

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
Monday 29 June 2026		
12:00	13:00	Registration, lunch and networking
12:45	13:00	Briefing for KNS, Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium
13:00	13:10	Welcome and introductions <i>Wellcome Connecting Science:</i> Nagehan Ramazanoglu Bahadir, Wellcome Connecting Science, UK <i>Scientific programme committee:</i> Melina Claussnitzer, Broad Institute, USA Craig Glastonbury, Human Technopole, Italy Jonathan Pritchard, Stanford University, USA Gosia Trynka, Wellcome Sanger Institute/Open Targets, UK
13:10	14:00	Keynote Chair: Gosia Trynka, Wellcome Sanger Institute/Open Targets, UK Moderator: Eva Holtkamp, Helmholtz Munich, Germany
13:10	14:00	Trait Causal Models: Harnessing GWAS and perturbations to understand human biology Jonathan Pritchard, Stanford University, USA
14:00	14:05	Comfort break
14:05	15:35	Session 1: Scalable genomic perturbations Chair: Melina Claussnitzer, Broad Institute, USA Moderator: Eva Holtkamp, Helmholtz Munich, Germany
14:05	14:35	A CRISPR way to understand neurodegenerative disease Andrew Bassett, Wellcome Sanger Institute, UK
14:35	15:05	Functional variation in the human genome: Lessons from population genomics and experimental perturbations Tuuli Lappalainen, New York Genome Center, USA
15:05	15:20	Saturation mutagenesis of 37 human splicing factor genes using pooled prime editing Michael Herger, Francis Crick Institute, UK
15:20	15:35	Using synthetic lineages to understand gene expression rules Connor Rogers, Wellcome Sanger Institute, UK
15:35	16:15	Refreshment break and networking
16:05	16:15	Briefing for session 2 speakers, chair & moderator - Auditorium
16:15	17:45	Session 2: Imaging technologies for cell profiling Chair: Bart Deplancke, École Polytechnique Fédérale de Lausanne, Switzerland Moderator: Jeffrey Pullin, MRC Biostatistics Unit, UK
16:15	16:45	Optical Pooled Screens for Neurodegenerative Diseases: High-Content Functional Genomics beyond the Genome-Wide Scale Owen Andrews, Broad Institute, USA
16:45	17:15	Perturbing cell fate regulators across biological contexts Silvia Domcke, University of Zurich, Switzerland
17:15	17:30	Phenotyping beyond gene expression with TGIow: a scalable imaging framework that captures non-transcriptomic hallmarks of human T cell activation Julie Matte, Wellcome Sanger Institute, UK
17:30	17:45	Characterizing the genetic regulation of cellular phenotypes in primary stem cell-derived adipocytes using single-cell high-content imaging Henry Taylor, Broad Institute, USA
17:45	18:15	Poster pitch talks for odd number posters
18:15	19:15	Poster session 1 - odd number posters
19:15		Bar open (card payments only)
19:15	21:00	Dinner

