

**Hybrid Conference Programme**

Start (BST)	Finish (BST)	Presenter details
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**Monday 23 June 2025**

10:00	11:00	Registration, refreshments and networking
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10:45	Briefing for Advisory Board, Session 1 speakers, microphone runners, chair, moderator - Auditorium	
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11:00	11:10	Welcome
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**Wellcome Connecting Science:**

*Nagehan Ramazanoglu Bahadır, Wellcome Connecting Science, UK*

**Advisory Board**

[Žiga Avsec, Google DeepMind, UK](#)

[Noelia Ferruz, Centre for Genomic Regulation, Spain](#)

[Patrick Hsu, University of California, Berkeley, USA](#)

[Ben Lehner, Wellcome Sanger Institute, UK](#)

[Mo Lotfollahi, Wellcome Sanger Institute, UK](#)

[Debra Marks, Harvard University, USA](#)

[Tingying Peng, Helmholtz Munich, Germany](#)

[Jussi Taipale, Karolinska Institutet, Sweden | University of Helsinki, Finland | Wellcome Sanger Institute, UK](#)

[Caroline Uhler, Massachusetts Institute of Technology \(MIT\), USA](#)

11:10	12:40	Session 1: Modelling, designing and engineering DNA and RNA I
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*Chair: Žiga Avsec, Google DeepMind, UK*

*Moderator: Smita Krishnaswamy, Yale University, USA*

11:10	11:40	Leveraging AI to reveal and leverage the mRNA code <a href="#">Hani Goodarzi, Arc Institute, USA</a>
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11:40	12:10	Interpreting and designing regulatory DNA with deep learning <a href="#">Peter Koo, Cold Spring Harbor Laboratory, USA</a>
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12:10	12:25	Testing genome models out of distribution: predicting the behaviour of an evolutionary distant chromosome grafted into human cells <i>Leopold Parts, Wellcome Sanger Institute, UK</i>
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12:25	12:40	A Genomic Language Model for Zero-Shot Prediction of Promoter Variant Effects <i>Courtney Shearer, Harvard University, USA</i>
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12:40	14:00	Lunch and networking
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13:45	Briefing for Session 2 speakers, chair & moderator - Auditorium	
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14:00	15:15	Session 2: Modelling, designing and engineering DNA and RNA II
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*Chair: Ben Lehner, Wellcome Sanger Institute, UK*

*Moderator: Tingying Peng, Helmholtz Munich, Germany*

14:00	14:30	A unifying multimodal masked modeling framework for functional genomics <a href="#">Gökçen Eraslan, Genentech, USA [virtual]</a>
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14:30	14:45	Assessment and Prediction of Gene Expression in Mammalian Cells <i>Josh Mayne, Imperial College London and University College London, UK</i>
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14:45	15:00	Inferring modes of gene regulation from time-resolved single-cell transcriptomics with mechanistic machine learning <i>Dimitris Volterras, Francis Crick Institute, UK</i>
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15:00	15:15	Nuclear targeting sequences <i>Dogancan Ozturan, University Of British Columbia, Canada</i>
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15:15	16:00	Refreshment break and networking
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15:45	Briefing for Session 3 speakers, chair & moderator - Auditorium	
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<b>16:00</b>	<b>17:30</b>	<b>Session 3: Designing Precision Molecules and Therapeutics</b>
		<i>Chair: Debora Marks, Harvard University, USA</i> <i>Moderator: Mo Lotfollahi, Wellcome Sanger Institute, UK</i>
16:00	16:30	Biological data in the age of AI <a href="#">Michael Bronstein, University of Oxford, UK   Vienna Biocenter, Austria</a>
16:30	17:00	Title <a href="#">Charlotte Deane, University of Oxford, UK [virtual]</a>
17:00	17:15	Programmable Proteome Editing with Language Model-Derived Peptide Guides <i>Lauren Hong, Duke University, USA</i>
17:15	17:30	Open Targets: AI x Genetics for Drug Target Identification & Prioritisation <i>David Hulcoop, EMBL-EBI, UK</i>
<b>17:30</b>	<b>18:15</b>	<b>Poster pitch talks for odd number posters</b>
<b>18:15</b>	<b>19:30</b>	<b>Poster session 1 - odd number posters</b>
19:30		Dinner
19:30		Bar open (card payments only)

