

**Hybrid Conference Programme**

Start (BST)	Finish (BST)	Presenter details	Location
<b>Monday 8 June 2026</b>			
09:00	10:00	<b>Registration, arrival refreshments and networking</b>	<i>Event space</i>
09:45		<i>Briefing for keynote speaker, microphone runners, chair, moderator and committee</i>	<i>Auditorium</i>
10:00	10:25	<b>Welcome and introductions</b>	<i>Auditorium</i>
		<p><b>Wellcome Connecting Science</b> Michelle Bishop, Associate Director, Learning and Training</p> <p><b>Wellcome Genome Campus Science and Tech Advisory Group</b> Nicole Mather, Chair, Wellcome Genome Campus Science and Tech Advisory Group, United Kingdom</p> <p><b>Scientific programme committee:</b>  <a href="#">Ben Lehner, Wellcome Sanger Institute, United Kingdom</a>  <a href="#">Mo Lotfollahi, Wellcome Sanger Institute, United Kingdom</a>  <a href="#">Debora Marks, Harvard University, United States</a>  <a href="#">Noelia Ferruz, Centre for Genomic Regulation, Spain</a>  <a href="#">Jussi Taipale, Wellcome Sanger Institute / Karolinska Institute, United Kingdom / Sweden</a>  <a href="#">Jun Cheng, Google DeepMind, United Kingdom</a></p>	
10:25	11:15	<b>Opening keynote</b>	<i>Auditorium</i>
		<p><i>Chair: Noelia Ferruz</i> <i>Moderator: Jun Cheng</i></p>	
10:25	11:15	Leveraging AI to advance biology <a href="#">Pushmeet Kohli, Google DeepMind, United Kingdom</a>	
11:15	11:45	Coffee break and networking	<i>Event Space</i>
11:30	11:45	<i>Briefing for Session 1 speakers, chair and moderator</i>	<i>Auditorium</i>
11:45	13:00	<b>Session 1: Solving the Gene Regulatory Code (DNA)</b>	<i>Auditorium</i>
		<p><i>Chair: Debbie Marks</i> <i>Moderator: Jussi Taipale</i></p>	
11:45	12:15	Improving Genomic Deep Learning with Perturbation Data <a href="#">Peter Koo, Cold Spring Harbor Laboratory, United States</a>	
12:15	12:45	Solving the genome regulatory code with AI-first synthetic genomic data generation and machine learning <a href="#">Carl de Boer, University of British Columbia, Canada</a>	
12:45	13:00	Deciphering gene regulation with a whole-organism sequence-to-expression model <i>Cas Blaauw, VIB-KU Leuven, Belgium</i>	
13:00	14:10	Lunch and networking	<i>Event Space</i>

13:55	14:10	Briefing for Session 2 speakers, chair and moderator	Auditorium
<b>14:10</b>	<b>15:40</b>	<b>Session 2: Solving the Gene Regulatory Code (RNA)</b>	<b>Auditorium</b>
		Chair: Jun Cheng Moderator: Mo Lotfollahi	
14:10	14:50	From protein-RNA interactions to their functional models <a href="#">Jernej Ule, King's College London, United Kingdom</a> <a href="#">Charlotte Capitanichik, The Francis Crick Institute, United Kingdom</a>	
14:50	15:10	Deep screening of biomolecular repertoires <a href="#">Phil Holliger, MRC Laboratory of Molecular Biology, United Kingdom</a>	
15:10	15:40	Model-guided sequence design for mRNA and gene therapy applications <a href="#">Georg Seelig, Botnar Institute Of Immune Engineering, United States</a>	
15:40	16:20	Refreshment break and networking	Event Space
16:05	16:20	Briefing for Session 3 speakers, chair and moderator	Auditorium
<b>16:20</b>	<b>17:50</b>	<b>Session 3: Solving Proteins (data)</b>	<b>Auditorium</b>
		Chair: Ben Lehner Moderator: Noelia Ferruz	
16:20	16:50	Large-scale discovery of protein stability and dynamics <a href="#">Gabriel Rocklin, Northwestern, United States</a>	
16:50	17:20	Decoding the protein dance <a href="#">Paola Picotti, ETH Zurich, Switzerland</a>	
17:20	17:35	Scaling data generation for chemical biology <a href="#">Simon d'Oelsnitz, Harvard Medical School, United States</a>	
17:35	17:50	Beyond Substitutions: Generating Protein Variants with Insertions and Deletions Constance Ferragu, Cradle, Switzerland	
<b>17:50</b>	<b>18:30</b>	<b>Poster pitch talks for odd number posters</b>	<b>Auditorium</b>
<b>18:30</b>	<b>19:45</b>	<b>Poster session 1 - odd number posters</b>	<b>Event Space</b>
19:45	21:00	Dinner	Hinxton Hall Restaurant
19:45		Bar open (card payments only)	Graham Cameron Bar

