## Virtual Conference Agenda

### Wednesday, 04 May 2022

<table>
<thead>
<tr>
<th>Start (BST)</th>
<th>Finish (BST)</th>
<th>Presenter details</th>
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<tbody>
<tr>
<td>13:00</td>
<td>13:15</td>
<td>Welcome</td>
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<td><strong>Scientific Programme Committee:</strong></td>
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<td></td>
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<td>Mark McCarthy, Genentech, USA</td>
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<td>Gitte Neubauer, GSK, Germany</td>
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<td>Oliver Stegle, German Cancer Research Center (DKFZ), Germany</td>
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<td>Gosia Trynka, Open Targets, UK</td>
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<tr>
<td>13:15</td>
<td>14:45</td>
<td><strong>Session 1: Genetics at scale</strong></td>
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<td>13:15</td>
<td>13:35</td>
<td>Translational genomics of osteoarthritis</td>
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<td>Eleftheria Zeggini, Helmholtz Zentrum Munich, Germany</td>
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<tr>
<td>13:35</td>
<td>13:55</td>
<td>Human genetics to predict adverse outcomes in clinical trials</td>
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<td></td>
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<td>Robert Plenge, Bristol Myers Squibb, USA</td>
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<tr>
<td>13:55</td>
<td>14:05</td>
<td>Prioritising new drug candidates using allelic series</td>
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<td></td>
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<td>Luca Stefanucci, Wellcome Sanger Institute, UK</td>
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<td>14:05</td>
<td>14:15</td>
<td>Mapping the functional impact of immune disease associated variants through single-cell CRISPR screens in primary T cells</td>
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<td>Radu Rapiteanu, GSK, UK</td>
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<td>14:15</td>
<td>14:45</td>
<td>Q&amp;A</td>
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<td>Chair: Mark McCarthy, Genentech, USA</td>
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<td>Moderator: Oliver Stegle, German Cancer Research Center (DKFZ), Germany</td>
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<tr>
<td>14:45</td>
<td>15:05</td>
<td>Spatial Networking</td>
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<tr>
<td>15:05</td>
<td>15:15</td>
<td>Break</td>
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<tr>
<td>Time</td>
<td>Session 2: Disease at scale</td>
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<tr>
<td>15:15</td>
<td>Introduction to the session</td>
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<td>Chair: Oliver Stegle, German Cancer Research Center (DKFZ), Germany</td>
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<tr>
<td>15:15</td>
<td>Somatic mutations in diseased tissues can yield insights into disease biology and aid generation of therapeutic hypotheses</td>
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<td>Carl Anderson, Wellcome Sanger Institute, UK</td>
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<td>15:35</td>
<td>Role of cohort diversity in the discovery, fine-mapping, and risk prediction of lipid traits from GWAS meta-analysis</td>
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<td>Cristen Willer, University of Michigan Medical School, USA</td>
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<td>15:55</td>
<td>Applying genetic feature engineering on blood cell traits to investigate the differential genetic architecture of immune-mediated diseases</td>
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<td>Guillermo Reales, University of Cambridge, UK</td>
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<td>16:05</td>
<td>Multi-omics profiling of collagen-induced arthritis mouse model reveals early metabolic dysregulation via SIRT1 axis</td>
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<td>Lingzi Li, Sanofi-Aventis Deutschland GmbH, Germany</td>
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<td>16:15</td>
<td>Q&amp;A</td>
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<td>Moderator: Gosia Trynka, Open Targets, UK</td>
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<td>16:45</td>
<td>Spatial Networking</td>
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<thead>
<tr>
<th>Time</th>
<th>Keynote Speaker</th>
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<tr>
<td>17:15</td>
<td>Introduction to the session</td>
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<tr>
<td></td>
<td>Chair: Gosia Trynka, Open Targets, UK</td>
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<tr>
<td>17:15</td>
<td>Cell, Tissue and Perturbation Genomics as Roadmaps for Target Discovery and Validation</td>
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<td>Aviv Regev, Genentech, USA</td>
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<td>17:45</td>
<td>Q&amp;A</td>
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<td>Moderator: Mark McCarthy, Genentech, USA</td>
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<td>18:00</td>
<td>Spatial Networking</td>
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## Thursday, 05 May 2022

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<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Topic</th>
<th>Speaker</th>
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<tr>
<td>13:00</td>
<td>Introduction to the session</td>
<td>Chair: Gosia Trynka, Open Targets, UK</td>
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<tr>
<td>13:00</td>
<td>13:20</td>
<td>The drug-induced phenotypic landscape of patient-derived colorectal cancer organoids</td>
<td>Michael Boutros, Germany Cancer Research Center, Germany</td>
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<td>13:20</td>
<td>13:40</td>
<td>Learnings on high throughput target validation in primary T cells</td>
<td>Klio Maratou, GlaxoSmithKline, UK</td>
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<td>13:40</td>
<td>13:50</td>
<td>Multi-ancestry meta-analysis of genome-wide association studies of lung function implicates novel putative causal genes and biological pathways for COPD</td>
<td>Abril Izquierdo, University of Leicester, UK</td>
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<td>13:50</td>
<td>14:00</td>
<td>Cellular genome-wide association study identifies common genetic variation influencing lithium induced neural progenitor proliferation</td>
<td>Brandon Le, University of North Carolina at Chapel Hill, USA</td>
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<td>14:00</td>
<td>14:30</td>
<td>Q&amp;A</td>
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<td>Moderator: Gitte Neubauer, GSK, Germany</td>
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<td>14:30</td>
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<td>14:50</td>
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<td>Break</td>
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<td>15:00</td>
<td>16:30</td>
<td>Poster Session</td>
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<td>15:00</td>
<td>15:45</td>
<td>Poster session lightning talks</td>
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<td>16:30</td>
<td>Poster session</td>
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<td>16:30</td>
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<td>Break</td>
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<tr>
<td>16:40</td>
<td>18:10</td>
<td>Session 4: Understanding and validation of drug function</td>
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<td>16:40</td>
<td>17:00</td>
<td>Informatics approaches for drug target safety assessment</td>
<td>James Sidaway, Apconix, UK</td>
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<td>Time</td>
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| 17:00 | Beyond target-disease association: using Open Targets in safety, tractability and therapeutic hypothesis assessment  
       | Ellen McDonagh, EMBL-EBI, UK                                             |
| 17:20 | Interplay between longitudinally-measured gene expression and metabolite levels in whole blood in the MultiMuTHER study  
       | Kerrin Small, Kings College London, UK                                   |
| 17:30 | Computational pharmacogenomics identifies synergistic drug combinations targeting the mevalonate pathway for breast cancer therapy  
       | Deena Gendoo, University of Birmingham, UK                              |
| 17:40 | Q&A                                                                      
       | Chair: Gitte Neubauer, GSK, Germany  
       | Moderator: Gosia Trynka, Open Targets, UK                              |
| 18:10 | Q&A                                                                      
       | Chair: Gitte Neubauer, GSK, Germany  
       | Moderator: Gosia Trynka, Open Targets, UK                              |
| 18:10 | Spatial Networking                                                       |
### Session 5: Clinical trials - translation in the clinic

**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

### Session 6: Emerging technologies for drug discovery

**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
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<tr>
<td>15:50</td>
<td>Mantis-ML v2: Identifying novel disease genes combining knowledge graphs with engineered structured features via Graph Convolutional Networks (Dimitrios Vitsios, AstraZeneca, UK)</td>
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<td>16:00</td>
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<td>Break</td>
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<tr>
<td>17:00</td>
<td>Closing remarks</td>
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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