

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details
-------------	--------------	-------------------

Wednesday, 28 September 2022

11:30	13:00	Registration, lunch and networking
-------	-------	------------------------------------

12:30		Session 1 speakers, chair, moderator and mic runners briefing session - auditorium
-------	--	--

13:00 13:10 Welcome

Scientific Programme Committee:
[John Doench, Broad Institute, USA](#)
[Leopold Parts, Wellcome Sanger Institute, UK](#)
[Lea Starita, University of Washington, USA](#)
[Jolanda van Leeuwen, University of Lausanne, Switzerland](#)

13:10 14:40 Session 1: Emerging technologies and models

Introduction to the session
 Chair: [Lea Starita, University of Washington, USA](#)
 Moderator: [Leopold Parts, Wellcome Sanger Institute, UK](#)

13:10	13:40	Genome-scale functional genomics screens with CRISPR/Cas9 and high-speed image-enabled cell sorting Daniel Schraivogel, EMBL, Germany
-------	-------	--

13:40	14:10	Defining the regulation of the response to exposure using multiplex single-cell genomics Jose McFaline-Figueroa, Columbia University, USA
-------	-------	--

14:10	14:25	Genome scale fitness screens and 2-, 3-, and 4-way paralog synthetic lethality with just 44k clones: the enAsCas12a IN4MER 4-plex one-component knockout library Traver Hart, MD Anderson Cancer Center, USA
-------	-------	---

14:25	14:40	Bulk and single-cell loss-of-function CRISPR screening reveals mechanisms of human endocrine and beta cell in vitro differentiation Aubrey Faust, Harvard University, USA
-------	-------	--

14:40	15:25	Refreshment Break
-------	-------	-------------------

15:10		Session 2 speakers, chair, moderator and mic runners briefing session - auditorium
-------	--	--

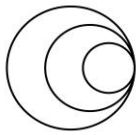
15:25 16:55 Session 2: Computational models

Introduction to the session
 Chair: [Leopold Parts, Wellcome Sanger Institute, UK](#)
 Moderator: [John Doench, Broad Institute, USA](#)

15:25	15:55	Dissecting context-dependent cancer signalling networks using CRISPR-based approaches Evangelia Petsalaki, EMBL-EBI, UK
-------	-------	--

15:55	16:10	Sensitivity to gene inhibition in cancer cells is better predicted by mRNA abundance than by gene regulatory network-inferred activity Cosmin Tudose, Systems Biology Ireland, UCD, Ireland
-------	-------	--

16:10	16:25	Mapping the protein universe with high-throughput deep learning variant effect prediction Alistair Dunham, Wellcome Sanger Institute, UK
-------	-------	---



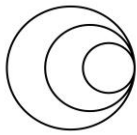
16:25	16:40	MoCHI: a package to infer mechanistic models, free energies, energetic couplings and global epistasis from deep mutational scanning data <i>Andre Faure, CRG, Spain</i>
16:40	16:55	GEARS: Predicting transcriptional outcomes of novel multi-gene perturbations <i>Yusuf Roohani, Stanford University, USA</i>

17:00 Dinner

Bar Open (card payment only)

