

Hybrid Conference Programme

Monday 22 April 2024 12:00 13:00 Registration, lunch and networking 12:45 13:00 Briefing for Keynole & Session 1 speakers, microphone runners, chair, moderator & committee - Auditorum 13:00 13:15 Welcome 13:00 13:05 Welcome Connecting Science: Nagehan Ramazanogli Bahadir, Welcome Connecting Science, UK 13:05 13:15 Scientific Programme Committee: Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany Leopold Parts, Welcome Sanger Institute, UK Lea Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Lea Starita, University of Toronto, Canade 14:15 14:20 15:50 Session 1: Emerging technologies and models Chair: Leopolar break Chair: Stift Adamson, Princeton University, USA Moderator: Michael Herger – Francis Circk Institute, UK 14:20 15:50 Session 1: Emerging technologies and models Chair: Stift Adamson, Princeton University, USA Moderator: Michael Herger – Francis Circk Institute, UK 14:20 15:50 Session 1: Emerging technologies and models Chair: Stift Adamson, Princeton University, USA Moderator: Michael Herger – Francis Circk Institute, UK Saturation resistance profiling of EGFR varinants against tyrosine kinase inhibibtors us	Start (BST)	Finish (BST)	Presenter details		
 12:45 13:00 Brieling for Keynote & Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium 13:00 13:15 Welcome 13:00 13:05 Welcome Connecting Science: Nagehan Ramazanoglu Bahadir, Wolcome Connecting Science, UK 13:05 13:15 Scientific Programme Committee: Britt Adamson, Princeton University, USA Marin Kircher, Berlin Institute of Health, Germany Leopold Parts, Welcome Sanger Institute, UK Lee Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Welcome Sanger Institute, UK Moderator: Nazanin Esmaelli Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:30 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:30 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	Monday 22 April 2024				
13:00 13:15 Welcome 13:00 13:05 Welcome Connecting Science: Nagehan Ramazanoglu Bahadir, Welcome Connecting Science, UK 13:05 13:15 Scientific Programme Committee: Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany Leopold Parts, Welcome Sanger Institute, UK Lee Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaeill Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:31 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA	12:00	13:00	Registration, lunch and networking		
 13:00 13:05 Wellcome Connecting Science: Nagehan Ramazanoglu Bahadir, Wellcome Connecting Science, UK 13:05 13:15 Scientific Programme Committee: Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany Leopold Parts, Wellcome Sanger Institute, UK Lea Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randell Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	12:45	13:00	Briefing for Keynote & Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium		
 Nagehan Ramazanoglu Bahadir, Wellcome Connecting Science, UK 13:05 13:15 Scientific Programme Committee: Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany Leopold Parts, Wellcome Sanger Institute, UK Lee Starte, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaelii Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongburn Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	13:00	13:15	Welcome		
 13:05 13:15 Scientific Programme Committee: Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany Leopold Parts, Wellcome Sanger Institute, UK Lee Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaelli Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyondburn Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	13:00	13:05	•		
Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany Leopold Parts, Wellcome Sanger Institute, UK Lea Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 15:0 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA	13:05	13:15			
Leopold Parts, Wellcome Sanger Institute, UK Lea Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaelil Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 14:20 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hvongburn Henry Kim, Yonsei University, South Korea 14:50 15:20 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randell Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			•		
