

Hybrid Conference Programme

Start (BST)	Finish (BST)	Presenter details	Location
Monday 8 June 2026			
09:00	10:00	Registration, arrival refreshments and networking	<i>Event space</i>
09:45		<i>Briefing for keynote speaker, microphone runners, chair, moderator and committee</i>	<i>Auditorium</i>
10:00	10:20	Welcome and introductions	<i>Auditorium</i>
		Wellcome Genome Campus Science and Tech Advisory Group Nicole Mather, Chair, Wellcome Genome Campus Science and Tech Advisory Group Scientific programme committee: Ben Lehner, Wellcome Sanger Institute, United Kingdom Mo Lotfollahi, Wellcome Sanger Institute, United Kingdom Debra Marks, Harvard University, United States Noelia Ferruz, Centre for Genomic Regulation, Spain Jussi Taipale, Wellcome Sanger Institute / Karolinska Institute, United Kingdom / Sweden Jun Cheng, Google DeepMind, United Kingdom	
10:20	11:10	Opening keynote	<i>Auditorium</i>
		<i>Chair: Noelia Ferruz</i> <i>Moderator: Jun Cheng</i>	
10:20	11:10	Leveraging AI to advance biology Pushmeet Kohli, Google DeepMind, United Kingdom	
11:10	11:40	Coffee break and networking	
11:30	11:45	<i>Briefing for Session 1 speakers, chair and moderator</i>	<i>Auditorium</i>
11:40	12:55	Session 1: Solving the Gene Regulatory Code (DNA)	<i>Auditorium</i>
		<i>Chair: Debbie Marks</i> <i>Moderator: Jussi Taipale</i>	
11:40	12:10	Improving Genomic Deep Learning with Perturbation Data Peter Koo, Cold Spring Harbor Laboratory, United States	
12:10	12:40	Solving the genome regulatory code with AI-first synthetic genomic data generation and machine learning Carl de Boer, University of British Columbia, Canada	
12:40	12:55	Deciphering gene regulation with a whole-organism sequence-to-expression model Cas Blaauw, VIB-KU Leuven, Belgium	
12:55	14:10	Lunch and networking	<i>Event Space</i>

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

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

Wednesday 10 June 2026			
08:45	09:00	Briefing for Session 7 speakers, chair and moderator	Auditorium
09:00	10:30	Session 7: Solving Cells, Tissues and Organs	Auditorium
		<i>Chair: Mo Lotfollahi</i>	
		<i>Moderator: Debbie Marks</i>	
09:00	09:30	Modeling cellular migration and differentiation with spatial transcriptomic data Joshua Welch, University of Michigan, United States	
09:30	10:00	Towards Multimodal Foundation Modeling in Pathology Guillaume Jaume, University of Lausanne, Switzerland	
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>Lélia Polit, Oraki Oncology, France</i>	
10:30	11:10	Refreshment break and networking	Event Space
10:55	11:10	Briefing for keynote, chair, moderator and committee	Auditorium
11:10	12:10	Session 7: Solving Cells, Tissues and Organs (continued)	Auditorium
		<i>Chair: Mo Lotfollahi</i>	
		<i>Moderator: Noelia Ferruz</i>	
11:10	11:40	Multimodal learning for single-cell multi-omics data integration Laura Cantini, Institut Pasteur, France	
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 Kingdom</i>	
12:10	12:20	Closing remarks	Auditorium
		Scientific Programme Committee:	
		Ben Lehner, Wellcome Sanger Institute, United Kingdom	
		Mo Lotfollahi, Wellcome Sanger Institute, United Kingdom	
		Debra Marks, Harvard University, United States	
		Noelia Ferruz, Centre for Genomic Regulation, Spain	
		Jussi Taipale, Wellcome Sanger Institute / Karolinska Institute, United Kingdom / Sweden	
		Jun Cheng, Google DeepMind, United Kingdom	
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