications”
11:50 am – 12:30 pm	Ben Shirley, Cytogenomix “Interpreting Variants in Complete Genes and Genome Sequences”
12:30 pm – 1:30 pm 12:45 pm – 1:00 pm 1:00 pm – 1:15 pm 1:15 pm – 1:30 pm	Lunch – Foyer, Ben Sadowski Auditorium, Vendor Presentations During Lunch Pac Bio - “The most comprehensive view of genome complexity with single-molecule, long reads” Perkin Elmer – “Automating Solutions: Kapa Hyperplus on the Sciclone NGSx Workstation” Thermo Fisher - “New Developments from Ion Torrent™”
1:30 pm – 2:10 pm	Scott Bratman, Princess Margaret Cancer Centre “NGS Based Detection of Circulating Tumor DNA”
2:10 pm – 2:50 pm	Michael Wilson, SickKids Hospital “Exploring the Structure and Function of The Mammalian Genome with Comparative Epigenomics”
2:50 pm – 3:30 pm	Jeff Wrana, Mount Sinai Hospital “Why Stop at 21? Delivering Whole Transcriptomes to the Clinic”
3:30 – 5:00 pm	Poster Competition & Social – Foyer See reverse for poster titles and for our sponsors

Thank you to our Sponsors!



Please Join Us for the Poster Competition and Social at 3:30 PM !!

Posters Featured:

“Mutation analysis of five Hypertrophic Cardiomyopathy genes using targeted next-generation sequencing in clinical setting” – Nasim Vasli, Children’s Hospital of Eastern Ontario

“Mapping Loci and Genes using a Hidden Markov Model for Bipolar Affective Disorder” – Ricardo Harripaul, CAMH

“Loss of function variants in the genome of Parkinson’s disease patients” - Mahdi Gani, University of Toronto

“Whole Exome Sequencing identifies 1 base pair deletion, in BCL2-associated athanogene 3 (BAG3) gene associated with severe Dilated Cardiomyopathy (DCM) requiring heart transplant in multiple members of a family” – Arshad Rafiq, SickKid’s Hospital

“Pathogen-host omics of HPV16 variants in an organotypic model of human skin” – Robert Jackson, Lakehead University

“Comparative and Evolutionary analysis of 386 *Pseudomonas syringae* strains reveals ecological and evolutionary cohesion” – Shalabh Thakur, University of Toronto

“Creating a Complex Genotype to Phenotype Map of Drug Resistance in *Saccharomyces cerevisiae* using an Engineered Population” Albi Celaj, University of Toronto

“Spatial genomic heterogeneity in diffuse intrinsic pontine and midline high-grade glioma: implications for diagnostic biopsy and targeted therapeutics” – Scott Ryall, University of Toronto

“Identification of defects in equine innate infectious disease resistance through targeted resequencing of the collagenous lectin gene family” – Russell Fraser, University of Guelph

“Towards a platform for global mapping of binary protein interactions under diverse conditions” – Dayag Sheykhkarimli, University of Toronto

“Using Antibody Phage Display and Deep-Sequencing For Cancer Drug-Discovery” – Sunandan Banerjee, Gino Gallo, University of Toronto