

CRISPR and Beyond: Perturbations at Scale to Understand Genomes

22-25 September 2020

Virtual Conference Agenda

Tuesday, 22 September		
13:00	13:05	Welcome <i>Scientific Programme Committee:</i> <i>John Doench, Broad Institute, USA</i> <i>Leopold Parts, Wellcome Sanger Institute, UK</i> <i>Lea Starita, University of Washington, USA</i> <i>Jolanda van Leeuwen, University of Lausanne, Switzerland</i>
13:05	14:35	Session 1: Links to Disease Introduction to the session <i>Chair: Leopold Parts, Wellcome Sanger Institute, UK</i> 13:05 13:25 Genome-wide characterisation of BRCA I functioning in DNA damage repair <i>Sylvie Noordermeer, Leiden University Medical Centre, Netherlands</i> 13:25 13:45 Using Stem Cells to Explore the Genetics Underlying Neuropsychiatric Disease <i>Kristen Brennand, Icahn School of Medicine at Mount Sinai, USA</i> 13:45 13:55 Whole genome CRISPR screen for entry of extracellular tau in human neurons <i>Lewis Evans, UCL Great Ormond Street, ICH, UK</i> 13:55 14:05 Transforming diagnostic confidence in developmental disorders using CRISPR-based saturation genome editing <i>Hong Kee Tan, Wellcome Sanger Institute, UK</i> 14:05 14:35 Q&A <i>Chair: Leopold Parts, Wellcome Sanger Institute, UK</i> <i>Moderator: Lea Starita, University of Washington, USA</i>
14:35	14:55	Break
14:55	16:25	Session 2: Coding Variation Introduction to the session <i>Chair: John Doench, Broad Institute, USA</i> 14:55 15:15 High throughput human genetics in yeast <i>Maitreya Dunham, University of Washington, USA</i> 15:15 15:35 Understanding the functional effects of coding variation, at scale <i>Lea Starita, University of Washington, USA</i> 15:35 15:45 Massively parallel assessment of human variants with base editor screens <i>Ruth Hanna, Broad Institute, USA</i> 15:45 15:55 Large-scale phenotypic characterization of genetic variants of the DNA damage response using CRISPR-dependent base editing <i>Alberto Ciccia, Columbia University, USA</i> 15:55 16:25 Q&A <i>Chair: John Doench, Broad Institute, USA</i> <i>Moderator: Leopold Parts, Wellcome Sanger Institute, UK</i>
16:25	16:45	Break
16:45	17:25	Poster lightning talks
17:25	18:25	Poster session

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Wednesday, 23 September

13:00 14:30 Session 3: Genetic Screens		
Introduction to the session <i>Chair: Sylvie Noordermeer, Leuden University, Netherlands</i>		
13:00	13:20	CRISPR screening for cancer drug discovery <i>Mathew Garnett, Wellcome Sanger Institute, UK</i>
13:20	13:40	Optimisation and meta-analysis of genome-scale signals <i>Kenneth Baille, University of Edinburgh, UK</i>
13:40	13:50	Major functional bias in genome-wide CRISPR screens for mitochondrial complexes <i>Maximilian Billmann, University of Minnesota, USA</i>
13:50	14:00	Temporal analysis of time-series CRISPR screen data using mixed linear models. <i>Lorena Sofia Lopez Zepeda, Berlin Institute of Medical Systems Biology, Germany</i>
14:00	14:30	Q&A <i>Chair: Jolanda van Leeuwen, University of Lausaane, Switzerland</i> <i>Moderator: Sylvie Noordermeer, Leuden University, Netherlands</i>
14:30 14:50 Break		
14:50 16:20 Session 4: Rewriting DNA		
Introduction to the session <i>Chair: Tom Ellis, Imperial College London, UK</i>		
14:50	15:10	Gene editing and high-throughput functional genomics <i>Wensheng Wei, Peking University, China</i>
15:10	15:30	Recording cellular and molecular events in DNA <i>Nozomu Yachie, University of British Columbia, Canada</i>
15:30	15:40	Pooled protein tagging, cellular imaging and in situ sequencing for monitoring drug action in real time <i>Andreas Reicher, CeMM Research Center for Molecular Medicine, Austria</i>
15:40	15:50	Characterization of synthetic single guide RNAs for CRISPR/Cas9 genome editing – An extensive evaluation of gRNA formats, purity, and delivery methods <i>Garrett Rettig, Integrated DNA Technologies, USA</i>
15:50	16:20	Q&A <i>Chair: Lea Staria, University of Washington, USA</i> <i>Moderator: Tom Ellis, Imperial College London, UK</i>
16:20 16:40 Break		
16:40	17:15	Poster lightning talks
17:15	18:15	Poster session