Tuesday 30 June 2026

09:15	09:30	Briefing for Session 3 speakers, chair & moderator - Auditorium
09:30	11:00	Session 3: Linking polygenic signals to gene programs <i>Chair: Gosia Trynka, Wellcome Sanger Institute/Open Targets, UK</i> <i>Moderator: Jeffrey Pullin, MRC Biostatistics Unit, UK</i>
09:30	10:00	A Universal Translator of Transcriptome to Protein Interactome Algorithm Stephen Michnick, Université de Montréal, Canada
10:00	10:30	Insights from process specific polygenic scores in diabetes Miriam Udler, Harvard Medical School, USA
10:30	10:45	Genome-scale perturb-seq in primary human CD4+ T cells maps context-specific regulators of human immune traits <i>Emma Dann, Stanford University & Gladstone Institutes, USA</i>
10:45	11:00	Integration of GWAS, 3D genomics, and CRISPRi screens in microglia implicates causal variants and genes at Alzheimer's disease loci, including an enhancer variant regulating TSPAN14 expression <i>Shannon Laub, University Of Pennsylvania, USA</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: From genetic and induced perturbation to phenotype through imaging <i>Chair: Jonathan Pritchard, Stanford University, USA</i> <i>Moderator: Marina Simunovic, European Molecular Biology Laboratory, Germany</i>
11:45	12:15	Title TBC Melina Claussnitzer, Broad Institute, USA
12:15	12:45	Image-based profiling to investigate how environmental contaminants impact cell function Jessica Ewald, EMBL/EBI, UK
12:45	13:00	Genome-scale profiling of genetic determinants of micronucleus formation in human cells using optical pooled screening <i>Louise Morlot, Danish Cancer Institute, Denmark</i>
13:00	13:15	Dissecting the heterogeneity of secondary senescence using paired single-cell transcriptomics and high-resolution imaging <i>Augoustina Maria Economou, Ecole Polytechnique Fédérale de Lausanne, Switzerland</i>
13:15	14:30	Lunch and networking
14:15	14:30	Briefing for Session 5 speakers, chair & moderator - Auditorium
14:30	16:00	Session 5: Generating high-resolution trait descriptors <i>Chair: Miriam Udler, Harvard Medical School, USA</i> <i>Moderator: Marina Simunovic, European Molecular Biology Laboratory, Germany</i>
14:30	15:00	A picture's worth a thousand data points: leveraging biomedical imaging to dissect the impact of genetic variation on human biology Hannah Curren, University of Oxford, UK
15:00	15:30	Title TBC Sarah Teichmann, Cambridge Stem Cell Institute, University of Cambridge, UK
15:30	15:45	Spatial molecular profiling and tissue architecture define subtype, outcome and genetic specificity in inflammatory bowel disease <i>Francesco Cisternino, Human Technopole, Italy</i>
15:45	16:00	Endophenotype-aware colocalisation prioritises shared effector genes in fibrosis <i>Elena Bernabeu, Genomics England, United Kingdom</i>
16:00	16:45	Refreshment break and networking
16:45	17:15	Poster pitch talks for even number posters
17:15	18:15	Poster session 2 - even number posters
18:15		Bar open (card payments only)
18:15	20:15	Dinner

Wednesday 1 July 2026		
09:15	09:30	Briefing for Session 6 speakers, chair & moderator - Auditorium
09:30	11:00	Session 6: Charting cellular function at high-throughput <i>Chair: Jessica Ewald, EMBL/EBI, UK</i> <i>Moderator: Haerin Jang, Wellcome Sanger Institute, UK</i>
09:30	10:00	The role of protein mislocalization in human genetic disorders Mikko Taipale, University of Toronto, Canada
10:00	10:30	Bridging Cellular Morphology and Molecular State through Single-Cell Phenomics Bart Deplancke, École Polytechnique Fédérale de Lausanne, Switzerland
10:30	10:45	A genetic interaction map for a human cell line <i>Maximilian Billmann, University of Bonn, Germany</i>
10:45	11:00	Decoding the genetic interaction network of a multi-functional regulator through kinetics perturbations <i>Judith Notbohm, University Of Zurich, Switzerland</i>
11:00	11:30	Refreshment break and networking
11:15	11:30	Briefing for Session 7 speakers, chair & moderator - Auditorium
11:30	13:00	Session 7: Computational methods for multimodal data integration <i>Chair: Craig Glastonbury, Human Technopole, Italy</i> <i>Moderator: Haerin Jang, Wellcome Sanger Institute, UK</i>
11:30	12:00	Massively Multiplexed Multi-Modal Chemical Screens at Single-cell Resolution Romain Lopez, New York University, USA
12:00	12:30	Representation learning for cell and tissue biology: from multimodal integration to biomarkers and function Xinyi Zhang, AITHYRA Research Institute for Biomedical Artificial Intelligence, Austria
12:30	12:45	Stage-resolved multi-omic annotations from human prefrontal cortex refine psychiatric diseases heritability estimation and polygenic prediction. <i>Ang Li, University of Oxford, UK</i>
12:45	13:00	Integrating GWAS heritability and genome-scale CRISPR screens to map condition-specific T cell regulatory programs in immune-mediated diseases <i>Boris Vasilev, University Of Cambridge, UK</i>
13:00	13:10	Closing Remarks Scientific Programme Committee: Melina Claussnitzer, Broad Institute, USA Craig Glastonbury, Human Technopole, Italy Jonathan Pritchard, Stanford University, USA Gosia Trynka, Wellcome Sanger Institute/Open Targets, UK
13:10	14:00	Lunch and departures
14:00		Coach departures for Stansted and Heathrow airports
14:10		Coach departures for Cambridge train station and city centre