

DRAFT Symposium Program



Wednesday March 25th			
Time	Speaker	Institution	Title
10:00-10:15 Welcome to Country			
10:15-11:00	Fumitaka Inoue	Kyoto University	Deciphering human functional genome using Massively Parallel Reporter Assays
11:00-11:15	Chanodya Pasansi Ranwala	Adelaide, Australia	Unraveling Regulatory Complexity: Functional Characterisation of Enhancer Variants associated with Common Epilepsy
11:15-11:30	Asfar Lathif Salaudeen	The University of British Columbia	Expanding the gene editing toolkit to decipher endogenous causal variants
11:30-11:45 Coffee break			
11:45-12:00	Daniel V Brown	Walter and Eliza Hall Institute	Active learning of the sequence-function landscape in a far-red fluorescent protein
12:00-12:15	Maddy Comerford	University of Melbourne	Mapping the gene regulatory landscape of archaic hominin introgression in modern Papuans
12:15-12:30	Justine Shih	Broad Institute of MIT and Harvard	Mapping Genetic Variation to Cellular Phenotypes with Targeted Optical Endogenous Sequencing
12:30-12:45	Twist Biosciences	Bernd Willems	TBC
12:45-13:45 Lunch + posters on your own			
13:45-14:15	Bryony Thompson	Royal Melbourne Hospital	Lessons Learned from Applying Functional Data in Real-World Clinical Variant Classification
14:15-14:30	Melissa Gilbert	The Children's Hospital of Philadelphia & University of Pennsylvania	The clinical utility of Multiplexed Assays of Variant Effects (MAVEs) in a pediatric cohort
14:30-14:45	Richard James	Seattle Children's Research Institute	Functional Assessment of Genetic Variants of CARD11 and BCL10 with Saturation Genome Editing
14:45-15:00	Jeremy Stone	Brotman Baty Institute at the University of Washington	MaveMD: A functional data resource for genomic medicine
15:00-15:15	Emmylou C. Nicolas-Martinez	Adelaide University, Adelaide, Australia	RNA variants resolved in non-expressed genes by transactivation
15:15-15:45 Coffee Break			
15:45-16:15	Alex Wagner	Nationwide Children's Hospital	TBC
16:15-16:30	Steven E. Brenner	University of California, Berkeley	Findings from the Critical Assessment of Genome Interpretation (CAGI), seventh edition: a community experiment to evaluate phenotype prediction
16:30-16:45	Ashley P.L. Marsh	Ambry Genetics Corporation, Aliso Viejo, CA	Clinical translation of a MUTYH MAVE into a diagnostic laboratory workflow enables large-scale VUS resolution
16:45-17:00	Frederick P. Roth	Pittsburgh, PA, USA	Landscapes of human AAT missense-variant effects reveal pathogenic variation and genetic suppressors