<b>Tuesday 9 June 2026</b>			
09:15	09:30	Briefing for Session 4 speakers, chair and moderator	Auditorium
<b>09:30</b>	<b>10:45</b>	<b>Session 4: AI Methods and Development</b>	<b>Auditorium</b>
		Chair: Debbie Marks Moderator: Ben Lehner	
09:30	10:00	Large Language Models for Therapeutics and Biology - virtual <a href="#">Shek Azizi, Google DeepMind, Canada</a>	
10:00	10:30	BoltzGen: Toward Universal Binder Design <a href="#">Hannes Stark, Massachusetts Institute of Technology, United States</a>	
10:30	10:45	DeepMechanisticModels: Combining mechanistic models and deep learning to discover drivers of ERK signalling heterogeneity <i>Fabian Frohlich, The Francis Crick Institute, United Kingdom</i>	
10:45	11:30	Refreshment break and networking	Event Space
11:15	11:30	Briefing for Session 5 speakers, chair and moderator	Auditorium
<b>11:30</b>	<b>13:00</b>	<b>Session 5: Solving Chemistry and Therapeutics</b>	<b>Auditorium</b>
		Chair: Jussi Taipale Moderator: Ben Lehner	
11:30	12:00	Designing Programmable Biologics with Generative Sequence Models <a href="#">Pranam Chatterjee, University of Pennsylvania, United States</a>	
12:00	12:30	Beyond the Funnel: Machine Learning Powered Lab-in-the-Loop for Drug Discovery <a href="#">Richard Bonneau, Genentech / Roche, United States</a>	
12:30	12:45	Learning to predict aptamer sensors for any metabolite or drug target <i>Andrew Fraser, University of Toronto, Canada</i>	
12:45	13:00	Temporally-faithful heterogeneous biomedical knowledge graphs for quasi-prospective clinical advancement prediction <i>Jacky Siu, Queen Mary University of London, United Kingdom</i>	
<b>13:00</b>	<b>13:30</b>	<b>Session 5: Solving Chemistry and Therapeutics (continued)</b>	<b>Auditorium</b>
		Chair: Ben Lehner Moderator: Jun Cheng	
13:00	13:30	How AI Unifies an Ecosystem of Biotechnology <a href="#">Matt Davis, Flagship Pioneering, United States</a>	
13:30	14:45	Lunch and networking	Hinxton Hall Restaurant
14:30	14:45	Briefing for Session 6 speakers, chair and moderator	Auditorium
<b>14:45</b>	<b>16:15</b>	<b>Session 6: Solving Proteins (design)</b>	<b>Auditorium</b>
		Chair: Noelia Ferruz Moderator: Mo Lotfollahi	
14:45	15:15	Natural Language-Guided Protein Mining and Design System <a href="#">Fajie Yuan, Westlake University, China</a>	
15:15	15:45	Biophysics in the age of AI <a href="#">Frank Noe, Microsoft Research, Germany</a>	
15:45	16:00	Capturing transient protein interactions using in-cell photo-crosslinking <i>Santosh Shivakumaraswamy, The Francis Crick Institute, United Kingdom</i>	
16:00	16:15	Proteina-Complexa: Atomistic Generative Design of de novo Protein Binders with Experimental Validation <i>Kieran Didi, Oxford University, United Kingdom</i>	
16:15	16:45	Refreshment break and networking	Event Space
<b>16:45</b>	<b>17:25</b>	<b>Poster pitch talks for even number posters</b>	<b>Auditorium</b>
		Chair: Jussi Taipale	
<b>17:25</b>	<b>18:45</b>	<b>Poster session 2 - even number posters</b>	<b>Event Space</b>
18:45	20:30	Dinner	Hinxton Hall Restaurant
18:45		Bar open (card payments only)	Graham Cameron Bar

<b>Wednesday 10 June 2026</b>			
08:45	09:00	Briefing for Session 7 speakers, chair and moderator	Auditorium
<b>09:00</b>	<b>10:30</b>	<b>Session 7: Solving Cells, Tissues and Organs</b>	<b>Auditorium</b>
		<i>Chair: Mo Lotfollahi</i>	
		<i>Moderator: Debbie Marks</i>	
09:00	09:30	Modeling cellular migration and differentiation with spatial transcriptomic data <a href="#">Joshua Welch, University of Michigan, United States</a>	
09:30	10:00	Towards Multimodal Foundation Modeling in Pathology <a href="#">Guillaume Jaume, University of Lausanne, Switzerland</a>	
10:00	10:15	Universal model-free cell annotation for high definition spatial transcriptomics data from Visium HD 11mm arrays <i>Preyas Shah, 10x Genomics, United States</i>	
10:15	10:30	Stress-testing drug response prediction: a modular framework, dataset-suitability benchmark, and a functionally aware embedding model <i>Nico Trummer, Orakl Oncology, France</i>	
10:30	11:10	Refreshment break and networking	Event Space
10:55	11:10	Briefing for session 7 (continued), chair, moderator and committee	Auditorium
<b>11:10</b>	<b>12:10</b>	<b>Session 7: Solving Cells, Tissues and Organs (continued)</b>	<b>Auditorium</b>
		<i>Chair: Mo Lotfollahi</i>	
		<i>Moderator: Noelia Ferruz</i>	
11:10	11:40	Multimodal learning for single-cell multi-omics data integration <a href="#">Laura Cantini, Institut Pasteur, France</a>	
11:40	11:55	InterScale reveals multi-scale cellular interaction programs in spatial transcriptomics <i>Francesca Drummer, EBI-EMBL, United Kingdom</i>	
11:55	12:10	Mapping the AI x Bio Capability Landscape <i>Nelly Mak, SecureBio, United States</i>	
<b>12:10</b>	<b>12:20</b>	<b>Closing remarks</b>	<b>Auditorium</b>
		<b>Scientific Programme Committee:</b>	
		<a href="#">Ben Lehner, Wellcome Sanger Institute, United Kingdom</a>	
		<a href="#">Mo Lotfollahi, Wellcome Sanger Institute, United Kingdom</a>	
		<a href="#">Debora Marks, Harvard University, United States</a>	
		<a href="#">Noelia Ferruz, Centre for Genomic Regulation, Spain</a>	
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		<a href="#">Jun Cheng, Google DeepMind, United Kingdom</a>	
12:20	13:30	Lunch	Hinxton Hall Restaurant
13:30		Coach departures for Stansted and Heathrow airports	Main entrance
13:45		Coach departures for Cambridge train station and city centre	Main entrance