Genomics of Rare Disease
25-27 March 2020

**Wellcome Genome Campus,
Hinxton, Cambridge, UK**

Conference Programme

Wednesday 25 March 2020

12:00-13:30 **Registration with lunch**

13:30-13:40 **Welcome and introduction**
Programme Committee: Kaitlin Samocha, Wellcome Sanger Institute, UK

13:40-14:40 **Lupski lecture**
Chair: Kaitlin Samocha, Wellcome Sanger Institute, UK

Rare variation, rare subtypes of common disease: neuropsychiatry and neurodevelopment
Mark Daly
FIMM, University of Helsinki, Finland

14:40-15:55 **Session 1: What's new in rare disease?**
Chair: Lisenka Vissers, Radboudumc University, Netherlands

14:40 Delineating the structure of chromosome rearrangements using multiple WGS technologies
Anna Lindstrand
Karolinska Institutet, Sweden

15:10 Functional genetics in inborn errors of immunity
Cecilia Poli
Universidad del Desarrollo, Chile

15:40 Patterns of mitochondrial DNA variation across 15,000 individuals in the gnomAD database
Nicole Lake
Yale University, USA

15:55-16:30 **Afternoon tea**

16:30-17:00 **Session 1 continued: What's new in rare disease?**
Chair: Lisenka Vissers, Radboudumc University, Netherlands

16:30 Integrating healthcare and research genetic data empowers the discovery of 48 novel developmental disorders
Kaitlin Samocha
Wellcome Sanger Institute, UK

16:45 The Androgen Receptor CAG repeat expansion is unexpectedly common in the general population
Arianna Tucci
Queen Mary University, UK

17:00-17:30 **Lightning talks**
Chair: Kaitlin Samocha, Wellcome Sanger Institute, UK

17:30-19:00 **Poster session 1 (odd numbers) with drinks reception**

19:00 **Dinner**

Thursday 26 March 2020

09:00-10:45 **Session 2: Beyond the coding genome**
Chair: James Ware, Imperial College London, UK

09:00 Polygenic contribution to rare inherited cardiac disorders
Connie Bezzina
Amsterdam University Medical Center, Netherlands

09.30 Coding plus non-coding, common plus rare: lessons learned from TBX6-associated congenital scoliosis (TACS)
Nan Wu
Peking Union Medical College Hospital, China

10.00 Unveiling the regulation of CDH1/E-Cadherin expression by intronic cis-regulatory elements
Rita Matos
IPATIMUP/i3S, Portugal

10.15 Pervasive and CpG-dependent promoter-like characteristics of transcribed enhancers
Robin Steinhaus
Charité – Universitätsmedizin Berlin, Germany

10:30 Identification of repeat expansions with whole exome and whole genome sequencing in epilepsy patients
Melanie Bahlo
Walter and Eliza Hall Institute, Australia

10:45-11:20 **Morning coffee**

11:20-12:50 **Session 3: Informatics**
Chair: Kaitlin Samocha, Wellcome Sanger Institute, UK

11:20 Phenotype aware prioritisation of rare disease variants
Damian Smedley
Queen Mary University of London and Genomics England, UK

11:50 CADD-SV – a framework to score the effect of structural variants in health and disease
Philip Kleinert
Berlin Institute of Health, Germany

12:05 InDelible: detection and evaluation of clinically-relevant structural variation from whole exome sequencing
Eugene Gardner
Wellcome Sanger Institute, UK

12:20 Genetic intolerance across homologous protein domains identifies TTN missense variants with a role in dilated cardiomyopathy
Xiaolei Zhang
Imperial College London, UK

12:35 Gene-specific modelling of mutational hotspots and in-silico evidence in a large hypertrophic cardiomyopathy cohort
Adam Waring
University of Oxford, UK

12:50-14:15 **Lunch**

14:15-15:45 **Session 4: Functional genomics**
Chair: Mark Daly, FIMM, University of Helsinki, Finland

14:15 Understanding the functional effects of coding variation at scale
Lea Starita
University of Washington, USA

14:45 Phenotypic impacts of mono- and biallelic variation at a locus
Tamar Harel
Hadassah-Hebrew University Medical Center, Israel

15:15 Saturation genome editing of developmental disorder genes
Hong Kee Tan
Wellcome Sanger Institute, UK

15:30 The role of genetic modifiers in a mild LAMA2-RD case associated with a LAMA2 loss-of-function mutation
Veronica Pini
UCL, UK

15:45-16:20 **Afternoon tea**

16:20-17:35 **Session 5: New therapeutic approaches**
Chair: Clare Turnbull, Institute of Cancer Research, UK

16:20 Targeted therapy in patients with PIK3CA-related overgrowth syndrome
Guillaume Canaud
Hôpital Necker Enfants Malades, France

16:50 Splice modulation therapy in inherited retinal diseases
Rob Collin
Radboudumc University Medical Center, Netherlands

17.20 Fast and scalable RNA-seq splicing analysis for the clinical setting
Joseph Aicher
University of Pennsylvania, USA

17:35-18:00 **Lightning talks**
Chair: James Ware, Imperial College London, UK

18:00-19:30 **Poster session 2 (even numbers) with drinks reception**

19:30 **Conference dinner**

Friday 27 March 2020

09:00-10:30 **Session 6: Clinical genetics**
Chair: Jennifer Posey, Baylor College of Medicine, USA

09:00 Identifying diagnoses beyond the exome: lessons from genetically undiagnosed cases with compelling clinical phenotypes
Anne O'Donnell-Luria
The Broad Institute and Boston Children's Hospital, USA

09:30 Cancer susceptibility genomics: harnessing the full spectrum of variant frequency-penetrance
Clare Turnbull
Institute of Cancer Research, UK

10:00 The Heart Hive (thehearthive.org) - a scalable solution for 21st century cardiovascular genomics research
Angharad Roberts
Imperial College London, UK

10:15 The added value of RNA sequencing on top of WES for variant interpretation and diagnosis of patients with Mendelian disorders
Vicente Yepez
Technical University of Munich, Germany

10:30-11:10 **Morning coffee**

11:10-12:40 **Session 7: Developmental genetics**
Chair: Tamar Harel, Hadassah-Hebrew University Medical Center, Israel

11:10 Neurodevelopmental proteasomopathies
Sébastien Kury
CHU de Nantes, France

11:40 Mutation-specific pathophysiological mechanisms in a new SATB1-associated neurodevelopmental disorder
Elke de Boer
Radboud University Medical Center, Netherlands

11:55 Detection of mosaic chromosomal alterations in children with developmental disorders
Ruth Eberhardt
Wellcome Sanger Institute, UK

12:10 Heterozygous variants disturbing the transcriptional repressor activity of FOXP4 cause a disorder with congenital abnormalities, expressive language deficits and divergent growth parameters
Lot Snijders Blok
Radboud University Medical Center, Netherlands

12:25 GREB1L variants contribute to the development of Mayer Rokitansky Kuster Hauser syndrome
Angad Jolly
Baylor College of Medicine, USA

12:40-12:50 **Closing remarks**
Chair: Lisenka Vissers, Radboudumc, Netherlands

12:50-14:00 **Lunch**

13:45 **Coach to Heathrow airport via Stansted airport departs**

14:00 **Coach to Cambridge departs**