Lea Starita, University of Washington, USA 13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 Comfort break 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			Martin Kircher, Berlin Institute of Health, Germany		
13:15 14:15 Keynote Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 Comfort break 14:15 14:20 Comfort break 14:10 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			Leopold Parts, Wellcome Sanger Institute, UK		
 Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale <u>Brenda Andrews, University of Toronto, Canada</u> 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing <u>Hyongburn Henry Kim, Yonsei University, South Korea</u> 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq <u>Randall Platt, ETH Zurich, Switzerland</u> 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 			Lea Starita, University of Washington, USA		
 Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA Mapping genetic networks at scale Brenda Andrews, University of Toronto, Canada 14:15 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	13:15	14:15	Keynote		
 Mapping genetic networks at scale <u>Brenda Andrews, University of Toronto, Canada</u> 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 			Chair: Leopold Parts, Wellcome Sanger Institute, UK		
Brenda Andrews, University of Toronto, Canada 14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			Moderator: Nazanin Esmaeili Anvar - MD Anderson Cancer Center, USA		
14:15 14:20 Comfort break 14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			Mapping genetic networks at scale		
14:20 15:50 Session 1: Emerging technologies and models Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			Brenda Andrews, University of Toronto, Canada		
 Chair: Britt Adamson, Princeton University, USA Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing <u>Hyongbum Henry Kim, Yonsei University, South Korea</u> 15:20 15:20 Transcriptional linkage analysis with AAV-Perturb-seq <u>Randall Platt, ETH Zurich, Switzerland</u> 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	14:15	14:20	Comfort break		
 Moderator: Michael Herger – Francis Crick Institute, UK 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing <u>Hyongbum Henry Kim, Yonsei University, South Korea</u> 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq <u>Randall Platt, ETH Zurich, Switzerland</u> 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	14:20	15:50	Session 1: Emerging technologies and models		
 14:20 14:50 Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing <i>Hyongbum Henry Kim, Yonsei University, South Korea</i> 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq <i>Randall Platt, ETH Zurich, Switzerland</i> 15:20 15:35 Building a genome-wide atlas of human cell morphology <i>JT Neal, Broad Institute of MIT & Harvard, USA</i> 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators <i>Caroline Wilson, UCSF/Arc Institute, USA</i> 			Chair: Britt Adamson, Princeton University, USA		
Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA			Moderator: Michael Herger – Francis Crick Institute, UK		
Hyongbum Henry Kim, Yonsei University, South Korea 14:50 15:20 Transcriptional linkage analysis with AAV-Perturb-seq Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA	14:20	14:50	Saturation resistance profiling of EGFR variants against tyrosine kinase inhibitors using prime editing		
 Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 					
 Randall Platt, ETH Zurich, Switzerland 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	14.50	15:20	Transprintional linkage analysis with AAV Darturh and		
 15:20 15:35 Building a genome-wide atlas of human cell morphology JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA 	14.50	15.20			
JT Neal, Broad Institute of MIT & Harvard, USA 15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA					
15:35 15:50 High-throughput screening for combinatorial transcriptional modulators Caroline Wilson, UCSF/Arc Institute, USA	15:20	15:35			
Caroline Wilson, UCSF/Arc Institute, USA			JI Neal, Broad Institute of MII & Harvard, USA		
	15:35	15:50	High-throughput screening for combinatorial transcriptional modulators		
15:50 16:25 Refreshment break and networking			Caroline Wilson, UCSF/Arc Institute, USA		
	15:50	16:25	Refreshment break and networking		