Thursday, 29 September 2022

07:30	09:30	Breakfast
09:15		Session 3 speakers, chair, moderator and mic runners briefing session - auditorium
09:30	11:00	Session 3: Controlling transcription
		Introduction to the session <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i> <i>Moderator: Lea Starita, University of Washington, USA</i>
09:30	10:00	Systematic investigation of allelic regulatory activity of schizophrenia-associated common variants Hyejung Won, University of North Carolina, USA
10:00	10:30	Functional genomics by induced proximity Mikko Taipale, University of Toronto, Canada
10:30	10:45	Modular Vector Assembly Enables Rapid Assessment of Emerging CRISPR Technologies <i>Abby McGee, Broad Institute, USA</i>
10:45	11:00	CRISPRa-QTL identifies regulatory elements that can rescue haploinsufficient neurodevelopmental disorders <i>Florence Chardon, University of Washington, USA</i>
11:00	11:30	Refreshment Break
11:30	12:20	Lightning talks for onsite posters
		Introduction to the session <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i>
12:20	14:30	Lunch with posters
14:15		Session 4 speakers, chair, moderator and mic runners briefing session - auditorium
14:30	16:00	Session 4: Protein engineering
		Introduction to the session <i>Chair: John Doench, Broad Institute, USA</i> <i>Moderator: Leopold Parts, Wellcome Sanger Institute, UK</i>
14:30	15:00	Cellular functions of regulator proteins – or why biochemistry needs high-throughput genetic interaction screens Tina Perica, ETHZ, Switzerland
15:00	15:30	Massively Parallel Approaches to Study Membrane Protein Trafficking, Folding, and Regulation <i>Willow Coyote Maestas, University of California, San Francisco, USA</i>
15:30	15:45	Saturation Genome Editing Reveals 10% of Missense SNV Alleles in Functional Domains of PALB2 as Functionally Abnormal <i>Moez Dawood, Baylor College of Medicine, USA</i>
15:45	16:00	Systematic mutational scanning of the entire human leucine zipper interaction network <i>Alexandra Bendel, Friedrich Miescher Institute for Biomedical Research, Switzerland</i>
16:00	16:45	Refreshment Break



16:30 Session 5 speakers, chair, moderator and mic runners briefing session - auditorium

16:45 18:15 Session 5: Highly parallel readouts

Introduction to the session

Chair: Lea Starita, University of Washington, USA

Moderator: John Doench, Broad Institute, USA

16:45 17:15 Massively parallel biophysics

[Ben Lehner, CRG, Spain](#)

17:15 17:45 Saturation genome editing of DDX3X clarifies pathogenicity of germline and somatic variation

[Elizabeth Radford, Wellcome Sanger Institute, UK](#)

17:45 18:00 Genome-Wide Optical Pooled Screens Identify Regulators of Host-Pathogen Interactions

Rebecca Carlson, Broad Institute, USA

18:00 18:15 Environmental challenge induces rewiring of functional connections among human genes

Luke Gilbert, University of California, San Francisco, USA

18:15 19:15 Presentation and Drinks Reception - sponsored by Collecta, Inc. USA

19:15 Dinner

Bar Open (card payment only)

Friday, 30 September 2022

07:30 09:30 Breakfast

09:15 Session 6 Speakers, chair, moderator and mic runners briefing session - auditorium

09:30 11:00 Session 6: Precision Editing

Introduction to the session
Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland
Moderator: Leopold Parts, Wellcome Sanger Institute, UK

09:30 10:00 Molecular recording using precision genome editing
[Junhong Choi, University of Washington, USA](#)

10:00 10:30 Base editing – a next-generation genome editing technology
[Holly Rees, Beam Tx, USA](#)

10:30 10:45 Assessing missense mutation effects at scale using CRISPR-Cas9 base editors
Uyen Linh Ho, University of Lausanne, Switzerland

10:45 11:00 Dissecting the molecular repair dynamics induced by Cas9 DNA cleavage
Rhythm Phutela, CSIR IGIB, India - VIRTUAL

11:00 11:45 Refreshment Break

11:35 Session 7 Speakers, chair, moderator and mic runners briefing session - auditorium

11:45 12:45 Session 7: Functional genomics in drug discovery - panel discussion

Introduction to the session
Chair: John Doench, Broad Institute, USA
Moderator: Jolanda van Leeuwen, University of Lausanne, Switzerland

Fiona Behan, GSK, UK
Paul Diehl, Collecta, Inc. USA
Laralynne Przybyla, University of California, San Francisco, USA
Euan Stronach, GSK, UK
Ceri Wiggins, AstraZeneca, UK

12:45 13:00 Closing remarks and poster prize presentation

Scientific Programme Committee:
[John Doench, Broad Institute, USA](#)
[Leopold Parts, Wellcome Sanger Institute, UK](#)
[Lea Starita, University of Washington, USA](#)
[Jolanda van Leeuwen, University of Lausanne, Switzerland](#)

13:00 13:50 Lunch & departures

13:50 Coach departures for Stansted and Heathrow airports

14:00 Coach departures for Cambridge train station