

Hybrid Conference Programme		
Start (GMT)	Finish (GMT)	Presenter details
Wednesday 4 November 2026		
12:00	13:00	Registration, lunch and networking
12:45	13:00	Briefing for Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium
13:00	13:10	Welcome and introductions Wellcome Connecting Science: Andy Mains, Wellcome Connecting Science, UK Scientific programme committee: Jordana Bell, King's College London, UK Christoph Bock, CeMM Research Center for Molecular Medicine, Austria Claudia Kleinman, McGill University, Canada Charlotte Ling, Lund University, Sweden
13:10	14:00	Keynote 1 Chair: Charlotte Ling, Lund University, Sweden Moderator: TBC 13:10 14:00 DNA methylation: the beauty and the beast in population studies Bas Heijmans, Leiden University, The Netherlands 14:00 14:05 Comfort break (no refreshments)
14:05	15:35	Session 1: Epigenetics, development and disease Chair: Claudia Kleinman, McGill University, Canada Moderator: TBC 14:05 14:35 Synthetic Ex Utero Embryogenesis: from Naive Pluripotent Cells to bona fide Embryo Models Jacob Hanna, Weizmann Institute of Science, Israel 14:35 15:05 Deep learning approaches to dissect transcription factor binding syntax in the human genome Selin Jassia, Stanford University, USA 15:05 15:20 Placental epigenetic dysregulation predicts early child developmental outcomes Lucas Casten, Max Planck Institute Of Psychiatry, Germany 15:20 15:35 DNA methylation captures shared and protein-specific variation in the inflammatory proteome across development Wim Schalkwijk, University Medical Center Utrecht, Netherlands 15:35 16:15 Refreshment break and networking 16:00 16:15 Briefing for session 2 speakers, chair & moderator - Auditorium
16:15	17:45	Session 2: Epigenetic mechanisms in ageing and age-related diseases Chair: Charlotte Ling, Lund University, Sweden Moderator: TBC 16:15 16:45 Developing cfDNA DNA Methylation Biomarkers for Neurodegenerative Disease Emma Dempster, University of Exeter, UK 16:45 17:15 Title TBC Duqu Ucar, The Jackson Laboratory, USA 17:15 17:30 Shared and clock-specific genetic architecture across three generations of epigenetic clocks Siyi Wang, University Of Exeter, UK 17:30 17:45 Cell-to-cell variability and gain of methylation at polycomb CpG islands as a hallmark of aging Tommy Kaplan, Queen Mary University of London, UK
17:45	18:15	Poster pitch talks for odd number posters
18:15	19:15	Poster session 1 - odd number posters
19:15	20:30	Dinner
19:15		Bar open (card payments only)