16:10	16:25	Briefing for Session 2 speakers, chair & moderator - Auditorium
16:25	17:55	Session 2: Precision editing and delivery systems
		Chair: Lea Starita, University of Washington, USA Moderator: Jan Gleixner - German Cancer Research Center (DKFZ), Germany
16:25	16:55	Base editing rescue of spinal muscular atrophy in cells and in mice - VIRTUAL Mandana Arbab, Boston Children's Hospital, USA
16:55	17:25	Precision editing for gene therapy in Fanconi anemia
		Paula Rio, The Centre for Energy, Environmental and Technological Research, Spain
17:25	17:40	Cas13d effectively targets the transcriptome in a functional genomic screen
		Fernanda G. Arriaga-González, Wellcome Sanger Institute, UK
17:40	17:55	A prime editing platform for multiplexed dropout screening
		Ann Cirincione, Princeton University, USA
17:55	18:40	Poster pitch talks for odd number posters
18:40	19:40	Poster session 1 - odd number posters with drinks reception
19:40	21:40	Dinner
19:40		Bar open (card payments only)



Tuesday 23 April 2024				
09:15	09:30	Briefing for Session 3 speakers, chair & moderator - Auditorium		
09:30	11:00	Session 3: Coding & non coding variation		
		Chair: Martin Kircher, Berlin Institute of Health, Germany Moderator: Veronica Yumiceba - Universität zu Lübeck, Germany		
09:30	10:00	Decoding large regulatory landscapes – one element at a time or start from scratch? <u>Wendy Bickmore, University of Edinburgh, UK</u>		
10:00	10:30	Non-linear transcriptional responses to gradual modulation of transcription factor dosage Tuuli Lappalainen, New York Genome Center, USA/KTH Royal Institute of Technology, Sweden		
10:30	10:45	Synthetic genomic dissection of enhancer context sensitivity and synergy Matthew Maurano, NYU Institute for Systems Genetics, USA		
10:45	11:00	Evolution and function of sex chromosome regulatory regions Hannah Harris, Whitehead Institute, USA		
11:00	11:35	Refreshment break and networking		
11:20	11:35	Briefing for Session 4 speakers, chair & moderator - Auditorium		
11:35	13:10	Session 4: Gene engineering technologies		
		Chair: Lea Starita, University of Washington, USA Moderator: Florence Lichou – Sanger Institute, UK		
11:35	12:05	Species-aware DNA language models Julien Gagneur, Technical University of Munich, Germany		
12:05	12:35	Generative modeling for cellular perturbation <u>Mo Lotfollahi, Wellcome Sanger Institute, UK</u>		
12:35	12:55	Multi-locus CRISPRi targeting with a single truncated guide RNA Fadi Najm, Broad Institute, USA		
12:55	13:10	Decoding the Role of Distal Enhancers in the Regulatory Circuitry of Human Astrocytes and their Impact on Neurodegeneration: Insights from Large-Scale Single-Cell CRISPRi Screening Nicole Green, University of New South Wales, Australia		
13:10	14:30	Lunch and networking		



14:15	14:30	Briefing for Session 5 speakers, chair & moderator - Auditorium
14:30	16:00	Session 5: Genetic interactions
		Chair: Britt Adamson, Princeton University, USA
		Moderator: Anjan Venkatesh - University College Dublin, Ireland
14:30	15:00	Engineering transcriptional state with Perturb-seq
		Thomas Norman, Memorial Sloan Kettering Cancer Center, USA
15:00	15:30	CRISPR+Retrons: Precise Editing and Transcriptional Recording
		Seth Shipman, University of California, San Francisco
15:30	15:45	Global analysis of genetic suppression of partial loss-of-function alleles
		Sabine van Schie, University of Lausanne, Switzerland
15:45	16:00	Sequential genetic dependencies identified by time-resolved orthogonal gene editing
		Ronay Cetin, Goethe University Frankfurt, Germany
16:00	16:35	Refreshment break and networking
16:20	16:35	Briefing for Sponsored talk speaker, chair & moderator - Auditorium
16:35	16:50	Sponsored talk by Parse Biosciences
		Chair: Britt Adamson, Princeton University, USA
16:35	16:50	Multi-million cell CRISPR screens - the future is now with Parse Biosciences
		Mike Day, Parse Biosciences
16:50	17:35	Poster pitch talks for even number posters
17:35	18:35	Poster session 2 - even number posters with drinks reception
18:35	20:35	Dinner
18:35		Bar open (card payments only)



Wednesday 24 April 2024

09:15	09:30	Briefing for Session 6 speakers, chair & moderator - Auditorium
09:30	11:00	Session 6: Computational models and integration
		Chair: Leopold Parts, Wellcome Sanger Institute, UK Moderator: Olivier Belli – ETH Zurich, Switzerland
09:30	10:00	Inferring regulatory mechanisms from single cell CRISPR screens Britta Velten, Heidelberg University, Germany
10:00	10:30	CRISPR-based second-generation of genetic-vulnerability-maps in cancer cells Francesco Iorio, Human Technopole, Italy
10:30	10:45	Differentiable and multimodal feature selection for compressed genome-scale CRISPR screens Aidan Winters, UCSF/Arc Institute, USA
10:45	11:00	Inferring context-specific essentiality networks using large-scale CRISPR- KO screens Paula Weidemüller, EMBL-EBI, UK
11:00	11:35	Refreshment break and networking
11:20	11:35	Briefing for Panel members, chair, moderator & committee - Auditorium
11:35	12:35	Session 7: Panel Discussion - will AI ever replace experiments?
		Chair: Martin Kircher, Berlin Institute of Health, Germany
		Moderator: Leopold Parts, Wellcome Sanger Institute, UK
		Panel members: Brenda Andrews, University of Toronto, Canada
		Julien Gagneur, Technical University of Munich, Germany
		Joshua Pan, Google DeepMind, UK
		Britta Velten, Heidelberg University, Germany
12:35	12:50	Closing remarks and prize presentation
		Scientific Programme Committee:
		Britt Adamson, Princeton University, USA Martin Kircher, Berlin Institute of Health, Germany
		Leopold Parts, Wellcome Sanger Institute, UK
		Lea Starita, University of Washington, USA
12:50	13:50	Lunch and departures
13:50		Coach departures for Stansted and Heathrow airports
14:00		Coach departures for Cambridge train station and city centre