

Virtual Conference Agenda

Start (BST)	Finish (BST)	Presenter details
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Wednesday, 04 May 2022

13:00	13:15	Welcome
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Scientific Programme Committee:

[*Mark McCarthy, Genentech, USA*](#)

[*Gitte Neubauer, GSK, Germany*](#)

[*Oliver Stegle, German Cancer Research Center \(DKFZ\), Germany*](#)

[*Gosia Trynka, Open Targets, UK*](#)

13:15	14:45	Session 1: Genetics at scale
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Introduction to the session

Chair: Mark McCarthy, Genentech, USA

13:15	13:35	Translational genomics of osteoarthritis <i>Eleftheria Zeggini, Helmholtz Zentrum Munich, Germany</i>
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13:35	13:55	Human genetics to predict adverse outcomes in clinical trials <i>Robert Plenge, Bristol Myers Squibb, USA</i>
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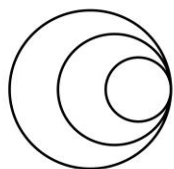
13:55	14:05	Prioritising new drug candidates using allelic series <i>Luca Stefanucci, Wellcome Sanger Institute, UK</i>
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14:05	14:15	Mapping the functional impact of immune disease associated variants through single-cell CRISPR screens in primary T cells <i>Radu Rapiteanu, GSK, UK</i>
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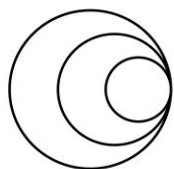
14:15	14:45	Q&A <i>Chair: Mark McCarthy, Genentech, USA</i> <i>Moderator: Oliver Stegle, German Cancer Research Center (DKFZ), Germany</i>
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14:45	15:05	Spatial Networking
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15:05	15:15	Break
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15:15	16:45	Session 2: Disease at scale
		Introduction to the session <i>Chair: Oliver Stegle, German Cancer Research Center (DKFZ), Germany</i>
15:15	15:35	Somatic mutations in diseased tissues can yield insights into disease biology and aid generation of therapeutic hypotheses <i>Carl Anderson, Wellcome Sanger Institute, UK</i>
15:35	15:55	Role of cohort diversity in the discovery, fine-mapping, and risk prediction of lipid traits from GWAS meta-analysis <i>Cristen Willer, University of Michigan Medical School, USA</i>
15:55	16:05	Applying genetic feature engineering on blood cell traits to investigate the differential genetic architecture of immune-mediated diseases <i>Guillermo Reales, University of Cambridge, UK</i>
16:05	16:15	Multi-omics profiling of collagen-induced arthritis mouse model reveals early metabolic dysregulation via SIRT1 axis <i>Lingzi Li, Sanofi-Aventis Deutschland GmbH, Germany</i>
16:15	16:45	Q&A <i>Chair: Oliver Stegle, German Cancer Research Center (DKFZ), Germany</i> <i>Moderator: Gosia Trynka, Open Targets, UK</i>
16:45	17:15	Spatial Networking
17:05	17:15	Break
17:15	18:00	Keynote Speaker
		Introduction to the session <i>Chair: Gosia Trynka, Open Targets, UK</i>
17:15	17:45	Cell, Tissue and Perturbation Genomics as Roadmaps for Target Discovery and Validation <i>Aviv Regev, Genentech, USA</i>
17:45	18:00	Q&A <i>Chair: Gosia Trynka, Open Targets, UK</i> <i>Moderator: Mark McCarthy, Genentech, USA</i>
18:00	18:30	Spatial Networking



Thursday, 05 May 2022

13:00 14:30 **Session 3: Understanding and validation of target function**

Introduction to the session

Chair: Gosia Trynka, Open Targets, UK

13:00 13:20 The drug-induced phenotypic landscape of patient-derived colorectal cancer organoids
[Michael Boutros, Germany Cancer Research Center, Germany](#)

13:20 13:40 Learnings on high throughput target validation in primary T cells
[Klio Maratou, GlaxoSmithKline, UK](#)