Thursday 5 November 2026		
09:15	09:30	Briefing for Session 3 speakers, chair & moderator - Auditorium
09:30	11:00	Session 3: Epigenetic cell plasticity Chair: <i>Claudia Kleinman, McGill University, Canada</i> Moderator: <i>TBC</i>
09:30	10:00	Epigenetic lineage tracing of cancer evolution <i>Trevor Graham, The Institute of Cancer Research, UK</i>
10:00	10:30	Targeting RNA Modifications in Cancer <i>Michaela Frey, DMPK, Germany</i>
10:30	10:45	Promoter-enhancer rewiring during terminal adipogenesis links epigenomic regulation to metabolic disease risk <i>Iona Sandovici, University of Cambridge, UK</i>
10:45	11:00	Effects of rituximab versus cladribine on the pace of biological aging in people with multiple sclerosis <i>Eirik Sandvik Gulbrandsen, Oslo University University, Norway</i>
11:00	11:45	Refreshment break and networking
11:30	11:45	Briefing for session 4 speakers, chair & moderator - Auditorium
11:45	13:15	Session 4: Genetics, epigenetics and environment Chair: <i>Jordana Bell, King's College London, UK</i> Moderator: <i>TBC</i>
11:45	12:15	Lessons from single cell epigenome in cardiometabolic disease and accelerated aging risk assessment <i>Pavni Pajkanta, UCLA, USA</i>
12:15	12:30	Nature vs nurture? Dissecting the contribution of genetics, environment, and their interaction to DNA methylation variability across the first 5 years of life <i>Erick Navarro-Delgado, The University Of British Columbia, Canada</i>
12:30	12:45	Identifying genetic impacts on DNA methylation variability to uncover gene-environment and gene-gene interactions in GoDMC <i>Xiaopu Zhang, King's College London, UK</i>
12:45	13:00	Cis and trans genetic control of DNA methylation in cord blood highlights neurodevelopmental and immune regulatory processes <i>Emilie Willoch Østad, University of Oslo, Norway</i>
13:00	14:15	Lunch and networking
14:00	14:15	Briefing for Session 5 speakers, chair & moderator - Auditorium
14:15	16:00	Session 5: Epigenetics and common disease: establishing causality Chair: <i>Charlotte Lina, Lund University, Sweden</i> Moderator: <i>TBC</i>
14:15	14:45	Title TBC <i>Maja Jagodic, Karolinska Institute, Sweden</i>
14:45	15:15	Title TBC <i>Yijun Ruan, Zhejiang University, China</i>
15:15	15:30	Epigenetic Signatures Classifying Brain Insulin Resistance in Humans <i>Meriem Ouni, German Institute of Human Nutrition Potsdam-Rehbrücke, Germany</i>
15:30	15:45	Decoding the Individual Vaccination response in Older adults through Immuno-Epigenetics <i>Anh Nouwen, Leiden University Medical Centre, Netherlands</i>
15:45	16:30	Refreshment break and networking
16:15	16:30	Briefing for Keynote speaker, chair & moderator - Auditorium
16:30	17:20	Keynote 2 Chair: <i>Jordana Bell, King's College London, UK</i> Moderator: <i>TBC</i> Decoding the tissue ecosystems of the human body <i>Muzlifah Haniffa, Wellcome Sanger Institute, UK</i>
17:20	17:50	Poster pitch talks for even number posters
17:50	18:05	Sponsored talk - Illumina Leading the epigenetics future: Illumina's expanding DNA methylation portfolio <i>Nicole Renke, Illumina, UK</i>
18:05	19:05	Poster session 1 - odd number posters
19:05	21:00	Dinner
19:05		Bar open (card payments only)

Friday 6 November 2026		
09:15	09:30	Briefing for Session 6 speakers, chair & moderator - Auditorium
09:30	11:00	Session 6: New frontiers in epigenomic technologies Chair: Claudia Kleinman, McGill University, Canada Moderator: TBC
09:30	10:00	Understanding epigenetic regulation during early human embryonic brain development at single cell resolution Fides Zerk, EPFL, Switzerland
10:00	10:30	Title TBC Juuso Taipale, Wellcome Sanger Institute, UK
10:30	10:45	Resolving cell-type-specific DNA methylation from heterogeneous tissues using long-read sequencing Ellis Hannon, University Of Exeter, UK
10:45	11:00	maxATAC-v2: Enhanced Genome-Wide TF Binding Site Prediction from (sc)ATAC-seq Akshata Rudrapatna, University Of Cincinnati/Cincinnati Children's Hospital Medical Center, USA
11:00	11:40	Refreshment break and networking
11:25	11:40	Briefing for Keynote, chair, moderator & committee - Auditorium
11:40	12:30	Keynote 3 Chair: Jordana Bell, King's College London, UK Moderator: TBC
11:40	12:30	Disturbances of DNA methylation and metabolic health in Asian populations John Chambers, Precision Health Research, Singapore
12:30	12:45	Closing Remarks Scientific Programme Committee: Jordana Bell, King's College London, UK Christoph Bock, CeMM Research Center for Molecular Medicine, Austria Claudia Kleinman, McGill University, Canada Charlotte Ling, Lund University, Sweden
12:45	13:45	Lunch and departures
13:45		Coach departures for Stansted and Heathrow airports
13:55		Coach departures for Cambridge train station and city centre