**Tuesday 24 June 2025**

09:00	<i>Briefing for Session 4 speakers, chair &amp; moderator - Auditorium</i>	
<b>09:15</b>	<b>11:00</b>	<b>Session 4: Modelling, designing and engineering proteins I</b> <i>Chair: Noelia Ferruz, Centre for Genomic Regulation, Spain</i> <i>Moderator: Žiga Avsec, Google DeepMind, UK</i>
09:15	09:45	Multimodal Representations for Contextual Biomolecular Analysis <a href="#">Smita Krishnaswamy, Yale University, USA</a>
09:45	10:15	Leveraging Evolutionary-Scale Enzymology to Map and Predict Catalytic Landscapes <a href="#">Marqaux Pinney, University of California, San Francisco (UCSF), USA</a>
10:15	10:45	Scaling Foundation Models for Protein Generation <a href="#">Ali Madani, Proficient, USA</a>
10:45	11:00	OpenFold3: an open-source biomolecular structure prediction model <i>Vinay Swamy, Columbia University, USA</i>
11:00	11:35	Refreshment break and networking
11:20	<i>Briefing for Session 5 speakers, chair &amp; moderator - Auditorium</i>	
<b>11:35</b>	<b>12:50</b>	<b>Session 5: Modelling, designing and engineering proteins II</b> <i>Chair: Tingying Peng, Helmholtz Munich, Germany</i> <i>Moderator: Ben Lehner, Wellcome Sanger Institute, UK</i>
11:35	12:05	Microfluidics for high-throughput and quantitative biophysics and biochemistry <a href="#">Poly Fordyce, Stanford University, USA</a>
12:05	12:20	Automated ML-guided lead optimization: surpassing human-level performance at protein engineering <i>Patrick Kidger, Cradle, Switzerland</i>
12:20	12:35	The Open Datasets Initiative and Protein Engineering Tournament — Scaling Open Science for Protein Function Prediction <i>Kasia Barranowski, The Align Foundation, USA</i>
12:35	12:50	Evaluating the sensitivity of genomic foundation models to interindividual variation using biobank-scale personalized genomes <i>Brian Schilder, Cold Spring Harbor Laboratory, USA</i>
12:50	14:10	Lunch and networking
13:55	<i>Briefing for Session 6 speakers, chair &amp; moderator - Auditorium</i>	
<b>14:10</b>	<b>16:10</b>	<b>Session 6: Modelling, designing and engineering cells</b> <i>Chair: Jussi Taipale, Karolinska Institutet, Sweden   University of Helsinki, Finland   Wellcome Sanger Institute, UK</i> <i>Moderator: Debora Marks, Harvard University, USA</i>
14:10	14:40	Reprogramming the Genetic Code <a href="#">Jason Chin, Medical Research Council Laboratory of Molecular Biology (MRC-LMB), UK [not livestreamed]</a>
14:40	15:10	How to build an AI-driven Digital Organism through multiscale foundation models <a href="#">Eric Xing, Mohamed bin Zayed University of Artificial Intelligence, UAE   Carnegie Mellon University, USA   GenBio AI, UAE</a>
15:10	15:25	Iterative SCRaMble for Engineering Synthetic Genome Modules and Chromosomes <i>Xinyu Lu, Imperial College London, UK</i>
15:25	15:40	CellFlow enables generative single-cell phenotype modeling with flow matching <i>Dominik Klein, Helmholtz Munich, Germany</i>
15:40	16:10	Designing Life <a href="#">Craig Venter, J. Craig Venter Institute, USA [virtual]</a>
16:10	16:50	Refreshment break and networking
<b>16:50</b>	<b>17:35</b>	<b>Poster pitch talks for even number posters</b> <i>Chair: Jussi Taipale, Karolinska Institutet, Sweden   University of Helsinki, Finland   Wellcome Sanger Institute, UK</i>
<b>17:35</b>	<b>18:50</b>	<b>Poster session 2 - even number posters</b>
18:50	Dinner	
18:50	Bar open (card payments only)	