Thursday March 26th			
Time	Speaker	Institution	Title
9:00-9:45	Matthew Hurles	Wellcome Sanger Institute	Plenary Speaker - Title TBC
9:45-10:15	Chai-Ann Ng	Victor Chang Cardiac Research Institute	Integrating MAVE and patch clamp data to improve classification and risk prediction in KCNH2-LQTS
10:15-10:30	Andrew Glazer	Vanderbilt University Medical Center	Three Multimodal Assays of SCN5A Variant Function Inform Arrhythmia Risk Prediction
10:30-10:45	Sujatha Jagannathan	University of Colorado Anschutz Medical Campus, Aurora, CO, USA	Single-codon resolution mapping of nonsense-mediated mRNA decay via genomic stop codon scanning of LMNA
10:45-11:00	Lea Starita	University of Washington	260,000 variant effect measurements and novel calibration methods drive resolution of VUS
11:00-11:30	Coffee Break		
11:30-12:00	Nilah Ioannidis	University of California, Santa Cruz	Modeling the impact of personal genome variation on molecular phenotypes
12:00-12:15	Omar Tariq	University of British Columbia	tfGPRA: A High Throughput Platform for Transcription Factor Characterization
12:15-12:30	Vanessa Burns	Wellcome Sanger Institute	Saturation Genome Editing to Clarify Variant Effect within 5'UTRs of Neurodevelopmental Disorder Genes
12:30-12:45	Lorenzo Vaccaro	Telethon Institute of Genetics and Medicine, Department of Translational Medicine	Genotype-phenotype single-cell transcriptomics for massive parallel assessment of genetic variants
12:45-13:00	Daniel Zimmerman	Ambry Genetics	MAVE Progress Report, How Ambry Genetics Validates and Deploys High-Throughput Functional Assays
13:00-14:00	Lunch + posters on your own		
14:00-14:30	Jian-Rong Yang	Sun Yat-sen University, Guangzhou	Phenotypic Mutations in Collision: Negative Epistasis Between Transcription Errors and Translation Errors Revealed by DMS
14:30-14:45	Srivatsan Raman	University of Wisconsin-Madison	From Variant Maps to Functional Design: Using Deep Mutational Scanning and Machine Learning to Engineer Programmable Bacteriophages
14:45-15:00	Guillaume Diss	Friedrich Miescher Institute	The genetic architecture of the human bZIP interaction network
15:00-15:15	Maximilian Stammnitz	Centre for Genomic Regulation	The genetic architecture of allosteric plant hormone receptors
15:15-15:30	Rosa De Santis	Telethon Institute of Genetics and Medicine	From bulk to single cell: benchmarking analytical tools for Deep Mutational Scanning experiments
15:30-16:00	Coffee Break		
16:00-16:30	Chris Hahn	SA Pathology and University of South Australia	Deep mutational scanning to measure the transactivational effect of GATA2 variants to benefit clinical interpretation
16:30-16:45	Xinyu Wu	Walter and Eliza Hall Institute of Medical Research	Elucidate the active conformation of cytokine receptors using deep mutational scanning
16:45-17:00	Polina V Polunina	University of Freiburg	Modeling Viral Evolution as Sequence Transitions: A Transformer Approach Using Time-Resolved SARS-CoV-2 Spike Data
17:00-17:30	Poster short talks		
17:30-19:30	Catered poster reception		

Friday March 27th			
Time	Speaker	Institution	Title
9:00-9:45	Maitreya Dunham	University of Washington	Plenary Speaker: From ARS1 to ZWF1: some adventures in deep mutational scanning
9:45-10:15	Mark Dawson	Peter MacCallum Cancer Centre	TBC
10:15-10:30	Jun J Yang	St. Jude Children's Research Hospital	MAVE-informed Protein Language Models for Predicting Pharmacogenetic Variant Function at Scale
10:30-10:45	Jacob Purcell	Monash University	High-resolution functional assessment of SMAD4 variants
10:45-11:00	Douglas M. Fowler	University of Washington	Biochemical profiling of ~315,000 MAP kinase pathway protein variants in human cells with LABEL-seq
11:00-11:30	Coffee Break		
11:30-12:00	Amelie Stein	University of Copenhagen	TBC
12:00-12:15	Alistair Dunham	Wellcome Sanger Institute	Standardisation and joint analysis of 2,041 MAVES
12:15-12:30	Yu-Jen (Jennifer) Lin	University of California	Critical Assessment of Genome Interpretation (CAGI) 7 ARSA missense stability prediction challenge identifies computational advances over state-of-the-art variant impact predictors
12:30-12:45	Brendan Larsen	Fred Hutch Cancer Center	Functional and antigenic landscape of the Nipah virus entry proteins
12:45-13:00	Linda Wijaya	The Kids Research Institute Australia, University of Western Australia	Unravelling the RASopathy Syndromes using iPSC-derived neural disease modelling
13:00-14:00	Lunch no posters		
14:00-14:30	Melissa Call	Walter & Eliza Hall Institute	TBC
14:30-14:45	Awards and closing		
	Coffee Break		
15:00-17:00	Workshops		Clinical Application Workshop