Hybrid Conference Programme

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

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*
		Chair: Jun Cheng *Moderator: Mo Lotfollahi*	
14:10	14:40	From protein-RNA interactions to their functional models *Jernej Ule, King's College London, United Kingdom* *Charlotte Capitanchik, The Francis Crick Institute, United Kingdom*	
14:40	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*
		Chair: Ben Lehner *Moderator: Noelia Ferruz*	
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 *Constance Ferragu, Cradle, Switzerland*	
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 - *virtual* *Shek Azizi, Google DeepMind, Canada*	
10:00	10:30	BoltzGen: Toward Universal Binder Design *Hannes Stark, Massachussetts 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	**13:00**	**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	How AI Unifies an Ecosystem of Biotechnology *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*
		Chair: Mo Lotfohalli *Moderator: Debbie Marks*	
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 *Preyas Shah, 10x Genomics, United States*	
10:15	10:30	Stress-testing drug response prediction: a modular framework, dataset-suitability benchmark, and a functionally aware embedding model *Nico Trummer, Orakl Oncology, France*	
10:30	11:10	Refreshment break and networking	*Event Space*
10:55	*11:10*	*Briefing for session 7 (continued), chair, moderator and committee*	*Auditorium*
11:10	**12:10**	**Session 7: Solving Cells, Tissues and Organs (continued)**	*Auditorium*
		Chair: Mo Lotfollahi *Moderator: Noelia Ferruz*	
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 *Francesca Drummer, EBI-EMBL, United Kingdom*	
11:55	12:10	Mapping the AI x Bio Capability Landscape *Nelly Mak, SecureBio, United States*	
12:10	**12:20**	**Closing remarks**	*Auditorium*
		Scientific Programme Committee: Ben Lehner, Wellcome Sanger Institute, United Kingdom Mo Lotfollahi, Wellcome Sanger Institute, United Kingdom Debora 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*