**Wednesday 25 June 2025**

09:00		<i>Briefing for Session 7 speakers, chair &amp; moderator - Auditorium</i>
<b>09:15</b>	<b>10:30</b>	<b>Session 7: Imaging and Pathology- Clinical Foundation Models</b> <i>Chair: Mo Lotfollahi, Wellcome Sanger Institute, UK</i> <i>Moderator: Jussi Taipale, Karolinska Institutet, Sweden   University of Helsinki, Finland   Wellcome Sanger Institute, UK</i>
09:15	09:45	Multimodal, Generative, and Agentic AI for Pathology <a href="#">Faisal Mahmood, Harvard University, USA</a>
09:45	10:15	Title <a href="#">Tingying Peng, Helmholtz Munich, Germany</a>
10:15	10:30	BioX-CPath: Biologically-driven Explainable Diagnostics for Multistain IHC Computational Pathology <i>Amaya Gallagher-Syed, Queen Mary University of London, UK</i>
10:30	11:15	Refreshment break and networking
11:00		<i>Briefing for session 8 speakers, chair, moderator &amp; committee - Auditorium</i>
<b>11:15</b>	<b>12:30</b>	<b>Session 8: Spatial omics and multi-omics I</b> <i>Chair: Marianna Rapsomaniki, University of Lausanne, Switzerland</i> <i>Moderator: Ben Lehner, Wellcome Sanger Institute, UK</i>
11:15	11:45	Generative AI for Unlocking the Complexity of Cells <a href="#">Maria Brbic, École Polytechnique Fédérale de Lausanne (EPFL), Switzerland</a>
11:45	12:00	Estimation of single-cell and tissue perturbation effect in spatial transcriptomics via Spatial Causal Disentanglement <i>Stathis Megas, University Of Cambridge, UK</i>
12:00	12:15	Deep Archetypal Analysis for Interpretable Multi-Omic Data Integration <i>Salvatore Milite, Fondazione Human Technopole, Italy</i>
12:15	12:30	Mapping and reprogramming microenvironment-induced cell states in human disease using generative AI <i>Marta R Sallase, Wellcome Sanger Institute, UK</i>
12:30	14:00	Lunch and networking
13:45		<i>Briefing for Session 9 speakers, chair &amp; moderator - Auditorium</i>
<b>14:00</b>	<b>15:45</b>	<b>Session 9: Spatial omics and multi-omics II</b> <i>Chair: Mo Lotfollahi, Wellcome Sanger Institute, UK</i> <i>Moderator: Tingying Peng, Helmholtz Munich, Germany</i>
14:00	14:30	Virtual Cells and Digital Twins: AI in Personalized Oncology <a href="#">Charlotte Bunne, École Polytechnique Fédérale de Lausanne (EPFL), Switzerland</a>
14:30	14:45	Predicting RNA-seq coverage from DNA in <i>S. Cerevisiae</i> <i>Timon Schneider, Imperial College London, UK</i>
14:45	15:15	Virtual Stains, Real Illusions: accelerating histopathology with virtually multiplexed staining <a href="#">Marianna Rapsomaniki, University of Lausanne, Switzerland</a>
15:15	15:45	Leveraging AI-driven sequence models for decoding cellular plasticity <a href="#">Oliver Stegle, German Cancer Research Center (DKFZ), Germany</a>

15:45 16:00 Closing remarks and prize presentation

**Advisory Board**

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[Caroline Uhler, Massachusetts Institute of Technology \(MIT\), USA](#)

16:00 16:45 Refreshments and departures

16:45 Coach departures for Stansted and Heathrow airports

17:00 Coach departures for Cambridge train station and city centre