13:40 13:50 Multi-ancestry meta-analysis of genome-wide association studies of lung function implicates novel putative causal genes and biological pathways for COPD
Abril Izquierdo, University of Leicester, UK

13:50 14:00 Cellular genome-wide association study identifies common genetic variation influencing lithium induced neural progenitor proliferation
Brandon Le, University of North Carolina at Chapel Hill, USA

14:00 14:30 Q&A
Chair: Gosia Trynka, Open Targets, UK
Moderator: Gitte Neubauer, GSK, Germany

14:30 14:50 Spatial Networking

14:50 15:00 Break

15:00 16:30 **Poster Session**

15:00 15:45 Poster session lightning talks

15:45 16:30 Poster session

16:30 16:40 Break

16:40 18:10 **Session 4: Understanding and validation of drug function**

Introduction to the session

Chair: Gitte Neubauer, GSK, Germany

16:40 17:00 Informatics approaches for drug target safety assessment
[James Sidaway, Apconix, UK](#)

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| 17:00 | 17:20 | Beyond target-disease association: using Open Targets in safety, tractability and therapeutic hypothesis assessment
<i>Ellen McDonagh, EMBL-EBI, UK</i> |
| 17:20 | 17:30 | Interplay between longitudinally-measured gene expression and metabolite levels in whole blood in the MultiMuTHER study
<i>Kerrin Small, Kings College London, UK</i> |
| 17:30 | 17:40 | Computational pharmacogenomics identifies synergistic drug combinations targeting the mevalonate pathway for breast cancer therapy
<i>Deena Gendoo, University of Birmingham, UK</i> |
| 17:40 | 18:10 | Q&A
<i>Chair: Gilte Neubauer, GSK, Germany</i>
<i>Moderator: Gosia Trynka, Open Targets, UK</i> |
| 18:10 | 18:40 | Spatial Networking |

Friday, 06 May 2022

13:00 14:30 Session 5: Clinical trials - translation in the clinic

Introduction to the session

Chair: Oliver Stegle, German Cancer Research Center (DKFZ), Germany

13:00 13:20 Implementing a genetics-first strategy in clinical development for rare brain diseases

[Adele Mitchell, Biogen, USA](#)

13:20 13:40 Bridging the gap between the genome and clinical phenotypes

[Kari Stefansson, deCODE genetics, Iceland](#)

13:40 13:50 Why Clinical Trials Stop: The role of Genetics

Olesya Razuvayevskaya, EMBL-EBI, UK

13:50 14:00 Prioritization of Covalent Antimicrobial Drug Targets by CRISPR-based Oligo Recombineering

Matthew Child, Imperial College London, UK

14:00 14:30 Q&A

Chair: Oliver Stegle, German Cancer Research Center (DKFZ), Germany

Moderator: Mark McCarthy, Genentech, USA

14:30 14:50 Spatial Networking

14:50 15:00 Break

15:00 16:30 Session 6: Emerging technologies for drug discovery

Introduction to the session

Chair: Gitte Neubauer, GSK, Germany

15:00 15:20 Machine learning on high-content phenotypes for target discovery and validation

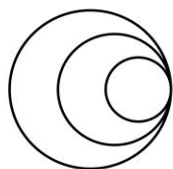
[Daphne Koller, Insitro, USA](#)

15:20 15:40 CROP-seq and scifi-RNA-seq: Single-cell CRISPR sequencing at scale

[Christoph Bock, CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria](#)

15:40 15:50 Systematic targeting and inhibiting of noncoding GWAS loci with single-cell sequencing

John Morris, New York Genome Center, USA



15:50 16:00 Mantis-ML v2: Identifying novel disease genes combining knowledge graphs with engineered structured features via Graph Convolutional Networks
Dimitrios Vitsios, AstraZeneca, UK

16:00 16:30 Q&A
Chair: Gitte Neubauer, GSK, Germany
Moderator: Mark McCarthy, Genentech, USA

16:30 16:50 Spatial Networking

16:50 17:00 Break

17:00 17:30 Closing remarks

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