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Thursday, 24 September

13:00	14:10	Session 5: Genetic Interactions
Introduction to the session <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i>		
13:00	13:20	Engagement of DNA repair pathways in the repair of CRISPR-Cas-induced breaks <i>Joanna Louzou, Research Centre for Molecular Medicine, Austria</i>
13:20	13:30	Comprehensive prediction of synthetic lethality between paralog pairs in cancer cell lines Barbara De Kegel, University College Dublin, Ireland
13:30	13:40	Understanding Chemical-Genetic Interactions <i>Loan Vulliard, CeMM Research Center for Molecular Biology, Austria</i>
13:40	14:10	Q&A <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i> <i>Moderator: John Doench, Broad Institute, USA</i>
14:10	14:30	Break

14:30	16:00	Session 6: Single Cell + Perturbation
Introduction to the session <i>Chair: Shondra Pruett-Miller, St Jude Children's Research Hospital, USA</i>		
14:30	14:50	Biochemistry at single-cell resolution: a new approach to understand functional heterogeneity <i>Jay Hesselberth, University of Colorado School of Medicine, USA</i>
14:50	15:10	Human tissues & Cellular Phenotypes <i>Sarah Teichman, Wellcome Sanger Institute, UK</i>
15:10	15:20	Relating thousands of variants to function with massively parallel pooled genetic screens <i>Kathryn Geiger Schuller, Broad Institute of MIT and Harvard, USA</i>
15:20	15:30	Towards genome-scale CROP-seq screens <i>Tilmann Buerckstuemmer, Aelian Biotechnology GmbH, Austria</i>
15:30	16:00	Q&A <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i> <i>Moderator: Shondra Pruett-Miller, St Jude Children's Research Hospital, USA</i>
16:00	16:20	Break
16:20	17:00	Poster lightning talks
17:00	18:00	Poster session

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Friday, 25 September

13:00		14:40		Session 7: Technology
				Introduction to the session <i>Chair: Mathew Garnett, Wellcome Sanger Institute, UK</i>
13:00	13:20	Tricks of the Trade: Functionalizing Genome Editing for a Broad Range of Cellular Targets <i>Shondra Pruett-Miller, St Jude Children's Research Hospital, USA</i>		
13:20	13:40	Exploring the flexibility of a eukaryotic genome using synthetic yeast <i>Tom Ellis, Imperial College London, UK</i>		
13:40	13:50	Massively parallel kinetic profiling of natural and engineered CRISPR nucleases <i>Stephen Jones, University of Texas at Austin, USA</i>		
13:50	14:00	A benchtop platform for generating highly multiplexed variant libraries <i>Deanna Church, Inscripta, Inc. USA</i>		
14:00	14:10	Discovery and characterization of transcriptional effectors with high-throughput protein domain screens in human cells <i>Josh Tycko, Bassik Lab, USA</i>		
14:10	14:40	Q&A <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i> <i>Moderator: John Doench, Broad Institute, USA</i>		
14:40	15:00	Break		

15:00		16:10		Session 8: Non-coding Variation
				Introduction to the session <i>Chair: Leopold Parts, Wellcome Sanger Institute, UK</i>
15:00	15:20	CRISPR, cancer and long noncoding RNAs <i>Rory Johnson, University College Dublin, Ireland</i>		
15:20	15:30	Systematic characterisation of functional circular RNAs <i>Matt Neve, Monash University, Australia</i>		
15:30	15:40	High-throughput screening of engineered microRNA target sites enables precise control of gene expression patterns in mammalian cells <i>Yale Michaels, University of British Columbia, Canada</i>		
15:40	16:10	Q&A <i>Chair: Jolanda van Leeuwen, University of Lausanne, Switzerland</i> <i>Moderator: Shondra Pruett-Miller, St Jude Children's Research Hospital, USA</i>		

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16:10 16:20 Closing remarks

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