Epigenomics of Common Diseases
6-8 November 2019
Wellcome Genome Campus,
Hinxton, Cambridge, UK

Conference Programme

Wednesday, 6 November

12:30-13:50  Registration with lunch

13:50-14:00  Welcome and Introductions
Doug Higgs, University of Oxford, UK

14:00-15:00  Keynote Lecture
Session Chair: Doug Higgs, University of Oxford, UK

Epigenomics and Genome Function at Nucleotide Resolution
John Stamatoyannopoulos
University of Washington & Altius Institute, USA

15:00-15:45  Session 1: The numerous faces of epigenomics: from Waddington to epigenetic editing
Chair: Art Petronis, University of Toronto, Canada

15:00  The somatic cellular genomics of common disease
John Greally
Albert Einstein College of Medicine, USA

15:30  Functional characterisation of GWAS loci using epigenetic editing
Emma Dempster
University of Exeter, UK

15:45-16:15  Afternoon Tea

16:15-17:00  Session I continued:

16:15  The disease epigenotype: Why is it so variable?
Eva Jablonka
Tel Aviv University, Israel
16:45 Changes to the transcriptome and methylome of human α and β cells during aging provide insight into the epigenomic basis of their dysfunction in T2D
Dana Avrahami Tzfati
Hebrew University School of Medicine, Israel

17:00-17:30 Lightning talks
Session Chair: Doug Higgs & Art Petronis

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

19:00 Dinner

19:00 Cash bar

Thursday, 7 November

09:00-10:30 Session 2: PRC
Chair: Nada Jabado, Montreal Children’s Hospital, Canada

09:00 Mechanistic insights into alterations of the Polycomb machinery in cancers
Raphaël Margueron
Institut Curie, France

09:30 Role of the Polycomb Repressive Complex 2 (PRC2) in transcriptional regulation and cancer
Kristian Helin
Memorial Sloan Kettering Cancer Centre, USA

10:00 Dppa2/4 target chromatin bivalency enabling multi-lineage commitment
Melanie Eckersley Maslin
Babraham Institute, UK

10:15 Index and vocabulary of accessible DNA elements in the human genome
Wouter Meuleman
Altius Institute for Biomedical Sciences, USA

10:30-11:00 Morning Coffee

11:00-12:30 Session 3: Cancer
Chair: Nada Jabado Montreal Children’s Hospital, Canada

11:00 Epigenetics of cancer
Mathieu Lupien
University of Toronto, Canada

11:30 Targetable Mechanisms of Tumor Immortality and Evolution
Joe Costello
UCSF Helen Diller Family Comprehensive Cancer Center, USA
12:00 The histone demethylase LSD1 mediates chemoresistance in breast cancer via induction of a stem cell programme  
John Verigos  
IMBB-FORTH, Greece

12:15 Complex pattern of histone acetylations at enhancer elements  
Pradeepa Madapura  
Blizard Institute, QMUL, UK

12:30-14:00 Lunch

14:00-15:30 Session 4: Population and Epidemiologic Studies  
Chair: Daniele Fallin, Johns Hopkins University, USA

14:00 Pleiotropic effects of trait-associated genetic variation on DNA methylation: Utility for refining GWAS loci  
Eilis Hannon  
University of Exeter, UK

14:30 Offspring health and DNA methylation profile following conception by assisted reproduction  
Richard Saffery  
Murdoch Children’s Research Institute, Australia

15:00 Characterisation of an inflammation-related epigenetic score and its associations with cognitive ability  
Anna Stevenson  
University of Edinburgh, UK

15:15 Meta-analysis of epigenome-wide association studies in Alzheimer’s disease highlights 220 differentially methylated loci across cortex  
Katie Lunnon  
University of Exeter, UK

15:30-16:00 Afternoon Tea

16:00-17:30 Session 5: Brain  
Chair: Art Petronis, University of Toronto, Canada

16:00 Molecular function of specific histone residues in neurodevelopment and diseases  
Kyung-Min Noh  
EMBL, Germany

16:30 Epigenetic mechanisms underlying dopaminergic abnormalities in psychosis  
Viviane Labrie  
Van Andel Institute, USA

17:00 Epigenomic and transcriptional signatures of progressive neuropathology in transgenic models of Alzheimer’s disease  
Isabel Castanho  
University of Exeter, UK
17:15 Identification of age of onset-associated genetic variants in cell type-specific regulatory elements in LRRK2 Parkinson’s disease
Jochen Ohnmacht
University of Luxembourg, Luxembourg

17:30-18:00 Lightning talks
Session Chair: Daniele Fallin & Nada Jabado

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

19:30 Silver service conference dinner (Please arrive prompt)
19:30 Cash bar

Friday, 8 November

09:00-10:30 Session 6: Environment
Chair: Daniele Fallin, Johns Hopkins University, USA

09:00 Methylation in relation to in utero exposures and child health: epigenome-wide meta-analyses in the Pregnancy and Childhood Epigenetics Consortium
Stephanie London
NIH, USA

09:30 Mammalian Ribosomal DNA as an environmental sensor
Vardhman Rakyan
Queen Mary, University of London, UK

10:00 Circadian DNA modification is involved in aging and complex disease
Akhil Nair
University of Toronto, Canada

10:15 Altered epigenetic profiles in the brains of young adult urbanites and mice chronically exposed to air pollution
Nur Jury Garfe
Andres Bello University, Chile

10:30-11:00 Morning Coffee

11:00-12:30 Session 7: Development
Chair: Daniele Fallin, Johns Hopkins University, USA

11:00 The dichotomy of DNA methylation in spermatogenesis
Déborah Bourc’his
Institut Curie, France

11:30 X-chromosome inactivation in human
Claire Rougeulle
Paris Diderot University, France
12:00  Endogenous retroviral insertions drive non-canonical imprinting in extra-embryonic tissues  
   Courtney Hanna  
   University of Cambridge, UK

12:15  KHDC3L is essential for establishment of DNA methylation in the human oocyte  
   Hannah Demond  
   Babraham Institute, UK

12:30-13:30  **Keynote Lecture**  
   **Session Chair: Art Petronis, University of Toronto, Canada**

   Probing the epigenome for therapeutic opportunities  
   Cheryl Arrowsmith  
   University of Toronto, Canada

13:30 -13:40  Closing remarks by Art Petronis

13:40  **Packed lunch**

14:00  **Coach departs to Heathrow Airport via Stansted Airport**

14:15  **Coach departs to Cambridge City Centre and Train Station**